Spot 1

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	Accession	Mass	Score	Description
1.	gi|222624156	99391	103	hypothetical protein OsJ_09326 [Oryza sativa Japonica Group]
2.	gi|115450595	106862	101	Os03g0136900 [Oryza sativa (japonica cultivar-group)]
3.	gi|218192045	106860	101	hypothetical protein OsI_09921 [Oryza sativa Indica Group]
4.	gi|3309243	98654	94	aconitase-iron regulated protein 1 [Citrus limon]
5.	gi|157329909	97645	65	unnamed protein product [Vitis vinifera]
6.	gi|34851120	99444	65	putative aconitase [Prunus avium]
7.	gi|157337907	110671	60	unnamed protein product [Vitis vinifera]
8.	gi|15233349	98774	58	aconitate hydratase, cytoplasmic / citrate hydro-lyase / aconitase (ACO) [Arabidopsis thalian
9.	gi|223529808	99108	57	aconitase, putative [Ricinus communis]
10.	gi|223536553	109346	56	aconitase, putative [Ricinus communis]

Results List

1. gi|222624156 **Mass:** 99391 **Score:** 103 **Expect:** 3e-005 **Queries matched:** 15

hypothetical protein OsJ_09326 [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
748.4287	747.4214	747.4279	-0.0065	48	53	0	---	LPYSIR
778.4234	777.4161	777.4133	0.0028	735	741	0	---	GTFANIR
914.5710	913.5637	913.5596	0.0041	54	61	0	---	ILLESAIR
945.4064	944.3991	944.3988	0.0004	718	725	0	---	DFNSYGSR
1013.5051	1012.4978	1012.4977	0.0001	593	600	1	---	DGKEVYFR
1073.5093	1072.5020	1072.4937	0.0083	717	725	1	---	KDFNSYGSR
1101.5094	1100.5021	1100.4999	0.0023	718	726	1	---	DFNSYGSRR
1146.6630	1145.6557	1145.6556	0.0001	45	53	1	---	IERLPYSIR
1146.6630	1145.6557	1145.6556	0.0001	45	53	1	17	IERLPYSIR
1184.6803	1183.6730	1183.6713	0.0017	86	95	0	---	QVEIPFKPAR
1184.6803	1183.6730	1183.6713	0.0017	86	95	0	30	QVEIPFKPAR
1299.6857	1298.6784	1298.6843	-0.0059	550	560	1	---	NFEGRVHALTR
1914.0151	1913.0078	1913.0258	-0.0179	755	772	1	---	TIHIPSGEKLSVFDAATK
2104.0850	2103.0777	2103.0856	-0.0079	96	114	0	---	VLLQDFTGVPAVVDLACMR
2120.0969	2119.0896	2119.0805	0.0091	96	114	0	---	VLLQDFTGVPAVVDLACMR + Oxidation (M)

No match to: 713.4077, 734.4895, 736.4941, 750.5085, 768.5223, 864.5479, 1129.5642, 1167.6704, 1167.6704, 1193.6896, 1265.6547, 1267.6661, 1279.7706, 1308.6721, 1334.8806, 1375.7246, 1402.8367, 1448.9188, 1485.6892, 1501.6815, 1527.7122, 1571.7610, 1640.7932, 1656.9176, 1724.8003, 1727.8501, 1740.7899, 1801.8282, 1801.8282, 1817.8153, 1817.8153, 1848.9139, 1928.9861, 2162.2378, 2326.1069, 2342.2144, 2414.1614, 2610.3076, 2780.9812, 2847.4150, 2854.5432, 3010.6689

2. gi|115450595 **Mass:** 106862 **Score:** 101 **Expect:** 4.8e-005 **Queries matched:** 16

Os03g0136900 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
748.4287	747.4214	747.4279	-0.0065	127	132	0	---	LPYSIR
778.4234	777.4161	777.4133	0.0028	814	820	0	---	GTFANIR
914.5710	913.5637	913.5596	0.0041	133	140	0	---	ILLESAIR
945.4064	944.3991	944.3988	0.0004	797	804	0	---	DFNSYGSR
1013.5051	1012.4978	1012.4977	0.0001	672	679	1	---	DGKEVYFR
1073.5093	1072.5020	1072.4937	0.0083	796	804	1	---	KDFNSYGSR
1101.5094	1100.5021	1100.4999	0.0023	797	805	1	---	DFNSYGSRR
1146.6630	1145.6557	1145.6556	0.0001	124	132	1	---	IERLPYSIR
1146.6630	1145.6557	1145.6556	0.0001	124	132	1	17	IERLPYSIR
1184.6803	1183.6730	1183.6713	0.0017	165	174	0	---	QVEIPFKPAR
1184.6803	1183.6730	1183.6713	0.0017	165	174	0	30	QVEIPFKPAR
1267.6661	1266.6588	1266.6316	0.0272	73	84	1	---	SSSSAAAVFERR
1299.6857	1298.6784	1298.6843	-0.0059	629	639	1	---	NFEGRVHALTR
1914.0151	1913.0078	1913.0258	-0.0179	834	851	1	---	TIHIPSGEKLSVFDAATK
2104.0850	2103.0777	2103.0856	-0.0079	175	193	0	---	VLLQDFTGVPAVVDLACMR
2120.0969	2119.0896	2119.0805	0.0091	175	193	0	---	VLLQDFTGVPAVVDLACMR + Oxidation (M)

No match to: 713.4077, 734.4895, 736.4941, 750.5085, 768.5223, 864.5479, 1129.5642, 1167.6704, 1167.6704, 1193.6896, 1265.6547, 1279.7706, 1308.6721, 1334.8806, 1375.7246, 1402.8367, 1448.9188, 1485.6892, 1501.6815, 1527.7122, 1571.7610, 1640.7932, 1656.9176, 1724.8003, 1727.8501, 1740.7899, 1801.8282, 1801.8282, 1817.8153, 1817.8153, 1848.9139, 1928.9861, 2162.2378, 2326.1069, 2342.2144, 2414.1614, 2610.3076, 2780.9812, 2847.4150, 2854.5432, 3010.6689

3. gi|218192045 **Mass:** 106860 **Score:** 101 **Expect:** 4.8e-005 **Queries matched:** 16

hypothetical protein OsI_09921 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
748.4287	747.4214	747.4279	-0.0065	127	132	0	---	LPYSIR
778.4234	777.4161	777.4133	0.0028	814	820	0	---	GTFANIR
914.5710	913.5637	913.5596	0.0041	133	140	0	---	ILLESAIR
945.4064	944.3991	944.3988	0.0004	797	804	0	---	DFNSYGSR
1013.5051	1012.4978	1012.4977	0.0001	672	679	1	---	DGKEVYFR
1073.5093	1072.5020	1072.4937	0.0083	796	804	1	---	KDFNSYGSR
1101.5094	1100.5021	1100.4999	0.0023	797	805	1	---	DFNSYGSRR
1146.6630	1145.6557	1145.6556	0.0001	124	132	1	---	IERLPYSIR
1146.6630	1145.6557	1145.6556	0.0001	124	132	1	17	IERLPYSIR
1184.6803	1183.6730	1183.6713	0.0017	165	174	0	---	QVEIPFKPAR
1184.6803	1183.6730	1183.6713	0.0017	165	174	0	30	QVEIPFKPAR
1267.6661	1266.6588	1266.6316	0.0272	73	84	1	---	SSSSAAAVFERR
1299.6857	1298.6784	1298.6843	-0.0059	629	639	1	---	NFEGRVHALTR
1914.0151	1913.0078	1913.0258	-0.0179	834	851	1	---	TIHIPSGEKLSVFDAATK
2104.0850	2103.0777	2103.0856	-0.0079	175	193	0	---	VLLQDFTGVPAVVDLACMR

2120.0969	2119.0896	2119.0805	0.0091	175 - 193	0	---	VLLQDFTGVPAVVDLACMR + Oxidation (M)

No match to: 713.4077, 734.4895, 736.4941, 750.5085, 768.5223, 864.5479, 1129.5642, 1167.6704, 1167.6704, 1193.6896, 1265.6547, 1279.7706, 1308.6721, 1334.8806, 1375.7246, 1402.8367, 1448.9188, 1485.6892, 1501.6815, 1527.7122, 1571.7610, 1640.7932, 1656.9176, 1724.8003, 1727.8501, 1740.7899, 1801.8282, 1801.8282, 1817.8153, 1817.8153, 1848.9139, 1928.9861, 2162.2378, 2326.1069, 2342.2144, 2414.1614, 2610.3076, 2780.9812, 2847.4150, 2854.5432, 3010.6689

4. gi|3309243 **Mass:** 98654 **Score:** 94 **Expect:** 0.00024 **Queries matched:** 14

aconitase-iron regulated protein 1 [Citrus limon]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
748.4287	747.4214	747.4279	-0.0065	39 -	44	0	---	LPYSIR
778.4234	777.4161	777.4133	0.0028	726 -	732	0	---	GTFANIR
914.5710	913.5637	913.5596	0.0041	45 -	52	0	---	ILLESAIR
945.4064	944.3991	944.3988	0.0004	709 -	716	0	---	DFNSYGSR
1073.5093	1072.5020	1072.4937	0.0083	708 -	716	1	---	KDFNSYGSR
1101.5094	1100.5021	1100.4999	0.0023	709 -	717	1	---	DFNSYGSRR
1184.6803	1183.6730	1183.6713	0.0017	77 -	86	0	---	QVEIPFKPAR
1184.6803	1183.6730	1183.6713	0.0017	77 -	86	0	30	QVEIPFKPAR
1571.7610	1570.7537	1570.7184	0.0353	330 -	342	0	---	SDETVSMIEEYLR
1656.9176	1655.9103	1655.9068	0.0035	459 -	472	1	---	KACELGLEVKPWVK
1848.9139	1847.9066	1847.9662	-0.0596	257 -	273	0	---	DGVTATDLVLTVTQMLR + Oxidation (M)
1928.9861	1927.9788	1927.9137	0.0651	281 -	297	0	---	FVEFYGEGMGQLPLADR
2162.2378	2161.2305	2161.1742	0.0563	473 -	493	1	---	TSLAPGSGVVTKYLQQSGLQK
2342.2144	2341.2071	2341.1147	0.0924	358 -	378	0	---	SYSSYLQLDLADVEPCISGPK

No match to: 713.4077, 734.4895, 736.4941, 750.5085, 768.5223, 864.5479, 1013.5051, 1129.5642, 1146.6630, 1146.6630, 1167.6704, 1167.6704, 1193.6896, 1265.6547, 1267.6661, 1279.7706, 1299.6857, 1308.6721, 1334.8806, 1375.7246, 1402.8367, 1448.9188, 1485.6892, 1501.6815, 1527.7122, 1640.7932, 1724.8003, 1727.8501, 1740.7899, 1801.8282, 1801.8282, 1817.8153, 1817.8153, 1914.0151, 2104.0850, 2120.0969, 2326.1069, 2414.1614, 2610.3076, 2780.9812, 2847.4150, 2854.5432, 3010.6689

5. gi|157329909 **Mass:** 97645 **Score:** 65 **Expect:** 0.17 **Queries matched:** 13

unnamed protein product [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
748.4287	747.4214	747.4279	-0.0065	29 -	34	0	---	LPYSIR
778.4234	777.4161	777.4133	0.0028	714 -	720	0	---	GTFANIR
914.5710	913.5637	913.5596	0.0041	35 -	42	0	---	ILLESAIR
945.4064	944.3991	944.3988	0.0004	697 -	704	0	---	DFNSYGSR
1101.5094	1100.5021	1100.4999	0.0023	697 -	705	1	---	DFNSYGSRR
1184.6803	1183.6730	1183.6713	0.0017	67 -	76	0	---	QVEIPFKPAR
1184.6803	1183.6730	1183.6713	0.0017	67 -	76	0	30	QVEIPFKPAR
1308.6721	1307.6648	1307.6292	0.0356	681 -	691	1	---	DSPAARYLMER
1485.6892	1484.6819	1484.7485	-0.0666	1 -	14	0	---	MFGLFKPAGGEFGK
1501.6815	1500.6742	1500.7434	-0.0692	1 -	14	0	---	MFGLFKPAGGEFGK + Oxidation (M)

1848.9139	1847.9066	1847.9662	-0.0596	247 - 263	0	---	DGVTATDLVLTVTQMLR + Oxidation (M)
2104.0850	2103.0777	2103.0856	-0.0079	77 - 95	0	---	VLLQDFTGVPAVVDLACMR
2120.0969	2119.0896	2119.0805	0.0091	77 - 95	0	---	VLLQDFTGVPAVVDLACMR + Oxidation (M)

No match to: 713.4077, 734.4895, 736.4941, 750.5085, 768.5223, 864.5479, 1013.5051, 1073.5093, 1129.5642, 1146.6630, 1146.6630, 1167.6704, 1167.6704, 1193.6896, 1265.6547, 1267.6661, 1279.7706, 1299.6857, 1334.8806, 1375.7246, 1402.8367, 1448.9188, 1527.7122, 1571.7610, 1640.7932, 1656.9176, 1724.8003, 1727.8501, 1740.7899, 1801.8282, 1801.8282, 1817.8153, 1817.8153, 1914.0151, 1928.9861, 2162.2378, 2326.1069, 2342.2144, 2414.1614, 2610.3076, 2780.9812, 2847.4150, 2854.5432, 3010.6689

6. gi|34851120 **Mass:** 99444 **Score:** 65 **Expect:** 0.21 **Queries matched:** 11

putative aconitase [Prunus avium]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
778.4234	777.4161	777.4133	0.0028	730 - 736		0	---	GTFANIR
864.5479	863.5406	863.5116	0.0290	319 - 325		0	---	VTLQYLK
914.5710	913.5637	913.5596	0.0041	45 - 52		0	---	ILLESAIR
945.4064	944.3991	944.3988	0.0004	713 - 720		0	---	DFNSYGSR
1101.5094	1100.5021	1100.4999	0.0023	713 - 721		1	---	DFNSYGSRR
1184.6803	1183.6730	1183.6713	0.0017	77 - 86		0	---	QVEIPFKPAR
1184.6803	1183.6730	1183.6713	0.0017	77 - 86		0	30	QVEIPFKPAR
1308.6721	1307.6648	1307.6510	0.0139	25 - 35		0	---	YYSLPALNDPR
1571.7610	1570.7537	1570.8255	-0.0718	420 - 433		0	---	VVEFAFHGTPAQLR
1848.9139	1847.9066	1847.9662	-0.0596	257 - 273		0	---	DGVTATDLVLTVTQMLR + Oxidation (M)
2104.0850	2103.0777	2103.0492	0.0285	87 - 105		0	---	VPLQDFTGVPAVVDLACMR + Oxidation (M)

No match to: 713.4077, 734.4895, 736.4941, 748.4287, 750.5085, 768.5223, 1013.5051, 1073.5093, 1129.5642, 1146.6630, 1146.6630, 1167.6704, 1167.6704, 1193.6896, 1265.6547, 1267.6661, 1279.7706, 1299.6857, 1334.8806, 1375.7246, 1402.8367, 1448.9188, 1485.6892, 1501.6815, 1527.7122, 1640.7932, 1656.9176, 1724.8003, 1727.8501, 1740.7899, 1801.8282, 1801.8282, 1817.8153, 1817.8153, 1914.0151, 1928.9861, 2120.0969, 2162.2378, 2326.1069, 2342.2144, 2414.1614, 2610.3076, 2780.9812, 2847.4150, 2854.5432, 3010.6689

7. gi|157337907 **Mass:** 110671 **Score:** 60 **Expect:** 0.65 **Queries matched:** 11

unnamed protein product [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
748.4287	747.4214	747.4279	-0.0065	150 - 155		0	---	LPYSIR
778.4234	777.4161	777.4133	0.0028	837 - 843		0	---	GTFANIR
914.5710	913.5637	913.5596	0.0041	156 - 163		0	---	ILLESAIR
945.4064	944.3991	944.3988	0.0004	820 - 827		0	---	DFNSYGSR
1101.5094	1100.5021	1100.4999	0.0023	820 - 828		1	---	DFNSYGSRR
1184.6803	1183.6730	1183.6713	0.0017	188 - 197		0	---	QVEIPFKPAR
1184.6803	1183.6730	1183.6713	0.0017	188 - 197		0	30	QVEIPFKPAR
1299.6857	1298.6784	1298.6843	-0.0059	652 - 662		1	---	NFEGRVHALTR
1375.7246	1374.7173	1374.6965	0.0208	108 - 119		1	---	KMATIASEHPFK + Oxidation (M)
2104.0850	2103.0777	2103.0856	-0.0079	198 - 216		0	---	VLLQDFTGVPAVVDLACMR
2120.0969	2119.0896	2119.0805	0.0091	198 - 216		0	---	VLLQDFTGVPAVVDLACMR + Oxidation (M)

No match to: 713.4077, 734.4895, 736.4941, 750.5085, 768.5223, 864.5479, 1013.5051, 1073.5093, 1129.5642, 1146.6630, 1146.6630, 1167.6704, 1167.6704, 1193.6896, 1265.6547, 1267.6661, 1279.7706, 1308.6721, 1334.8806, 1402.8367, 1448.9188, 1485.6892, 1501.6815, 1527.7122, 1571.7610, 1640.7932, 1656.9176, 1724.8003, 1727.8501, 1740.7899, 1801.8282, 1801.8282, 1817.8153, 1817.8153, 1848.9139, 1914.0151, 1928.9861, 2162.2378, 2326.1069, 2342.2144, 2414.1614, 2610.3076, 2780.9812, 2847.4150, 2854.5432, 3010.6689

8. gi|15233349 **Mass:** 98774 **Score:** 58 **Expect:** 0.89 **Queries matched:** 12

aconitate hydratase, cytoplasmic / citrate hydro-lyase / aconitase (ACO) [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
748.4287	747.4214	747.4279	-0.0065	39	44	0	---	LPYSIR
778.4234	777.4161	777.4133	0.0028	726	732	0	---	GTFANIR
914.5710	913.5637	913.5596	0.0041	45	52	0	---	ILLESAIR
945.4064	944.3991	944.3988	0.0004	709	716	0	---	DFNSYGSR
1101.5094	1100.5021	1100.4999	0.0023	709	717	1	---	DFNSYGSRR
1184.6803	1183.6730	1183.6713	0.0017	77	86	0	---	QVEIPFKPAR
1184.6803	1183.6730	1183.6713	0.0017	77	86	0	30	QVEIPFKPAR
1656.9176	1655.9103	1655.9068	0.0035	459	472	1	---	KACDLGLEVKPWIK
1801.8282	1800.8209	1800.8728	-0.0519	275	290	1	---	HGVVGKFVEFHGEGMR + Oxidation (M)
1801.8282	1800.8209	1800.8728	-0.0519	275	290	1	---	HGVVGKFVEFHGEGMR + Oxidation (M)
2104.0850	2103.0777	2103.0856	-0.0079	87	105	0	---	VLLQDFTGVPAVVDLACMR
2120.0969	2119.0896	2119.0805	0.0091	87	105	0	---	VLLQDFTGVPAVVDLACMR + Oxidation (M)

No match to: 713.4077, 734.4895, 736.4941, 750.5085, 768.5223, 864.5479, 1013.5051, 1073.5093, 1129.5642, 1146.6630, 1146.6630, 1167.6704, 1167.6704, 1193.6896, 1265.6547, 1267.6661, 1279.7706, 1299.6857, 1308.6721, 1334.8806, 1375.7246, 1402.8367, 1448.9188, 1485.6892, 1501.6815, 1527.7122, 1571.7610, 1640.7932, 1724.8003, 1727.8501, 1740.7899, 1817.8153, 1817.8153, 1848.9139, 1914.0151, 1928.9861, 2162.2378, 2326.1069, 2342.2144, 2414.1614, 2610.3076, 2780.9812, 2847.4150, 2854.5432, 3010.6689

9. gi|223529808 **Mass:** 99108 **Score:** 57 **Expect:** 1.4 **Queries matched:** 11

aconitase, putative [Ricinus communis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
748.4287	747.4214	747.4279	-0.0065	39	44	0	---	LPYSIR
778.4234	777.4161	777.4133	0.0028	726	732	0	---	GTFANIR
914.5710	913.5637	913.5596	0.0041	45	52	0	---	ILLESAIR
945.4064	944.3991	944.3988	0.0004	709	716	0	---	DFNSYGSR
1101.5094	1100.5021	1100.4999	0.0023	709	717	1	---	DFNSYGSRR
1184.6803	1183.6730	1183.6713	0.0017	77	86	0	---	QVEIPFKPAR
1184.6803	1183.6730	1183.6713	0.0017	77	86	0	30	QVEIPFKPAR
1308.6721	1307.6648	1307.6510	0.0139	25	35	0	---	YYSLPALNDPR
1848.9139	1847.9066	1847.9662	-0.0596	257	273	0	---	DGVTATDLVLTVTQMLR + Oxidation (M)
2104.0850	2103.0777	2103.0856	-0.0079	87	105	0	---	VLLQDFTGVPAVVDLACMR
2120.0969	2119.0896	2119.0805	0.0091	87	105	0	---	VLLQDFTGVPAVVDLACMR + Oxidation (M)

No match to: 713.4077, 734.4895, 736.4941, 750.5085, 768.5223, 864.5479, 1013.5051, 1073.5093, 1129.5642, 1146.6630, 1146.6630, 1167.6704, 1167.6704, 1193.6896, 1265.6547, 1267.6661, 1279.7706, 1299.6857, 1334.8806,

1375.7246, 1402.8367, 1448.9188, 1485.6892, 1501.6815, 1527.7122, 1571.7610, 1640.7932, 1656.9176, 1724.8003, 1727.8501, 1740.7899, 1801.8282, 1801.8282, 1817.8153, 1817.8153, 1914.0151, 1928.9861, 2162.2378, 2326.1069, 2342.2144, 2414.1614, 2610.3076, 2780.9812, 2847.4150, 2854.5432, 3010.6689

10. gi|223536553 **Mass:** 109346 **Score:** 56 **Expect:** 1.5 **Queries matched:** 10

aconitase, putative [Ricinus communis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
748.4287	747.4214	747.4279	-0.0065	137	142	0	---	LPYSIR
778.4234	777.4161	777.4133	0.0028	824	830	0	---	GTFANIR
914.5710	913.5637	913.5596	0.0041	143	150	0	---	ILLESAIR
1073.5093	1072.5020	1072.4573	0.0447	806	814	0	---	QDFNSYGSR
1184.6803	1183.6730	1183.6713	0.0017	175	184	0	---	QVEIPFKPAR
1184.6803	1183.6730	1183.6713	0.0017	175	184	0	30	QVEIPFKPAR
1299.6857	1298.6784	1298.6843	-0.0059	639	649	1	---	NFEGRVHALTR
1308.6721	1307.6648	1307.6656	-0.0007	753	765	0	---	SMTLNPPGAHGVK
1375.7246	1374.7173	1374.6965	0.0208	95	106	1	---	KISTMAAEHPFK + Oxidation (M)
1724.8003	1723.7930	1723.7835	0.0095	151	164	1	---	NCDNFQVTKQDVEK

No match to: 713.4077, 734.4895, 736.4941, 750.5085, 768.5223, 864.5479, 945.4064, 1013.5051, 1101.5094, 1129.5642, 1146.6630, 1146.6630, 1167.6704, 1167.6704, 1193.6896, 1265.6547, 1267.6661, 1279.7706, 1334.8806, 1402.8367, 1448.9188, 1485.6892, 1501.6815, 1527.7122, 1571.7610, 1640.7932, 1656.9176, 1727.8501, 1740.7899, 1801.8282, 1801.8282, 1817.8153, 1817.8153, 1848.9139, 1914.0151, 1928.9861, 2104.0850, 2120.0969, 2162.2378, 2326.1069, 2342.2144, 2414.1614, 2610.3076, 2780.9812, 2847.4150, 2854.5432, 3010.6689

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 57

Protein View

Match to: **gi|222624156** Score: **103** Expect: **3e-005**
hypothetical protein OsJ_09326 [Oryza sativa Japonica Group]

Nominal mass (M_r): **99391**; Calculated pI value: **5.80**
NCBI BLAST search of gi|222624156 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Oryza sativa Japonica Group

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **11%**

Matched peptides shown in **Bold Red**

```
   1 MTIFPLPQSP AKNSYDEILT GLAKPGGGAE FGKYYSLPAL SDPRIERLPY
  51 SIRILLESAI RNCDEFQVTG KDVEKILDWE NSAPKQVEIP FKPARVLLQD
 101 FTGVPAVVDL ACMRDAMSKL GSDPNKINPL VPVDLVIDHS VQVDVARSEN
 151 AVQANMELEF HRNKERFGFL KWGSTAFRNM LVVPPGSGIV HQVNLEYLAR
 201 VVFNNGGILY PDSVVGTDSH TTMIDGLGVA GWGVGGIEAE ATMLGQPMSM
 251 VLPGVVGFKL TGKLRNGVTA TDLVLTVTQM LRKHGVVGKF VEFYGGGMSE
 301 LSLADRATIA NMSPEYGATM GFFPVDGKTL DYLKLTGRSD DTVAMIESYL
 351 RANKMFVDYN QPEAERVYSS YLELNLEEVE PCLSGPKRPH DRVTLKNMKS
 401 DWLSCLDNDV GFKGFAVPKE SQGKVAEFSF HGTPAKLKHG DVVIAAITSC
 451 TNTSNPNVML GAALVAKKAC ELGLEVKPWI KTSLAPGSGV VKKYLDKSGL
 501 QKYLDQLGFH IVGYGCTTCI GNSGELDETV SAAISDNDIV AAAVLSGNRN
 551 FEGRVHALTR ANYLASPPLV VAYALAGTVN IDFEKEPIGI SKDGKEVYFR
 601 DIWPSTEEIA EVVKSSVLPD MFKSTYEAIT KGNPMWNELS VSASTLYPWD
 651 PTSTYIHEPP YFKDMTMSPP GPRPVKDAYC LLNFGDSITT DHISPAGSIH
 701 PDSPAARYLK ERGVERKDFN SYGSRRGNDE IMARGTFANI RLVNKFLKGE
 751 VGPKTIHIPS GEKLSVFDAA TKYKNEGHDT IILAGAEYGS GSSRDWAAKG
 801 PMLQGVKAVI AKSFERIHRS NLAGMGIIPL CFKSGEDADT LGLTGHERFT
 851 VHLPANVSEI KPGQDVTVTT DNGKSFTCTL RFDTEVELAY YDNGGILPYV
 901 IRKIAEQ
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
45 - 53	1146.6630	1145.6557	1145.6556	0.0001	1	IERLPYSIR (No match)
45 - 53	1146.6630	1145.6557	1145.6556	0.0001	1	IERLPYSIR (Ions score 17)
48 - 53	748.4287	747.4214	747.4279	-0.0065	0	LPYSIR (No match)
54 - 61	914.5710	913.5637	913.5596	0.0041	0	ILLESAIR (No match)
86 - 95	1184.6803	1183.6730	1183.6713	0.0017	0	QVEIPFKPAR (No match)
86 - 95	1184.6803	1183.6730	1183.6713	0.0017	0	QVEIPFKPAR (Ions score 30)
96 - 114	2104.0850	2103.0777	2103.0856	-0.0079	0	VLLQDFTGVPAVVDLACMR (No match)
96 - 114	2120.0969	2119.0896	2119.0805	0.0091	0	VLLQDFTGVPAVVDLACMR Oxidation (M) (No match)
550 - 560	1299.6857	1298.6784	1298.6843	-0.0059	1	NFEGRVHALTR (No match)
593 - 600	1013.5051	1012.4978	1012.4977	0.0001	1	DGKEVYFR (No match)
717 - 725	1073.5093	1072.5020	1072.4937	0.0083	1	KDFNSYGSR (No match)
718 - 725	945.4064	944.3991	944.3988	0.0004	0	DFNSYGSR (No match)
718 - 726	1101.5094	1100.5021	1100.4999	0.0023	1	DFNSYGSRR (No match)
735 - 741	778.4234	777.4161	777.4133	0.0028	0	GTFANIR (No match)
755 - 772	1914.0151	1913.0078	1913.0258	-0.0179	1	TIHIPSGEKLSVFDAATK (No match)

Spot 2

Index

	Accession	Mass	Score	Description
1.	gi|222624156	99391	162	hypothetical protein OsJ_09326 [Oryza sativa Japonica Group]
2.	gi|115450595	106862	160	Os03g0136900 [Oryza sativa (japonica cultivar-group)]
3.	gi|218192045	106860	160	hypothetical protein OsI_09921 [Oryza sativa Indica Group]
4.	gi|3309243	98654	86	aconitase-iron regulated protein 1 [Citrus limon]
5.	gi|34851120	99444	75	putative aconitase [Prunus avium]
6.	gi|223529808	99108	75	aconitase, putative [Ricinus communis]
7.	gi|4586021	98720	71	cytoplasmic aconitate hydratase [Arabidopsis thaliana]
8.	gi|157329909	97645	70	unnamed protein product [Vitis vinifera]
9.	gi|15233349	98774	68	aconitate hydratase, cytoplasmic / citrate hydro-lyase / aconitase (ACO) [Arabidopsis thalian
10.	gi|168057341	95476	61	predicted protein [Physcomitrella patens subsp. patens]

Results List

1. gi|222624156 **Mass:** 99391 **Score:** 162 **Expect:** 3.8e-011 **Queries matched:** 20

hypothetical protein OsJ_09326 [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
748.4346	747.4273	747.4279	-0.0006	48	53	0	---	LPYSIR
778.4242	777.4169	777.4133	0.0036	735	741	0	---	GTFANIR
914.5702	913.5629	913.5596	0.0033	54	61	0	---	ILLESAIR
945.4101	944.4028	944.3988	0.0041	718	725	0	---	DFNSYGSR
1013.5090	1012.5017	1012.4977	0.0040	593	600	1	---	DGKEVYFR
1023.5128	1022.5055	1022.5106	-0.0051	615	623	0	---	SSVLPDMFK
1061.5195	1060.5122	1060.5083	0.0039	726	734	1	---	RGNDEIMAR
1073.5051	1072.4978	1072.4937	0.0041	717	725	1	---	KDFNSYGSR
1077.5089	1076.5016	1076.5032	-0.0016	726	734	1	---	RGNDEIMAR + Oxidation (M)
1101.5071	1100.4998	1100.4999	-0.0000	718	726	1	---	DFNSYGSRR
1121.6525	1120.6452	1120.6465	-0.0013	388	396	1	---	RPHDRVTLK
1146.6636	1145.6563	1145.6556	0.0007	45	53	1	36	IERLPYSIR
1146.6636	1145.6563	1145.6556	0.0007	45	53	1	---	IERLPYSIR
1184.6810	1183.6737	1183.6713	0.0024	86	95	0	---	QVEIPFKPAR
1184.6810	1183.6737	1183.6713	0.0024	86	95	0	39	QVEIPFKPAR
1299.6910	1298.6837	1298.6843	-0.0006	550	560	1	---	NFEGRVHALTR
1668.7482	1667.7409	1667.7460	-0.0051	62	75	1	---	NCDEFQVTGKDVEK
2104.0957	2103.0884	2103.0856	0.0028	96	114	0	---	VLLQDFTGVPAVVDLACMR
2120.0881	2119.0808	2119.0805	0.0003	96	114	0	---	VLLQDFTGVPAVVDLACMR + Oxidation (M)
3009.6250	3008.6177	3008.6294	-0.0117	120	147	1	---	LGSDPNKINPLVPVDLVIDHSVQVDVAR

No match to: 713.4078, 734.4946, 750.5013, 768.5232, 813.4132, 886.9876, 967.4979, 1167.6635, 1176.5972,

1193.6886, 1229.6062, 1265.6515, 1267.6628, 1279.7657, 1334.8781, 1402.8402, 1402.8402, 1448.9122, 1485.6979, 1501.6788, 1508.8214, 1522.7649, 1527.7059, 1571.7571, 1656.9066, 1724.7947, 1727.8440, 1740.7786, 1755.4257, 1801.8174, 1801.8174, 1817.8101, 1817.8101, 1847.8879, 1863.8594, 1912.9987, 1928.9893, 1977.0912, 2162.2390, 2326.0974, 2342.2439, 2413.1497, 2564.2971, 2626.2878, 3443.6943

2. gi|115450595 **Mass:** 106862 **Score:** 160 **Expect:** 6e-011 **Queries matched:** 21

Os03g0136900 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
748.4346	747.4273	747.4279	-0.0006	127	132	0	---	LPYSIR
778.4242	777.4169	777.4133	0.0036	814	820	0	---	GTFANIR
914.5702	913.5629	913.5596	0.0033	133	140	0	---	ILLESAIR
945.4101	944.4028	944.3988	0.0041	797	804	0	---	DFNSYGSR
1013.5090	1012.5017	1012.4977	0.0040	672	679	1	---	DGKEVYFR
1023.5128	1022.5055	1022.5106	-0.0051	694	702	0	---	SSVLPDMFK
1061.5195	1060.5122	1060.5083	0.0039	805	813	1	---	RGNDEIMAR
1073.5051	1072.4978	1072.4937	0.0041	796	804	1	---	KDFNSYGSR
1077.5089	1076.5016	1076.5032	-0.0016	805	813	1	---	RGNDEIMAR + Oxidation (M)
1101.5071	1100.4998	1100.4999	-0.0000	797	805	1	---	DFNSYGSRR
1121.6525	1120.6452	1120.6465	-0.0013	467	475	1	---	RPHDRVTLK
1146.6636	1145.6563	1145.6556	0.0007	124	132	1	36	IERLPYSIR
1146.6636	1145.6563	1145.6556	0.0007	124	132	1	---	IERLPYSIR
1184.6810	1183.6737	1183.6713	0.0024	165	174	0	---	QVEIPFKPAR
1184.6810	1183.6737	1183.6713	0.0024	165	174	0	39	QVEIPFKPAR
1267.6628	1266.6555	1266.6316	0.0239	73	84	1	---	SSSSAAAVFERR
1299.6910	1298.6837	1298.6843	-0.0006	629	639	1	---	NFEGRVHALTR
1668.7482	1667.7409	1667.7460	-0.0051	141	154	1	---	NCDEFQVTGKDVEK
2104.0957	2103.0884	2103.0856	0.0028	175	193	0	---	VLLQDFTGVPAVVDLACMR
2120.0881	2119.0808	2119.0805	0.0003	175	193	0	---	VLLQDFTGVPAVVDLACMR + Oxidation (M)
3009.6250	3008.6177	3008.6294	-0.0117	199	226	1	---	LGSDPNKINPLVPVDLVIDHSVQVDVAR

No match to: 713.4078, 734.4946, 750.5013, 768.5232, 813.4132, 886.9876, 967.4979, 1167.6635, 1176.5972, 1193.6886, 1229.6062, 1265.6515, 1279.7657, 1334.8781, 1402.8402, 1402.8402, 1448.9122, 1485.6979, 1501.6788, 1508.8214, 1522.7649, 1527.7059, 1571.7571, 1656.9066, 1724.7947, 1727.8440, 1740.7786, 1755.4257, 1801.8174, 1801.8174, 1817.8101, 1817.8101, 1847.8879, 1863.8594, 1912.9987, 1928.9893, 1977.0912, 2162.2390, 2326.0974, 2342.2439, 2413.1497, 2564.2971, 2626.2878, 3443.6943

3. gi|218192045 **Mass:** 106860 **Score:** 160 **Expect:** 6e-011 **Queries matched:** 21

hypothetical protein OsI_09921 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
748.4346	747.4273	747.4279	-0.0006	127	132	0	---	LPYSIR
778.4242	777.4169	777.4133	0.0036	814	820	0	---	GTFANIR
914.5702	913.5629	913.5596	0.0033	133	140	0	---	ILLESAIR
945.4101	944.4028	944.3988	0.0041	797	804	0	---	DFNSYGSR

1013.5090	1012.5017	1012.4977	0.0040	672 - 679	1	---	DGKEVYFR
1023.5128	1022.5055	1022.5106	-0.0051	694 - 702	0	---	SSVLPDMFK
1061.5195	1060.5122	1060.5083	0.0039	805 - 813	1	---	RGNDEIMAR
1073.5051	1072.4978	1072.4937	0.0041	796 - 804	1	---	KDFNSYGSR
1077.5089	1076.5016	1076.5032	-0.0016	805 - 813	1	---	RGNDEIMAR + Oxidation (M)
1101.5071	1100.4998	1100.4999	-0.0000	797 - 805	1	---	DFNSYGSRR
1121.6525	1120.6452	1120.6465	-0.0013	467 - 475	1	---	RPHDRVTLK
1146.6636	1145.6563	1145.6556	0.0007	124 - 132	1	36	IERLPYSIR
1146.6636	1145.6563	1145.6556	0.0007	124 - 132	1	---	IERLPYSIR
1184.6810	1183.6737	1183.6713	0.0024	165 - 174	0	---	QVEIPFKPAR
1184.6810	1183.6737	1183.6713	0.0024	165 - 174	0	39	QVEIPFKPAR
1267.6628	1266.6555	1266.6316	0.0239	73 - 84	1	---	SSSSAAAVFERR
1299.6910	1298.6837	1298.6843	-0.0006	629 - 639	1	---	NFEGRVHALTR
1668.7482	1667.7409	1667.7460	-0.0051	141 - 154	1	---	NCDEFQVTGKDVEK
2104.0957	2103.0884	2103.0856	0.0028	175 - 193	0	---	VLLQDFTGVPAVVDLACMR
2120.0881	2119.0808	2119.0805	0.0003	175 - 193	0	---	VLLQDFTGVPAVVDLACMR + Oxidation (M)
3009.6250	3008.6177	3008.6294	-0.0117	199 - 226	1	---	LGSDPNKINPLVPVDLVIDHSVQVDVAR

No match to: 713.4078, 734.4946, 750.5013, 768.5232, 813.4132, 886.9876, 967.4979, 1167.6635, 1176.5972, 1193.6886, 1229.6062, 1265.6515, 1279.7657, 1334.8781, 1402.8402, 1402.8402, 1448.9122, 1485.6979, 1501.6788, 1508.8214, 1522.7649, 1527.7059, 1571.7571, 1656.9066, 1724.7947, 1727.8440, 1740.7786, 1755.4257, 1801.8174, 1801.8174, 1817.8101, 1817.8101, 1847.8879, 1863.8594, 1912.9987, 1928.9893, 1977.0912, 2162.2390, 2326.0974, 2342.2439, 2413.1497, 2564.2971, 2626.2878, 3443.6943

4. gi|3309243 **Mass:** 98654 **Score:** 86 **Expect:** 0.0014 **Queries matched:** 13

aconitase-iron regulated protein 1 [Citrus limon]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
748.4346	747.4273	747.4279	-0.0006	39 - 44		0	---	LPYSIR
778.4242	777.4169	777.4133	0.0036	726 - 732		0	---	GTFANIR
914.5702	913.5629	913.5596	0.0033	45 - 52		0	---	ILLESAIR
945.4101	944.4028	944.3988	0.0041	709 - 716		0	---	DFNSYGSR
1073.5051	1072.4978	1072.4937	0.0041	708 - 716		1	---	KDFNSYGSR
1101.5071	1100.4998	1100.4999	-0.0000	709 - 717		1	---	DFNSYGSRR
1184.6810	1183.6737	1183.6713	0.0024	77 - 86		0	---	QVEIPFKPAR
1184.6810	1183.6737	1183.6713	0.0024	77 - 86		0	39	QVEIPFKPAR
1571.7571	1570.7498	1570.7184	0.0314	330 - 342		0	---	SDETVSMIEEYLR
1656.9066	1655.8993	1655.9068	-0.0075	459 - 472		1	---	KACELGLEVKPWVK
1928.9893	1927.9820	1927.9137	0.0683	281 - 297		0	---	FVEFYGEGMGQLPLADR
1977.0912	1976.0839	1976.0612	0.0228	257 - 274		1	---	DGVTATDLVLTVTQMLRK + Oxidation (M)
2162.2390	2161.2317	2161.1742	0.0575	473 - 493		1	---	TSLAPGSGVVTKYLQQSGLQK

No match to: 713.4078, 734.4946, 750.5013, 768.5232, 813.4132, 886.9876, 967.4979, 1013.5090, 1023.5128, 1061.5195, 1077.5089, 1121.6525, 1146.6636, 1146.6636, 1167.6635, 1176.5972, 1193.6886, 1229.6062, 1265.6515, 1267.6628, 1279.7657, 1299.6910, 1334.8781, 1402.8402, 1402.8402, 1448.9122, 1485.6979, 1501.6788, 1508.8214,

1522.7649, 1527.7059, 1668.7482, 1724.7947, 1727.8440, 1740.7786, 1755.4257, 1801.8174, 1801.8174, 1817.8101, 1817.8101, 1847.8879, 1863.8594, 1912.9987, 2104.0957, 2120.0881, 2326.0974, 2342.2439, 2413.1497, 2564.2971, 2626.2878, 3009.6250, 3443.6943

5. gi|34851120 **Mass:** 99444 **Score:** 75 **Expect:** 0.02 **Queries matched:** 13

putative aconitase [Prunus avium]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
778.4242	777.4169	777.4133	0.0036	730	736	0	---	GTFANIR
914.5702	913.5629	913.5596	0.0033	45	52	0	---	ILLESAIR
945.4101	944.4028	944.3988	0.0041	713	720	0	---	DFNSYGSR
1023.5128	1022.5055	1022.4855	0.0200	1	9	0	---	MATANPFQK + Oxidation (M)
1061.5195	1060.5122	1060.5083	0.0039	721	729	1	---	RGNDEIMAR
1077.5089	1076.5016	1076.5032	-0.0016	721	729	1	---	RGNDEIMAR + Oxidation (M)
1101.5071	1100.4998	1100.4999	-0.0000	713	721	1	---	DFNSYGSRR
1184.6810	1183.6737	1183.6713	0.0024	77	86	0	---	QVEIPFKPAR
1184.6810	1183.6737	1183.6713	0.0024	77	86	0	39	QVEIPFKPAR
1508.8214	1507.8141	1507.7882	0.0260	330	342	1	---	SDDKVALIESYLR
1571.7571	1570.7498	1570.8255	-0.0757	420	433	0	---	VVEFAFHGTPAQLR
1977.0912	1976.0839	1976.0612	0.0228	257	274	1	---	DGVTATDLVLTVTQMLRK + Oxidation (M)
2104.0957	2103.0884	2103.0492	0.0392	87	105	0	---	VPLQDFTGVPAVVDLACMR + Oxidation (M)

No match to: 713.4078, 734.4946, 748.4346, 750.5013, 768.5232, 813.4132, 886.9876, 967.4979, 1013.5090, 1073.5051, 1121.6525, 1146.6636, 1146.6636, 1167.6635, 1176.5972, 1193.6886, 1229.6062, 1265.6515, 1267.6628, 1279.7657, 1299.6910, 1334.8781, 1402.8402, 1402.8402, 1448.9122, 1485.6979, 1501.6788, 1522.7649, 1527.7059, 1656.9066, 1668.7482, 1724.7947, 1727.8440, 1740.7786, 1755.4257, 1801.8174, 1801.8174, 1817.8101, 1817.8101, 1847.8879, 1863.8594, 1912.9987, 1928.9893, 2120.0881, 2162.2390, 2326.0974, 2342.2439, 2413.1497, 2564.2971, 2626.2878, 3009.6250, 3443.6943

6. gi|223529808 **Mass:** 99108 **Score:** 75 **Expect:** 0.021 **Queries matched:** 14

aconitase, putative [Ricinus communis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
748.4346	747.4273	747.4279	-0.0006	39	44	0	---	LPYSIR
778.4242	777.4169	777.4133	0.0036	726	732	0	---	GTFANIR
914.5702	913.5629	913.5596	0.0033	45	52	0	---	ILLESAIR
945.4101	944.4028	944.3988	0.0041	709	716	0	---	DFNSYGSR
967.4979	966.4906	966.5134	-0.0228	746	754	0	---	TVHIPSGEK
1061.5195	1060.5122	1060.5083	0.0039	717	725	1	---	RGNDEIMAR
1077.5089	1076.5016	1076.5032	-0.0016	717	725	1	---	RGNDEIMAR + Oxidation (M)
1101.5071	1100.4998	1100.4999	-0.0000	709	717	1	---	DFNSYGSRR
1184.6810	1183.6737	1183.6713	0.0024	77	86	0	---	QVEIPFKPAR
1184.6810	1183.6737	1183.6713	0.0024	77	86	0	39	QVEIPFKPAR
1977.0912	1976.0839	1976.0612	0.0228	257	274	1	---	DGVTATDLVLTVTQMLRK + Oxidation (M)
2104.0957	2103.0884	2103.0856	0.0028	87	105	0	---	VLLQDFTGVPAVVDLACMR

2120.0881	2119.0808	2119.0805	0.0003	87 - 105	0	---	VLLQDFTGVPAVVDLACMR + Oxidation (M)
2564.2971	2563.2898	2563.1938	0.0960	766 - 790	1	---	SEGHDTVILAGAEYGSGSSRDWAAK

No match to: 713.4078, 734.4946, 750.5013, 768.5232, 813.4132, 886.9876, 1013.5090, 1023.5128, 1073.5051, 1121.6525, 1146.6636, 1146.6636, 1167.6635, 1176.5972, 1193.6886, 1229.6062, 1265.6515, 1267.6628, 1279.7657, 1299.6910, 1334.8781, 1402.8402, 1402.8402, 1448.9122, 1485.6979, 1501.6788, 1508.8214, 1522.7649, 1527.7059, 1571.7571, 1656.9066, 1668.7482, 1724.7947, 1727.8440, 1740.7786, 1755.4257, 1801.8174, 1801.8174, 1817.8101, 1817.8101, 1847.8879, 1863.8594, 1912.9987, 1928.9893, 2162.2390, 2326.0974, 2342.2439, 2413.1497, 2626.2878, 3009.6250, 3443.6943

7. gi|4586021 **Mass:** 98720 **Score:** 71 **Expect:** 0.046 **Queries matched:** 14

cytoplasmic aconitate hydratase [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
748.4346	747.4273	747.4279	-0.0006	39 -	44	0	---	LPYSIR
778.4242	777.4169	777.4133	0.0036	726 -	732	0	---	GTFANIR
914.5702	913.5629	913.5596	0.0033	45 -	52	0	---	ILLESAIR
945.4101	944.4028	944.3988	0.0041	709 -	716	0	---	DFNSYGSR
967.4979	966.4906	966.5134	-0.0228	746 -	754	0	---	TVHIPSGEK
1061.5195	1060.5122	1060.5083	0.0039	717 -	725	1	---	RGNDEIMAR
1073.5051	1072.4978	1072.4937	0.0041	708 -	716	1	---	KDFNSYGSR
1077.5089	1076.5016	1076.5032	-0.0016	717 -	725	1	---	RGNDEIMAR + Oxidation (M)
1101.5071	1100.4998	1100.4999	-0.0000	709 -	717	1	---	DFNSYGSRR
1121.6525	1120.6452	1120.6465	-0.0013	379 -	387	1	---	RPHDRVTLK
1184.6810	1183.6737	1183.6713	0.0024	77 -	86	0	---	QVEIPFKPAR
1184.6810	1183.6737	1183.6713	0.0024	77 -	86	0	39	QVEIPFKPAR
2104.0957	2103.0884	2103.0856	0.0028	87 -	105	0	---	VLLQDFTGVPAVVDLACMR
2120.0881	2119.0808	2119.0805	0.0003	87 -	105	0	---	VLLQDFTGVPAVVDLACMR + Oxidation (M)

No match to: 713.4078, 734.4946, 750.5013, 768.5232, 813.4132, 886.9876, 1013.5090, 1023.5128, 1146.6636, 1146.6636, 1167.6635, 1176.5972, 1193.6886, 1229.6062, 1265.6515, 1267.6628, 1279.7657, 1299.6910, 1334.8781, 1402.8402, 1402.8402, 1448.9122, 1485.6979, 1501.6788, 1508.8214, 1522.7649, 1527.7059, 1571.7571, 1656.9066, 1668.7482, 1724.7947, 1727.8440, 1740.7786, 1755.4257, 1801.8174, 1801.8174, 1817.8101, 1817.8101, 1847.8879, 1863.8594, 1912.9987, 1928.9893, 1977.0912, 2162.2390, 2326.0974, 2342.2439, 2413.1497, 2564.2971, 2626.2878, 3009.6250, 3443.6943

8. gi|157329909 **Mass:** 97645 **Score:** 70 **Expect:** 0.065 **Queries matched:** 14

unnamed protein product [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
748.4346	747.4273	747.4279	-0.0006	29 -	34	0	---	LPYSIR
778.4242	777.4169	777.4133	0.0036	714 -	720	0	---	GTFANIR
914.5702	913.5629	913.5596	0.0033	35 -	42	0	---	ILLESAIR
945.4101	944.4028	944.3988	0.0041	697 -	704	0	---	DFNSYGSR
1061.5195	1060.5122	1060.5083	0.0039	705 -	713	1	---	RGNDEIMAR
1077.5089	1076.5016	1076.5032	-0.0016	705 -	713	1	---	RGNDEIMAR + Oxidation (M)
1101.5071	1100.4998	1100.4999	-0.0000	697 -	705	1	---	DFNSYGSRR

1184.6810	1183.6737	1183.6713	0.0024	67 - 76	0	---	QVEIPFKPAR
1184.6810	1183.6737	1183.6713	0.0024	67 - 76	0	39	QVEIPFKPAR
1485.6979	1484.6906	1484.7485	-0.0579	1 - 14	0	---	MFGLFKPAGGEFGK
1501.6788	1500.6715	1500.7434	-0.0719	1 - 14	0	---	MFGLFKPAGGEFGK + Oxidation (M)
1977.0912	1976.0839	1976.0612	0.0228	247 - 264	1	---	DGVTATDLVLTVTQMLRK + Oxidation (M)
2104.0957	2103.0884	2103.0856	0.0028	77 - 95	0	---	VLLQDFTGVPAVVDLACMR
2120.0881	2119.0808	2119.0805	0.0003	77 - 95	0	---	VLLQDFTGVPAVVDLACMR + Oxidation (M)

No match to: 713.4078, 734.4946, 750.5013, 768.5232, 813.4132, 886.9876, 967.4979, 1013.5090, 1023.5128, 1073.5051, 1121.6525, 1146.6636, 1146.6636, 1167.6635, 1176.5972, 1193.6886, 1229.6062, 1265.6515, 1267.6628, 1279.7657, 1299.6910, 1334.8781, 1402.8402, 1402.8402, 1448.9122, 1508.8214, 1522.7649, 1527.7059, 1571.7571, 1656.9066, 1668.7482, 1724.7947, 1727.8440, 1740.7786, 1755.4257, 1801.8174, 1801.8174, 1817.8101, 1817.8101, 1847.8879, 1863.8594, 1912.9987, 1928.9893, 2162.2390, 2326.0974, 2342.2439, 2413.1497, 2564.2971, 2626.2878, 3009.6250, 3443.6943

9. gi|15233349 **Mass:** 98774 **Score:** 68 **Expect:** 0.098 **Queries matched:** 14

aconitate hydratase, cytoplasmic / citrate hydro-lyase / aconitase (ACO) [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
748.4346	747.4273	747.4279	-0.0006	39 -	44	0	---	LPYSIR
778.4242	777.4169	777.4133	0.0036	726 -	732	0	---	GTFANIR
914.5702	913.5629	913.5596	0.0033	45 -	52	0	---	ILLESAIR
945.4101	944.4028	944.3988	0.0041	709 -	716	0	---	DFNSYGSR
1061.5195	1060.5122	1060.5083	0.0039	717 -	725	1	---	RGNDEIMAR
1077.5089	1076.5016	1076.5032	-0.0016	717 -	725	1	---	RGNDEIMAR + Oxidation (M)
1101.5071	1100.4998	1100.4999	-0.0000	709 -	717	1	---	DFNSYGSRR
1184.6810	1183.6737	1183.6713	0.0024	77 -	86	0	---	QVEIPFKPAR
1184.6810	1183.6737	1183.6713	0.0024	77 -	86	0	39	QVEIPFKPAR
1656.9066	1655.8993	1655.9068	-0.0075	459 -	472	1	---	KACDLGLEVKPWIK
1801.8174	1800.8101	1800.8728	-0.0627	275 -	290	1	---	HGVVGKFVEFHGEGMR + Oxidation (M)
1801.8174	1800.8101	1800.8728	-0.0627	275 -	290	1	---	HGVVGKFVEFHGEGMR + Oxidation (M)
2104.0957	2103.0884	2103.0856	0.0028	87 -	105	0	---	VLLQDFTGVPAVVDLACMR
2120.0881	2119.0808	2119.0805	0.0003	87 -	105	0	---	VLLQDFTGVPAVVDLACMR + Oxidation (M)

No match to: 713.4078, 734.4946, 750.5013, 768.5232, 813.4132, 886.9876, 967.4979, 1013.5090, 1023.5128, 1073.5051, 1121.6525, 1146.6636, 1146.6636, 1167.6635, 1176.5972, 1193.6886, 1229.6062, 1265.6515, 1267.6628, 1279.7657, 1299.6910, 1334.8781, 1402.8402, 1402.8402, 1448.9122, 1485.6979, 1501.6788, 1508.8214, 1522.7649, 1527.7059, 1571.7571, 1668.7482, 1724.7947, 1727.8440, 1740.7786, 1755.4257, 1817.8101, 1817.8101, 1847.8879, 1863.8594, 1912.9987, 1928.9893, 1977.0912, 2162.2390, 2326.0974, 2342.2439, 2413.1497, 2564.2971, 2626.2878, 3009.6250, 3443.6943

10. gi|168057341 **Mass:** 95476 **Score:** 61 **Expect:** 0.45 **Queries matched:** 13

predicted protein [Physcomitrella patens subsp. patens]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
778.4242	777.4169	777.4133	0.0036	695 -	701	0	---	GTFANIR
914.5702	913.5629	913.5596	0.0033	14 -	21	0	---	ILLESAIR

945.4101	944.4028	944.3988	0.0041	678 - 685	0	---	DFNSYGSR
1061.5195	1060.5122	1060.5083	0.0039	686 - 694	1	---	RGNDEIMAR
1073.5051	1072.4978	1072.4937	0.0041	677 - 685	1	---	KDFNSYGSR
1077.5089	1076.5016	1076.5032	-0.0016	686 - 694	1	---	RGNDEIMAR + Oxidation (M)
1101.5071	1100.4998	1100.4999	-0.0000	678 - 686	1	---	DFNSYGSRR
1184.6810	1183.6737	1183.6713	0.0024	46 - 55	0	---	QVEIPFKPAR
1184.6810	1183.6737	1183.6713	0.0024	46 - 55	0	39	QVEIPFKPAR
1265.6515	1264.6442	1264.7027	-0.0584	288 - 298	0	---	ITLDYLTLTGR
2104.0957	2103.0884	2103.0856	0.0028	56 - 74	0	---	VILQDFTGVPCVVDLAAMR
2120.0881	2119.0808	2119.0805	0.0003	56 - 74	0	---	VILQDFTGVPCVVDLAAMR + Oxidation (M)
2326.0974	2325.0901	2325.0872	0.0029	733 - 754	1	---	YKDEGHDTIILAGAEYGSGSSR

No match to: 713.4078, 734.4946, 748.4346, 750.5013, 768.5232, 813.4132, 886.9876, 967.4979, 1013.5090, 1023.5128, 1121.6525, 1146.6636, 1146.6636, 1167.6635, 1176.5972, 1193.6886, 1229.6062, 1267.6628, 1279.7657, 1299.6910, 1334.8781, 1402.8402, 1402.8402, 1448.9122, 1485.6979, 1501.6788, 1508.8214, 1522.7649, 1527.7059, 1571.7571, 1656.9066, 1668.7482, 1724.7947, 1727.8440, 1740.7786, 1755.4257, 1801.8174, 1801.8174, 1817.8101, 1817.8101, 1847.8879, 1863.8594, 1912.9987, 1928.9893, 1977.0912, 2162.2390, 2342.2439, 2413.1497, 2564.2971, 2626.2878, 3009.6250, 3443.6943

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 65

Protein View

Match to: **gi|222624156** Score: **162** Expect: **3.8e-011**
hypothetical protein OsJ_09326 [Oryza sativa Japonica Group]

Nominal mass (M_r): **99391**; Calculated pI value: **5.80**
NCBI BLAST search of gi|222624156 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Oryza sativa Japonica Group

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **16%**

Matched peptides shown in **Bold Red**

```
   1 MTIFPLPQSP AKNSYDEILT GLAKPGGGAE FGKYYSLPAL SDPRIERLPY
  51 SIRILLESAI RNCDEFQVTG KDVEKILDWE NSAPKQVEIP FKPARVLLQD
 101 FTGVPAVVDL ACMRDAMSKL GSDPNKINPL VPVDLVIDHS VQVDVARSEN
 151 AVQANMELEF HRNKERFGFL KWGSTAFRNM LVVPPGSGIV HQVNLEYLAR
 201 VVFNNGGILY PDSVVGTDSH TTMIDGLGVA GWGVGGIEAE ATMLGQPMSM
 251 VLPGVVGFKL TGKLRNGVTA TDLVLTVTQM LRKHGVVGKF VEFYGGGMSE
 301 LSLADRATIA NMSPEYGATM GFFPVDGKTL DYLKLTGRSD DTVAMIESYL
 351 RANKMFVDYN QPEAERVYSS YLELNLEEVE PCLSGPKRPH DRVTLKNMKS
 401 DWLSCLDNDV GFKGFAVPKE SQGKVAEFSF HGTPAKLKHG DVVIAAITSC
 451 TNTSNPNVML GAALVAKKAC ELGLEVKPWI KTSLAPGSGV VKKYLDKSGL
 501 QKYLDQLGFH IVGYGCTTCI GNSGELDETV SAAISDNDIV AAAVLSGNRN
 551 FEGRVHALTR ANYLASPPLV VAYALAGTVN IDFEKEPIGI SKDGKEVYFR
 601 DIWPSTEEIA EVVKSSVLPD MFKSTYEAIT KGNPMWNELS VSASTLYPWD
 651 PTSTYIHEPP YFKDMTMSPP GPRPVKDAYC LLNFGDSITT DHISPAGSIH
 701 PDSPAARYLK ERGVERKDFN SYGSRRGNDE IMARGTFANI RLVNKFLKGE
 751 VGPKTIHIPS GEKLSVFDAA TKYKNEGHDT IILAGAEYGS GSSRDWAAKG
 801 PMLQGVKAVI AKSFERIHRS NLAGMGIIPL CFKSGEDADT LGLTGHERFT
 851 VHLPANVSEI KPGQDVTVTT DNGKSFTCTL RFDTEVELAY YDNGGILPYV
 901 IRKIAEQ
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
45 - 53	1146.6636	1145.6563	1145.6556	0.0007	1	**IERLPYSIR** (Ions score 36)
45 - 53	1146.6636	1145.6563	1145.6556	0.0007	1	**IERLPYSIR** (No match)
48 - 53	748.4346	747.4273	747.4279	-0.0006	0	**LPYSIR** (No match)
54 - 61	914.5702	913.5629	913.5596	0.0033	0	**ILLESAIR** (No match)
62 - 75	1668.7482	1667.7409	1667.7460	-0.0051	1	**NCDEFQVTGKDVEK** (No match)
86 - 95	1184.6810	1183.6737	1183.6713	0.0024	0	**QVEIPFKPAR** (No match)
86 - 95	1184.6810	1183.6737	1183.6713	0.0024	0	**QVEIPFKPAR** (Ions score 39)
96 - 114	2104.0957	2103.0884	2103.0856	0.0028	0	**VLLQDFTGVPAVVDLACMR** (No match)
96 - 114	2120.0881	2119.0808	2119.0805	0.0003	0	**VLLQDFTGVPAVVDLACMR** Oxidation (M) (No match)
120 - 147	3009.6250	3008.6177	3008.6294	-0.0117	1	**LGSDPNKINPLVPVDLVIDHSVQVDVAR** (No match)
388 - 396	1121.6525	1120.6452	1120.6465	-0.0013	1	**RPHDRVTLK** (No match)
550 - 560	1299.6910	1298.6837	1298.6843	-0.0006	1	**NFEGRVHALTR** (No match)
593 - 600	1013.5090	1012.5017	1012.4977	0.0040	1	**DGKEVYFR** (No match)
615 - 623	1023.5128	1022.5055	1022.5106	-0.0051	0	**SSVLPDMFK** (No match)
717 - 725	1073.5051	1072.4978	1072.4937	0.0041	1	**KDFNSYGSR** (No match)
718 - 725	945.4101	944.4028	944.3988	0.0041	0	**DFNSYGSR** (No match)
718 - 726	1101.5071	1100.4998	1100.4999	-0.0000	1	**DFNSYGSRR** (No match)
726 - 734	1061.5195	1060.5122	1060.5083	0.0039	1	**RGNDEIMAR** (No match)
726 - 734	1077.5089	1076.5016	1076.5032	-0.0016	1	**RGNDEIMAR** Oxidation (M) (No match)
735 - 741	778.4242	777.4169	777.4133	0.0036	0	**GTFANIR** (No match)

Spot 3

Index

	Accession	Mass	Score	Description
1.	gi|12025466	91833	81	alpha 1,4-glucan phosphorylase H isozyme [Oryza sativa]
2.	gi|115441087	94867	80	Os01g0851700 [Oryza sativa (japonica cultivar-group)]
3.	gi|218189392	94840	80	hypothetical protein OsI_04460 [Oryza sativa Indica Group]
4.	gi|226494853	94850	74	LOC100285259 [Zea mays]
5.	gi|14916632	93952	74	RecName: Full=Alpha-glucan phosphorylase, H isozyme; AltName: Full=Starch phosphorylase H
6.	gi|19908257	26554	52	N-hydroxycinnamoyl-CoA:tyramine N-hydroxycinnamoyl transferase THT1-3 [Lycopersicon esculentum
7.	gi|10140790	58765	46	putative glutamyl-tRNA reductase [Oryza sativa (japonica cultivar-group)]
8.	gi|125532547	58781	46	hypothetical protein OsI_34217 [Oryza sativa Indica Group]
9.	gi|2920320	59115	46	glutamyl-tRNA reductase [Oryza sativa Indica Group]
10.	gi|115482796	58896	46	Os10g0502400 [Oryza sativa (japonica cultivar-group)]

Results List

1. gi|12025466 **Mass:** 91833 **Score:** 81 **Expect:** 0.005 **Queries matched:** 9

alpha 1,4-glucan phosphorylase H isozyme [Oryza sativa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
946.5215	945.5142	945.5072	0.0071	131	137	1	---	YRYGLFK
1133.6989	1132.6916	1132.6240	0.0676	711	719	1	---	FEEAKQLIR
1386.7255	1385.7182	1385.6939	0.0243	787	798	1	---	FSSDRTIAQYAK
1386.7255	1385.7182	1385.6939	0.0243	787	798	1	---	FSSDRTIAQYAK
1443.7333	1442.7260	1442.7266	-0.0005	699	710	1	---	DRENGLFKPDPR
1482.7474	1481.7401	1481.7401	0.0000	85	97	0	---	FGYELEALVGQEK
1651.7950	1650.7877	1650.7711	0.0166	51	63	0	---	QTYYLSMEYLQGR
2332.2068	2331.1995	2331.1892	0.0103	244	264	1	50	AQQICAVLYPGDATEEGKLLR
2332.2068	2331.1995	2331.1892	0.0103	244	264	1	---	AQQICAVLYPGDATEEGKLLR

No match to: 713.4024, 734.4888, 750.5057, 768.5154, 782.4682, 848.5264, 864.5364, 1183.6193, 1183.6193, 1230.6814, 1260.6824, 1276.6733, 1279.7549, 1334.8684, 1403.7279, 1403.7279, 1447.7212, 1448.9141, 1562.9406, 1732.0822, 1830.9354, 2144.0400, 2214.1680, 2215.1843, 2230.2134, 2440.3196, 2564.1919, 2608.3223, 2662.3896, 2824.3262, 2845.2925, 2908.4395, 2921.3589, 3333.5625, 3349.5981, 3349.5981

2. gi|115441087 **Mass:** 94867 **Score:** 80 **Expect:** 0.0062 **Queries matched:** 9

Os01g0851700 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
946.5215	945.5142	945.5072	0.0071	163	169	1	---	YRYGLFK
1133.6989	1132.6916	1132.6240	0.0676	743	751	1	---	FEEAKQLIR
1386.7255	1385.7182	1385.6939	0.0243	819	830	1	---	FSSDRTIAQYAK
1386.7255	1385.7182	1385.6939	0.0243	819	830	1	---	FSSDRTIAQYAK

1443.7333	1442.7260	1442.7266	-0.0005	731 - 742	1	---	DRENGLFKPDPR
1482.7474	1481.7401	1481.7401	0.0000	117 - 129	0	---	FGYELEALVGQEK
1651.7950	1650.7877	1650.7711	0.0166	83 - 95	0	---	QTYYLSMEYLQGR
2332.2068	2331.1995	2331.1892	0.0103	276 - 296	1	50	AQQICAVLYPGDATEEGKLLR
2332.2068	2331.1995	2331.1892	0.0103	276 - 296	1	---	AQQICAVLYPGDATEEGKLLR

No match to: 713.4024, 734.4888, 750.5057, 768.5154, 782.4682, 848.5264, 864.5364, 1183.6193, 1183.6193, 1230.6814, 1260.6824, 1276.6733, 1279.7549, 1334.8684, 1403.7279, 1403.7279, 1447.7212, 1448.9141, 1562.9406, 1732.0822, 1830.9354, 2144.0400, 2214.1680, 2215.1843, 2230.2134, 2440.3196, 2564.1919, 2608.3223, 2662.3896, 2824.3262, 2845.2925, 2908.4395, 2921.3589, 3333.5625, 3349.5981, 3349.5981

3. gi|218189392 **Mass:** 94840 **Score:** 80 **Expect:** 0.0062 **Queries matched:** 9

hypothetical protein OsI_04460 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
946.5215	945.5142	945.5072	0.0071	163 - 169	1	---	YRYGLFK
1133.6989	1132.6916	1132.6240	0.0676	743 - 751	1	---	FEEAKQLIR
1386.7255	1385.7182	1385.6939	0.0243	819 - 830	1	---	FSSDRTIAQYAK
1386.7255	1385.7182	1385.6939	0.0243	819 - 830	1	---	FSSDRTIAQYAK
1443.7333	1442.7260	1442.7266	-0.0005	731 - 742	1	---	DRENGLFKPDPR
1482.7474	1481.7401	1481.7401	0.0000	117 - 129	0	---	FGYELEALVGQEK
1651.7950	1650.7877	1650.7711	0.0166	83 - 95	0	---	QTYYLSMEYLQGR
2332.2068	2331.1995	2331.1892	0.0103	276 - 296	1	50	AQQICAVLYPGDATEEGKLLR
2332.2068	2331.1995	2331.1892	0.0103	276 - 296	1	---	AQQICAVLYPGDATEEGKLLR

No match to: 713.4024, 734.4888, 750.5057, 768.5154, 782.4682, 848.5264, 864.5364, 1183.6193, 1183.6193, 1230.6814, 1260.6824, 1276.6733, 1279.7549, 1334.8684, 1403.7279, 1403.7279, 1447.7212, 1448.9141, 1562.9406, 1732.0822, 1830.9354, 2144.0400, 2214.1680, 2215.1843, 2230.2134, 2440.3196, 2564.1919, 2608.3223, 2662.3896, 2824.3262, 2845.2925, 2908.4395, 2921.3589, 3333.5625, 3349.5981, 3349.5981

4. gi|226494853 **Mass:** 94850 **Score:** 74 **Expect:** 0.022 **Queries matched:** 8

LOC100285259 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
946.5215	945.5142	945.5072	0.0071	160 - 166	1	---	YRYGLFK
1386.7255	1385.7182	1385.6939	0.0243	816 - 827	1	---	FSSDRTIAQYAK
1386.7255	1385.7182	1385.6939	0.0243	816 - 827	1	---	FSSDRTIAQYAK
1443.7333	1442.7260	1442.7266	-0.0005	728 - 739	1	---	DRENGLFKPDPR
1651.7950	1650.7877	1650.7711	0.0166	80 - 92	0	---	QTYYLSMEYLQGR
2214.1680	2213.1607	2213.1156	0.0451	465 - 482	1	---	QELFADYVSIWPTKFQNK
2332.2068	2331.1995	2331.1892	0.0103	273 - 293	1	50	AQQICAVLYPGDATEEGKLLR
2332.2068	2331.1995	2331.1892	0.0103	273 - 293	1	---	AQQICAVLYPGDATEEGKLLR

No match to: 713.4024, 734.4888, 750.5057, 768.5154, 782.4682, 848.5264, 864.5364, 1133.6989, 1183.6193, 1183.6193, 1230.6814, 1260.6824, 1276.6733, 1279.7549, 1334.8684, 1403.7279, 1403.7279, 1447.7212, 1448.9141, 1482.7474, 1562.9406, 1732.0822, 1830.9354, 2144.0400, 2215.1843, 2230.2134, 2440.3196, 2564.1919, 2608.3223, 2662.3896, 2824.3262, 2845.2925, 2908.4395, 2921.3589, 3333.5625, 3349.5981, 3349.5981

5. gi|14916632 **Mass:** 93952 **Score:** 74 **Expect:** 0.023 **Queries matched:** 7

RecName: Full=Alpha-glucan phosphorylase, H isozyme; AltName: Full=Starch phosphorylase H

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
946.5215	945.5142	945.5072	0.0071	155	161	1	---	YRYGLFK
1443.7333	1442.7260	1442.7266	-0.0005	722	733	1	---	DRENGLFKPDPR
1482.7474	1481.7401	1481.7150	0.0252	109	121	0	---	FGYELEAIAGQER
1651.7950	1650.7877	1650.7711	0.0166	75	87	0	---	QTYYLSMEYLQGR
2230.2134	2229.2061	2229.1615	0.0446	289	306	1	---	LKQQYFLCSASLQDIIFR
2332.2068	2331.1995	2331.1892	0.0103	268	288	1	50	AQQICAVLYPGDATEEGKLLR
2332.2068	2331.1995	2331.1892	0.0103	268	288	1	---	AQQICAVLYPGDATEEGKLLR

No match to: 713.4024, 734.4888, 750.5057, 768.5154, 782.4682, 848.5264, 864.5364, 1133.6989, 1183.6193, 1183.6193, 1230.6814, 1260.6824, 1276.6733, 1279.7549, 1334.8684, 1386.7255, 1386.7255, 1403.7279, 1403.7279, 1447.7212, 1448.9141, 1562.9406, 1732.0822, 1830.9354, 2144.0400, 2214.1680, 2215.1843, 2440.3196, 2564.1919, 2608.3223, 2662.3896, 2824.3262, 2845.2925, 2908.4395, 2921.3589, 3333.5625, 3349.5981, 3349.5981

6. gi|19908257 **Mass:** 26554 **Score:** 52 **Expect:** 4.1 **Queries matched:** 6

N-hydroxycinnamoyl-CoA:tyramine N-hydroxycinnamoyl transferase THT1-3 [Lycopersicon esculentum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1403.7279	1402.7206	1402.7568	-0.0362	29	40	1	---	LATKSDLSHIYR
1403.7279	1402.7206	1402.7568	-0.0362	29	40	1	---	LATKSDLSHIYR
1651.7950	1650.7877	1650.8252	-0.0375	112	125	1	---	FPVVEGEVEEFRSK
2608.3223	2607.3150	2607.3391	-0.0241	2	26	1	---	APALEQAITSDASSDVTITGKIYTR
3349.5981	3348.5908	3348.7902	-0.1994	166	198	1	---	KLGMGSLLFGTVASIAANNGFVSVEGIVAVWNK
3349.5981	3348.5908	3348.7902	-0.1994	167	199	1	---	LGMGSLLFGTVASIAANNGFVSVEGIVAVWNKK

No match to: 713.4024, 734.4888, 750.5057, 768.5154, 782.4682, 848.5264, 864.5364, 946.5215, 1133.6989, 1183.6193, 1183.6193, 1230.6814, 1260.6824, 1276.6733, 1279.7549, 1334.8684, 1386.7255, 1386.7255, 1443.7333, 1447.7212, 1448.9141, 1482.7474, 1562.9406, 1732.0822, 1830.9354, 2144.0400, 2214.1680, 2215.1843, 2230.2134, 2332.2068, 2332.2068, 2440.3196, 2564.1919, 2662.3896, 2824.3262, 2845.2925, 2908.4395, 2921.3589, 3333.5625

7. gi|10140790 **Mass:** 58765 **Score:** 46 **Expect:** 15 **Queries matched:** 10

putative glutamyl-tRNA reductase [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1183.6193	1182.6120	1182.6396	-0.0276	105	114	0	---	LAVAEELWPR
1183.6193	1182.6120	1182.6396	-0.0276	105	114	0	---	LAVAEELWPR
1230.6814	1229.6741	1229.6867	-0.0126	428	438	1	---	DSLETVPTIKK
1386.7255	1385.7182	1385.7374	-0.0192	207	220	1	---	QVVRSGQNSGGLGK
1386.7255	1385.7182	1385.7374	-0.0192	207	220	1	---	QVVRSGQNSGGLGK
2214.1680	2213.1607	2213.1221	0.0386	42	63	1	---	SGVVVRCDAGVEAQAQAQAVAK
2332.2068	2331.1995	2331.1276	0.0719	375	395	1	---	NVSACVSEVGHARVYNVDDLK
2332.2068	2331.1995	2331.1276	0.0719	375	395	1	---	NVSACVSEVGHARVYNVDDLK

2608.3223	2607.3150	2607.2308	0.0842	499 - 520	1	---	TLDETLENMHALNRMFSLDTEK
2662.3896	2661.3823	2661.3716	0.0107	238 - 263	1	---	CETNISSGAVSVSSAAVELALMKLPK

No match to: 713.4024, 734.4888, 750.5057, 768.5154, 782.4682, 848.5264, 864.5364, 946.5215, 1133.6989, 1260.6824, 1276.6733, 1279.7549, 1334.8684, 1403.7279, 1403.7279, 1443.7333, 1447.7212, 1448.9141, 1482.7474, 1562.9406, 1651.7950, 1732.0822, 1830.9354, 2144.0400, 2215.1843, 2230.2134, 2440.3196, 2564.1919, 2824.3262, 2845.2925, 2908.4395, 2921.3589, 3333.5625, 3349.5981, 3349.5981

8. gi|125532547 **Mass:** 58781 **Score:** 46 **Expect:** 15 **Queries matched:** 10

hypothetical protein OsI_34217 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1183.6193	1182.6120	1182.6396	-0.0276	105 - 114	0	---	LAVAEELWPR
1183.6193	1182.6120	1182.6396	-0.0276	105 - 114	0	---	LAVAEELWPR
1230.6814	1229.6741	1229.6867	-0.0126	428 - 438	1	---	DSLETVPTIKK
1386.7255	1385.7182	1385.7374	-0.0192	207 - 220	1	---	QVVRSGQNSGGLGK
1386.7255	1385.7182	1385.7374	-0.0192	207 - 220	1	---	QVVRSGQNSGGLGK
2214.1680	2213.1607	2213.1221	0.0386	42 - 63	1	---	SGVVVRCDAGVEAQAQAQAVAK
2332.2068	2331.1995	2331.1276	0.0719	375 - 395	1	---	NVSACVSEVGHARVYNVDDLK
2332.2068	2331.1995	2331.1276	0.0719	375 - 395	1	---	NVSACVSEVGHARVYNVDDLK
2608.3223	2607.3150	2607.2308	0.0842	499 - 520	1	---	TLDETLENMHALNRMFSLDTEK
2662.3896	2661.3823	2661.3716	0.0107	238 - 263	1	---	CETNISSGAVSVSSAAVELALMKLPK

No match to: 713.4024, 734.4888, 750.5057, 768.5154, 782.4682, 848.5264, 864.5364, 946.5215, 1133.6989, 1260.6824, 1276.6733, 1279.7549, 1334.8684, 1403.7279, 1403.7279, 1443.7333, 1447.7212, 1448.9141, 1482.7474, 1562.9406, 1651.7950, 1732.0822, 1830.9354, 2144.0400, 2215.1843, 2230.2134, 2440.3196, 2564.1919, 2824.3262, 2845.2925, 2908.4395, 2921.3589, 3333.5625, 3349.5981, 3349.5981

9. gi|2920320 **Mass:** 59115 **Score:** 46 **Expect:** 16 **Queries matched:** 10

glutamyl-tRNA reductase [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1183.6193	1182.6120	1182.6396	-0.0276	105 - 114	0	---	LAVAEELWPR
1183.6193	1182.6120	1182.6396	-0.0276	105 - 114	0	---	LAVAEELWPR
1230.6814	1229.6741	1229.6867	-0.0126	428 - 438	1	---	DSLETVPTIKK
1386.7255	1385.7182	1385.7374	-0.0192	207 - 220	1	---	QVVRSGQNSGGLGK
1386.7255	1385.7182	1385.7374	-0.0192	207 - 220	1	---	QVVRSGQNSGGLGK
2214.1680	2213.1607	2213.1221	0.0386	42 - 63	1	---	SGVVVRCDAGVEAQAQAQAVAK
2332.2068	2331.1995	2331.1276	0.0719	375 - 395	1	---	NVSACVSEVGHARVYNVDDLK
2332.2068	2331.1995	2331.1276	0.0719	375 - 395	1	---	NVSACVSEVGHARVYNVDDLK
2608.3223	2607.3150	2607.2308	0.0842	499 - 520	1	---	TLDETLENMHALNRMFSLDTEK
2662.3896	2661.3823	2661.3716	0.0107	238 - 263	1	---	CETNISSGAVSVSSAAVELALMKLPK

No match to: 713.4024, 734.4888, 750.5057, 768.5154, 782.4682, 848.5264, 864.5364, 946.5215, 1133.6989, 1260.6824, 1276.6733, 1279.7549, 1334.8684, 1403.7279, 1403.7279, 1443.7333, 1447.7212, 1448.9141, 1482.7474, 1562.9406, 1651.7950, 1732.0822, 1830.9354, 2144.0400, 2215.1843, 2230.2134, 2440.3196, 2564.1919, 2824.3262, 2845.2925, 2908.4395, 2921.3589, 3333.5625, 3349.5981, 3349.5981

10. gi|115482796 **Mass:** 58896 **Score:** 46 **Expect:** 17 **Queries matched:** 10

Os10g0502400 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1183.6193	1182.6120	1182.6396	-0.0276	106	115	0	---	LAVAEELWPR
1183.6193	1182.6120	1182.6396	-0.0276	106	115	0	---	LAVAEELWPR
1230.6814	1229.6741	1229.6867	-0.0126	429	439	1	---	DSLETVPTIKK
1386.7255	1385.7182	1385.7374	-0.0192	208	221	1	---	QVVRSGQNSGGLGK
1386.7255	1385.7182	1385.7374	-0.0192	208	221	1	---	QVVRSGQNSGGLGK
2214.1680	2213.1607	2213.1221	0.0386	43	64	1	---	SGVVVRCDAGVEAQAQAQAVAK
2332.2068	2331.1995	2331.1276	0.0719	376	396	1	---	NVSACVSEVGHARVYNVDDLK
2332.2068	2331.1995	2331.1276	0.0719	376	396	1	---	NVSACVSEVGHARVYNVDDLK
2608.3223	2607.3150	2607.2308	0.0842	500	521	1	---	TLDETLENMHALNRMFSLDTEK
2662.3896	2661.3823	2661.3716	0.0107	239	264	1	---	CETNISSGAVSVSSAAVELALMKLPK

No match to: 713.4024, 734.4888, 750.5057, 768.5154, 782.4682, 848.5264, 864.5364, 946.5215, 1133.6989, 1260.6824, 1276.6733, 1279.7549, 1334.8684, 1403.7279, 1403.7279, 1443.7333, 1447.7212, 1448.9141, 1482.7474, 1562.9406, 1651.7950, 1732.0822, 1830.9354, 2144.0400, 2215.1843, 2230.2134, 2440.3196, 2564.1919, 2824.3262, 2845.2925, 2908.4395, 2921.3589, 3333.5625, 3349.5981, 3349.5981

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 45

Protein View

Match to: **gi|12025466** Score: **81** Expect: **0.005**
alpha 1,4-glucan phosphorylase H isozyme [Oryza sativa]

Nominal mass (M_r): **91833**; Calculated pI value: **7.36**
NCBI BLAST search of gi|12025466 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Oryza sativa

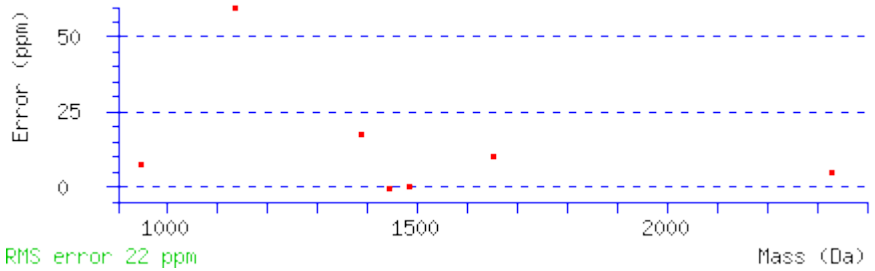
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **10%**

Matched peptides shown in **Bold Red**

```
   1 ISFHAQYSPH FSPLAFGPEQ AFYSTAESVR DHLVQRWNET YLHFHKTDPK
  51 QTYYLSMEYL QGRALTNAVG NLGITGAYAE AVKKFGYELE ALVGQEKDAA
 101 LGNGGLGRLA SCFLDSMATL NLPAWGYGLR YRYGLFKQCI TKEGQEEIAE
 151 DWLEKFSPWE IVRHDIVYPI RFFGHVEILP DGSRKWVGGE VLNALAYDVP
 201 IPGYKTKNAI SLRLWDAKAS AEDFNLFQFN DGQYESAAQL HARAQQICAV
 251 LYPGDATEEG KLLRLKQQYF LCSASLQDIF FRFKERKADR VSGKWSEFPA
 301 KVAVQLNDTH PTLAIPELMR LLMDVEGLGW DEAWDITNKT IAYTNHTVLP
 351 EALEKWSQIV MRKLLPRHME IIEEIDKRFK EMVISTRKEM EGKIDSMRIL
 401 DNSNPQKPVV RMANLCVVSA HTVNGVAELH SNILKEELFA DYLSIWPNKF
 451 QNKTNGITPR RWLRFCNPEL SEIVTKWLKT DQWTSNLDLL TGLRKFADDE
 501 KLHAEWASAK LASKKRLAKH VLDVTGVTID PNSLFDIQIK RIHEYKRQLL
 551 NILGAVYRYK KLKGMSAEER QKVTPRTVMI GGKAFATYTN AKRIVKLVND
 601 VGAVVNNDPD VNKYLKVVFI PNYNVSVAEV LIPGSELSQH ISTAGMEASG
 651 TSNMKFSLNG CVIIGTLDGA NVEIREEVGQ ENFFLFGAKA DQVAGLRKDR
 701 ENGLFKPDPR FEEAKQLIRS GAFGTYDYAP LLDSLEGNSG FGRGDYFLVG
 751 YDFPSYIDAQ AQVDEAYKDK KKWIKMSILN TAGSGKFSSD RTIAQYAKEI
 801 WGITASPVS
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
51 - 63	1651.7950	1650.7877	1650.7711	0.0166	0	QTYYLSMEYLQGR	(No match)
85 - 97	1482.7474	1481.7401	1481.7401	0.0000	0	FGYELEALVGQEK	(No match)
131 - 137	946.5215	945.5142	945.5072	0.0071	1	YRYGLFK	(No match)
244 - 264	2332.2068	2331.1995	2331.1892	0.0103	1	AQQICAVLYPGDATEEGKLLR	(Ions score 50)
244 - 264	2332.2068	2331.1995	2331.1892	0.0103	1	AQQICAVLYPGDATEEGKLLR	(No match)
699 - 710	1443.7333	1442.7260	1442.7266	-0.0005	1	DRENGLFKPDPR	(No match)
711 - 719	1133.6989	1132.6916	1132.6240	0.0676	1	FEEAKQLIR	(No match)
787 - 798	1386.7255	1385.7182	1385.6939	0.0243	1	FSSDRTIAQYAK	(No match)
787 - 798	1386.7255	1385.7182	1385.6939	0.0243	1	FSSDRTIAQYAK	(No match)



Spot 4

Index

	Accession	Mass	Score	Description
1.	gi|12025466	91833	96	alpha 1,4-glucan phosphorylase H isozyme [Oryza sativa]
2.	gi|194740440	94850	96	starch phosphorylase 2 precursor [Zea mays]
3.	gi|115441087	94867	94	Os01g0851700 [Oryza sativa (japonica cultivar-group)]
4.	gi|218189392	94840	94	hypothetical protein OsI_04460 [Oryza sativa Indica Group]
5.	gi|14916632	93952	93	RecName: Full=Alpha-glucan phosphorylase, H isozyme; AltName: Full=Starch phosphorylase H

Results List

1. gi|12025466 **Mass:** 91833 **Score:** 96 **Expect:** 0.00015 **Queries matched:** 11

alpha 1,4-glucan phosphorylase H isozyme [Oryza sativa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
946.5114	945.5041	945.5072	-0.0030	131	137	1	---	YRYGLFK
946.5114	945.5041	945.5072	-0.0030	131	137	1	---	YRYGLFK
1142.5887	1141.5814	1141.5880	-0.0065	584	593	1	---	AFATYTNAKR
1386.7029	1385.6956	1385.6939	0.0017	787	798	1	---	FSSDRTIAQYAK
1436.6925	1435.6852	1435.7017	-0.0164	465	476	0	---	FCNPELSEIVTK
1443.7275	1442.7202	1442.7266	-0.0063	699	710	1	11	DRENGLFKPDPR
1443.7275	1442.7202	1442.7266	-0.0063	699	710	1	---	DRENGLFKPDPR
1482.7206	1481.7133	1481.7401	-0.0268	85	97	0	---	FGYELEALVGQEK
1575.7821	1574.7748	1574.7100	0.0649	143	155	0	---	EGQEEIAEDWLEK
2332.1855	2331.1782	2331.1892	-0.0110	244	264	1	---	AQQICAVLYPGDATEEGKLLR
2332.1855	2331.1782	2331.1892	-0.0110	244	264	1	39	AQQICAVLYPGDATEEGKLLR

No match to: 713.4120, 724.5015, 736.5021, 750.5233, 768.5256, 838.5318, 864.5406, 911.5117, 1133.7001, 1183.6066, 1183.6066, 1230.6703, 1279.7584, 1334.8746, 1403.7191, 1403.7191, 1419.7026, 1447.6920, 1448.9092, 1562.9381, 1618.0436, 1652.7708, 1701.8165, 1732.0732, 1814.9587, 1830.9232, 2153.0862, 2187.1521, 2609.3208

2. gi|194740440 **Mass:** 94850 **Score:** 96 **Expect:** 0.00017 **Queries matched:** 11

starch phosphorylase 2 precursor [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
946.5114	945.5041	945.5072	-0.0030	160	166	1	---	YRYGLFK
946.5114	945.5041	945.5072	-0.0030	160	166	1	---	YRYGLFK
1142.5887	1141.5814	1141.5880	-0.0065	613	622	1	---	AFATYTNAKR
1386.7029	1385.6956	1385.6939	0.0017	816	827	1	---	FSSDRTIAQYAK
1436.6925	1435.6852	1435.7017	-0.0164	494	505	0	---	FCNPELSEIVTK
1443.7275	1442.7202	1442.7266	-0.0063	728	739	1	11	DRENGLFKPDPR
1443.7275	1442.7202	1442.7266	-0.0063	728	739	1	---	DRENGLFKPDPR
1701.8165	1700.8092	1700.8158	-0.0065	525	539	1	---	FADDEKLHAEWAAAK

2332.1855	2331.1782	2331.1892	-0.0110	273 - 293	1	---	AQQICAVLYPGDATEEGKLLR
2332.1855	2331.1782	2331.1892	-0.0110	273 - 293	1	39	AQQICAVLYPGDATEEGKLLR
2609.3208	2608.3135	2608.3100	0.0035	441 - 464	0	---	MANLCVVSSHTVNGVAELHSNILK + Oxidation (M)

No match to: 713.4120, 724.5015, 736.5021, 750.5233, 768.5256, 838.5318, 864.5406, 911.5117, 1133.7001, 1183.6066, 1183.6066, 1230.6703, 1279.7584, 1334.8746, 1403.7191, 1403.7191, 1419.7026, 1447.6920, 1448.9092, 1482.7206, 1562.9381, 1575.7821, 1618.0436, 1652.7708, 1732.0732, 1814.9587, 1830.9232, 2153.0862, 2187.1521

3. gi|115441087 **Mass:** 94867 **Score:** 94 **Expect:** 0.00027 **Queries matched:** 11

Os01g0851700 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
946.5114	945.5041	945.5072	-0.0030	163 - 169	1	---	YRYGLFK
946.5114	945.5041	945.5072	-0.0030	163 - 169	1	---	YRYGLFK
1142.5887	1141.5814	1141.5880	-0.0065	616 - 625	1	---	AFATYTNAKR
1386.7029	1385.6956	1385.6939	0.0017	819 - 830	1	---	FSSDRTIAQYAK
1436.6925	1435.6852	1435.7017	-0.0164	497 - 508	0	---	FCNPELSEIVTK
1443.7275	1442.7202	1442.7266	-0.0063	731 - 742	1	11	DRENGLFKPDPR
1443.7275	1442.7202	1442.7266	-0.0063	731 - 742	1	---	DRENGLFKPDPR
1482.7206	1481.7133	1481.7401	-0.0268	117 - 129	0	---	FGYELEALVGQEK
1575.7821	1574.7748	1574.7100	0.0649	175 - 187	0	---	EGQEEIAEDWLEK
2332.1855	2331.1782	2331.1892	-0.0110	276 - 296	1	---	AQQICAVLYPGDATEEGKLLR
2332.1855	2331.1782	2331.1892	-0.0110	276 - 296	1	39	AQQICAVLYPGDATEEGKLLR

No match to: 713.4120, 724.5015, 736.5021, 750.5233, 768.5256, 838.5318, 864.5406, 911.5117, 1133.7001, 1183.6066, 1183.6066, 1230.6703, 1279.7584, 1334.8746, 1403.7191, 1403.7191, 1419.7026, 1447.6920, 1448.9092, 1562.9381, 1618.0436, 1652.7708, 1701.8165, 1732.0732, 1814.9587, 1830.9232, 2153.0862, 2187.1521, 2609.3208

4. gi|218189392 **Mass:** 94840 **Score:** 94 **Expect:** 0.00027 **Queries matched:** 11

hypothetical protein OsI_04460 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
946.5114	945.5041	945.5072	-0.0030	163 - 169	1	---	YRYGLFK
946.5114	945.5041	945.5072	-0.0030	163 - 169	1	---	YRYGLFK
1142.5887	1141.5814	1141.5880	-0.0065	616 - 625	1	---	AFATYTNAKR
1386.7029	1385.6956	1385.6939	0.0017	819 - 830	1	---	FSSDRTIAQYAK
1436.6925	1435.6852	1435.7017	-0.0164	497 - 508	0	---	FCNPELSEIVTK
1443.7275	1442.7202	1442.7266	-0.0063	731 - 742	1	11	DRENGLFKPDPR
1443.7275	1442.7202	1442.7266	-0.0063	731 - 742	1	---	DRENGLFKPDPR
1482.7206	1481.7133	1481.7401	-0.0268	117 - 129	0	---	FGYELEALVGQEK
1575.7821	1574.7748	1574.7100	0.0649	175 - 187	0	---	EGQEEIAEDWLEK
2332.1855	2331.1782	2331.1892	-0.0110	276 - 296	1	---	AQQICAVLYPGDATEEGKLLR
2332.1855	2331.1782	2331.1892	-0.0110	276 - 296	1	39	AQQICAVLYPGDATEEGKLLR

No match to: 713.4120, 724.5015, 736.5021, 750.5233, 768.5256, 838.5318, 864.5406, 911.5117, 1133.7001, 1183.6066, 1183.6066, 1230.6703, 1279.7584, 1334.8746, 1403.7191, 1403.7191, 1419.7026, 1447.6920, 1448.9092, 1562.9381, 1618.0436, 1652.7708, 1701.8165, 1732.0732, 1814.9587, 1830.9232, 2153.0862, 2187.1521, 2609.3208

5. gi|14916632 **Mass:** 93952 **Score:** 93 **Expect:** 0.00028 **Queries matched:** 11

RecName: Full=Alpha-glucan phosphorylase, H isozyme; AltName: Full=Starch phosphorylase H

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
911.5117	910.5044	910.5024	0.0020	157	163	1	---	YGLFKQR
946.5114	945.5041	945.5072	-0.0030	155	161	1	---	YRYGLFK
946.5114	945.5041	945.5072	-0.0030	155	161	1	---	YRYGLFK
1142.5887	1141.5814	1141.5880	-0.0065	607	616	1	---	AFATYTNAKR
1436.6925	1435.6852	1435.7017	-0.0164	488	499	0	---	FCNPELSEIVTK
1443.7275	1442.7202	1442.7266	-0.0063	722	733	1	11	DRENGLFKPDPR
1443.7275	1442.7202	1442.7266	-0.0063	722	733	1	---	DRENGLFKPDPR
1482.7206	1481.7133	1481.7150	-0.0016	109	121	0	---	FGYELEAIAGQER
1701.8165	1700.8092	1700.8158	-0.0065	519	533	1	---	FADDEKLHAEWAAAK
2332.1855	2331.1782	2331.1892	-0.0110	268	288	1	---	AQQICAVLYPGDATEEGKLLR
2332.1855	2331.1782	2331.1892	-0.0110	268	288	1	39	AQQICAVLYPGDATEEGKLLR

No match to: 713.4120, 724.5015, 736.5021, 750.5233, 768.5256, 838.5318, 864.5406, 1133.7001, 1183.6066, 1183.6066, 1230.6703, 1279.7584, 1334.8746, 1386.7029, 1403.7191, 1403.7191, 1419.7026, 1447.6920, 1448.9092, 1562.9381, 1575.7821, 1618.0436, 1652.7708, 1732.0732, 1814.9587, 1830.9232, 2153.0862, 2187.1521, 2609.3208

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 40

Protein View

Match to: **gi|12025466** Score: **96** Expect: **0.00015**
alpha 1,4-glucan phosphorylase H isozyme [Oryza sativa]

Nominal mass (M_r): **91833**; Calculated pI value: **7.36**
NCBI BLAST search of gi|12025466 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Oryza sativa

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **12%**

Matched peptides shown in **Bold Red**

```
   1 ISFHAQYSPH FSPLAFGPEQ AFYSTAESVR DHLVQRWNET YLHFHKTDPK
  51 QTYYLSMEYL QGRALTNAVG NLGITGAYAE AVKKFGYELE ALVGQEKDAA
 101 LGNGGLGRLA SCFLDSMATL NLPAWGYGLR YRYGLFKQCI TKEGQEEIAE
 151 DWLEKFSPWE IVRHDIVYPI RFFGHVEILP DGSRKWVGGE VLNALAYDVP
 201 IPGYKTKNAI SLRLWDAKAS AEDFNLFQFN DGQYESAAQL HARAQQICAV
 251 LYPGDATEEG KLLRLKQQYF LCSASLQDIF FRFKERKADR VSGKWSEFPA
 301 KVAVQLNDTH PTLAIPELMR LLMDVEGLGW DEAWDITNKT IAYTNHTVLP
 351 EALEKWSQIV MRKLLPRHME IIEEIDKRFK EMVISTRKEM EGKIDSMRIL
 401 DNSNPQKPVV RMANLCVVSA HTVNGVAELH SNILKEELFA DYLSIWPNKF
 451 QNKTNGITPR RWLRFCNPEL SEIVTKWLKT DQWTSNLDLL TGLRKFADDE
 501 KLHAEWASAK LASKKRLAKH VLDVTGVTID PNSLFDIQIK RIHEYKRQLL
 551 NILGAVYRYK KLKGMSAEER QKVTPRTVMI GGKAFATYTN AKRIVKLVND
 601 VGAVVNNDPD VNKYLKVVFI PNYNVSVAEV LIPGSELSQH ISTAGMEASG
 651 TSNMKFSLNG CVIIGTLDGA NVEIREEVGQ ENFFLFGAKA DQVAGLRKDR
 701 ENGLFKPDPR FEEAKQLIRS GAFGTYDYAP LLDSLEGNSG FGRGDYFLVG
 751 YDFPSYIDAQ AQVDEAYKDK KKWIKMSILN TAGSGKFSSD RTIAQYAKEI
 801 WGITASPVS
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
85 - 97	1482.7206	1481.7133	1481.7401	-0.0268	0	FGYELEALVGQEK (No match)
131 - 137	946.5114	945.5041	945.5072	-0.0030	1	YRYGLFK (No match)
131 - 137	946.5114	945.5041	945.5072	-0.0030	1	YRYGLFK (No match)
143 - 155	1575.7821	1574.7748	1574.7100	0.0649	0	EGQEEIAEDWLEK (No match)
244 - 264	2332.1855	2331.1782	2331.1892	-0.0110	1	AQQICAVLYPGDATEEGKLLR (No match)
244 - 264	2332.1855	2331.1782	2331.1892	-0.0110	1	AQQICAVLYPGDATEEGKLLR (Ions score 39)
465 - 476	1436.6925	1435.6852	1435.7017	-0.0164	0	FCNPELSEIVTK (No match)
584 - 593	1142.5887	1141.5814	1141.5880	-0.0065	1	AFATYTNAKR (No match)
699 - 710	1443.7275	1442.7202	1442.7266	-0.0063	1	DRENGLFKPDPR (Ions score 11)
699 - 710	1443.7275	1442.7202	1442.7266	-0.0063	1	DRENGLFKPDPR (No match)
787 - 798	1386.7029	1385.6956	1385.6939	0.0017	1	FSSDRTIAQYAK (No match)

Spot 5

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	Accession	Mass	Score	Description
1.	gi|14916632	93952	132	RecName: Full=Alpha-glucan phosphorylase, H isozyme; AltName: Full=Starch phosphorylase H
2.	gi|12025466	91833	119	alpha 1,4-glucan phosphorylase H isozyme [Oryza sativa]
3.	gi|115441087	94867	117	Os01g0851700 [Oryza sativa (japonica cultivar-group)]
4.	gi|218189392	94840	117	hypothetical protein OsI_04460 [Oryza sativa Indica Group]
5.	gi|226494853	94850	109	LOC100285259 [Zea mays]
6.	gi|67772809	6263	56	putative LEA protein [Pinus gerardiana]
7.	gi|116057674	48359	50	putative porphobilinogen deaminase (ISS) [Ostreococcus tauri]
8.	gi|3915783	15433	49	RecName: Full=Probable non-specific lipid-transfer protein; Short=LTP; AltName: Full=Major pol
9.	gi|95007033	15447	49	par j1.0103 protein [Parietaria judaica]
10.	gi|62132439	11107	48	putative LEA protein [Pinus monophylla]

Results List

1. gi|14916632 **Mass:** 93952 **Score:** 132 **Expect:** 3.8e-008 **Queries matched:** 20

RecName: Full=Alpha-glucan phosphorylase, H isozyme; AltName: Full=Starch phosphorylase H

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
845.4825	844.4752	844.4555	0.0197	565	570	1	---	IHEYKR
911.5127	910.5054	910.5024	0.0030	157	163	1	---	YGLFKQR
946.5179	945.5106	945.5072	0.0035	155	161	1	---	YRYGLFK
1033.5721	1032.5648	1032.5392	0.0256	180	187	0	---	FSPWEIVR
1138.6040	1137.5967	1137.5964	0.0003	403	411	1	---	FREMVISTR
1142.6011	1141.5938	1141.5880	0.0059	607	616	1	---	AFATYTNAKR
1154.5992	1153.5919	1153.5913	0.0006	403	411	1	---	FREMVISTR + Oxidation (M)
1436.7216	1435.7143	1435.7017	0.0127	488	499	0	---	FCNPELSEIVTK
1443.7349	1442.7276	1442.7266	0.0011	722	733	1	---	DRENGLFKPDPR
1443.7349	1442.7276	1442.7266	0.0011	722	733	1	11	DRENGLFKPDPR
1482.7306	1481.7233	1481.7150	0.0084	109	121	0	---	FGYELEAIAGQER
1651.7887	1650.7814	1650.7711	0.0103	75	87	0	---	QTYYLSMEYLQGR
1667.7795	1666.7722	1666.7661	0.0062	75	87	0	---	QTYYLSMEYLQGR + Oxidation (M)
1701.8275	1700.8202	1700.8158	0.0045	519	533	1	---	FADDEKLHAEWAAAK
2136.1069	2135.0996	2135.0867	0.0129	326	344	0	---	VAVQMNDTHPTLAIPELMR
2152.0977	2151.0904	2151.0816	0.0088	326	344	0	---	VAVQMNDTHPTLAIPELMR + Oxidation (M)
2197.0430	2196.0357	2196.0163	0.0194	767	785	0	---	GDYFLVGYDFPSYIDAQAR
2230.2109	2229.2036	2229.1615	0.0421	289	306	1	---	LKQQYFLCSASLQDIIFR
2332.2034	2331.1961	2331.1892	0.0069	268	288	1	41	AQQICAVLYPGDATEEGKLLR
2332.2034	2331.1961	2331.1892	0.0069	268	288	1	---	AQQICAVLYPGDATEEGKLLR

No match to: 713.4016, 724.4961, 734.4911, 750.5103, 768.5095, 782.4717, 838.5148, 848.5263, 864.5408, 984.5296, 1017.6736, 1183.6167, 1183.6167, 1230.6737, 1260.6870, 1276.6666, 1279.7520, 1286.7300, 1334.8766, 1386.7174, 1386.7174, 1403.7255, 1403.7255, 1419.7145, 1447.7067, 1448.9009, 1562.9395, 1575.7968, 1732.0865, 1814.9707, 1829.9282, 2061.1213, 2214.1685, 2439.3262, 2541.2637, 2554.1797, 2564.1943, 2608.3162, 2662.3716, 2825.3342, 2845.2798, 2921.3489, 3332.5593, 3348.6086, 3459.6030

2. gi|12025466 **Mass:** 91833 **Score:** 119 **Expect:** 7.6e-007 **Queries matched:** 17

alpha 1,4-glucan phosphorylase H isozyme [Oryza sativa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
845.4825	844.4752	844.4555	0.0197	542	547	1	---	IHEYKR
946.5179	945.5106	945.5072	0.0035	131	137	1	---	YRYGLFK
1033.5721	1032.5648	1032.5392	0.0256	156	163	0	---	FSPWEIVR
1142.6011	1141.5938	1141.5880	0.0059	584	593	1	---	AFATYTNAKR
1286.7300	1285.7227	1285.7142	0.0085	208	218	1	---	NAISLRLWDAK
1386.7174	1385.7101	1385.6939	0.0162	787	798	1	---	FSSDRTIAQYAK
1386.7174	1385.7101	1385.6939	0.0162	787	798	1	---	FSSDRTIAQYAK
1436.7216	1435.7143	1435.7017	0.0127	465	476	0	---	FCNPELSEIVTK
1443.7349	1442.7276	1442.7266	0.0011	699	710	1	---	DRENGLFKPDPR
1443.7349	1442.7276	1442.7266	0.0011	699	710	1	11	DRENGLFKPDPR
1482.7306	1481.7233	1481.7401	-0.0168	85	97	0	---	FGYELEALVGQEK
1575.7968	1574.7895	1574.7100	0.0796	143	155	0	---	EGQEEIAEDWLEK
1651.7887	1650.7814	1650.7711	0.0103	51	63	0	---	QTYYLSMEYLQGR
1667.7795	1666.7722	1666.7661	0.0062	51	63	0	---	QTYYLSMEYLQGR + Oxidation (M)
2061.1213	2060.1140	2060.1265	-0.0125	64	84	1	---	ALTNAVGNLGITGAYAEAVKK
2332.2034	2331.1961	2331.1892	0.0069	244	264	1	41	AQQICAVLYPGDATEEGKLLR
2332.2034	2331.1961	2331.1892	0.0069	244	264	1	---	AQQICAVLYPGDATEEGKLLR

No match to: 713.4016, 724.4961, 734.4911, 750.5103, 768.5095, 782.4717, 838.5148, 848.5263, 864.5408, 911.5127, 984.5296, 1017.6736, 1138.6040, 1154.5992, 1183.6167, 1183.6167, 1230.6737, 1260.6870, 1276.6666, 1279.7520, 1334.8766, 1403.7255, 1403.7255, 1419.7145, 1447.7067, 1448.9009, 1562.9395, 1701.8275, 1732.0865, 1814.9707, 1829.9282, 2136.1069, 2152.0977, 2197.0430, 2214.1685, 2230.2109, 2439.3262, 2541.2637, 2554.1797, 2564.1943, 2608.3162, 2662.3716, 2825.3342, 2845.2798, 2921.3489, 3332.5593, 3348.6086, 3459.6030

3. gi|115441087 **Mass:** 94867 **Score:** 117 **Expect:** 1.2e-006 **Queries matched:** 17

Os01g0851700 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
845.4825	844.4752	844.4555	0.0197	574	579	1	---	IHEYKR
946.5179	945.5106	945.5072	0.0035	163	169	1	---	YRYGLFK
1033.5721	1032.5648	1032.5392	0.0256	188	195	0	---	FSPWEIVR
1142.6011	1141.5938	1141.5880	0.0059	616	625	1	---	AFATYTNAKR
1286.7300	1285.7227	1285.7142	0.0085	240	250	1	---	NAISLRLWDAK
1386.7174	1385.7101	1385.6939	0.0162	819	830	1	---	FSSDRTIAQYAK
1386.7174	1385.7101	1385.6939	0.0162	819	830	1	---	FSSDRTIAQYAK

1436.7216	1435.7143	1435.7017	0.0127	497 - 508	0	---	FCNPELSEIVTK
1443.7349	1442.7276	1442.7266	0.0011	731 - 742	1	---	DRENGLFKPDPR
1443.7349	1442.7276	1442.7266	0.0011	731 - 742	1	11	DRENGLFKPDPR
1482.7306	1481.7233	1481.7401	-0.0168	117 - 129	0	---	FGYELEALVGQEK
1575.7968	1574.7895	1574.7100	0.0796	175 - 187	0	---	EGQEEIAEDWLEK
1651.7887	1650.7814	1650.7711	0.0103	83 - 95	0	---	QTYYLSMEYLQGR
1667.7795	1666.7722	1666.7661	0.0062	83 - 95	0	---	QTYYLSMEYLQGR + Oxidation (M)
2061.1213	2060.1140	2060.1265	-0.0125	96 - 116	1	---	ALTNAVGNLGITGAYAEAVKK
2332.2034	2331.1961	2331.1892	0.0069	276 - 296	1	41	AQQICAVLYPGDATEEGKLLR
2332.2034	2331.1961	2331.1892	0.0069	276 - 296	1	---	AQQICAVLYPGDATEEGKLLR

No match to: 713.4016, 724.4961, 734.4911, 750.5103, 768.5095, 782.4717, 838.5148, 848.5263, 864.5408, 911.5127, 984.5296, 1017.6736, 1138.6040, 1154.5992, 1183.6167, 1183.6167, 1230.6737, 1260.6870, 1276.6666, 1279.7520, 1334.8766, 1403.7255, 1403.7255, 1419.7145, 1447.7067, 1448.9009, 1562.9395, 1701.8275, 1732.0865, 1814.9707, 1829.9282, 2136.1069, 2152.0977, 2197.0430, 2214.1685, 2230.2109, 2439.3262, 2541.2637, 2554.1797, 2564.1943, 2608.3162, 2662.3716, 2825.3342, 2845.2798, 2921.3489, 3332.5593, 3348.6086, 3459.6030

4. gi|218189392 **Mass:** 94840 **Score:** 117 **Expect:** 1.2e-006 **Queries matched:** 17

hypothetical protein OsI_04460 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
845.4825	844.4752	844.4555	0.0197	574 - 579	1	---	IHEYKR
946.5179	945.5106	945.5072	0.0035	163 - 169	1	---	YRYGLFK
1033.5721	1032.5648	1032.5392	0.0256	188 - 195	0	---	FSPWEIVR
1142.6011	1141.5938	1141.5880	0.0059	616 - 625	1	---	AFATYTNAKR
1286.7300	1285.7227	1285.7142	0.0085	240 - 250	1	---	NAISLRLWDAK
1386.7174	1385.7101	1385.6939	0.0162	819 - 830	1	---	FSSDRTIAQYAK
1386.7174	1385.7101	1385.6939	0.0162	819 - 830	1	---	FSSDRTIAQYAK
1436.7216	1435.7143	1435.7017	0.0127	497 - 508	0	---	FCNPELSEIVTK
1443.7349	1442.7276	1442.7266	0.0011	731 - 742	1	---	DRENGLFKPDPR
1443.7349	1442.7276	1442.7266	0.0011	731 - 742	1	11	DRENGLFKPDPR
1482.7306	1481.7233	1481.7401	-0.0168	117 - 129	0	---	FGYELEALVGQEK
1575.7968	1574.7895	1574.7100	0.0796	175 - 187	0	---	EGQEEIAEDWLEK
1651.7887	1650.7814	1650.7711	0.0103	83 - 95	0	---	QTYYLSMEYLQGR
1667.7795	1666.7722	1666.7661	0.0062	83 - 95	0	---	QTYYLSMEYLQGR + Oxidation (M)
2061.1213	2060.1140	2060.1265	-0.0125	96 - 116	1	---	ALTNAVGNLGITGAYAEAVKK
2332.2034	2331.1961	2331.1892	0.0069	276 - 296	1	41	AQQICAVLYPGDATEEGKLLR
2332.2034	2331.1961	2331.1892	0.0069	276 - 296	1	---	AQQICAVLYPGDATEEGKLLR

No match to: 713.4016, 724.4961, 734.4911, 750.5103, 768.5095, 782.4717, 838.5148, 848.5263, 864.5408, 911.5127, 984.5296, 1017.6736, 1138.6040, 1154.5992, 1183.6167, 1183.6167, 1230.6737, 1260.6870, 1276.6666, 1279.7520, 1334.8766, 1403.7255, 1403.7255, 1419.7145, 1447.7067, 1448.9009, 1562.9395, 1701.8275, 1732.0865, 1814.9707, 1829.9282, 2136.1069, 2152.0977, 2197.0430, 2214.1685, 2230.2109, 2439.3262, 2541.2637, 2554.1797, 2564.1943, 2608.3162, 2662.3716, 2825.3342, 2845.2798, 2921.3489, 3332.5593, 3348.6086, 3459.6030

5. gi|226494853 **Mass:** 94850 **Score:** 109 **Expect:** 7.6e-006 **Queries matched:** 16

LOC100285259 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
845.4825	844.4752	844.4555	0.0197	571 -	576	1	---	IHEYKR
946.5179	945.5106	945.5072	0.0035	160 -	166	1	---	YRYGLFK
1142.6011	1141.5938	1141.5880	0.0059	613 -	622	1	---	AFATYTNAKR
1386.7174	1385.7101	1385.6939	0.0162	816 -	827	1	---	FSSDRTIAQYAK
1386.7174	1385.7101	1385.6939	0.0162	816 -	827	1	---	FSSDRTIAQYAK
1436.7216	1435.7143	1435.7017	0.0127	494 -	505	0	---	FCNPELSEIVTK
1443.7349	1442.7276	1442.7266	0.0011	728 -	739	1	---	DRENGLFKPDPR
1443.7349	1442.7276	1442.7266	0.0011	728 -	739	1	11	DRENGLFKPDPR
1651.7887	1650.7814	1650.7711	0.0103	80 -	92	0	---	QTYYLSMEYLQGR
1667.7795	1666.7722	1666.7661	0.0062	80 -	92	0	---	QTYYLSMEYLQGR + Oxidation (M)
1701.8275	1700.8202	1700.8158	0.0045	525 -	539	1	---	FADDEKLHAEWAAAK
2061.1213	2060.1140	2060.1265	-0.0125	93 -	113	1	---	ALTNAVGNLGITGAYAEAVKK
2136.1069	2135.0996	2135.1585	-0.0589	623 -	642	1	---	IVKLVNDVGAVVNNDPEVNK
2214.1685	2213.1612	2213.1156	0.0456	465 -	482	1	---	QELFADYVSIWPTKFQNK
2332.2034	2331.1961	2331.1892	0.0069	273 -	293	1	41	AQQICAVLYPGDATEEGKLLR
2332.2034	2331.1961	2331.1892	0.0069	273 -	293	1	---	AQQICAVLYPGDATEEGKLLR

No match to: 713.4016, 724.4961, 734.4911, 750.5103, 768.5095, 782.4717, 838.5148, 848.5263, 864.5408, 911.5127, 984.5296, 1017.6736, 1033.5721, 1138.6040, 1154.5992, 1183.6167, 1183.6167, 1230.6737, 1260.6870, 1276.6666, 1279.7520, 1286.7300, 1334.8766, 1403.7255, 1403.7255, 1419.7145, 1447.7067, 1448.9009, 1482.7306, 1562.9395, 1575.7968, 1732.0865, 1814.9707, 1829.9282, 2152.0977, 2197.0430, 2230.2109, 2439.3262, 2541.2637, 2554.1797, 2564.1943, 2608.3162, 2662.3716, 2825.3342, 2845.2798, 2921.3489, 3332.5593, 3348.6086, 3459.6030

6. gi|67772809 **Mass:** 6263 **Score:** 56 **Expect:** 1.5 **Queries matched:** 5

putative LEA protein [Pinus gerardiana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1386.7174	1385.7101	1385.7401	-0.0300	1 -	14	0	---	EIASGTILDPGSVK
1386.7174	1385.7101	1385.7401	-0.0300	1 -	14	0	7	EIASGTILDPGSVK
1814.9707	1813.9634	1813.9421	0.0213	1 -	18	1	---	EIASGTILDPGSVKANDK
2197.0430	2196.0357	2196.1574	-0.1216	19 -	37	0	---	TGMIIPVTVPYDFLLNIMK + 2 Oxidation (M)
2608.3162	2607.3089	2607.3804	-0.0714	19 -	41	1	---	TGMIIPVTVPYDFLLNIMKDVGR + Oxidation (M)

No match to: 713.4016, 724.4961, 734.4911, 750.5103, 768.5095, 782.4717, 838.5148, 845.4825, 848.5263, 864.5408, 911.5127, 946.5179, 984.5296, 1017.6736, 1033.5721, 1138.6040, 1142.6011, 1154.5992, 1183.6167, 1183.6167, 1230.6737, 1260.6870, 1276.6666, 1279.7520, 1286.7300, 1334.8766, 1403.7255, 1403.7255, 1419.7145, 1436.7216, 1443.7349, 1443.7349, 1447.7067, 1448.9009, 1482.7306, 1562.9395, 1575.7968, 1651.7887, 1667.7795, 1701.8275, 1732.0865, 1829.9282, 2061.1213, 2136.1069, 2152.0977, 2214.1685, 2230.2109, 2332.2034, 2332.2034, 2439.3262, 2541.2637, 2554.1797, 2564.1943, 2662.3716, 2825.3342, 2845.2798, 2921.3489, 3332.5593, 3348.6086, 3459.6030

7. gi|116057674 **Mass:** 48359 **Score:** 50 **Expect:** 6.5 **Queries matched:** 8

putative porphobilinogen deaminase (ISS) [Ostreococcus tauri]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
911.5127	910.5054	910.5236	-0.0181	40	48	0	---	AAVDAPIVR
1419.7145	1418.7072	1418.6724	0.0348	289	301	0	---	TPIAAHCHNVDGK
1562.9395	1561.9322	1561.8576	0.0746	367	381	1	---	SQTSPALPNVPRAPK
1667.7795	1666.7722	1666.8031	-0.0309	409	423	1	---	CPMDVGAHIPRASTR
1701.8275	1700.8202	1700.9308	-0.1106	306	321	1	---	GLIASLDGKEVLETTR
2061.1213	2060.1140	2060.0135	0.1005	70	87	0	---	ENFPELAEDGALEICIIK
2825.3342	2824.3269	2824.3952	-0.0683	151	176	1	---	DAFLCLKYDSLDDLPEGAVVGTASLR
2845.2798	2844.2725	2844.4140	-0.1415	315	342	1	---	EVLETTREGAWDAASLLAAGTDAGAELK

No match to: 713.4016, 724.4961, 734.4911, 750.5103, 768.5095, 782.4717, 838.5148, 845.4825, 848.5263, 864.5408, 946.5179, 984.5296, 1017.6736, 1033.5721, 1138.6040, 1142.6011, 1154.5992, 1183.6167, 1183.6167, 1230.6737, 1260.6870, 1276.6666, 1279.7520, 1286.7300, 1334.8766, 1386.7174, 1386.7174, 1403.7255, 1403.7255, 1436.7216, 1443.7349, 1443.7349, 1447.7067, 1448.9009, 1482.7306, 1575.7968, 1651.7887, 1732.0865, 1814.9707, 1829.9282, 2136.1069, 2152.0977, 2197.0430, 2214.1685, 2230.2109, 2332.2034, 2332.2034, 2439.3262, 2541.2637, 2554.1797, 2564.1943, 2608.3162, 2662.3716, 2921.3489, 3332.5593, 3348.6086, 3459.6030

8. gi|3915783 **Mass:** 15433 **Score:** 49 **Expect:** 7.8 **Queries matched:** 6

RecName: Full=Probable non-specific lipid-transfer protein; Short=LTP; AltName: Full=Major pollen a

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
911.5127	910.5054	910.5348	-0.0294	124	130	0	---	LERPQIR
1138.6040	1137.5967	1137.6730	-0.0763	122	130	1	---	ARLERPQIR
1447.7067	1446.6994	1446.6418	0.0577	47	58	0	---	VHACECIQTAMK
1667.7795	1666.7722	1666.8712	-0.0989	67	81	1	---	LVSEVPKHCGIVDSK
2214.1685	2213.1612	2213.0278	0.1334	74	92	1	---	HCGIVDSKLPPIDVNMDCK + Oxidation (M)
2439.3262	2438.3189	2438.1578	0.1611	1	21	1	---	QETCGTMVRALMPCLPFVQGK + Oxidation (M)

No match to: 713.4016, 724.4961, 734.4911, 750.5103, 768.5095, 782.4717, 838.5148, 845.4825, 848.5263, 864.5408, 946.5179, 984.5296, 1017.6736, 1033.5721, 1142.6011, 1154.5992, 1183.6167, 1183.6167, 1230.6737, 1260.6870, 1276.6666, 1279.7520, 1286.7300, 1334.8766, 1386.7174, 1386.7174, 1403.7255, 1403.7255, 1419.7145, 1436.7216, 1443.7349, 1443.7349, 1448.9009, 1482.7306, 1562.9395, 1575.7968, 1651.7887, 1701.8275, 1732.0865, 1814.9707, 1829.9282, 2061.1213, 2136.1069, 2152.0977, 2197.0430, 2230.2109, 2332.2034, 2332.2034, 2541.2637, 2554.1797, 2564.1943, 2608.3162, 2662.3716, 2825.3342, 2845.2798, 2921.3489, 3332.5593, 3348.6086, 3459.6030

9. gi|95007033 **Mass:** 15447 **Score:** 49 **Expect:** 7.8 **Queries matched:** 6

par j1.0103 protein [Parietaria judaica]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
911.5127	910.5054	910.5348	-0.0294	124	130	0	---	LERPQIR
1138.6040	1137.5967	1137.6730	-0.0763	122	130	1	---	ARLERPQIR
1447.7067	1446.6994	1446.6418	0.0577	47	58	0	---	VHACECIQTAMK
1667.7795	1666.7722	1666.8712	-0.0989	67	81	1	---	LVSEVPKHCGIVDSK
2214.1685	2213.1612	2213.0278	0.1334	74	92	1	---	HCGIVDSKLPPIDVNMDCK + Oxidation (M)
2439.3262	2438.3189	2438.1578	0.1611	1	21	1	---	QETCGTMVRALMPCLPFVQGK + Oxidation (M)

No match to: 713.4016, 724.4961, 734.4911, 750.5103, 768.5095, 782.4717, 838.5148, 845.4825, 848.5263, 864.5408, 946.5179, 984.5296, 1017.6736, 1033.5721, 1142.6011, 1154.5992, 1183.6167, 1183.6167, 1230.6737, 1260.6870, 1276.6666, 1279.7520, 1286.7300, 1334.8766, 1386.7174, 1386.7174, 1403.7255, 1403.7255, 1419.7145, 1436.7216, 1443.7349, 1443.7349, 1448.9009, 1482.7306, 1562.9395, 1575.7968, 1651.7887, 1701.8275, 1732.0865, 1814.9707, 1829.9282, 2061.1213, 2136.1069, 2152.0977, 2197.0430, 2230.2109, 2332.2034, 2332.2034, 2541.2637, 2554.1797, 2564.1943, 2608.3162, 2662.3716, 2825.3342, 2845.2798, 2921.3489, 3332.5593, 3348.6086, 3459.6030

10. gi|62132439 **Mass:** 11107 **Score:** 48 **Expect:** 9.8 **Queries matched:** 5

putative LEA protein [Pinus monophylla]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1386.7174	1385.7101	1385.7401	-0.0300	30	-	43	0	---	EIASGTILDPGSVK
1386.7174	1385.7101	1385.7401	-0.0300	30	-	43	0	7	EIASGTILDPGSVK
1814.9707	1813.9634	1813.9421	0.0213	30	-	47	1	---	EIASGTILDPGSVKANDK
2197.0430	2196.0357	2196.1574	-0.1216	48	-	66	0	---	TGMIIPVTVPYDFLLNIMK + 2 Oxidation (M)
2608.3162	2607.3089	2607.3804	-0.0714	48	-	70	1	---	TGMIIPVTVPYDFLLNIMKDVGR + Oxidation (M)

No match to: 713.4016, 724.4961, 734.4911, 750.5103, 768.5095, 782.4717, 838.5148, 845.4825, 848.5263, 864.5408, 911.5127, 946.5179, 984.5296, 1017.6736, 1033.5721, 1138.6040, 1142.6011, 1154.5992, 1183.6167, 1183.6167, 1230.6737, 1260.6870, 1276.6666, 1279.7520, 1286.7300, 1334.8766, 1403.7255, 1403.7255, 1419.7145, 1436.7216, 1443.7349, 1443.7349, 1447.7067, 1448.9009, 1482.7306, 1562.9395, 1575.7968, 1651.7887, 1667.7795, 1701.8275, 1732.0865, 1829.9282, 2061.1213, 2136.1069, 2152.0977, 2214.1685, 2230.2109, 2332.2034, 2332.2034, 2439.3262, 2541.2637, 2554.1797, 2564.1943, 2662.3716, 2825.3342, 2845.2798, 2921.3489, 3332.5593, 3348.6086, 3459.6030

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 65

Protein View

Match to: **gi|14916632** Score: **132** Expect: **3.8e-008**
RecName: Full=Alpha-glucan phosphorylase, H isozyme; AltName: Full=Starch phosphorylase H

Nominal mass (M_r): **93952**; Calculated pI value: **7.27**
NCBI BLAST search of gi|14916632 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Triticum aestivum
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|9082278 from Triticum aestivum

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **22%**

Matched peptides shown in **Bold Red**

```
    1 MSAADKVKPA ASPASEDPSA IAGNISYHAQ YSPHFSPLAF GPEQAFYATA
   51 ESVRDHLLQR WNDTYLHFHK TDPKQTYYLS MEYLQGRALT NAVGNLAITG
  101 AYADALKKFG YELEAIAGQE RDAALGNGGL GRLASCFLDS MATLNLPSWG
  151 YGLRYRYGLF KQRIAKEGQE EIAEDWLDKF SPWEIVRHDV VYPIRFFGHV
  201 EISPDGKRKW AGGEVLNALA YDVPIPGYKT KNAISLRLWD ATATAEDFNL
  251 FQFNDGQYES AAQLHSRAQQ ICAVLYPGDA TEEGKLLRLK QQYFLCSASL
  301 QDIIFRFKER KADRVSGKWS EFPSKVAVQM NDTHPTLAIP ELMRLLMDVE
  351 GLGWDEAWAV TNKTVAYTNH TVLPEALEKW SQAVMKKLLP RHMEIIEEID
  401 KRFREMVIST RKDMEGKIES MRVLDNNPEK PVVRMANLCV VAGHTVNGVA
  451 ELHSNILKQE LFADYVSIWP NKFQNKTNGI TPRRWLRFCN PELSEIVTKW
  501 LKTDQWTSNL DLLTGLRKFA DDEKLHAEWA AAKLASKKRL AKHVLDVTGV
  551 TIDPDSLFDI QIKRIHEYKR QLMNILGAVY RYKKLKEMSA ADRQKVTPRT
  601 VMVGGKAFAT YTNAKRIVKL VNDVGAVVNN DADVNKYLKV VFIPNYNVSV
  651 AEVLIPGSEL SQHISTAGME ASGTSNMKFS LNGCVIIGTL DGANVEIREE
  701 VGQDNFFLFG AKADQVAGLR KDRENGLFKP DPRFEEAKQF IRSGAFGTYD
  751 YTPLLDSLEG NTGFGRGDYF LVGYDFPSYI DAQARVDEAY KDKKKWVKMS
  801 ILNTAGSGKF SSDRTIDQYA KEIWGISACP VP
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
75 - 87	1651.7887	1650.7814	1650.7711	0.0103	0	QTYYLSMEYLQGR (No match)
75 - 87	1667.7795	1666.7722	1666.7661	0.0062	0	QTYYLSMEYLQGR Oxidation (M) (No match)
109 - 121	1482.7306	1481.7233	1481.7150	0.0084	0	FGYELEAIAGQER (No match)
155 - 161	946.5179	945.5106	945.5072	0.0035	1	YRYGLFK (No match)
157 - 163	911.5127	910.5054	910.5024	0.0030	1	YGLFKQR (No match)
180 - 187	1033.5721	1032.5648	1032.5392	0.0256	0	FSPWEIVR (No match)
268 - 288	2332.2034	2331.1961	2331.1892	0.0069	1	AQQICAVLYPGDATEEGKLLR (Ions score 41)
268 - 288	2332.2034	2331.1961	2331.1892	0.0069	1	AQQICAVLYPGDATEEGKLLR (No match)
289 - 306	2230.2109	2229.2036	2229.1615	0.0421	1	LKQQYFLCSASLQDIIFR (No match)
326 - 344	2136.1069	2135.0996	2135.0867	0.0129	0	VAVQMNDTHPTLAIPELMR (No match)
326 - 344	2152.0977	2151.0904	2151.0816	0.0088	0	VAVQMNDTHPTLAIPELMR Oxidation (M) (No match)
403 - 411	1138.6040	1137.5967	1137.5964	0.0003	1	FREMVISTR (No match)
403 - 411	1154.5992	1153.5919	1153.5913	0.0006	1	FREMVISTR Oxidation (M) (No match)
488 - 499	1436.7216	1435.7143	1435.7017	0.0127	0	FCNPELSEIVTK (No match)
519 - 533	1701.8275	1700.8202	1700.8158	0.0045	1	FADDEKLHAEWAAAK (No match)
565 - 570	845.4825	844.4752	844.4555	0.0197	1	IHEYKR (No match)
607 - 616	1142.6011	1141.5938	1141.5880	0.0059	1	AFATYTNAKR (No match)
722 - 733	1443.7349	1442.7276	1442.7266	0.0011	1	DRENGLFKPDPR (No match)
722 - 733	1443.7349	1442.7276	1442.7266	0.0011	1	DRENGLFKPDPR (Ions score 11)
767 - 785	2197.0430	2196.0357	2196.0163	0.0194	0	GDYFLVGYDFPSYIDAQAR (No match)

Spot 6

Index

	Accession	Mass	Score	Description
1.	gi|14916632	93952	182	RecName: Full=Alpha-glucan phosphorylase, H isozyme; AltName: Full=Starch phosphorylase H
2.	gi|12025466	91833	179	alpha 1,4-glucan phosphorylase H isozyme [Oryza sativa]
3.	gi|115441087	94867	177	Os01g0851700 [Oryza sativa (japonica cultivar-group)]
4.	gi|218189392	94840	177	hypothetical protein OsI_04460 [Oryza sativa Indica Group]
5.	gi|226494853	94850	167	LOC100285259 [Zea mays]
6.	gi|125558706	79522	57	hypothetical protein OsI_26387 [Oryza sativa Indica Group]
7.	gi|61097780	45413	54	NADH-Ubiquinone oxidoreductase subunit 7 [Nicotiana sylvestris]
8.	gi|10140790	58765	53	putative glutamyl-tRNA reductase [Oryza sativa (japonica cultivar-group)]
9.	gi|125532547	58781	53	hypothetical protein OsI_34217 [Oryza sativa Indica Group]
10.	gi|2920320	59115	53	glutamyl-tRNA reductase [Oryza sativa Indica Group]

Results List

1. gi|14916632 **Mass:** 93952 **Score:** 182 **Expect:** 3.8e-013 **Queries matched:** 21

RecName: Full=Alpha-glucan phosphorylase, H isozyme; AltName: Full=Starch phosphorylase H

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
911.5097	910.5024	910.5024	-0.0000	157	163	1	---	YGLFKQR
946.5131	945.5058	945.5072	-0.0013	155	161	1	---	YRYGLFK
1033.5568	1032.5495	1032.5392	0.0103	180	187	0	---	FSPWEIVR
1138.6040	1137.5967	1137.5964	0.0003	403	411	1	---	FREMVISTR
1142.5974	1141.5901	1141.5880	0.0022	607	616	1	---	AFATYTNAKR
1154.5870	1153.5797	1153.5913	-0.0116	403	411	1	---	FREMVISTR + Oxidation (M)
1277.6727	1276.6654	1276.6961	-0.0307	571	581	0	---	QLMNILGAVYR
1436.7157	1435.7084	1435.7017	0.0068	488	499	0	---	FCNPELSEIVTK
1443.7225	1442.7152	1442.7266	-0.0113	722	733	1	---	DRENGLFKPDPR
1443.7225	1442.7152	1442.7266	-0.0113	722	733	1	14	DRENGLFKPDPR
1482.7289	1481.7216	1481.7150	0.0067	109	121	0	---	FGYELEAIAGQER
1651.7767	1650.7694	1650.7711	-0.0017	75	87	0	---	QTYYLSMEYLQGR
1667.7607	1666.7534	1666.7661	-0.0126	75	87	0	---	QTYYLSMEYLQGR + Oxidation (M)
1701.8160	1700.8087	1700.8158	-0.0070	519	533	1	---	FADDEKLHAEWAAAK
1860.9697	1859.9624	1859.9741	-0.0117	503	518	1	---	TDQWTSNLDLLTGLRK
2136.0972	2135.0899	2135.0867	0.0032	326	344	0	---	VAVQMNDTHPTLAIPELMR
2152.0815	2151.0742	2151.0816	-0.0074	326	344	0	---	VAVQMNDTHPTLAIPELMR + Oxidation (M)
2168.0930	2167.0857	2167.0765	0.0092	326	344	0	---	VAVQMNDTHPTLAIPELMR + 2 Oxidation (M)
2230.2063	2229.1990	2229.1615	0.0375	289	306	1	---	LKQQYFLCSASLQDIIFR
2332.1980	2331.1907	2331.1892	0.0015	268	288	1	---	AQQICAVLYPGDATEEGKLLR

2332.1980	2331.1907	2331.1892	0.0015	268 - 288	1	87	AQQICAVLYPGDATEEGKLLR

No match to: 713.4000, 734.4866, 750.5250, 768.5093, 782.4626, 848.5183, 864.5323, 984.5283, 1183.6097, 1183.6097, 1230.6704, 1260.6819, 1276.6522, 1279.7296, 1286.7244, 1334.8633, 1386.7120, 1386.7120, 1402.6910, 1403.7192, 1403.7192, 1419.6974, 1447.7036, 1448.8943, 1542.8066, 1575.7903, 1814.9574, 1829.9056, 1830.9283, 1884.9893, 2034.0367, 2061.1270, 2186.1396, 2214.1663, 2263.1914, 2439.3152, 2555.1829, 2565.1882, 2608.3137, 2662.3735, 2825.3191, 2845.2861, 2921.3730, 3348.6106

2. gi|12025466 **Mass:** 91833 **Score:** 179 **Expect:** 7.6e-013 **Queries matched:** 18

alpha 1,4-glucan phosphorylase H isozyme [Oryza sativa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
946.5131	945.5058	945.5072	-0.0013	131 -	137	1	---	YRYGLFK
1033.5568	1032.5495	1032.5392	0.0103	156 -	163	0	---	FSPWEIVR
1142.5974	1141.5901	1141.5880	0.0022	584 -	593	1	---	AFATYTNAKR
1286.7244	1285.7171	1285.7142	0.0029	208 -	218	1	---	NAISLRLWDAK
1386.7120	1385.7047	1385.6939	0.0108	787 -	798	1	---	FSSDRTIAQYAK
1386.7120	1385.7047	1385.6939	0.0108	787 -	798	1	---	FSSDRTIAQYAK
1436.7157	1435.7084	1435.7017	0.0068	465 -	476	0	---	FCNPELSEIVTK
1443.7225	1442.7152	1442.7266	-0.0113	699 -	710	1	---	DRENGLFKPDPR
1443.7225	1442.7152	1442.7266	-0.0113	699 -	710	1	14	DRENGLFKPDPR
1482.7289	1481.7216	1481.7401	-0.0185	85 -	97	0	---	FGYELEALVGQEK
1575.7903	1574.7830	1574.7100	0.0731	143 -	155	0	---	EGQEEIAEDWLEK
1651.7767	1650.7694	1650.7711	-0.0017	51 -	63	0	---	QTYYLSMEYLQGR
1667.7607	1666.7534	1666.7661	-0.0126	51 -	63	0	---	QTYYLSMEYLQGR + Oxidation (M)
1860.9697	1859.9624	1859.9741	-0.0117	480 -	495	1	---	TDQWTSNLDLLTGLRK
2061.1270	2060.1197	2060.1265	-0.0068	64 -	84	1	---	ALTNAVGNLGITGAYAEAVKK
2186.1396	2185.1323	2185.1378	-0.0055	597 -	616	1	---	LVNDVGAVVNNDPDVNKYLK
2332.1980	2331.1907	2331.1892	0.0015	244 -	264	1	---	AQQICAVLYPGDATEEGKLLR
2332.1980	2331.1907	2331.1892	0.0015	244 -	264	1	87	AQQICAVLYPGDATEEGKLLR

No match to: 713.4000, 734.4866, 750.5250, 768.5093, 782.4626, 848.5183, 864.5323, 911.5097, 984.5283, 1138.6040, 1154.5870, 1183.6097, 1183.6097, 1230.6704, 1260.6819, 1276.6522, 1277.6727, 1279.7296, 1334.8633, 1402.6910, 1403.7192, 1403.7192, 1419.6974, 1447.7036, 1448.8943, 1542.8066, 1701.8160, 1814.9574, 1829.9056, 1830.9283, 1884.9893, 2034.0367, 2136.0972, 2152.0815, 2168.0930, 2214.1663, 2230.2063, 2263.1914, 2439.3152, 2555.1829, 2565.1882, 2608.3137, 2662.3735, 2825.3191, 2845.2861, 2921.3730, 3348.6106

3. gi|115441087 **Mass:** 94867 **Score:** 177 **Expect:** 1.2e-012 **Queries matched:** 18

Os01g0851700 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
946.5131	945.5058	945.5072	-0.0013	163 -	169	1	---	YRYGLFK
1033.5568	1032.5495	1032.5392	0.0103	188 -	195	0	---	FSPWEIVR
1142.5974	1141.5901	1141.5880	0.0022	616 -	625	1	---	AFATYTNAKR
1286.7244	1285.7171	1285.7142	0.0029	240 -	250	1	---	NAISLRLWDAK
1386.7120	1385.7047	1385.6939	0.0108	819 -	830	1	---	FSSDRTIAQYAK

1386.7120	1385.7047	1385.6939	0.0108	819 - 830	1	---	FSSDRTIAQYAK
1436.7157	1435.7084	1435.7017	0.0068	497 - 508	0	---	FCNPELSEIVTK
1443.7225	1442.7152	1442.7266	-0.0113	731 - 742	1	---	DRENGLFKPDPR
1443.7225	1442.7152	1442.7266	-0.0113	731 - 742	1	14	DRENGLFKPDPR
1482.7289	1481.7216	1481.7401	-0.0185	117 - 129	0	---	FGYELEALVGQEK
1575.7903	1574.7830	1574.7100	0.0731	175 - 187	0	---	EGQEEIAEDWLEK
1651.7767	1650.7694	1650.7711	-0.0017	83 - 95	0	---	QTYYLSMEYLQGR
1667.7607	1666.7534	1666.7661	-0.0126	83 - 95	0	---	QTYYLSMEYLQGR + Oxidation (M)
1860.9697	1859.9624	1859.9741	-0.0117	512 - 527	1	---	TDQWTSNLDLLTGLRK
2061.1270	2060.1197	2060.1265	-0.0068	96 - 116	1	---	ALTNAVGNLGITGAYAEAVKK
2186.1396	2185.1323	2185.1378	-0.0055	629 - 648	1	---	LVNDVGAVVNNDPDVNKYLK
2332.1980	2331.1907	2331.1892	0.0015	276 - 296	1	---	AQQICAVLYPGDATEEGKLLR
2332.1980	2331.1907	2331.1892	0.0015	276 - 296	1	87	AQQICAVLYPGDATEEGKLLR

No match to: 713.4000, 734.4866, 750.5250, 768.5093, 782.4626, 848.5183, 864.5323, 911.5097, 984.5283, 1138.6040, 1154.5870, 1183.6097, 1183.6097, 1230.6704, 1260.6819, 1276.6522, 1277.6727, 1279.7296, 1334.8633, 1402.6910, 1403.7192, 1403.7192, 1419.6974, 1447.7036, 1448.8943, 1542.8066, 1701.8160, 1814.9574, 1829.9056, 1830.9283, 1884.9893, 2034.0367, 2136.0972, 2152.0815, 2168.0930, 2214.1663, 2230.2063, 2263.1914, 2439.3152, 2555.1829, 2565.1882, 2608.3137, 2662.3735, 2825.3191, 2845.2861, 2921.3730, 3348.6106

4. gi|218189392 **Mass:** 94840 **Score:** 177 **Expect:** 1.2e-012 **Queries matched:** 18

hypothetical protein OsI_04460 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
946.5131	945.5058	945.5072	-0.0013	163 - 169	1	---	YRYGLFK
1033.5568	1032.5495	1032.5392	0.0103	188 - 195	0	---	FSPWEIVR
1142.5974	1141.5901	1141.5880	0.0022	616 - 625	1	---	AFATYTNAKR
1286.7244	1285.7171	1285.7142	0.0029	240 - 250	1	---	NAISLRLWDAK
1386.7120	1385.7047	1385.6939	0.0108	819 - 830	1	---	FSSDRTIAQYAK
1386.7120	1385.7047	1385.6939	0.0108	819 - 830	1	---	FSSDRTIAQYAK
1436.7157	1435.7084	1435.7017	0.0068	497 - 508	0	---	FCNPELSEIVTK
1443.7225	1442.7152	1442.7266	-0.0113	731 - 742	1	---	DRENGLFKPDPR
1443.7225	1442.7152	1442.7266	-0.0113	731 - 742	1	14	DRENGLFKPDPR
1482.7289	1481.7216	1481.7401	-0.0185	117 - 129	0	---	FGYELEALVGQEK
1575.7903	1574.7830	1574.7100	0.0731	175 - 187	0	---	EGQEEIAEDWLEK
1651.7767	1650.7694	1650.7711	-0.0017	83 - 95	0	---	QTYYLSMEYLQGR
1667.7607	1666.7534	1666.7661	-0.0126	83 - 95	0	---	QTYYLSMEYLQGR + Oxidation (M)
1860.9697	1859.9624	1859.9741	-0.0117	512 - 527	1	---	TDQWTSNLDLLTGLRK
2061.1270	2060.1197	2060.1265	-0.0068	96 - 116	1	---	ALTNAVGNLGITGAYAEAVKK
2186.1396	2185.1323	2185.1378	-0.0055	629 - 648	1	---	LVNDVGAVVNNDPDVNKYLK
2332.1980	2331.1907	2331.1892	0.0015	276 - 296	1	---	AQQICAVLYPGDATEEGKLLR
2332.1980	2331.1907	2331.1892	0.0015	276 - 296	1	87	AQQICAVLYPGDATEEGKLLR

No match to: 713.4000, 734.4866, 750.5250, 768.5093, 782.4626, 848.5183, 864.5323, 911.5097, 984.5283, 1138.6040,

1154.5870, 1183.6097, 1183.6097, 1230.6704, 1260.6819, 1276.6522, 1277.6727, 1279.7296, 1334.8633, 1402.6910, 1403.7192, 1403.7192, 1419.6974, 1447.7036, 1448.8943, 1542.8066, 1701.8160, 1814.9574, 1829.9056, 1830.9283, 1884.9893, 2034.0367, 2136.0972, 2152.0815, 2168.0930, 2214.1663, 2230.2063, 2263.1914, 2439.3152, 2555.1829, 2565.1882, 2608.3137, 2662.3735, 2825.3191, 2845.2861, 2921.3730, 3348.6106

5. gi|226494853 **Mass:** 94850 **Score:** 167 **Expect:** 1.2e-011 **Queries matched:** 17

LOC100285259 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
946.5131	945.5058	945.5072	-0.0013	160	166	1	---	YRYGLFK
1142.5974	1141.5901	1141.5880	0.0022	613	622	1	---	AFATYTNAKR
1183.6097	1182.6024	1182.5260	0.0764	418	427	1	7	EMEGKIDSMK + Oxidation (M)
1183.6097	1182.6024	1182.5260	0.0764	418	427	1	---	EMEGKIDSMK + Oxidation (M)
1386.7120	1385.7047	1385.6939	0.0108	816	827	1	---	FSSDRTIAQYAK
1386.7120	1385.7047	1385.6939	0.0108	816	827	1	---	FSSDRTIAQYAK
1436.7157	1435.7084	1435.7017	0.0068	494	505	0	---	FCNPELSEIVTK
1443.7225	1442.7152	1442.7266	-0.0113	728	739	1	---	DRENGLFKPDPR
1443.7225	1442.7152	1442.7266	-0.0113	728	739	1	14	DRENGLFKPDPR
1651.7767	1650.7694	1650.7711	-0.0017	80	92	0	---	QTYYLSMEYLQGR
1667.7607	1666.7534	1666.7661	-0.0126	80	92	0	---	QTYYLSMEYLQGR + Oxidation (M)
1701.8160	1700.8087	1700.8158	-0.0070	525	539	1	---	FADDEKLHAEWAAAK
2061.1270	2060.1197	2060.1265	-0.0068	93	113	1	---	ALTNAVGNLGITGAYAEAVKK
2136.0972	2135.0899	2135.1585	-0.0686	623	642	1	---	IVKLVNDVGAVVNNDPEVNK
2214.1663	2213.1590	2213.1156	0.0434	465	482	1	---	QELFADYVSIWPTKFQNK
2332.1980	2331.1907	2331.1892	0.0015	273	293	1	---	AQQICAVLYPGDATEEGKLLR
2332.1980	2331.1907	2331.1892	0.0015	273	293	1	87	AQQICAVLYPGDATEEGKLLR

No match to: 713.4000, 734.4866, 750.5250, 768.5093, 782.4626, 848.5183, 864.5323, 911.5097, 984.5283, 1033.5568, 1138.6040, 1154.5870, 1230.6704, 1260.6819, 1276.6522, 1277.6727, 1279.7296, 1286.7244, 1334.8633, 1402.6910, 1403.7192, 1403.7192, 1419.6974, 1447.7036, 1448.8943, 1482.7289, 1542.8066, 1575.7903, 1814.9574, 1829.9056, 1830.9283, 1860.9697, 1884.9893, 2034.0367, 2152.0815, 2168.0930, 2186.1396, 2230.2063, 2263.1914, 2439.3152, 2555.1829, 2565.1882, 2608.3137, 2662.3735, 2825.3191, 2845.2861, 2921.3730, 3348.6106

6. gi|125558706 **Mass:** 79522 **Score:** 57 **Expect:** 1.4 **Queries matched:** 12

hypothetical protein OsI_26387 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1154.5870	1153.5797	1153.5740	0.0057	294	304	1	---	SGPGNAWGPRR
1277.6727	1276.6654	1276.5968	0.0686	571	582	0	---	VEAMSINPSGEK + Oxidation (M)
1386.7120	1385.7047	1385.7262	-0.0215	378	390	1	---	SVGVRELDGGIER
1386.7120	1385.7047	1385.7262	-0.0215	378	390	1	---	SVGVRELDGGIER
1402.6910	1401.6837	1401.7099	-0.0262	541	553	1	---	ERGIDALASDLDK
1447.7036	1446.6963	1446.7942	-0.0979	245	257	1	---	SLSFLTNPSRIGR
1448.8943	1447.8870	1447.8735	0.0135	499	510	1	---	AVERPRLNLKPR

1542.8066	1541.7993	1541.8929	-0.0936	641 - 654	0	---	KPVEPPKPEVVAPR
1829.9056	1828.8983	1828.9543	-0.0560	237 - 254	1	---	LNGGGGPRSLSFLTNPSR
1860.9697	1859.9624	1859.9642	-0.0017	275 - 293	0	---	RPAPSPPSFAPSPAAGPTR
2186.1396	2185.1323	2185.0408	0.0915	42 - 58	1	---	YNCHLMEKIESENLLHR
2608.3137	2607.3064	2607.1468	0.1596	20 - 41	0	---	LMFDDECILVDEQDNVVGHESK + Oxidation (M)

No match to: 713.4000, 734.4866, 750.5250, 768.5093, 782.4626, 848.5183, 864.5323, 911.5097, 946.5131, 984.5283, 1033.5568, 1138.6040, 1142.5974, 1183.6097, 1183.6097, 1230.6704, 1260.6819, 1276.6522, 1279.7296, 1286.7244, 1334.8633, 1403.7192, 1403.7192, 1419.6974, 1436.7157, 1443.7225, 1443.7225, 1482.7289, 1575.7903, 1651.7767, 1667.7607, 1701.8160, 1814.9574, 1830.9283, 1884.9893, 2034.0367, 2061.1270, 2136.0972, 2152.0815, 2168.0930, 2214.1663, 2230.2063, 2263.1914, 2332.1980, 2332.1980, 2439.3152, 2555.1829, 2565.1882, 2662.3735, 2825.3191, 2845.2861, 2921.3730, 3348.6106

7. gi|61097780 **Mass:** 45413 **Score:** 54 **Expect:** 2.7 **Queries matched:** 11

NADH-Ubiquinone oxidoreductase subunit 7 [Nicotiana sylvestris]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1142.5974	1141.5901	1141.6356	-0.0454	40 - 49	0	---	AEPHIGLLHR
1183.6097	1182.6024	1182.5491	0.0533	216 - 225	0	---	DWGFSGVMLR + Oxidation (M)
1183.6097	1182.6024	1182.5491	0.0533	216 - 225	0	---	DWGFSGVMLR + Oxidation (M)
1386.7120	1385.7047	1385.6979	0.0068	59 - 69	0	---	TYLQALPYFDR
1386.7120	1385.7047	1385.6979	0.0068	59 - 69	0	---	TYLQALPYFDR
1403.7192	1402.7119	1402.7125	-0.0006	28 - 39	0	---	LVLEMNGEVVER + Oxidation (M)
1403.7192	1402.7119	1402.7125	-0.0006	28 - 39	0	4	LVLEMNGEVVER + Oxidation (M)
1419.6974	1418.6901	1418.6711	0.0190	186 - 197	0	---	IDELEEMLTGNR
2214.1663	2213.1590	2213.0145	0.1445	216 - 234	1	---	DWGFSGVMLRGSGVCWDLR + Oxidation (M)
2565.1882	2564.1809	2564.3056	-0.1247	372 - 394	0	---	HHMLADVVTIIGTQDIVFGEVDR
2921.3730	2920.3657	2920.2973	0.0684	236 - 260	1	---	AAPYDVYDQLDFDIPVGTRGDCYDR

No match to: 713.4000, 734.4866, 750.5250, 768.5093, 782.4626, 848.5183, 864.5323, 911.5097, 946.5131, 984.5283, 1033.5568, 1138.6040, 1154.5870, 1230.6704, 1260.6819, 1276.6522, 1277.6727, 1279.7296, 1286.7244, 1334.8633, 1402.6910, 1436.7157, 1443.7225, 1443.7225, 1447.7036, 1448.8943, 1482.7289, 1542.8066, 1575.7903, 1651.7767, 1667.7607, 1701.8160, 1814.9574, 1829.9056, 1830.9283, 1860.9697, 1884.9893, 2034.0367, 2061.1270, 2136.0972, 2152.0815, 2168.0930, 2186.1396, 2230.2063, 2263.1914, 2332.1980, 2332.1980, 2439.3152, 2555.1829, 2608.3137, 2662.3735, 2825.3191, 2845.2861, 3348.6106

8. gi|10140790 **Mass:** 58765 **Score:** 53 **Expect:** 3 **Queries matched:** 13

putative glutamyl-tRNA reductase [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1183.6097	1182.6024	1182.6396	-0.0372	105 - 114	0	---	LAVAEELWPR
1183.6097	1182.6024	1182.6396	-0.0372	105 - 114	0	---	LAVAEELWPR
1230.6704	1229.6631	1229.6867	-0.0236	428 - 438	1	---	DSLETVPTIKK
1386.7120	1385.7047	1385.7374	-0.0327	207 - 220	1	---	QVVRSGQNSGGLGK
1386.7120	1385.7047	1385.7374	-0.0327	207 - 220	1	---	QVVRSGQNSGGLGK
1402.6910	1401.6837	1401.6960	-0.0122	211 - 224	1	---	SGQNSGGLGKNIDR

2152.0815	2151.0742	2151.1469	-0.0727	83 - 102	1	---	ERSSIAVIGLSVHTAPVEMR
2168.0930	2167.0857	2167.1418	-0.0561	83 - 102	1	---	ERSSIAVIGLSVHTAPVEMR + Oxidation (M)
2214.1663	2213.1590	2213.1221	0.0369	42 - 63	1	---	SGVVVRCDAGVEAQAQAQAVAK
2332.1980	2331.1907	2331.1276	0.0631	375 - 395	1	---	NVSACVSEVGHARVYNVDDLK
2332.1980	2331.1907	2331.1276	0.0631	375 - 395	1	---	NVSACVSEVGHARVYNVDDLK
2608.3137	2607.3064	2607.2308	0.0756	499 - 520	1	---	TLDETLENMHALNRMFSLDTEK
2662.3735	2661.3662	2661.3716	-0.0054	238 - 263	1	---	CETNISSGAVSVSSAAVELALMKLPK

No match to: 713.4000, 734.4866, 750.5250, 768.5093, 782.4626, 848.5183, 864.5323, 911.5097, 946.5131, 984.5283, 1033.5568, 1138.6040, 1142.5974, 1154.5870, 1260.6819, 1276.6522, 1277.6727, 1279.7296, 1286.7244, 1334.8633, 1403.7192, 1403.7192, 1419.6974, 1436.7157, 1443.7225, 1443.7225, 1447.7036, 1448.8943, 1482.7289, 1542.8066, 1575.7903, 1651.7767, 1667.7607, 1701.8160, 1814.9574, 1829.9056, 1830.9283, 1860.9697, 1884.9893, 2034.0367, 2061.1270, 2136.0972, 2186.1396, 2230.2063, 2263.1914, 2439.3152, 2555.1829, 2565.1882, 2825.3191, 2845.2861, 2921.3730, 3348.6106

9. gi|125532547 **Mass:** 58781 **Score:** 53 **Expect:** 3 **Queries matched:** 13

hypothetical protein OsI_34217 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1183.6097	1182.6024	1182.6396	-0.0372	105 - 114	0	---	LAVAEELWPR
1183.6097	1182.6024	1182.6396	-0.0372	105 - 114	0	---	LAVAEELWPR
1230.6704	1229.6631	1229.6867	-0.0236	428 - 438	1	---	DSLETVPTIKK
1386.7120	1385.7047	1385.7374	-0.0327	207 - 220	1	---	QVVRSGQNSGGLGK
1386.7120	1385.7047	1385.7374	-0.0327	207 - 220	1	---	QVVRSGQNSGGLGK
1402.6910	1401.6837	1401.6960	-0.0122	211 - 224	1	---	SGQNSGGLGKNIDR
2152.0815	2151.0742	2151.1469	-0.0727	83 - 102	1	---	ERSSIAVIGLSVHTAPVEMR
2168.0930	2167.0857	2167.1418	-0.0561	83 - 102	1	---	ERSSIAVIGLSVHTAPVEMR + Oxidation (M)
2214.1663	2213.1590	2213.1221	0.0369	42 - 63	1	---	SGVVVRCDAGVEAQAQAQAVAK
2332.1980	2331.1907	2331.1276	0.0631	375 - 395	1	---	NVSACVSEVGHARVYNVDDLK
2332.1980	2331.1907	2331.1276	0.0631	375 - 395	1	---	NVSACVSEVGHARVYNVDDLK
2608.3137	2607.3064	2607.2308	0.0756	499 - 520	1	---	TLDETLENMHALNRMFSLDTEK
2662.3735	2661.3662	2661.3716	-0.0054	238 - 263	1	---	CETNISSGAVSVSSAAVELALMKLPK

No match to: 713.4000, 734.4866, 750.5250, 768.5093, 782.4626, 848.5183, 864.5323, 911.5097, 946.5131, 984.5283, 1033.5568, 1138.6040, 1142.5974, 1154.5870, 1260.6819, 1276.6522, 1277.6727, 1279.7296, 1286.7244, 1334.8633, 1403.7192, 1403.7192, 1419.6974, 1436.7157, 1443.7225, 1443.7225, 1447.7036, 1448.8943, 1482.7289, 1542.8066, 1575.7903, 1651.7767, 1667.7607, 1701.8160, 1814.9574, 1829.9056, 1830.9283, 1860.9697, 1884.9893, 2034.0367, 2061.1270, 2136.0972, 2186.1396, 2230.2063, 2263.1914, 2439.3152, 2555.1829, 2565.1882, 2825.3191, 2845.2861, 2921.3730, 3348.6106

10. gi|2920320 **Mass:** 59115 **Score:** 53 **Expect:** 3.3 **Queries matched:** 13

glutamyl-tRNA reductase [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1183.6097	1182.6024	1182.6396	-0.0372	105 - 114	0	---	LAVAEELWPR
1183.6097	1182.6024	1182.6396	-0.0372	105 - 114	0	---	LAVAEELWPR

1230.6704	1229.6631	1229.6867	-0.0236	428 - 438	1	---	DSLETVPTIKK
1386.7120	1385.7047	1385.7374	-0.0327	207 - 220	1	---	QVVRSGQNSGGLGK
1386.7120	1385.7047	1385.7374	-0.0327	207 - 220	1	---	QVVRSGQNSGGLGK
1402.6910	1401.6837	1401.6960	-0.0122	211 - 224	1	---	SGQNSGGLGKNIDR
2152.0815	2151.0742	2151.1469	-0.0727	83 - 102	1	---	ERSSIAVIGLSVHTAPVEMR
2168.0930	2167.0857	2167.1418	-0.0561	83 - 102	1	---	ERSSIAVIGLSVHTAPVEMR + Oxidation (M)
2214.1663	2213.1590	2213.1221	0.0369	42 - 63	1	---	SGVVVRCDAGVEAQAQAQAVAK
2332.1980	2331.1907	2331.1276	0.0631	375 - 395	1	---	NVSACVSEVGHARVYNVDDLK
2332.1980	2331.1907	2331.1276	0.0631	375 - 395	1	---	NVSACVSEVGHARVYNVDDLK
2608.3137	2607.3064	2607.2308	0.0756	499 - 520	1	---	TLDETLENMHALNRMFSLDTEK
2662.3735	2661.3662	2661.3716	-0.0054	238 - 263	1	---	CETNISSGAVSVSSAAVELALMKLPK

No match to: 713.4000, 734.4866, 750.5250, 768.5093, 782.4626, 848.5183, 864.5323, 911.5097, 946.5131, 984.5283, 1033.5568, 1138.6040, 1142.5974, 1154.5870, 1260.6819, 1276.6522, 1277.6727, 1279.7296, 1286.7244, 1334.8633, 1403.7192, 1403.7192, 1419.6974, 1436.7157, 1443.7225, 1443.7225, 1447.7036, 1448.8943, 1482.7289, 1542.8066, 1575.7903, 1651.7767, 1667.7607, 1701.8160, 1814.9574, 1829.9056, 1830.9283, 1860.9697, 1884.9893, 2034.0367, 2061.1270, 2136.0972, 2186.1396, 2230.2063, 2263.1914, 2439.3152, 2555.1829, 2565.1882, 2825.3191, 2845.2861, 2921.3730, 3348.6106

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 65

Protein View

Match to: **gi|14916632** Score: **182** Expect: **3.8e-013**
RecName: Full=Alpha-glucan phosphorylase, H isozyme; AltName: Full=Starch phosphorylase H

Nominal mass (M_r): **93952**; Calculated pI value: **7.27**
NCBI BLAST search of gi|14916632 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Triticum aestivum
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|9082278 from Triticum aestivum

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **22%**

Matched peptides shown in **Bold Red**

```
   1 MSAADKVKPA ASPASEDPSA IAGNISYHAQ YSPHFSPLAF GPEQAFYATA
  51 ESVRDHLLQR WNDTYLHFHK TDPKQTYYLS MEYLQGRALT NAVGNLAITG
 101 AYADALKKFG YELEAIAGQE RDAALGNGGL GRLASCFLDS MATLNLPSWG
 151 YGLRYRYGLF KQRIAKEGQE EIAEDWLDKF SPWEIVRHDV VYPIRFFGHV
 201 EISPDGKRKW AGGEVLNALA YDVPIPGYKT KNAISLRLWD ATATAEDFNL
 251 FQFNDGQYES AAQLHSRAQQ ICAVLYPGDA TEEGKLLRLK QQYFLCSASL
 301 QDIIFRFKER KADRVSGKWS EFPSKVAVQM NDTHPTLAIP ELMRLLMDVE
 351 GLGWDEAWAV TNKTVAYTNH TVLPEALEKW SQAVMKKLLP RHMEIIEEID
 401 KRFREMVIST RKDMEGKIES MRVLDNNPEK PVVRMANLCV VAGHTVNGVA
 451 ELHSNILKQE LFADYVSIWP NKFQNKTNGI TPRRWLRFCN PELSEIVTKW
 501 LKTDQWTSNL DLLTGLRKFA DDEKLHAEWA AAKLASKKRL AKHVLDVTGV
 551 TIDPDSLFDI QIKRIHEYKR QLMNILGAVY RYKKLKEMSA ADRQKVTPRT
 601 VMVGGKAFAT YTNAKRIVKL VNDVGAVVNN DADVNKYLKV VFIPNYNVSV
 651 AEVLIPGSEL SQHISTAGME ASGTSNMKFS LNGCVIIGTL DGANVEIREE
 701 VGQDNFFLFG AKADQVAGLR KDRENGLFKP DPRFEEAKQF IRSGAFGTYD
 751 YTPLLDSLEG NTGFGRGDYF LVGYDFPSYI DAQARVDEAY KDKKKWVKMS
 801 ILNTAGSGKF SSDRTIDQYA KEIWGISACP VP
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
75 - 87	1651.7767	1650.7694	1650.7711	-0.0017	0	QTYYLSMEYLQGR (No match)
75 - 87	1667.7607	1666.7534	1666.7661	-0.0126	0	QTYYLSMEYLQGR Oxidation (M) (No match)
109 - 121	1482.7289	1481.7216	1481.7150	0.0067	0	FGYELEAIAGQER (No match)
155 - 161	946.5131	945.5058	945.5072	-0.0013	1	YRYGLFK (No match)
157 - 163	911.5097	910.5024	910.5024	-0.0000	1	YGLFKQR (No match)
180 - 187	1033.5568	1032.5495	1032.5392	0.0103	0	FSPWEIVR (No match)
268 - 288	2332.1980	2331.1907	2331.1892	0.0015	1	AQQICAVLYPGDATEEGKLLR (No match)
268 - 288	2332.1980	2331.1907	2331.1892	0.0015	1	AQQICAVLYPGDATEEGKLLR (Ions score 87)
289 - 306	2230.2063	2229.1990	2229.1615	0.0375	1	LKQQYFLCSASLQDIIFR (No match)
326 - 344	2136.0972	2135.0899	2135.0867	0.0032	0	VAVQMNDTHPTLAIPELMR (No match)
326 - 344	2152.0815	2151.0742	2151.0816	-0.0074	0	VAVQMNDTHPTLAIPELMR Oxidation (M) (No match)
326 - 344	2168.0930	2167.0857	2167.0765	0.0092	0	VAVQMNDTHPTLAIPELMR 2 Oxidation (M) (No match)
403 - 411	1138.6040	1137.5967	1137.5964	0.0003	1	FREMVISTR (No match)
403 - 411	1154.5870	1153.5797	1153.5913	-0.0116	1	FREMVISTR Oxidation (M) (No match)
488 - 499	1436.7157	1435.7084	1435.7017	0.0068	0	FCNPELSEIVTK (No match)
503 - 518	1860.9697	1859.9624	1859.9741	-0.0117	1	TDQWTSNLDLLTGLRK (No match)
519 - 533	1701.8160	1700.8087	1700.8158	-0.0070	1	FADDEKLHAEWAAAK (No match)
571 - 581	1277.6727	1276.6654	1276.6961	-0.0307	0	QLMNILGAVYR (No match)
607 - 616	1142.5974	1141.5901	1141.5880	0.0022	1	AFATYTNAKR (No match)
722 - 733	1443.7225	1442.7152	1442.7266	-0.0113	1	DRENGLFKPDPR (No match)
722 - 733	1443.7225	1442.7152	1442.7266	-0.0113	1	DRENGLFKPDPR (Ions score 14)

Spot 7

Index

	Accession	Mass	Score	Description
1.	gi|14916632	93952	161	RecName: Full=Alpha-glucan phosphorylase, H isozyme; AltName: Full=Starch phosphorylase H
2.	gi|12025466	91833	153	alpha 1,4-glucan phosphorylase H isozyme [Oryza sativa]
3.	gi|115441087	94867	152	Os01g0851700 [Oryza sativa (japonica cultivar-group)]
4.	gi|218189392	94840	152	hypothetical protein OsI_04460 [Oryza sativa Indica Group]
5.	gi|226494853	94850	148	LOC100285259 [Zea mays]
6.	gi|417488	95451	56	RecName: Full=Alpha-glucan phosphorylase, H isozyme; AltName: Full=Starch phosphorylase H
7.	gi|168016360	49345	51	predicted protein [Physcomitrella patens subsp. patens]
8.	gi|168000234	64796	51	predicted protein [Physcomitrella patens subsp. patens]
9.	gi|116057674	48359	51	putative porphobilinogen deaminase (ISS) [Ostreococcus tauri]
10.	gi|3915783	15433	49	RecName: Full=Probable non-specific lipid-transfer protein; Short=LTP; AltName: Full=Major pol

Results List

1. gi|14916632 **Mass:** 93952 **Score:** 161 **Expect:** 4.8e-011 **Queries matched:** 19

RecName: Full=Alpha-glucan phosphorylase, H isozyme; AltName: Full=Starch phosphorylase H

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
911.5172	910.5099	910.5024	0.0075	157	163	1	---	YGLFKQR
946.5131	945.5058	945.5072	-0.0013	155	161	1	---	YRYGLFK
1138.6066	1137.5993	1137.5964	0.0029	403	411	1	---	FREMVISTR
1142.6122	1141.6049	1141.5880	0.0170	607	616	1	---	AFATYTNAKR
1154.5930	1153.5857	1153.5913	-0.0056	403	411	1	---	FREMVISTR + Oxidation (M)
1436.7255	1435.7182	1435.7017	0.0166	488	499	0	---	FCNPELSEIVTK
1443.7375	1442.7302	1442.7266	0.0037	722	733	1	---	DRENGLFKPDPR
1443.7375	1442.7302	1442.7266	0.0037	722	733	1	16	DRENGLFKPDPR
1482.7467	1481.7394	1481.7150	0.0245	109	121	0	---	FGYELEAIAGQER
1651.7783	1650.7710	1650.7711	-0.0001	75	87	0	---	QTYYLSMEYLQGR
1667.7695	1666.7622	1666.7661	-0.0038	75	87	0	---	QTYYLSMEYLQGR + Oxidation (M)
1701.8246	1700.8173	1700.8158	0.0016	519	533	1	---	FADDEKLHAEWAAAK
1860.9924	1859.9851	1859.9741	0.0110	503	518	1	---	TDQWTSNLDLLTGLRK
2048.0464	2047.0391	2047.0084	0.0307	815	832	1	---	TIDQYAKEIWGISACPVP
2136.1042	2135.0969	2135.0867	0.0102	326	344	0	---	VAVQMNDTHPTLAIPELMR
2152.0886	2151.0813	2151.0816	-0.0003	326	344	0	---	VAVQMNDTHPTLAIPELMR + Oxidation (M)
2168.1096	2167.1023	2167.0765	0.0258	326	344	0	---	VAVQMNDTHPTLAIPELMR + 2 Oxidation (M)
2332.2039	2331.1966	2331.1892	0.0074	268	288	1	---	AQQICAVLYPGDATEEGKLLR
2332.2039	2331.1966	2331.1892	0.0074	268	288	1	77	AQQICAVLYPGDATEEGKLLR

No match to: 713.3970, 734.4929, 750.5135, 768.5093, 782.4641, 848.5261, 864.5320, 984.5320, 1183.6147,

1183.6147, 1230.6731, 1260.6840, 1276.6632, 1279.7448, 1286.7258, 1334.8624, 1386.7183, 1386.7183, 1402.6913, 1403.7231, 1403.7231, 1419.7095, 1447.7135, 1448.8988, 1542.8176, 1562.9264, 1575.7908, 1732.0847, 1814.9642, 1830.9380, 2034.0474, 2062.1301, 2186.1475, 2198.0315, 2214.1609, 2263.1943, 2352.2332, 2439.3186, 2565.2075, 2608.3313, 2663.3779, 2824.3289, 2845.2898, 2922.3645, 3333.5713, 3349.6025

2. gi|12025466 **Mass:** 91833 **Score:** 153 **Expect:** 3e-010 **Queries matched:** 16

alpha 1,4-glucan phosphorylase H isozyme [Oryza sativa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
946.5131	945.5058	945.5072	-0.0013	131	137	1	---	YRYGLFK
1142.6122	1141.6049	1141.5880	0.0170	584	593	1	---	AFATYTNAKR
1286.7258	1285.7185	1285.7142	0.0043	208	218	1	---	NAISLRLWDAK
1386.7183	1385.7110	1385.6939	0.0171	787	798	1	---	FSSDRTIAQYAK
1386.7183	1385.7110	1385.6939	0.0171	787	798	1	---	FSSDRTIAQYAK
1436.7255	1435.7182	1435.7017	0.0166	465	476	0	---	FCNPELSEIVTK
1443.7375	1442.7302	1442.7266	0.0037	699	710	1	---	DRENGLFKPDPR
1443.7375	1442.7302	1442.7266	0.0037	699	710	1	16	DRENGLFKPDPR
1482.7467	1481.7394	1481.7401	-0.0007	85	97	0	---	FGYELEALVGQEK
1575.7908	1574.7835	1574.7100	0.0736	143	155	0	---	EGQEEIAEDWLEK
1651.7783	1650.7710	1650.7711	-0.0001	51	63	0	---	QTYYLSMEYLQGR
1667.7695	1666.7622	1666.7661	-0.0038	51	63	0	---	QTYYLSMEYLQGR + Oxidation (M)
1860.9924	1859.9851	1859.9741	0.0110	480	495	1	---	TDQWTSNLDLLTGLRK
2186.1475	2185.1402	2185.1378	0.0024	597	616	1	---	LVNDVGAVVNNDPDVNKYLK
2332.2039	2331.1966	2331.1892	0.0074	244	264	1	---	AQQICAVLYPGDATEEGKLLR
2332.2039	2331.1966	2331.1892	0.0074	244	264	1	77	AQQICAVLYPGDATEEGKLLR

No match to: 713.3970, 734.4929, 750.5135, 768.5093, 782.4641, 848.5261, 864.5320, 911.5172, 984.5320, 1138.6066, 1154.5930, 1183.6147, 1183.6147, 1230.6731, 1260.6840, 1276.6632, 1279.7448, 1334.8624, 1402.6913, 1403.7231, 1403.7231, 1419.7095, 1447.7135, 1448.8988, 1542.8176, 1562.9264, 1701.8246, 1732.0847, 1814.9642, 1830.9380, 2034.0474, 2048.0464, 2062.1301, 2136.1042, 2152.0886, 2168.1096, 2198.0315, 2214.1609, 2263.1943, 2352.2332, 2439.3186, 2565.2075, 2608.3313, 2663.3779, 2824.3289, 2845.2898, 2922.3645, 3333.5713, 3349.6025

3. gi|115441087 **Mass:** 94867 **Score:** 152 **Expect:** 3.8e-010 **Queries matched:** 16

Os01g0851700 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
946.5131	945.5058	945.5072	-0.0013	163	169	1	---	YRYGLFK
1142.6122	1141.6049	1141.5880	0.0170	616	625	1	---	AFATYTNAKR
1286.7258	1285.7185	1285.7142	0.0043	240	250	1	---	NAISLRLWDAK
1386.7183	1385.7110	1385.6939	0.0171	819	830	1	---	FSSDRTIAQYAK
1386.7183	1385.7110	1385.6939	0.0171	819	830	1	---	FSSDRTIAQYAK
1436.7255	1435.7182	1435.7017	0.0166	497	508	0	---	FCNPELSEIVTK
1443.7375	1442.7302	1442.7266	0.0037	731	742	1	---	DRENGLFKPDPR
1443.7375	1442.7302	1442.7266	0.0037	731	742	1	16	DRENGLFKPDPR

1482.7467	1481.7394	1481.7401	-0.0007	117 - 129	0	---	FGYELEALVGQEK
1575.7908	1574.7835	1574.7100	0.0736	175 - 187	0	---	EGQEEIAEDWLEK
1651.7783	1650.7710	1650.7711	-0.0001	83 - 95	0	---	QTYYLSMEYLQGR
1667.7695	1666.7622	1666.7661	-0.0038	83 - 95	0	---	QTYYLSMEYLQGR + Oxidation (M)
1860.9924	1859.9851	1859.9741	0.0110	512 - 527	1	---	TDQWTSNLDLLTGLRK
2186.1475	2185.1402	2185.1378	0.0024	629 - 648	1	---	LVNDVGAVVNNDPDVNKYLK
2332.2039	2331.1966	2331.1892	0.0074	276 - 296	1	---	AQQICAVLYPGDATEEGKLLR
2332.2039	2331.1966	2331.1892	0.0074	276 - 296	1	77	AQQICAVLYPGDATEEGKLLR

No match to: 713.3970, 734.4929, 750.5135, 768.5093, 782.4641, 848.5261, 864.5320, 911.5172, 984.5320, 1138.6066, 1154.5930, 1183.6147, 1183.6147, 1230.6731, 1260.6840, 1276.6632, 1279.7448, 1334.8624, 1402.6913, 1403.7231, 1403.7231, 1419.7095, 1447.7135, 1448.8988, 1542.8176, 1562.9264, 1701.8246, 1732.0847, 1814.9642, 1830.9380, 2034.0474, 2048.0464, 2062.1301, 2136.1042, 2152.0886, 2168.1096, 2198.0315, 2214.1609, 2263.1943, 2352.2332, 2439.3186, 2565.2075, 2608.3313, 2663.3779, 2824.3289, 2845.2898, 2922.3645, 3333.5713, 3349.6025

4. gi|218189392 **Mass:** 94840 **Score:** 152 **Expect:** 3.8e-010 **Queries matched:** 16

hypothetical protein OsI_04460 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
946.5131	945.5058	945.5072	-0.0013	163 - 169	1	---	YRYGLFK
1142.6122	1141.6049	1141.5880	0.0170	616 - 625	1	---	AFATYTNAKR
1286.7258	1285.7185	1285.7142	0.0043	240 - 250	1	---	NAISLRLWDAK
1386.7183	1385.7110	1385.6939	0.0171	819 - 830	1	---	FSSDRTIAQYAK
1386.7183	1385.7110	1385.6939	0.0171	819 - 830	1	---	FSSDRTIAQYAK
1436.7255	1435.7182	1435.7017	0.0166	497 - 508	0	---	FCNPELSEIVTK
1443.7375	1442.7302	1442.7266	0.0037	731 - 742	1	---	DRENGLFKPDPR
1443.7375	1442.7302	1442.7266	0.0037	731 - 742	1	16	DRENGLFKPDPR
1482.7467	1481.7394	1481.7401	-0.0007	117 - 129	0	---	FGYELEALVGQEK
1575.7908	1574.7835	1574.7100	0.0736	175 - 187	0	---	EGQEEIAEDWLEK
1651.7783	1650.7710	1650.7711	-0.0001	83 - 95	0	---	QTYYLSMEYLQGR
1667.7695	1666.7622	1666.7661	-0.0038	83 - 95	0	---	QTYYLSMEYLQGR + Oxidation (M)
1860.9924	1859.9851	1859.9741	0.0110	512 - 527	1	---	TDQWTSNLDLLTGLRK
2186.1475	2185.1402	2185.1378	0.0024	629 - 648	1	---	LVNDVGAVVNNDPDVNKYLK
2332.2039	2331.1966	2331.1892	0.0074	276 - 296	1	---	AQQICAVLYPGDATEEGKLLR
2332.2039	2331.1966	2331.1892	0.0074	276 - 296	1	77	AQQICAVLYPGDATEEGKLLR

No match to: 713.3970, 734.4929, 750.5135, 768.5093, 782.4641, 848.5261, 864.5320, 911.5172, 984.5320, 1138.6066, 1154.5930, 1183.6147, 1183.6147, 1230.6731, 1260.6840, 1276.6632, 1279.7448, 1334.8624, 1402.6913, 1403.7231, 1403.7231, 1419.7095, 1447.7135, 1448.8988, 1542.8176, 1562.9264, 1701.8246, 1732.0847, 1814.9642, 1830.9380, 2034.0474, 2048.0464, 2062.1301, 2136.1042, 2152.0886, 2168.1096, 2198.0315, 2214.1609, 2263.1943, 2352.2332, 2439.3186, 2565.2075, 2608.3313, 2663.3779, 2824.3289, 2845.2898, 2922.3645, 3333.5713, 3349.6025

5. gi|226494853 **Mass:** 94850 **Score:** 148 **Expect:** 9.6e-010 **Queries matched:** 16

LOC100285259 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide

946.5131	945.5058	945.5072	-0.0013	160 - 166	1	---	YRYGLFK
1142.6122	1141.6049	1141.5880	0.0170	613 - 622	1	---	AFATYTNAKR
1183.6147	1182.6074	1182.5260	0.0814	418 - 427	1	7	EMEGKIDSMK + Oxidation (M)
1183.6147	1182.6074	1182.5260	0.0814	418 - 427	1	---	EMEGKIDSMK + Oxidation (M)
1386.7183	1385.7110	1385.6939	0.0171	816 - 827	1	---	FSSDRTIAQYAK
1386.7183	1385.7110	1385.6939	0.0171	816 - 827	1	---	FSSDRTIAQYAK
1436.7255	1435.7182	1435.7017	0.0166	494 - 505	0	---	FCNPELSEIVTK
1443.7375	1442.7302	1442.7266	0.0037	728 - 739	1	---	DRENGLFKPDPR
1443.7375	1442.7302	1442.7266	0.0037	728 - 739	1	16	DRENGLFKPDPR
1651.7783	1650.7710	1650.7711	-0.0001	80 - 92	0	---	QTYYLSMEYLQGR
1667.7695	1666.7622	1666.7661	-0.0038	80 - 92	0	---	QTYYLSMEYLQGR + Oxidation (M)
1701.8246	1700.8173	1700.8158	0.0016	525 - 539	1	---	FADDEKLHAEWAAAK
2136.1042	2135.0969	2135.1585	-0.0616	623 - 642	1	---	IVKLVNDVGAVVNNDPEVNK
2214.1609	2213.1536	2213.1156	0.0380	465 - 482	1	---	QELFADYVSIWPTKFQNK
2332.2039	2331.1966	2331.1892	0.0074	273 - 293	1	---	AQQICAVLYPGDATEEGKLLR
2332.2039	2331.1966	2331.1892	0.0074	273 - 293	1	77	AQQICAVLYPGDATEEGKLLR

No match to: 713.3970, 734.4929, 750.5135, 768.5093, 782.4641, 848.5261, 864.5320, 911.5172, 984.5320, 1138.6066, 1154.5930, 1230.6731, 1260.6840, 1276.6632, 1279.7448, 1286.7258, 1334.8624, 1402.6913, 1403.7231, 1403.7231, 1419.7095, 1447.7135, 1448.8988, 1482.7467, 1542.8176, 1562.9264, 1575.7908, 1732.0847, 1814.9642, 1830.9380, 1860.9924, 2034.0474, 2048.0464, 2062.1301, 2152.0886, 2168.1096, 2186.1475, 2198.0315, 2263.1943, 2352.2332, 2439.3186, 2565.2075, 2608.3313, 2663.3779, 2824.3289, 2845.2898, 2922.3645, 3333.5713, 3349.6025

6. gi|417488 **Mass:** 95451 **Score:** 56 **Expect:** 1.6 **Queries matched:** 12

RecName: Full=Alpha-glucan phosphorylase, H isozyme; AltName: Full=Starch phosphorylase H

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
946.5131	945.5058	945.5072	-0.0013	161 - 167	1	---	YRYGLFK
1142.6122	1141.6049	1141.5880	0.0170	613 - 622	1	---	AFATYTNAKR
1386.7183	1385.7110	1385.6761	0.0349	828 - 838	1	5	EIWNIAECRVP
1386.7183	1385.7110	1385.6761	0.0349	828 - 838	1	---	EIWNIAECRVP
1402.6913	1401.6840	1401.6888	-0.0048	816 - 827	1	---	FSSDRTISQYAK
1443.7375	1442.7302	1442.7266	0.0037	728 - 739	1	---	DRENGLFKPDPR
1443.7375	1442.7302	1442.7266	0.0037	728 - 739	1	16	DRENGLFKPDPR
1482.7467	1481.7394	1481.6575	0.0819	66 - 76	0	---	QWNDTYLHYDK
1651.7783	1650.7710	1650.7711	-0.0001	81 - 93	0	---	QTYYLSMEYLQGR
1667.7695	1666.7622	1666.7661	-0.0038	81 - 93	0	---	QTYYLSMEYLQGR + Oxidation (M)
2198.0315	2197.0242	2197.1127	-0.0884	94 - 114	0	---	ALTNAVGNLDIHNAYADALNK
2352.2332	2351.2259	2351.1436	0.0824	409 - 428	1	---	FVATIMSERPDLENKMPSMR

No match to: 713.3970, 734.4929, 750.5135, 768.5093, 782.4641, 848.5261, 864.5320, 911.5172, 984.5320, 1138.6066, 1154.5930, 1183.6147, 1183.6147, 1230.6731, 1260.6840, 1276.6632, 1279.7448, 1286.7258, 1334.8624, 1403.7231, 1403.7231, 1419.7095, 1436.7255, 1447.7135, 1448.8988, 1542.8176, 1562.9264, 1575.7908, 1701.8246, 1732.0847, 1814.9642, 1830.9380, 1860.9924, 2034.0474, 2048.0464, 2062.1301, 2136.1042, 2152.0886, 2168.1096, 2186.1475,

2214.1609, 2263.1943, 2332.2039, 2332.2039, 2439.3186, 2565.2075, 2608.3313, 2663.3779, 2824.3289, 2845.2898, 2922.3645, 3333.5713, 3349.6025

7. gi|168016360 **Mass:** 49345 **Score:** 51 **Expect:** 4.4 **Queries matched:** 8

predicted protein [Physcomitrella patens subsp. patens]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
864.5320	863.5247	863.4977	0.0270	180	-	186	0	---	QHTPLLR
911.5172	910.5099	910.4946	0.0153	1	-	7	1	---	MTKLYQK
1386.7183	1385.7110	1385.7626	-0.0516	392	-	404	1	25	EALRVTETIAAGR
1386.7183	1385.7110	1385.7626	-0.0516	392	-	404	1	---	EALRVTETIAAGR
1403.7231	1402.7158	1402.8044	-0.0886	23	-	34	0	---	LVEVTLRPHSPR
1403.7231	1402.7158	1402.8044	-0.0886	23	-	34	0	---	LVEVTLRPHSPR
1814.9642	1813.9569	1813.9468	0.0101	163	-	177	1	---	DTNDMLISKKPRPQR + Oxidation (M)
2186.1475	2185.1402	2185.0109	0.1293	214	-	233	0	---	SLSSPCGPELHQESGSWLSK

No match to: 713.3970, 734.4929, 750.5135, 768.5093, 782.4641, 848.5261, 946.5131, 984.5320, 1138.6066, 1142.6122, 1154.5930, 1183.6147, 1183.6147, 1230.6731, 1260.6840, 1276.6632, 1279.7448, 1286.7258, 1334.8624, 1402.6913, 1419.7095, 1436.7255, 1443.7375, 1443.7375, 1447.7135, 1448.8988, 1482.7467, 1542.8176, 1562.9264, 1575.7908, 1651.7783, 1667.7695, 1701.8246, 1732.0847, 1830.9380, 1860.9924, 2034.0474, 2048.0464, 2062.1301, 2136.1042, 2152.0886, 2168.1096, 2198.0315, 2214.1609, 2263.1943, 2332.2039, 2332.2039, 2352.2332, 2439.3186, 2565.2075, 2608.3313, 2663.3779, 2824.3289, 2845.2898, 2922.3645, 3333.5713, 3349.6025

8. gi|168000234 **Mass:** 64796 **Score:** 51 **Expect:** 5 **Queries matched:** 10

predicted protein [Physcomitrella patens subsp. patens]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
713.3970	712.3897	712.3544	0.0353	113	-	117	0	---	FYDIR
1276.6632	1275.6559	1275.6856	-0.0297	288	-	299	0	---	MTISSLNNVLGK
1402.6913	1401.6840	1401.7650	-0.0809	545	-	556	0	---	LLLLIQSDCTAR
1443.7375	1442.7302	1442.7663	-0.0361	387	-	398	1	---	LARENACVILER
1443.7375	1442.7302	1442.7663	-0.0361	387	-	398	1	---	LARENACVILER
1482.7467	1481.7394	1481.6568	0.0826	2	-	16	0	---	GEELMASQGGAGFGR + Oxidation (M)
1575.7908	1574.7835	1574.8403	-0.0567	476	-	490	0	---	ALATLELLSTTEEGK
2263.1943	2262.1870	2262.0294	0.1576	249	-	269	1	---	TSDQCSVHARSSIASDASDLR
2845.2898	2844.2825	2844.2336	0.0489	1	-	27	1	---	MGEELMASQGGAGFGRCGSSAQRPTDR + 2 Oxidation (M)
2922.3645	2921.3572	2921.3162	0.0411	219	-	248	0	---	SEVDIPLSGFVPGSPSASEGDNASSSASDR

No match to: 734.4929, 750.5135, 768.5093, 782.4641, 848.5261, 864.5320, 911.5172, 946.5131, 984.5320, 1138.6066, 1142.6122, 1154.5930, 1183.6147, 1183.6147, 1230.6731, 1260.6840, 1279.7448, 1286.7258, 1334.8624, 1386.7183, 1386.7183, 1403.7231, 1403.7231, 1419.7095, 1436.7255, 1447.7135, 1448.8988, 1542.8176, 1562.9264, 1651.7783, 1667.7695, 1701.8246, 1732.0847, 1814.9642, 1830.9380, 1860.9924, 2034.0474, 2048.0464, 2062.1301, 2136.1042, 2152.0886, 2168.1096, 2186.1475, 2198.0315, 2214.1609, 2332.2039, 2332.2039, 2352.2332, 2439.3186, 2565.2075, 2608.3313, 2663.3779, 2824.3289, 3333.5713, 3349.6025

9. gi|116057674 **Mass:** 48359 **Score:** 51 **Expect:** 5 **Queries matched:** 8

putative porphobilinogen deaminase (ISS) [Ostreococcus tauri]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
911.5172	910.5099	910.5236	-0.0136	40	48	0	---	AAVDAPIVR
1419.7095	1418.7022	1418.6724	0.0298	289	301	0	---	TPIAAHCHNVDGK
1562.9264	1561.9191	1561.8576	0.0615	367	381	1	---	SQTSPALPNVPRAPK
1667.7695	1666.7622	1666.8031	-0.0409	409	423	1	---	CPMDVGAHIPRASTR
1701.8246	1700.8173	1700.9308	-0.1135	306	321	1	---	GLIASLDGKEVLETTR
2352.2332	2351.2259	2351.2704	-0.0445	230	251	0	---	LIIPTEQMLPAVAQGAIGITCR
2824.3289	2823.3216	2823.4622	-0.1406	230	256	1	---	LIIPTEQMLPAVAQGAIGITCRGGDDK
2845.2898	2844.2825	2844.4140	-0.1315	315	342	1	---	EVLETTREGAWDAASLLAAGTDAGAELK

No match to: 713.3970, 734.4929, 750.5135, 768.5093, 782.4641, 848.5261, 864.5320, 946.5131, 984.5320, 1138.6066, 1142.6122, 1154.5930, 1183.6147, 1183.6147, 1230.6731, 1260.6840, 1276.6632, 1279.7448, 1286.7258, 1334.8624, 1386.7183, 1386.7183, 1402.6913, 1403.7231, 1403.7231, 1436.7255, 1443.7375, 1443.7375, 1447.7135, 1448.8988, 1482.7467, 1542.8176, 1575.7908, 1651.7783, 1732.0847, 1814.9642, 1830.9380, 1860.9924, 2034.0474, 2048.0464, 2062.1301, 2136.1042, 2152.0886, 2168.1096, 2186.1475, 2198.0315, 2214.1609, 2263.1943, 2332.2039, 2332.2039, 2439.3186, 2565.2075, 2608.3313, 2663.3779, 2922.3645, 3333.5713, 3349.6025

10. gi|3915783 **Mass:** 15433 **Score:** 49 **Expect:** 7.1 **Queries matched:** 7

RecName: Full=Probable non-specific lipid-transfer protein; Short=LTP; AltName: Full=Major pollen a

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
911.5172	910.5099	910.5348	-0.0249	124	130	0	---	LERPQIR
1138.6066	1137.5993	1137.6730	-0.0737	122	130	1	---	ARLERPQIR
1447.7135	1446.7062	1446.6418	0.0645	47	58	0	---	VHACECIQTAMK
1667.7695	1666.7622	1666.8712	-0.1089	67	81	1	---	LVSEVPKHCGIVDSK
2198.0315	2197.0242	2197.0329	-0.0087	74	92	1	---	HCGIVDSKLPPIDVNMDCK
2214.1609	2213.1536	2213.0278	0.1258	74	92	1	---	HCGIVDSKLPPIDVNMDCK + Oxidation (M)
2439.3186	2438.3113	2438.1578	0.1535	1	21	1	---	QETCGTMVRALMPCLPFVQGK + Oxidation (M)

No match to: 713.3970, 734.4929, 750.5135, 768.5093, 782.4641, 848.5261, 864.5320, 946.5131, 984.5320, 1142.6122, 1154.5930, 1183.6147, 1183.6147, 1230.6731, 1260.6840, 1276.6632, 1279.7448, 1286.7258, 1334.8624, 1386.7183, 1386.7183, 1402.6913, 1403.7231, 1403.7231, 1419.7095, 1436.7255, 1443.7375, 1443.7375, 1448.8988, 1482.7467, 1542.8176, 1562.9264, 1575.7908, 1651.7783, 1701.8246, 1732.0847, 1814.9642, 1830.9380, 1860.9924, 2034.0474, 2048.0464, 2062.1301, 2136.1042, 2152.0886, 2168.1096, 2186.1475, 2263.1943, 2332.2039, 2332.2039, 2352.2332, 2565.2075, 2608.3313, 2663.3779, 2824.3289, 2845.2898, 2922.3645, 3333.5713, 3349.6025

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 65

Protein View

Match to: **gi|14916632** Score: **161** Expect: **4.8e-011**
RecName: Full=Alpha-glucan phosphorylase, H isozyme; AltName: Full=Starch phosphorylase H

Nominal mass (M_r): **93952**; Calculated pI value: **7.27**
NCBI BLAST search of gi|14916632 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Triticum aestivum
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|9082278 from Triticum aestivum

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **20%**

Matched peptides shown in **Bold Red**

```
   1 MSAADKVKPA ASPASEDPSA IAGNISYHAQ YSPHFSPLAF GPEQAFYATA
  51 ESVRDHLLQR WNDTYLHFHK TDPKQTYYLS MEYLQGRALT NAVGNLAITG
 101 AYADALKKFG YELEAIAGQE RDAALGNGGL GRLASCFLDS MATLNLPSWG
 151 YGLRYRYGLF KQRIAKEGQE EIAEDWLDKF SPWEIVRHDV VYPIRFFGHV
 201 EISPDGKRKW AGGEVLNALA YDVPIPGYKT KNAISLRLWD ATATAEDFNL
 251 FQFNDGQYES AAQLHSRAQQ ICAVLYPGDA TEEGKLLRLK QQYFLCSASL
 301 QDIIFRFKER KADRVSGKWS EFPSKVAVQM NDTHPTLAIP ELMRLLMDVE
 351 GLGWDEAWAV TNKTVAYTNH TVLPEALEKW SQAVMKKLLP RHMEIIEEID
 401 KRFREMVIST RKDMEGKIES MRVLDNNPEK PVVRMANLCV VAGHTVNGVA
 451 ELHSNILKQE LFADYVSIWP NKFQNKTNGI TPRRWLRFCN PELSEIVTKW
 501 LKTDQWTSNL DLLTGLRKFA DDEKLHAEWA AAKLASKKRL AKHVLDVTGV
 551 TIDPDSLFDI QIKRIHEYKR QLMNILGAVY RYKKLKEMSA ADRQKVTPRT
 601 VMVGGKAFAT YTNAKRIVKL VNDVGAVVNN DADVNKYLKV VFIPNYNVSV
 651 AEVLIPGSEL SQHISTAGME ASGTSNMKFS LNGCVIIGTL DGANVEIREE
 701 VGQDNFFLFG AKADQVAGLR KDRENGLFKP DPRFEEAKQF IRSGAFGTYD
 751 YTPLLDSLEG NTGFGRGDYF LVGYDFPSYI DAQARVDEAY KDKKKWVKMS
 801 ILNTAGSGKF SSDRTIDQYA KEIWGISACP VP
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
75 - 87	1651.7783	1650.7710	1650.7711	-0.0001	0	**QTYYLSMEYLQGR** (No match)
75 - 87	1667.7695	1666.7622	1666.7661	-0.0038	0	**QTYYLSMEYLQGR** Oxidation (M) (No match)
109 - 121	1482.7467	1481.7394	1481.7150	0.0245	0	**FGYELEAIAGQER** (No match)
155 - 161	946.5131	945.5058	945.5072	-0.0013	1	**YRYGLFK** (No match)
157 - 163	911.5172	910.5099	910.5024	0.0075	1	**YGLFKQR** (No match)
268 - 288	2332.2039	2331.1966	2331.1892	0.0074	1	**AQQICAVLYPGDATEEGKLLR** (No match)
268 - 288	2332.2039	2331.1966	2331.1892	0.0074	1	**AQQICAVLYPGDATEEGKLLR** (Ions score 77)
326 - 344	2136.1042	2135.0969	2135.0867	0.0102	0	**VAVQMNDTHPTLAIPELMR** (No match)
326 - 344	2152.0886	2151.0813	2151.0816	-0.0003	0	**VAVQMNDTHPTLAIPELMR** Oxidation (M) (No match)
326 - 344	2168.1096	2167.1023	2167.0765	0.0258	0	**VAVQMNDTHPTLAIPELMR** 2 Oxidation (M) (No match)
403 - 411	1138.6066	1137.5993	1137.5964	0.0029	1	**FREMVISTR** (No match)
403 - 411	1154.5930	1153.5857	1153.5913	-0.0056	1	**FREMVISTR** Oxidation (M) (No match)
488 - 499	1436.7255	1435.7182	1435.7017	0.0166	0	**FCNPELSEIVTK** (No match)
503 - 518	1860.9924	1859.9851	1859.9741	0.0110	1	**TDQWTSNLDLLTGLRK** (No match)
519 - 533	1701.8246	1700.8173	1700.8158	0.0016	1	**FADDEKLHAEWAAAK** (No match)
607 - 616	1142.6122	1141.6049	1141.5880	0.0170	1	**AFATYTNAKR** (No match)
722 - 733	1443.7375	1442.7302	1442.7266	0.0037	1	**DRENGLFKPDPR** (No match)
722 - 733	1443.7375	1442.7302	1442.7266	0.0037	1	**DRENGLFKPDPR** (Ions score 16)
815 - 832	2048.0464	2047.0391	2047.0084	0.0307	1	**TIDQYAKEIWGISACPVP** (No match)

Spot 8

Index

	Accession	Mass	Score	Description
1.	gi|3914429	14269	194	RecName: Full=Profilin-3; AltName: Full=Pollen allergen Phl p 12; AltName: Full=Allergen Phl p
2.	gi|3914432	14255	194	RecName: Full=Profilin-2/4; AltName: Full=Pollen allergen Phl p 12; AltName: Full=Allergen Phl
3.	gi|121277849	14319	163	profilin [Caryota mitis]
4.	gi|121277814	14297	163	profilin [Cocos nucifera]
5.	gi|121277830	14323	163	profilin [Roystonea regia]
6.	gi|464471	14340	99	RecName: Full=Profilin-1; AltName: Full=Pollen allergen Phl p 12; AltName: Full=Allergen Phl p
7.	gi|47606031	14204	99	RecName: Full=Profilin; AltName: Full=Minor pollen allergen Che a 2; AltName: Allergen=Che a 2
8.	gi|3914426	14594	99	RecName: Full=Profilin-1; AltName: Full=Pollen allergen Ole e 2; AltName: Allergen=Ole e 2
9.	gi|205829383	2519	95	RecName: Full=Profilin; AltName: Full=Pollen allergen Beta v 2; AltName: Allergen=Beta v 2
10.	gi|1709779	14462	94	RecName: Full=Profilin-1

Results List

1. gi|3914429 **Mass:** 14269 **Score:** 194 **Expect:** 2.4e-014 **Queries matched:** 8

RecName: Full=Profilin-3; AltName: Full=Pollen allergen Phl p 12; AltName: Full=Allergen Phl p 11;

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1124.5073	1123.5000	1123.5219	-0.0219	122	131	0	---	LGDYLVEQGM
1124.5073	1123.5000	1123.5219	-0.0219	122	131	0	87	LGDYLVEQGM
1140.4902	1139.4829	1139.5168	-0.0339	122	131	0	(82)	LGDYLVEQGM + Oxidation (M)
1140.4902	1139.4829	1139.5168	-0.0339	122	131	0	---	LGDYLVEQGM + Oxidation (M)
1432.7612	1431.7539	1431.7543	-0.0004	72	84	0	---	YMVIQGEPGAVIR
1432.7612	1431.7539	1431.7543	-0.0004	72	84	0	75	YMVIQGEPGAVIR
1448.7452	1447.7379	1447.7493	-0.0113	72	84	0	---	YMVIQGEPGAVIR + Oxidation (M)
1448.7452	1447.7379	1447.7493	-0.0113	72	84	0	(16)	YMVIQGEPGAVIR + Oxidation (M)

No match to: 768.5288, 1146.4877, 1162.4921, 1736.8076

2. gi|3914432 **Mass:** 14255 **Score:** 194 **Expect:** 2.4e-014 **Queries matched:** 8

RecName: Full=Profilin-2/4; AltName: Full=Pollen allergen Phl p 12; AltName: Full=Allergen Phl p 11

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1124.5073	1123.5000	1123.5219	-0.0219	122	131	0	---	LGDYLVEQGM
1124.5073	1123.5000	1123.5219	-0.0219	122	131	0	87	LGDYLVEQGM
1140.4902	1139.4829	1139.5168	-0.0339	122	131	0	(82)	LGDYLVEQGM + Oxidation (M)
1140.4902	1139.4829	1139.5168	-0.0339	122	131	0	---	LGDYLVEQGM + Oxidation (M)
1432.7612	1431.7539	1431.7543	-0.0004	72	84	0	---	YMVIQGEPGAVIR
1432.7612	1431.7539	1431.7543	-0.0004	72	84	0	75	YMVIQGEPGAVIR
1448.7452	1447.7379	1447.7493	-0.0113	72	84	0	---	YMVIQGEPGAVIR + Oxidation (M)
1448.7452	1447.7379	1447.7493	-0.0113	72	84	0	(16)	YMVIQGEPGAVIR + Oxidation (M)

No match to: 768.5288, 1146.4877, 1162.4921, 1736.8076

3. gi|121277849 **Mass:** 14319 **Score:** 163 **Expect:** 3e-011 **Queries matched:** 6

profilin [Caryota mitis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1140.4902	1139.4829	1139.5498	-0.0669	122	131	0	58	LGDYLIDQGF
1140.4902	1139.4829	1139.5498	-0.0669	122	131	0	---	LGDYLIDQGF
1432.7612	1431.7539	1431.7543	-0.0004	72	84	0	---	YMVIQGEPGAVIR
1432.7612	1431.7539	1431.7543	-0.0004	72	84	0	75	YMVIQGEPGAVIR
1448.7452	1447.7379	1447.7493	-0.0113	72	84	0	---	YMVIQGEPGAVIR + Oxidation (M)
1448.7452	1447.7379	1447.7493	-0.0113	72	84	0	(16)	YMVIQGEPGAVIR + Oxidation (M)

No match to: 768.5288, 1124.5073, 1124.5073, 1146.4877, 1162.4921, 1736.8076

4. gi|121277814 **Mass:** 14297 **Score:** 163 **Expect:** 3e-011 **Queries matched:** 6

profilin [Cocos nucifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1140.4902	1139.4829	1139.5498	-0.0669	122	131	0	58	LGDYLIDQGF
1140.4902	1139.4829	1139.5498	-0.0669	122	131	0	---	LGDYLIDQGF
1432.7612	1431.7539	1431.7543	-0.0004	72	84	0	---	YMVIQGEPGAVIR
1432.7612	1431.7539	1431.7543	-0.0004	72	84	0	75	YMVIQGEPGAVIR
1448.7452	1447.7379	1447.7493	-0.0113	72	84	0	---	YMVIQGEPGAVIR + Oxidation (M)
1448.7452	1447.7379	1447.7493	-0.0113	72	84	0	(16)	YMVIQGEPGAVIR + Oxidation (M)

No match to: 768.5288, 1124.5073, 1124.5073, 1146.4877, 1162.4921, 1736.8076

5. gi|121277830 **Mass:** 14323 **Score:** 163 **Expect:** 3e-011 **Queries matched:** 6

profilin [Roystonea regia]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1140.4902	1139.4829	1139.5498	-0.0669	122	131	0	58	LGDYLIDQGF
1140.4902	1139.4829	1139.5498	-0.0669	122	131	0	---	LGDYLIDQGF
1432.7612	1431.7539	1431.7543	-0.0004	72	84	0	---	YMVIQGEPGAVIR
1432.7612	1431.7539	1431.7543	-0.0004	72	84	0	75	YMVIQGEPGAVIR
1448.7452	1447.7379	1447.7493	-0.0113	72	84	0	---	YMVIQGEPGAVIR + Oxidation (M)
1448.7452	1447.7379	1447.7493	-0.0113	72	84	0	(16)	YMVIQGEPGAVIR + Oxidation (M)

No match to: 768.5288, 1124.5073, 1124.5073, 1146.4877, 1162.4921, 1736.8076

6. gi|464471 **Mass:** 14340 **Score:** 99 **Expect:** 7.8e-005 **Queries matched:** 4

RecName: Full=Profilin-1; AltName: Full=Pollen allergen Phl p 12; AltName: Full=Allergen Phl p 11;

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1124.5073	1123.5000	1123.5219	-0.0219	122	131	0	---	LGDYLVEQGM
1124.5073	1123.5000	1123.5219	-0.0219	122	131	0	87	LGDYLVEQGM
1140.4902	1139.4829	1139.5168	-0.0339	122	131	0	(82)	LGDYLVEQGM + Oxidation (M)
1140.4902	1139.4829	1139.5168	-0.0339	122	131	0	---	LGDYLVEQGM + Oxidation (M)

No match to: 768.5288, 1146.4877, 1162.4921, 1432.7612, 1432.7612, 1448.7452, 1448.7452, 1736.8076

7. gi|47606031 **Mass:** 14204 **Score:** 99 **Expect:** 7.8e-005 **Queries matched:** 4

RecName: Full=Profilin; AltName: Full=Minor pollen allergen Che a 2; AltName: Allergen=Che a 2

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1124.5073	1123.5000	1123.5219	-0.0219	122	131	0	---	IGDYLVEQGM
1124.5073	1123.5000	1123.5219	-0.0219	122	131	0	87	IGDYLVEQGM
1140.4902	1139.4829	1139.5168	-0.0339	122	131	0	(82)	IGDYLVEQGM + Oxidation (M)
1140.4902	1139.4829	1139.5168	-0.0339	122	131	0	---	IGDYLVEQGM + Oxidation (M)

No match to: 768.5288, 1146.4877, 1162.4921, 1432.7612, 1432.7612, 1448.7452, 1448.7452, 1736.8076

8. gi|3914426 **Mass:** 14594 **Score:** 99 **Expect:** 8e-005 **Queries matched:** 4

RecName: Full=Profilin-1; AltName: Full=Pollen allergen Ole e 2; AltName: Allergen=Ole e 2

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1124.5073	1123.5000	1123.5219	-0.0219	125	134	0	---	LGDYLVEQGM
1124.5073	1123.5000	1123.5219	-0.0219	125	134	0	87	LGDYLVEQGM
1140.4902	1139.4829	1139.5168	-0.0339	125	134	0	(82)	LGDYLVEQGM + Oxidation (M)
1140.4902	1139.4829	1139.5168	-0.0339	125	134	0	---	LGDYLVEQGM + Oxidation (M)

No match to: 768.5288, 1146.4877, 1162.4921, 1432.7612, 1432.7612, 1448.7452, 1448.7452, 1736.8076

9. gi|205829383 **Mass:** 2519 **Score:** 95 **Expect:** 0.00022 **Queries matched:** 4

RecName: Full=Profilin; AltName: Full=Pollen allergen Beta v 2; AltName: Allergen=Beta v 2

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1432.7612	1431.7539	1431.7543	-0.0004	1	13	0	---	YMVIQGEPGAVIR
1432.7612	1431.7539	1431.7543	-0.0004	1	13	0	75	YMVIQGEPGAVIR
1448.7452	1447.7379	1447.7493	-0.0113	1	13	0	---	YMVIQGEPGAVIR + Oxidation (M)
1448.7452	1447.7379	1447.7493	-0.0113	1	13	0	(16)	YMVIQGEPGAVIR + Oxidation (M)

No match to: 768.5288, 1124.5073, 1124.5073, 1140.4902, 1140.4902, 1146.4877, 1162.4921, 1736.8076

10. gi|1709779 **Mass:** 14462 **Score:** 94 **Expect:** 0.00025 **Queries matched:** 2

RecName: Full=Profilin-1

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1140.4902	1139.4829	1139.5498	-0.0669	122	131	0	82	LGDYLVEQGF
1140.4902	1139.4829	1139.5498	-0.0669	122	131	0	---	LGDYLVEQGF

No match to: 768.5288, 1124.5073, 1124.5073, 1146.4877, 1162.4921, 1432.7612, 1432.7612, 1448.7452, 1448.7452, 1736.8076

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 12

Protein View

Match to: **gi|3914432** Score: **194** Expect: **2.4e-014**
RecName: Full=Profilin-2/4; AltName: Full=Pollen allergen Phl p 12; AltName: Full=Allergen Phl p 11

Nominal mass (M_r): **14255**; Calculated pI value: **4.92**
NCBI BLAST search of gi|3914432 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|2415698 from Phleum pratense
gi|2415702 from Phleum pratense

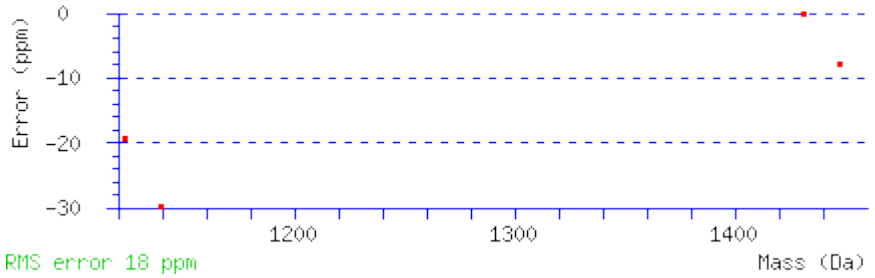
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **17%**

Matched peptides shown in **Bold Red**

```
     1 MSWQTYVDEH LMCEIEGHHL ASAAILGHDG TVWAQSADFP QFKPEEITGI
    51 MKDFDEPGHL APTGMFVAGA KYMVIQGEPG AVIRGKKGAG GITIKKTGQA
   101 LVVGIYDEPM TPGQCNMVVE RLGDYLVEQG M
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
72 - 84	1432.7612	1431.7539	1431.7543	-0.0004	0	**YMVIQGEPGAVIR**	(No match)
72 - 84	1432.7612	1431.7539	1431.7543	-0.0004	0	**YMVIQGEPGAVIR**	(Ions score 75)
72 - 84	1448.7452	1447.7379	1447.7493	-0.0113	0	**YMVIQGEPGAVIR**	Oxidation (M) (No match)
72 - 84	1448.7452	1447.7379	1447.7493	-0.0113	0	**YMVIQGEPGAVIR**	Oxidation (M) (Ions score 16)
122 - 131	1124.5073	1123.5000	1123.5219	-0.0219	0	**LGDYLVEQGM**	(No match)
122 - 131	1124.5073	1123.5000	1123.5219	-0.0219	0	**LGDYLVEQGM**	(Ions score 87)
122 - 131	1140.4902	1139.4829	1139.5168	-0.0339	0	**LGDYLVEQGM**	Oxidation (M) (Ions score 82)
122 - 131	1140.4902	1139.4829	1139.5168	-0.0339	0	**LGDYLVEQGM**	Oxidation (M) (No match)



Spot 9

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	Accession	Mass	Score	Description
1.	gi|3914432	14255	229	RecName: Full=Profilin-2/4; AltName: Full=Pollen allergen Phl p 12; AltName: Full=Allergen Phl
2.	gi|3914429	14269	208	RecName: Full=Profilin-3; AltName: Full=Pollen allergen Phl p 12; AltName: Full=Allergen Phl p
3.	gi|121277849	14319	157	profilin [Caryota mitis]
4.	gi|121277814	14297	157	profilin [Cocos nucifera]
5.	gi|121277830	14323	157	profilin [Roystonea regia]
6.	gi|109391821	14199	129	Ole e 2 allergen [Olea europaea]
7.	gi|109391827	14316	129	Ole e 2 allergen [Olea europaea]
8.	gi|215809491	4764	124	putative profilin [Pinus sylvestris]
9.	gi|215809483	5157	123	putative profilin [Pinus sylvestris]
10.	gi|215809495	5583	122	putative profilin [Pinus sylvestris]

Results List

1. gi|3914432 **Mass:** 14255 **Score:** 229 **Expect:** 7.6e-018 **Queries matched:** 12

RecName: Full=Profilin-2/4; AltName: Full=Pollen allergen Phl p 12; AltName: Full=Allergen Phl p 11

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1124.5006	1123.4933	1123.5219	-0.0286	122	131	0	---	LGDYLVEQGM
1124.5006	1123.4933	1123.5219	-0.0286	122	131	0	79	LGDYLVEQGM
1140.4985	1139.4912	1139.5168	-0.0256	122	131	0	(72)	LGDYLVEQGM + Oxidation (M)
1140.4985	1139.4912	1139.5168	-0.0256	122	131	0	---	LGDYLVEQGM + Oxidation (M)
1432.7551	1431.7478	1431.7543	-0.0065	72	84	0	---	YMVIQGEPGAVIR
1432.7551	1431.7478	1431.7543	-0.0065	72	84	0	70	YMVIQGEPGAVIR
1448.7463	1447.7390	1447.7493	-0.0102	72	84	0	---	YMVIQGEPGAVIR + Oxidation (M)
1448.7463	1447.7390	1447.7493	-0.0102	72	84	0	(39)	YMVIQGEPGAVIR + Oxidation (M)
1617.8850	1616.8777	1616.8708	0.0070	72	86	1	---	YMVIQGEPGAVIRGK
1959.9275	1958.9202	1958.9196	0.0007	53	71	0	---	DFDEPGHLAPTGMFVAGAK
1975.9238	1974.9165	1974.9145	0.0021	53	71	0	---	DFDEPGHLAPTGMFVAGAK + Oxidation (M)
2764.3281	2763.3208	2763.3029	0.0179	97	121	0	---	TGQALVVGIYDEPMTPGQCNMVVER

No match to: 768.5280, 845.1058, 864.5134, 1146.5085, 1162.5090, 1386.3390, 1454.7446, 1464.7532, 1464.7532, 1470.7283

2. gi|3914429 **Mass:** 14269 **Score:** 208 **Expect:** 9.6e-016 **Queries matched:** 10

RecName: Full=Profilin-3; AltName: Full=Pollen allergen Phl p 12; AltName: Full=Allergen Phl p 11;

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1124.5006	1123.4933	1123.5219	-0.0286	122	131	0	---	LGDYLVEQGM
1124.5006	1123.4933	1123.5219	-0.0286	122	131	0	79	LGDYLVEQGM
1140.4985	1139.4912	1139.5168	-0.0256	122	131	0	(72)	LGDYLVEQGM + Oxidation (M)
1140.4985	1139.4912	1139.5168	-0.0256	122	131	0	---	LGDYLVEQGM + Oxidation (M)

1432.7551	1431.7478	1431.7543	-0.0065	72 - 84	0	---	YMVIQGEPGAVIR
1432.7551	1431.7478	1431.7543	-0.0065	72 - 84	0	70	YMVIQGEPGAVIR
1448.7463	1447.7390	1447.7493	-0.0102	72 - 84	0	---	YMVIQGEPGAVIR + Oxidation (M)
1448.7463	1447.7390	1447.7493	-0.0102	72 - 84	0	(39)	YMVIQGEPGAVIR + Oxidation (M)
1617.8850	1616.8777	1616.8708	0.0070	72 - 86	1	---	YMVIQGEPGAVIRGK
2764.3281	2763.3208	2763.3029	0.0179	97 - 121	0	---	TGQALVVGIYDEPMTPGQCNMVVER

No match to: 768.5280, 845.1058, 864.5134, 1146.5085, 1162.5090, 1386.3390, 1454.7446, 1464.7532, 1464.7532, 1470.7283, 1959.9275, 1975.9238

3. gi|121277849 **Mass:** 14319 **Score:** 157 **Expect:** 1.2e-010 **Queries matched:** 7

profilin [Caryota mitis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1140.4985	1139.4912	1139.5498	-0.0586	122 - 131		0	49	LGDYLIDQGF
1140.4985	1139.4912	1139.5498	-0.0586	122 - 131		0	---	LGDYLIDQGF
1432.7551	1431.7478	1431.7543	-0.0065	72 - 84		0	---	YMVIQGEPGAVIR
1432.7551	1431.7478	1431.7543	-0.0065	72 - 84		0	70	YMVIQGEPGAVIR
1448.7463	1447.7390	1447.7493	-0.0102	72 - 84		0	---	YMVIQGEPGAVIR + Oxidation (M)
1448.7463	1447.7390	1447.7493	-0.0102	72 - 84		0	(39)	YMVIQGEPGAVIR + Oxidation (M)
1617.8850	1616.8777	1616.8708	0.0070	72 - 86		1	---	YMVIQGEPGAVIRGK

No match to: 768.5280, 845.1058, 864.5134, 1124.5006, 1124.5006, 1146.5085, 1162.5090, 1386.3390, 1454.7446, 1464.7532, 1464.7532, 1470.7283, 1959.9275, 1975.9238, 2764.3281

4. gi|121277814 **Mass:** 14297 **Score:** 157 **Expect:** 1.2e-010 **Queries matched:** 7

profilin [Cocos nucifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1140.4985	1139.4912	1139.5498	-0.0586	122 - 131		0	49	LGDYLIDQGF
1140.4985	1139.4912	1139.5498	-0.0586	122 - 131		0	---	LGDYLIDQGF
1432.7551	1431.7478	1431.7543	-0.0065	72 - 84		0	---	YMVIQGEPGAVIR
1432.7551	1431.7478	1431.7543	-0.0065	72 - 84		0	70	YMVIQGEPGAVIR
1448.7463	1447.7390	1447.7493	-0.0102	72 - 84		0	---	YMVIQGEPGAVIR + Oxidation (M)
1448.7463	1447.7390	1447.7493	-0.0102	72 - 84		0	(39)	YMVIQGEPGAVIR + Oxidation (M)
1617.8850	1616.8777	1616.8708	0.0070	72 - 86		1	---	YMVIQGEPGAVIRGK

No match to: 768.5280, 845.1058, 864.5134, 1124.5006, 1124.5006, 1146.5085, 1162.5090, 1386.3390, 1454.7446, 1464.7532, 1464.7532, 1470.7283, 1959.9275, 1975.9238, 2764.3281

5. gi|121277830 **Mass:** 14323 **Score:** 157 **Expect:** 1.2e-010 **Queries matched:** 7

profilin [Roystonea regia]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1140.4985	1139.4912	1139.5498	-0.0586	122 - 131		0	49	LGDYLIDQGF
1140.4985	1139.4912	1139.5498	-0.0586	122 - 131		0	---	LGDYLIDQGF
1432.7551	1431.7478	1431.7543	-0.0065	72 - 84		0	---	YMVIQGEPGAVIR
1432.7551	1431.7478	1431.7543	-0.0065	72 - 84		0	70	YMVIQGEPGAVIR

1448.7463	1447.7390	1447.7493	-0.0102	72 - 84	0	---	YMVIQGEPGAVIR + Oxidation (M)
1448.7463	1447.7390	1447.7493	-0.0102	72 - 84	0	(39)	YMVIQGEPGAVIR + Oxidation (M)
1617.8850	1616.8777	1616.8708	0.0070	72 - 86	1	---	YMVIQGEPGAVIRGK

No match to: 768.5280, 845.1058, 864.5134, 1124.5006, 1124.5006, 1146.5085, 1162.5090, 1386.3390, 1454.7446, 1464.7532, 1464.7532, 1470.7283, 1959.9275, 1975.9238, 2764.3281

6. gi|109391821 **Mass:** 14199 **Score:** 129 **Expect:** 7.6e-008 **Queries matched:** 8

Ole e 2 allergen [Olea europaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1432.7551	1431.7478	1431.7543	-0.0065	72 -	84	0	---	YMVIQGEPGAVIR
1432.7551	1431.7478	1431.7543	-0.0065	72 -	84	0	70	YMVIQGEPGAVIR
1448.7463	1447.7390	1447.7493	-0.0102	72 -	84	0	---	YMVIQGEPGAVIR + Oxidation (M)
1448.7463	1447.7390	1447.7493	-0.0102	72 -	84	0	(39)	YMVIQGEPGAVIR + Oxidation (M)
1617.8850	1616.8777	1616.8708	0.0070	72 -	86	1	---	YMVIQGEPGAVIRGK
1959.9275	1958.9202	1958.9196	0.0007	53 -	71	0	---	DFDEPGHLAPTGMFVAGAK
1975.9238	1974.9165	1974.9145	0.0021	53 -	71	0	---	DFDEPGHLAPTGMFVAGAK + Oxidation (M)
2764.3281	2763.3208	2763.3029	0.0179	97 -	121	0	---	TGQALVVGIYDEPMTPGQCNMVVER

No match to: 768.5280, 845.1058, 864.5134, 1124.5006, 1124.5006, 1140.4985, 1140.4985, 1146.5085, 1162.5090, 1386.3390, 1454.7446, 1464.7532, 1464.7532, 1470.7283

7. gi|109391827 **Mass:** 14316 **Score:** 129 **Expect:** 7.6e-008 **Queries matched:** 8

Ole e 2 allergen [Olea europaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1432.7551	1431.7478	1431.7543	-0.0065	72 -	84	0	---	YMVIQGEPGAVIR
1432.7551	1431.7478	1431.7543	-0.0065	72 -	84	0	70	YMVIQGEPGAVIR
1448.7463	1447.7390	1447.7493	-0.0102	72 -	84	0	---	YMVIQGEPGAVIR + Oxidation (M)
1448.7463	1447.7390	1447.7493	-0.0102	72 -	84	0	(39)	YMVIQGEPGAVIR + Oxidation (M)
1617.8850	1616.8777	1616.8708	0.0070	72 -	86	1	---	YMVIQGEPGAVIRGK
1959.9275	1958.9202	1958.9196	0.0007	53 -	71	0	---	DFDEPGHLAPTGMFVAGAK
1975.9238	1974.9165	1974.9145	0.0021	53 -	71	0	---	DFDEPGHLAPTGMFVAGAK + Oxidation (M)
2764.3281	2763.3208	2763.3029	0.0179	97 -	121	0	---	TGQALVVGIYDEPMTPGQCNMVVER

No match to: 768.5280, 845.1058, 864.5134, 1124.5006, 1124.5006, 1140.4985, 1140.4985, 1146.5085, 1162.5090, 1386.3390, 1454.7446, 1464.7532, 1464.7532, 1470.7283

8. gi|215809491 **Mass:** 4764 **Score:** 124 **Expect:** 2.4e-007 **Queries matched:** 6

putative profilin [Pinus sylvestris]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1432.7551	1431.7478	1431.7543	-0.0065	15 -	27	0	---	YMVIQGEPGAVIR
1432.7551	1431.7478	1431.7543	-0.0065	15 -	27	0	70	YMVIQGEPGAVIR
1448.7463	1447.7390	1447.7493	-0.0102	15 -	27	0	---	YMVIQGEPGAVIR + Oxidation (M)
1448.7463	1447.7390	1447.7493	-0.0102	15 -	27	0	(39)	YMVIQGEPGAVIR + Oxidation (M)
1617.8850	1616.8777	1616.8708	0.0070	15 -	29	1	---	YMVIQGEPGAVIRGK

2764.3281	2763.3208	2763.4628	-0.1420	1 - 27	1	---	GSLAPTGLYIGGTKYMVIQGEPGAVIR + Oxidation (M)

No match to: 768.5280, 845.1058, 864.5134, 1124.5006, 1124.5006, 1140.4985, 1140.4985, 1146.5085, 1162.5090, 1386.3390, 1454.7446, 1464.7532, 1464.7532, 1470.7283, 1959.9275, 1975.9238

9. gi|215809483 **Mass:** 5157 **Score:** 123 **Expect:** 3e-007 **Queries matched:** 6

putative profilin [Pinus sylvestris]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1432.7551	1431.7478	1431.7543	-0.0065	15 -	27	0	---	YMVIQGEPGAVIR
1432.7551	1431.7478	1431.7543	-0.0065	15 -	27	0	70	YMVIQGEPGAVIR
1448.7463	1447.7390	1447.7493	-0.0102	15 -	27	0	---	YMVIQGEPGAVIR + Oxidation (M)
1448.7463	1447.7390	1447.7493	-0.0102	15 -	27	0	(39)	YMVIQGEPGAVIR + Oxidation (M)
1617.8850	1616.8777	1616.8708	0.0070	15 -	29	1	---	YMVIQGEPGAVIRGK
2764.3281	2763.3208	2763.4628	-0.1420	1 -	27	1	---	GSLAPTGLYIGGTKYMVIQGEPGAVIR + Oxidation (M)

No match to: 768.5280, 845.1058, 864.5134, 1124.5006, 1124.5006, 1140.4985, 1140.4985, 1146.5085, 1162.5090, 1386.3390, 1454.7446, 1464.7532, 1464.7532, 1470.7283, 1959.9275, 1975.9238

10. gi|215809495 **Mass:** 5583 **Score:** 122 **Expect:** 3.8e-007 **Queries matched:** 6

putative profilin [Pinus sylvestris]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1432.7551	1431.7478	1431.7543	-0.0065	15 -	27	0	---	YMVIQGEPGAVIR
1432.7551	1431.7478	1431.7543	-0.0065	15 -	27	0	70	YMVIQGEPGAVIR
1448.7463	1447.7390	1447.7493	-0.0102	15 -	27	0	---	YMVIQGEPGAVIR + Oxidation (M)
1448.7463	1447.7390	1447.7493	-0.0102	15 -	27	0	(39)	YMVIQGEPGAVIR + Oxidation (M)
1617.8850	1616.8777	1616.8708	0.0070	15 -	29	1	---	YMVIQGEPGAVIRGK
2764.3281	2763.3208	2763.4628	-0.1420	1 -	27	1	---	GSLAPTGLYIGGTKYMVIQGEPGAVIR + Oxidation (M)

No match to: 768.5280, 845.1058, 864.5134, 1124.5006, 1124.5006, 1140.4985, 1140.4985, 1146.5085, 1162.5090, 1386.3390, 1454.7446, 1464.7532, 1464.7532, 1470.7283, 1959.9275, 1975.9238

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 22

Protein View

Match to: **gi|3914432** Score: **229** Expect: **7.6e-018**
RecName: Full=Profilin-2/4; AltName: Full=Pollen allergen Phl p 12; AltName: Full=Allergen Phl p 11

Nominal mass (M_r): **14255**; Calculated pI value: **4.92**
NCBI BLAST search of gi|3914432 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|2415698 from Phleum pratense
gi|2415702 from Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **52%**

Matched peptides shown in **Bold Red**

```
     1 MSWQTYVDEH LMCEIEGHHL ASAAILGHDG TVWAQSADFP QFKPEEITGI
    51 MKDFDEPGHL APTGMFVAGA KYMVIQGEPG AVIRGKKGAG GITIKKTGQA
   101 LVVGIYDEPM TPGQCNMVVE RLGDYLVEQG M
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
53 - 71	1959.9275	1958.9202	1958.9196	0.0007	0	**DFDEPGHLAPTGMFVAGAK** (No match)
53 - 71	1975.9238	1974.9165	1974.9145	0.0021	0	**DFDEPGHLAPTGMFVAGAK** Oxidation (M) (No match)
72 - 84	1432.7551	1431.7478	1431.7543	-0.0065	0	**YMVIQGEPGAVIR** (No match)
72 - 84	1432.7551	1431.7478	1431.7543	-0.0065	0	**YMVIQGEPGAVIR** (Ions score 70)
72 - 84	1448.7463	1447.7390	1447.7493	-0.0102	0	**YMVIQGEPGAVIR** Oxidation (M) (No match)
72 - 84	1448.7463	1447.7390	1447.7493	-0.0102	0	**YMVIQGEPGAVIR** Oxidation (M) (Ions score 39)
72 - 86	1617.8850	1616.8777	1616.8708	0.0070	1	**YMVIQGEPGAVIRGK** (No match)
97 - 121	2764.3281	2763.3208	2763.3029	0.0179	0	**TGQALVVGIYDEPMTPGQCNMVVER** (No match)
122 - 131	1124.5006	1123.4933	1123.5219	-0.0286	0	**LGDYLVEQGM** (No match)
122 - 131	1124.5006	1123.4933	1123.5219	-0.0286	0	**LGDYLVEQGM** (Ions score 79)
122 - 131	1140.4985	1139.4912	1139.5168	-0.0256	0	**LGDYLVEQGM** Oxidation (M) (Ions score 72)
122 - 131	1140.4985	1139.4912	1139.5168	-0.0256	0	**LGDYLVEQGM** Oxidation (M) (No match)

Spot 10

Index

	Accession	Mass	Score	Description
1.	gi|439586	47180	196	calreticulin
2.	gi|439588	47558	196	calreticulin
3.	gi|56606827	47404	195	calreticulin-like protein [Triticum aestivum]
4.	gi|6682833	48067	150	calcium-binding protein [Oryza sativa]
5.	gi|222631425	34042	52	hypothetical protein OsJ_18373 [Oryza sativa Japonica Group]

Results List

1. gi|439586 **Mass:** 47180 **Score:** 196 **Expect:** 1.5e-014 **Queries matched:** 7

calreticulin

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1061.5756	1060.5683	1060.5665	0.0018	280	288	1	---	IKNPNYQGK
1082.5070	1081.4997	1081.5080	-0.0083	341	349	0	---	TFAEETWAK
1082.5070	1081.4997	1081.5080	-0.0083	341	349	0	32	TFAEETWAK
1248.6884	1247.6811	1247.6913	-0.0102	313	322	0	---	YIGIELWQVK
1248.6884	1247.6811	1247.6913	-0.0102	313	322	0	35	YIGIELWQVK
1877.9799	1876.9726	1876.9781	-0.0055	323	340	0	99	SGTLFDNILITDDAALAK
1877.9799	1876.9726	1876.9781	-0.0055	323	340	0	---	SGTLFDNILITDDAALAK

No match to: 713.4117, 724.4991, 768.5263, 838.5314, 864.5148, 886.9918, 1189.6691, 1279.7660, 1334.8824, 1448.9146, 1618.0708, 1790.8652, 1918.8583, 1918.8583, 2101.0876, 2169.0742, 2332.1035, 2332.1035, 2565.1951

2. gi|439588 **Mass:** 47558 **Score:** 196 **Expect:** 1.5e-014 **Queries matched:** 7

calreticulin

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1061.5756	1060.5683	1060.5665	0.0018	283	291	1	---	IKNPNYQGK
1082.5070	1081.4997	1081.5080	-0.0083	344	352	0	---	TFAEETWAK
1082.5070	1081.4997	1081.5080	-0.0083	344	352	0	32	TFAEETWAK
1248.6884	1247.6811	1247.6913	-0.0102	316	325	0	---	YIGIELWQVK
1248.6884	1247.6811	1247.6913	-0.0102	316	325	0	35	YIGIELWQVK
1877.9799	1876.9726	1876.9781	-0.0055	326	343	0	99	SGTLFDNILITDDAALAK
1877.9799	1876.9726	1876.9781	-0.0055	326	343	0	---	SGTLFDNILITDDAALAK

No match to: 713.4117, 724.4991, 768.5263, 838.5314, 864.5148, 886.9918, 1189.6691, 1279.7660, 1334.8824, 1448.9146, 1618.0708, 1790.8652, 1918.8583, 1918.8583, 2101.0876, 2169.0742, 2332.1035, 2332.1035, 2565.1951

3. gi|56606827 **Mass:** 47404 **Score:** 195 **Expect:** 1.9e-014 **Queries matched:** 7

calreticulin-like protein [Triticum aestivum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide

1061.5756	1060.5683	1060.5665	0.0018	287 - 295	1	---	IKNPNYQGK
1082.5070	1081.4997	1081.5080	-0.0083	348 - 356	0	---	TFAEETWAK
1082.5070	1081.4997	1081.5080	-0.0083	348 - 356	0	32	TFAEETWAK
1248.6884	1247.6811	1247.6913	-0.0102	320 - 329	0	---	YIGIELWQVK
1248.6884	1247.6811	1247.6913	-0.0102	320 - 329	0	35	YIGIELWQVK
1877.9799	1876.9726	1876.9781	-0.0055	330 - 347	0	99	SGTLFDNILITDDAALAK
1877.9799	1876.9726	1876.9781	-0.0055	330 - 347	0	---	SGTLFDNILITDDAALAK

No match to: 713.4117, 724.4991, 768.5263, 838.5314, 864.5148, 886.9918, 1189.6691, 1279.7660, 1334.8824, 1448.9146, 1618.0708, 1790.8652, 1918.8583, 1918.8583, 2101.0876, 2169.0742, 2332.1035, 2332.1035, 2565.1951

4. gi|6682833 **Mass:** 48067 **Score:** 150 **Expect:** 6e-010 **Queries matched:** 5

calcium-binding protein [Oryza sativa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1061.5756	1060.5683	1060.5665	0.0018	291 - 299		1	---	IKNPNYQGK
1082.5070	1081.4997	1081.5080	-0.0083	352 - 360		0	---	TFAEETWAK
1082.5070	1081.4997	1081.5080	-0.0083	352 - 360		0	32	TFAEETWAK
1877.9799	1876.9726	1876.9781	-0.0055	334 - 351		0	99	SGTLFDNILITDDAALAK
1877.9799	1876.9726	1876.9781	-0.0055	334 - 351		0	---	SGTLFDNILITDDAALAK

No match to: 713.4117, 724.4991, 768.5263, 838.5314, 864.5148, 886.9918, 1189.6691, 1248.6884, 1248.6884, 1279.7660, 1334.8824, 1448.9146, 1618.0708, 1790.8652, 1918.8583, 1918.8583, 2101.0876, 2169.0742, 2332.1035, 2332.1035, 2565.1951

5. gi|222631425 **Mass:** 34042 **Score:** 52 **Expect:** 3.7 **Queries matched:** 8

hypothetical protein OsJ_18373 [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1061.5756	1060.5683	1060.5665	0.0018	35 -	43	1	---	QPEKLSGFR
1082.5070	1081.4997	1081.5516	-0.0519	2 -	10	0	---	ADEIQHLTR
1082.5070	1081.4997	1081.5516	-0.0519	2 -	10	0	---	ADEIQHLTR
1790.8652	1789.8579	1789.9474	-0.0895	291 - 307		1	---	AHGYYRDALLSLVAGGK
1918.8583	1917.8510	1917.9332	-0.0822	273 - 290		1	---	AAYHEQFGGRLEDAVAGK
1918.8583	1917.8510	1917.9332	-0.0822	273 - 290		1	---	AAYHEQFGGRLEDAVAGK
2332.1035	2331.0962	2331.2044	-0.1082	11 -	33	1	---	AFSGLGGLGVDEPAMVSALAKWR
2332.1035	2331.0962	2331.2044	-0.1082	11 -	33	1	---	AFSGLGGLGVDEPAMVSALAKWR

No match to: 713.4117, 724.4991, 768.5263, 838.5314, 864.5148, 886.9918, 1189.6691, 1248.6884, 1248.6884, 1279.7660, 1334.8824, 1448.9146, 1618.0708, 1877.9799, 1877.9799, 2101.0876, 2169.0742, 2565.1951

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 10

Protein View

Match to: **gi|439588** Score: **196** Expect: **1.5e-014**
calreticulin

Nominal mass (M_r): **47558**; Calculated pI value: **4.48**
NCBI BLAST search of gi|439588 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Hordeum vulgare subsp. vulgare

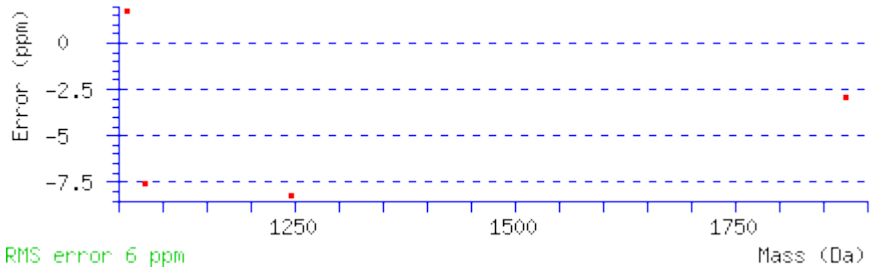
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **11%**

Matched peptides shown in **Bold Red**

```
     1 RIGKKALESR LVCASVAAVA ADVFFQEKFE DGWESRWVKS EWKKDENMAG
    51 EWNHTSGKWH GDAEDKGIQT SEDYRFYAIS AEYPEFSNKD KTLVLQFTVK
   101 HEQKLDCGGG YVKLLGGDVD QKKFGGDTPY GIMFGPDICG YSTKKVHTIL
   151 TKNGKNHLIK KDVPCETDQL SHVYTLIIRP DATYSILIDN EEKQTGSIYE
   201 HWDILPPKEI KDPEAKKPED WDDKEYIPDP EDVKPEGYDD IPKEVTDPDA
   251 KKPEDWDDEE DGEWTAPTIP NPEYKGPWKQ KKIKNPNYQG KWKAPMIANP
   301 DFQDDPYIYA FDSLKYIGIE LWQVKSGTLF DNILITDDAA LAKTFAEETW
   351 AKHKDAEKAA FDEAEKKKEE EDASKAGEDD DDLDDEDADD EDKDDKAGSD
   401 AEDDKDSDDE KHDEL
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
283 - 291	1061.5756	1060.5683	1060.5665	0.0018	1	IKNPNYQGK	(No match)
316 - 325	1248.6884	1247.6811	1247.6913	-0.0102	0	YIGIELWQVK	(No match)
316 - 325	1248.6884	1247.6811	1247.6913	-0.0102	0	YIGIELWQVK	(Ions score 35)
326 - 343	1877.9799	1876.9726	1876.9781	-0.0055	0	SGTLFDNILITDDAALAK	(Ions score 99)
326 - 343	1877.9799	1876.9726	1876.9781	-0.0055	0	SGTLFDNILITDDAALAK	(No match)
344 - 352	1082.5070	1081.4997	1081.5080	-0.0083	0	TFAEETWAK	(No match)
344 - 352	1082.5070	1081.4997	1081.5080	-0.0083	0	TFAEETWAK	(Ions score 32)



Spot 11

Index

	Accession	Mass	Score	Description
1.	gi|18076790	62978	265	phosphoglucomutase [Triticum aestivum]
2.	gi|12585326	62862	207	RecName: Full=Phosphoglucomutase, cytoplasmic; Short=PGM; AltName: Full=Glucose phosphomutase
3.	gi|162459678	63230	159	phosphoglucomutase 2 [Zea mays]
4.	gi|115454931	63138	149	Os03g0712700 [Oryza sativa (japonica cultivar-group)]
5.	gi|145864607	63600	148	phosphoglucomutase [Bambusa oldhamii]

Results List

1. gi|18076790 **Mass:** 62978 **Score:** 265 **Expect:** 1.9e-021 **Queries matched:** 24

phosphoglucomutase [Triticum aestivum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
739.3566	738.3493	738.3449	0.0044	441	445	0	---	HYYTR
789.4051	788.3978	788.3963	0.0016	77	84	0	---	MAAANGVR
866.4718	865.4645	865.4657	-0.0012	568	574	1	---	IKEYTGR
914.4339	913.4266	913.4293	-0.0027	511	518	0	---	YLFGDGSR
914.4339	913.4266	913.4293	-0.0027	511	518	0	57	YLFGDGSR
945.5009	944.4936	944.4974	-0.0037	77	85	1	---	MAAANGVRR
1110.5519	1109.5446	1109.5545	-0.0099	361	369	0	---	FFEVPTGWK
1118.6172	1117.6099	1117.6091	0.0009	523	534	0	---	LSGTGSVGATIR
1227.6565	1226.6492	1226.6546	-0.0054	206	215	1	---	TIFDFESIKK
1429.7534	1428.7461	1428.7513	-0.0052	511	522	1	---	YLFGDGSRLVFR
1502.7269	1501.7196	1501.7300	-0.0104	535	546	1	---	IYIEQYEKDSSK
1505.7485	1504.7412	1504.7534	-0.0122	506	518	1	---	HQGIRYLFGDGSR
1556.7988	1555.7915	1555.7994	-0.0078	54	68	1	---	GATIVVSGDGRYFSK
1633.9337	1632.9264	1632.9310	-0.0046	519	534	1	---	LVFRLSGTGSVGATIR
1717.7772	1716.7699	1716.7743	-0.0044	259	274	0	---	EDFGGGHPDPNLTYAK
1846.8502	1845.8429	1845.8507	-0.0078	222	238	0	---	FSFCFDGLHGVAGAYAK
1872.0240	1871.0167	1871.0186	-0.0018	343	360	1	---	SMPTSAALDVVAKNLNLK
2002.9625	2001.9552	2001.9518	0.0034	222	239	1	---	FSFCFDGLHGVAGAYAKR
2012.1093	2011.1020	2011.1102	-0.0081	86	104	0	---	VWVGQDSLLSTPAVSAIIR
2107.9238	2106.9165	2106.9282	-0.0117	441	457	1	---	HYYTRYDYENVDAEAAK
2168.2095	2167.2022	2167.2113	-0.0090	85	104	1	---	RVWVGQDSLLSTPAVSAIIR
2185.2002	2184.1929	2184.1425	0.0504	523	542	1	---	LSGTGSVGATIRIYIEQYEK
2297.2537	2296.2464	2296.2538	-0.0074	86	106	1	---	VWVGQDSLLSTPAVSAIIRER
2301.1543	2300.1470	2300.1436	0.0034	114	136	0	---	ATGAFILTASHNPGGPTEDFGIK

No match to: 713.4088, 724.4879, 768.5236, 1056.6530, 1190.7317, 1279.7683, 1334.8783, 1395.6573, 1396.1555, 1404.1484, 1412.2228, 1412.7672, 1446.7977, 1448.8859, 1462.7893, 1543.8142, 1673.0198, 1703.8633, 1703.8633,

1816.9021, 1816.9021, 1831.9589, 1831.9589, 1857.9866, 1901.9260, 1919.9579, 1960.0546, 1991.8529, 2186.1936, 2425.2939, 2453.3567, 2493.3384, 2507.3569, 2634.1863, 2773.7454, 2790.3242, 2790.3242, 2806.3213, 2952.4131, 3297.7358, 3543.7004

2. gi|12585326 **Mass:** 62862 **Score:** 207 **Expect:** 1.2e-015 **Queries matched:** 20

RecName: Full=Phosphoglucomutase, cytoplasmic; Short=PGM; AltName: Full=Glucose phosphomutase

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
739.3566	738.3493	738.3449	0.0044	441	445	0	---	HYYTR
789.4051	788.3978	788.3963	0.0016	77	84	0	---	MAAANGVR
914.4339	913.4266	913.4293	-0.0027	511	518	0	---	YLFGDGSR
914.4339	913.4266	913.4293	-0.0027	511	518	0	57	YLFGDGSR
945.5009	944.4936	944.4974	-0.0037	77	85	1	---	MAAANGVRR
1110.5519	1109.5446	1109.5545	-0.0099	361	369	0	---	FFEVPTGWK
1118.6172	1117.6099	1117.6091	0.0009	523	534	0	---	LSGTGSVGATIR
1227.6565	1226.6492	1226.6546	-0.0054	206	215	1	---	TIFDFESIKK
1429.7534	1428.7461	1428.7513	-0.0052	511	522	1	---	YLFGDGSRLVFR
1462.7893	1461.7820	1461.7861	-0.0040	466	478	1	---	MQSSLSDVNKLIK
1502.7269	1501.7196	1501.7300	-0.0104	535	546	1	---	IYIEQYEKDSSK
1505.7485	1504.7412	1504.7534	-0.0122	506	518	1	---	HQGIRYLFGDGSR
1543.8142	1542.8069	1542.8140	-0.0071	550	564	0	---	ESSDALSPLVDVALK
1556.7988	1555.7915	1555.7994	-0.0078	54	68	1	---	GATIVVSGDGRYFSK
1633.9337	1632.9264	1632.9310	-0.0046	519	534	1	---	LVFRLSGTGSVGATIR
1717.7772	1716.7699	1716.7743	-0.0044	259	274	0	---	EDFGGGHPDPNLTYAK
1857.9866	1856.9793	1856.9843	-0.0050	547	564	1	---	TGRESSDALSPLVDVALK
1872.0240	1871.0167	1871.0186	-0.0018	343	360	1	---	SMPTSAALDVVAKNLNLK
2107.9238	2106.9165	2106.9282	-0.0117	441	457	1	---	HYYTRYDYENVDAEAAK
2185.2002	2184.1929	2184.1425	0.0504	523	542	1	---	LSGTGSVGATIRIYIEQYEK

No match to: 713.4088, 724.4879, 768.5236, 866.4718, 1056.6530, 1190.7317, 1279.7683, 1334.8783, 1395.6573, 1396.1555, 1404.1484, 1412.2228, 1412.7672, 1446.7977, 1448.8859, 1673.0198, 1703.8633, 1703.8633, 1816.9021, 1816.9021, 1831.9589, 1831.9589, 1846.8502, 1901.9260, 1919.9579, 1960.0546, 1991.8529, 2002.9625, 2012.1093, 2168.2095, 2186.1936, 2297.2537, 2301.1543, 2425.2939, 2453.3567, 2493.3384, 2507.3569, 2634.1863, 2773.7454, 2790.3242, 2790.3242, 2806.3213, 2952.4131, 3297.7358, 3543.7004

3. gi|162459678 **Mass:** 63230 **Score:** 159 **Expect:** 7.6e-011 **Queries matched:** 16

phosphoglucomutase 2 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
739.3566	738.3493	738.3449	0.0044	443	447	0	---	HYYTR
789.4051	788.3978	788.3963	0.0016	78	85	0	---	MAAANGVR
914.4339	913.4266	913.4293	-0.0027	513	520	0	---	YLFGDGSR
914.4339	913.4266	913.4293	-0.0027	513	520	0	57	YLFGDGSR
945.5009	944.4936	944.4974	-0.0037	78	86	1	---	MAAANGVRR
1110.5519	1109.5446	1109.5545	-0.0099	363	371	0	---	FFEVPTGWK

1118.6172	1117.6099	1117.6091	0.0009	525 - 536	0	---	LSGTGSVGATIR
1412.7672	1411.7599	1411.7711	-0.0111	66 - 77	1	---	YFSKDAVQIITK
1429.7534	1428.7461	1428.7513	-0.0052	513 - 524	1	---	YLFGDGSRLVFR
1505.7485	1504.7412	1504.7534	-0.0122	508 - 520	1	---	HQGIRYLFGDGSR
1556.7988	1555.7915	1555.7994	-0.0078	55 - 69	1	---	GATIVVSGDGRYFSK
1633.9337	1632.9264	1632.9310	-0.0046	521 - 536	1	---	LVFRLSGTGSVGATIR
1717.7772	1716.7699	1716.7743	-0.0044	260 - 275	0	---	EDFGGGHPDPNLTYAK
1872.0240	1871.0167	1871.0186	-0.0018	345 - 362	1	---	SMPTSAALDVVAKNLNLK
1991.8529	1990.8456	1990.8504	-0.0047	286 - 305	0	---	SSSNVEPPEFGAAADGDADR
2301.1543	2300.1470	2300.1436	0.0034	115 - 137	0	---	ATGAFILTASHNPGGPTEDFGIK

No match to: 713.4088, 724.4879, 768.5236, 866.4718, 1056.6530, 1190.7317, 1227.6565, 1279.7683, 1334.8783, 1395.6573, 1396.1555, 1404.1484, 1412.2228, 1446.7977, 1448.8859, 1462.7893, 1502.7269, 1543.8142, 1673.0198, 1703.8633, 1703.8633, 1816.9021, 1816.9021, 1831.9589, 1831.9589, 1846.8502, 1857.9866, 1901.9260, 1919.9579, 1960.0546, 2002.9625, 2012.1093, 2107.9238, 2168.2095, 2185.2002, 2186.1936, 2297.2537, 2425.2939, 2453.3567, 2493.3384, 2507.3569, 2634.1863, 2773.7454, 2790.3242, 2790.3242, 2806.3213, 2952.4131, 3297.7358, 3543.7004

4. gi|115454931 **Mass:** 63138 **Score:** 149 **Expect:** 7.6e-010 **Queries matched:** 15

Os03g0712700 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
739.3566	738.3493	738.3449	0.0044	442 - 446	0	---	HYYTR
789.4051	788.3978	788.3963	0.0016	78 - 85	0	---	MAAANGVR
914.4339	913.4266	913.4293	-0.0027	512 - 519	0	---	YLFGDGSR
914.4339	913.4266	913.4293	-0.0027	512 - 519	0	57	YLFGDGSR
945.5009	944.4936	944.4974	-0.0037	78 - 86	1	---	MAAANGVRR
1110.5519	1109.5446	1109.5545	-0.0099	362 - 370	0	---	FFEVPTGWK
1118.6172	1117.6099	1117.6091	0.0009	524 - 535	0	---	LSGTGSVGATIR
1227.6565	1226.6492	1226.6546	-0.0054	207 - 216	1	---	TIFDFESIKK
1412.7672	1411.7599	1411.7711	-0.0111	66 - 77	1	---	YFSKDAVQIITK
1429.7534	1428.7461	1428.7513	-0.0052	512 - 523	1	---	YLFGDGSRLVFR
1556.7988	1555.7915	1555.7994	-0.0078	55 - 69	1	---	GATIVVSGDGRYFSK
1633.9337	1632.9264	1632.9310	-0.0046	520 - 535	1	---	LVFRLSGTGSVGATIR
1717.7772	1716.7699	1716.7743	-0.0044	260 - 275	0	---	EDFGGGHPDPNLTYAK
1872.0240	1871.0167	1871.0186	-0.0018	344 - 361	1	---	SMPTSAALDVVAKNLNLK
2301.1543	2300.1470	2300.1436	0.0034	115 - 137	0	---	ATGAFILTASHNPGGPTEDFGIK

No match to: 713.4088, 724.4879, 768.5236, 866.4718, 1056.6530, 1190.7317, 1279.7683, 1334.8783, 1395.6573, 1396.1555, 1404.1484, 1412.2228, 1446.7977, 1448.8859, 1462.7893, 1502.7269, 1505.7485, 1543.8142, 1673.0198, 1703.8633, 1703.8633, 1816.9021, 1816.9021, 1831.9589, 1831.9589, 1846.8502, 1857.9866, 1901.9260, 1919.9579, 1960.0546, 1991.8529, 2002.9625, 2012.1093, 2107.9238, 2168.2095, 2185.2002, 2186.1936, 2297.2537, 2425.2939, 2453.3567, 2493.3384, 2507.3569, 2634.1863, 2773.7454, 2790.3242, 2790.3242, 2806.3213, 2952.4131, 3297.7358, 3543.7004

5. gi|145864607 **Mass:** 63600 **Score:** 148 **Expect:** 9.6e-010 **Queries matched:** 15

phosphoglucomutase [Bambusa oldhamii]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
739.3566	738.3493	738.3449	0.0044	444	448	0	---	HYYTR
789.4051	788.3978	788.3963	0.0016	78	85	0	---	MAAANGVR
914.4339	913.4266	913.4293	-0.0027	514	521	0	---	YLFGDGSR
914.4339	913.4266	913.4293	-0.0027	514	521	0	57	YLFGDGSR
945.5009	944.4936	944.4974	-0.0037	78	86	1	---	MAAANGVRR
1110.5519	1109.5446	1109.5545	-0.0099	364	372	0	---	FFEVPTGWK
1118.6172	1117.6099	1117.6091	0.0009	526	537	0	---	LSGTGSVGATIR
1227.6565	1226.6492	1226.6546	-0.0054	208	217	1	---	TIFDFESIKK
1412.7672	1411.7599	1411.7711	-0.0111	66	77	1	---	YFSKDAVQIITK
1429.7534	1428.7461	1428.7513	-0.0052	514	525	1	---	YLFGDGSRLVFR
1505.7485	1504.7412	1504.7534	-0.0122	509	521	1	---	HQGIRYLFGDGSR
1556.7988	1555.7915	1555.7994	-0.0078	55	69	1	---	GATIVVSGDGRYFSK
1633.9337	1632.9264	1632.9310	-0.0046	522	537	1	---	LVFRLSGTGSVGATIR
1717.7772	1716.7699	1716.7743	-0.0044	261	276	0	---	EDFGGGHPDPNLTYAK
2301.1543	2300.1470	2300.1436	0.0034	115	137	0	---	ATGAFILTASHNPGGPTEDFGIK

No match to: 713.4088, 724.4879, 768.5236, 866.4718, 1056.6530, 1190.7317, 1279.7683, 1334.8783, 1395.6573, 1396.1555, 1404.1484, 1412.2228, 1446.7977, 1448.8859, 1462.7893, 1502.7269, 1543.8142, 1673.0198, 1703.8633, 1703.8633, 1816.9021, 1816.9021, 1831.9589, 1831.9589, 1846.8502, 1857.9866, 1872.0240, 1901.9260, 1919.9579, 1960.0546, 1991.8529, 2002.9625, 2012.1093, 2107.9238, 2168.2095, 2185.2002, 2186.1936, 2297.2537, 2425.2939, 2453.3567, 2493.3384, 2507.3569, 2634.1863, 2773.7454, 2790.3242, 2790.3242, 2806.3213, 2952.4131, 3297.7358, 3543.7004

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 65

Protein View

Match to: **gi|18076790** Score: **265** Expect: **1.9e-021**
phosphoglucomutase [Triticum aestivum]

Nominal mass (M_r): **62978**; Calculated pI value: **5.66**
NCBI BLAST search of gi|18076790 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Triticum aestivum

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **35%**

Matched peptides shown in **Bold Red**

```
   1 MVFSVTKKET KPYEGQKPGT SGLRKKVTVF QQPHYLANFV QSTFNALPAD
  51 QVKGATIVVS GDGRYFSKDA VQIIAKMAAA NGVRRVWVGQ DSLLSTPAVS
 101 AIIRERISAD GAKATGAFIL TASHNPGGPT EDFGIKYNMG NGGPAPESVT
 151 DKIFSNTKTV TEYLIAEDLP NVDISVIGVT SFTGPEGPFD VDVFDSATDY
 201 IKLMKTIFDF ESIKKLLASP KFSFCFDGLH GVAGAYAKRM FVDELGASES
 251 SLLNCVPKED FGGGHPDPNL TYAKELVDRM GLGKTSNVEP PEFGAAADGD
 301 ADRNMVLGKR FFVTPSDSVA IIAANAVQSI PYFASGLKGV ARSMPTSAAL
 351 DVVAKNLNLK FFEVPTGWKF FGNLMDAGMC SVCGEESFGT GSDHIREKDG
 401 IWAVLAWLSI LAYKNKDNLG GDKLVTVEDI VLQHWATYGR HYYTRYDYEN
 451 VDAEAAKELM ANLVKMQSSL SDVNKSIKEI QPTVADVVSA DEFEYKDPVD
 501 GSVSKHQGIR YLFGDGSRLV FRLSGTGSVG ATIRIYIEQY EKDSSKTGRA
 551 SSDALSPLVD VALKFSKIKE YTGRSAPTVI T
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
54 - 68	1556.7988	1555.7915	1555.7994	-0.0078	1	GATIVVSGDGRYFSK (No match)
77 - 84	789.4051	788.3978	788.3963	0.0016	0	MAAANGVR (No match)
77 - 85	945.5009	944.4936	944.4974	-0.0037	1	MAAANGVRR (No match)
85 - 104	2168.2095	2167.2022	2167.2113	-0.0090	1	RVWVGQDSLLSTPAVSAIIR (No match)
86 - 104	2012.1093	2011.1020	2011.1102	-0.0081	0	VWVGQDSLLSTPAVSAIIR (No match)
86 - 106	2297.2537	2296.2464	2296.2538	-0.0074	1	VWVGQDSLLSTPAVSAIIRER (No match)
114 - 136	2301.1543	2300.1470	2300.1436	0.0034	0	ATGAFILTASHNPGGPTEDFGIK (No match)
206 - 215	1227.6565	1226.6492	1226.6546	-0.0054	1	TIFDFESIKK (No match)
222 - 238	1846.8502	1845.8429	1845.8507	-0.0078	0	FSFCFDGLHGVAGAYAK (No match)
222 - 239	2002.9625	2001.9552	2001.9518	0.0034	1	FSFCFDGLHGVAGAYAKR (No match)
259 - 274	1717.7772	1716.7699	1716.7743	-0.0044	0	EDFGGGHPDPNLTYAK (No match)
343 - 360	1872.0240	1871.0167	1871.0186	-0.0018	1	SMPTSAALDVVAKNLNLK (No match)
361 - 369	1110.5519	1109.5446	1109.5545	-0.0099	0	FFEVPTGWK (No match)
441 - 445	739.3566	738.3493	738.3449	0.0044	0	HYYTR (No match)
441 - 457	2107.9238	2106.9165	2106.9282	-0.0117	1	HYYTRYDYENVDAEAAK (No match)
506 - 518	1505.7485	1504.7412	1504.7534	-0.0122	1	HQGIRYLFGDGSR (No match)
511 - 518	914.4339	913.4266	913.4293	-0.0027	0	YLFGDGSR (No match)
511 - 518	914.4339	913.4266	913.4293	-0.0027	0	YLFGDGSR (Ions score 57)
511 - 522	1429.7534	1428.7461	1428.7513	-0.0052	1	YLFGDGSRLVFR (No match)
519 - 534	1633.9337	1632.9264	1632.9310	-0.0046	1	LVFRLSGTGSVGATIR (No match)
523 - 534	1118.6172	1117.6099	1117.6091	0.0009	0	LSGTGSVGATIR (No match)
523 - 542	2185.2002	2184.1929	2184.1425	0.0504	1	LSGTGSVGATIRIYIEQYEK (No match)
535 - 546	1502.7269	1501.7196	1501.7300	-0.0104	1	IYIEQYEKDSSK (No match)
568 - 574	866.4718	865.4645	865.4657	-0.0012	1	IKEYTGR (No match)

Spot 12

Index

	Accession	Mass	Score	Description
1.	gi|115434270	67097	163	Os01g0125800 [Oryza sativa (japonica cultivar-group)]
2.	gi|223949659	66850	72	unknown [Zea mays]
3.	gi|212723938	66930	72	hypothetical protein LOC100192950 [Zea mays]
4.	gi|147860511	162244	60	hypothetical protein [Vitis vinifera]
5.	gi|38344458	89381	56	OSJNBa0017P10.6 [Oryza sativa (japonica cultivar-group)]
6.	gi|14517362	73621	53	AT3g61130/T20K12_30 [Arabidopsis thaliana]
7.	gi|240256469	72821	52	nucleic acid binding [Arabidopsis thaliana]
8.	gi|168015219	38489	50	predicted protein [Physcomitrella patens subsp. patens]
9.	gi|60547607	9651	50	hypothetical protein At1g33450 [Arabidopsis thaliana]
10.	gi|147797914	51075	48	hypothetical protein [Vitis vinifera]

Results List

1. gi|115434270 **Mass:** 67097 **Score:** 163 **Expect:** 3e-011 **Queries matched:** 14

Os01g0125800 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
830.4199	829.4126	829.4082	0.0044	108	114	0	---	WSPDGLR
1032.5616	1031.5543	1031.5512	0.0032	94	102	0	---	AEFRPLSGR
1092.5636	1091.5563	1091.5875	-0.0312	353	362	1	---	WIKGVGYGGR
1092.5636	1091.5563	1091.5875	-0.0312	353	362	1	66	WIKGVGYGGR
1261.5885	1260.5812	1260.5669	0.0143	186	195	0	---	DHSNFVNCIR
1344.7769	1343.7696	1343.7673	0.0023	91	102	1	---	ALKAEFRPLSGR
1428.7333	1427.7260	1427.7157	0.0103	103	114	1	---	VDDLRWSPDGLR
1455.7562	1454.7489	1454.7439	0.0050	340	352	0	---	TILSTSYDGVIMR
1471.7473	1470.7400	1470.7388	0.0012	340	352	0	---	TILSTSYDGVIMR + Oxidation (M)
1600.8933	1599.8860	1599.7780	0.1080	196	210	1	---	YAPDGSKFISVSSDK
1622.8430	1621.8357	1621.8398	-0.0041	148	160	0	---	VLSCDFKPTRPFR
1630.8540	1629.8467	1629.8586	-0.0119	94	107	1	---	AEFRPLSGRVDDLR
1754.8619	1753.8546	1753.8430	0.0116	182	195	1	---	HSIRDHSNFVNCIR
1979.9825	1978.9752	1978.8955	0.0797	186	202	1	---	DHSNFVNCIRYAPDGSK

No match to: 713.3978, 768.5062, 846.4267, 989.4948, 1155.5575, 1318.6300, 1318.6300, 1448.9115, 1570.7924, 1596.8088, 1596.8088, 1619.7943, 1635.7867, 1766.8069, 1766.8069, 1770.9160, 1786.9052, 1895.9664, 1895.9664, 1903.9036, 1943.0707, 2099.9321, 2115.9241, 2453.2244, 2547.2544

2. gi|223949659 **Mass:** 66850 **Score:** 72 **Expect:** 0.041 **Queries matched:** 11

unknown [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide

830.4199	829.4126	829.4082	0.0044	108 - 114	0	---	WSPDGLR
1032.5616	1031.5543	1031.5512	0.0032	94 - 102	0	---	AEFRPLSGR
1261.5885	1260.5812	1260.5669	0.0143	186 - 195	0	---	DHSNFVNCIR
1344.7769	1343.7696	1343.7673	0.0023	91 - 102	1	---	ALKAEFRPLSGR
1428.7333	1427.7260	1427.7157	0.0103	103 - 114	1	---	VDDLRWSPDGLR
1455.7562	1454.7489	1454.7439	0.0050	340 - 352	0	---	TILSTSYDGVIMR
1471.7473	1470.7400	1470.7388	0.0012	340 - 352	0	---	TILSTSYDGVIMR + Oxidation (M)
1622.8430	1621.8357	1621.8398	-0.0041	148 - 160	0	---	VLSCDFKPTRPFR
1630.8540	1629.8467	1629.8586	-0.0119	94 - 107	1	---	AEFRPLSGRVDDLR
1754.8619	1753.8546	1753.8430	0.0116	182 - 195	1	---	HSIRDHSNFVNCIR
1979.9825	1978.9752	1978.8955	0.0797	186 - 202	1	---	DHSNFVNCIRYAPDGSK

No match to: 713.3978, 768.5062, 846.4267, 989.4948, 1092.5636, 1092.5636, 1155.5575, 1318.6300, 1318.6300, 1448.9115, 1570.7924, 1596.8088, 1596.8088, 1600.8933, 1619.7943, 1635.7867, 1766.8069, 1766.8069, 1770.9160, 1786.9052, 1895.9664, 1895.9664, 1903.9036, 1943.0707, 2099.9321, 2115.9241, 2453.2244, 2547.2544

3. gi|212723938 **Mass:** 66930 **Score:** 72 **Expect:** 0.041 **Queries matched:** 11

hypothetical protein LOC100192950 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
830.4199	829.4126	829.4082	0.0044	108 - 114	0	---	WSPDGLR
1032.5616	1031.5543	1031.5512	0.0032	94 - 102	0	---	AEFRPLSGR
1261.5885	1260.5812	1260.5669	0.0143	186 - 195	0	---	DHSNFVNCIR
1344.7769	1343.7696	1343.7673	0.0023	91 - 102	1	---	ALKAEFRPLSGR
1428.7333	1427.7260	1427.7157	0.0103	103 - 114	1	---	VDDLRWSPDGLR
1455.7562	1454.7489	1454.7439	0.0050	340 - 352	0	---	TILSTSYDGVIMR
1471.7473	1470.7400	1470.7388	0.0012	340 - 352	0	---	TILSTSYDGVIMR + Oxidation (M)
1622.8430	1621.8357	1621.8398	-0.0041	148 - 160	0	---	VLSCDFKPTRPFR
1630.8540	1629.8467	1629.8586	-0.0119	94 - 107	1	---	AEFRPLSGRVDDLR
1754.8619	1753.8546	1753.8430	0.0116	182 - 195	1	---	HSIRDHSNFVNCIR
1979.9825	1978.9752	1978.8955	0.0797	186 - 202	1	---	DHSNFVNCIRYAPDGSK

No match to: 713.3978, 768.5062, 846.4267, 989.4948, 1092.5636, 1092.5636, 1155.5575, 1318.6300, 1318.6300, 1448.9115, 1570.7924, 1596.8088, 1596.8088, 1600.8933, 1619.7943, 1635.7867, 1766.8069, 1766.8069, 1770.9160, 1786.9052, 1895.9664, 1895.9664, 1903.9036, 1943.0707, 2099.9321, 2115.9241, 2453.2244, 2547.2544

4. gi|147860511 **Mass:** 162244 **Score:** 60 **Expect:** 0.64 **Queries matched:** 15

hypothetical protein [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
768.5062	767.4989	767.5017	-0.0028	916 -	922	1	---	LKAALPR
1032.5616	1031.5543	1031.5247	0.0297	698 -	707	0	---	GNGSSIQELK
1092.5636	1091.5563	1091.5579	-0.0016	824 -	832	1	---	ALRIQGMCK + Oxidation (M)
1092.5636	1091.5563	1091.5512	0.0051	358 -	366	0	---	NFEAHPHLK
1261.5885	1260.5812	1260.6462	-0.0650	48 -	58	0	---	IHAVLHDAEEK

1318.6300	1317.6227	1317.6421	-0.0193	16 - 26	0	---	LVDMLACPDLR + Oxidation (M)
1318.6300	1317.6227	1317.6421	-0.0193	16 - 26	0	---	LVDMLACPDLR + Oxidation (M)
1596.8088	1595.8015	1595.7579	0.0436	392 - 404	0	---	NELNHEAWDDILK
1596.8088	1595.8015	1595.7579	0.0436	392 - 404	0	---	NELNHEAWDDILK
1630.8540	1629.8467	1629.8685	-0.0218	941 - 955	0	---	NGVDLSSLTTLNIQR
1786.9052	1785.8979	1785.9182	-0.0203	1156 - 1172	0	---	CSSLPSLPTGELPSTLK
1895.9664	1894.9591	1894.9795	-0.0204	1028 - 1043	1	---	IENCANLQRLPNGLQR
1895.9664	1894.9591	1894.9795	-0.0204	1028 - 1043	1	---	IENCANLQRLPNGLQR
1943.0707	1942.0634	1942.0193	0.0441	1156 - 1173	1	---	CSSLPSLPTGELPSTLKR
2453.2244	2452.2171	2452.1844	0.0327	479 - 498	1	---	YFSELLSRSFFQQSSNIMPR + Oxidation (M)

No match to: 713.3978, 830.4199, 846.4267, 989.4948, 1155.5575, 1344.7769, 1428.7333, 1448.9115, 1455.7562, 1471.7473, 1570.7924, 1600.8933, 1619.7943, 1622.8430, 1635.7867, 1754.8619, 1766.8069, 1766.8069, 1770.9160, 1903.9036, 1979.9825, 2099.9321, 2115.9241, 2547.2544

5. gi|38344458 **Mass:** 89381 **Score:** 56 **Expect:** 1.5 **Queries matched:** 12

OSJNBa0017P10.6 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
830.4199	829.4126	829.4406	-0.0279	455 - 461	1	---	EAADRLR
989.4948	988.4875	988.4937	-0.0062	804 - 811	1	---	DALTERER
1092.5636	1091.5563	1091.5280	0.0283	653 - 662	0	---	SVEAMVEVGR + Oxidation (M)
1092.5636	1091.5563	1091.5280	0.0283	653 - 662	0	---	SVEAMVEVGR + Oxidation (M)
1261.5885	1260.5812	1260.5946	-0.0133	516 - 527	0	---	QDEALATSEAAR
1318.6300	1317.6227	1317.6272	-0.0045	736 - 747	1	---	EQRAAETEAASR
1318.6300	1317.6227	1317.6272	-0.0045	736 - 747	1	---	EQRAAETEAASR
1471.7473	1470.7400	1470.6746	0.0655	337 - 349	1	---	DRCPGSNRPADAR
1570.7924	1569.7851	1569.7099	0.0752	161 - 173	0	---	SDWFYTPLADEAR
1630.8540	1629.8467	1629.7820	0.0647	209 - 223	0	---	SQGLTGAMVYGDYLR
1754.8619	1753.8546	1753.9070	-0.0524	722 - 738	1	---	LDAAQGVLDAAAAREQR
1786.9052	1785.8979	1785.8831	0.0148	209 - 224	1	---	SQGLTGAMVYGDYLRR

No match to: 713.3978, 768.5062, 846.4267, 1032.5616, 1155.5575, 1344.7769, 1428.7333, 1448.9115, 1455.7562, 1596.8088, 1596.8088, 1600.8933, 1619.7943, 1622.8430, 1635.7867, 1766.8069, 1766.8069, 1770.9160, 1895.9664, 1895.9664, 1903.9036, 1943.0707, 1979.9825, 2099.9321, 2115.9241, 2453.2244, 2547.2544

6. gi|14517362 **Mass:** 73621 **Score:** 53 **Expect:** 2.8 **Queries matched:** 12

AT3g61130/T20K12_30 [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
846.4267	845.4194	845.4467	-0.0273	13 - 21	1	---	IRGSGGGSR
1032.5616	1031.5543	1031.5797	-0.0254	277 - 286	1	---	AMGQVLAKAK + Oxidation (M)
1155.5575	1154.5502	1154.6011	-0.0509	482 - 490	0	---	FYLPEVYPK
1261.5885	1260.5812	1260.6132	-0.0320	301 - 311	0	---	AMLQTADEQVR
1455.7562	1454.7489	1454.7261	0.0228	287 - 298	1	---	MQLYDCKLVTGK

1471.7473	1470.7400	1470.7210	0.0190	287 - 298	1	---	MQLYDCKLVTGK + Oxidation (M)
1619.7943	1618.7870	1618.7674	0.0196	579 - 590	1	---	WQNMNENRTLWK
1635.7867	1634.7794	1634.7762	0.0032	443 - 455	1	---	QLESAAMREYYFK
1766.8069	1765.7996	1765.8239	-0.0243	611 - 625	1	---	GGMCWDLDITRVSTR
1766.8069	1765.7996	1765.8239	-0.0243	611 - 625	1	---	GGMCWDLDITRVSTR
1895.9664	1894.9591	1894.9384	0.0207	257 - 274	1	---	VLGEATSDADLPRSAHEK
1895.9664	1894.9591	1894.9384	0.0207	257 - 274	1	---	VLGEATSDADLPRSAHEK

No match to: 713.3978, 768.5062, 830.4199, 989.4948, 1092.5636, 1092.5636, 1318.6300, 1318.6300, 1344.7769, 1428.7333, 1448.9115, 1570.7924, 1596.8088, 1596.8088, 1600.8933, 1622.8430, 1630.8540, 1754.8619, 1770.9160, 1786.9052, 1903.9036, 1943.0707, 1979.9825, 2099.9321, 2115.9241, 2453.2244, 2547.2544

7. gi|240256469 **Mass:** 72821 **Score:** 52 **Expect:** 3.5 **Queries matched:** 10

nucleic acid binding [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1032.5616	1031.5543	1031.5546	-0.0002	194 - 201		1	---	RELVCSLR
1092.5636	1091.5563	1091.5645	-0.0081	202 - 211		0	---	ALSMTTTPVR + Oxidation (M)
1092.5636	1091.5563	1091.5645	-0.0081	202 - 211		0	---	ALSMTTTPVR + Oxidation (M)
1344.7769	1343.7696	1343.7084	0.0612	485 - 497		1	---	VKGEASVPPGFEK
1455.7562	1454.7489	1454.7306	0.0183	527 - 538		1	---	DQSGKWVFGYIR
1630.8540	1629.8467	1629.8191	0.0277	418 - 430		0	---	TENFLWGFFLQTK
1770.9160	1769.9087	1770.0290	-0.1203	542 - 558		0	---	SIPEVVAGLLAIYQGLK
1895.9664	1894.9591	1894.9386	0.0205	349 - 364		0	---	SPTLLNVEMYLFPDEK
1895.9664	1894.9591	1894.9386	0.0205	349 - 364		0	---	SPTLLNVEMYLFPDEK
2547.2544	2546.2471	2546.3712	-0.1241	326 - 348		1	---	AMPALLKVELLPTCHILNDVSGR

No match to: 713.3978, 768.5062, 830.4199, 846.4267, 989.4948, 1155.5575, 1261.5885, 1318.6300, 1318.6300, 1428.7333, 1448.9115, 1471.7473, 1570.7924, 1596.8088, 1596.8088, 1600.8933, 1619.7943, 1622.8430, 1635.7867, 1754.8619, 1766.8069, 1766.8069, 1786.9052, 1903.9036, 1943.0707, 1979.9825, 2099.9321, 2115.9241, 2453.2244

8. gi|168015219 **Mass:** 38489 **Score:** 50 **Expect:** 5.5 **Queries matched:** 8

predicted protein [Physcomitrella patens subsp. patens]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1261.5885	1260.5812	1260.6098	-0.0286	159 - 168		0	---	EIENLSHYTR
1471.7473	1470.7400	1470.7830	-0.0430	96 - 107		1	---	EFHDVIIDSIKR
1570.7924	1569.7851	1569.7456	0.0395	274 - 287		1	---	METKVLNDGSAYAR + Oxidation (M)
1630.8540	1629.8467	1629.8150	0.0317	33 - 46		1	---	STKTSEFWAFAISR
1635.7867	1634.7794	1634.8892	-0.1098	295 - 308		1	---	KAVQFLTVPPNHER
1766.8069	1765.7996	1765.8722	-0.0726	210 - 223		1	1	QKWPIDMEHGWAIR
1766.8069	1765.7996	1765.8722	-0.0726	210 - 223		1	---	QKWPIDMEHGWAIR
1903.9036	1902.8963	1902.8934	0.0030	36 - 51		1	---	TSEFWAFAISRMQEGK + Oxidation (M)

No match to: 713.3978, 768.5062, 830.4199, 846.4267, 989.4948, 1032.5616, 1092.5636, 1092.5636, 1155.5575, 1318.6300, 1318.6300, 1344.7769, 1428.7333, 1448.9115, 1455.7562, 1596.8088, 1596.8088, 1600.8933, 1619.7943,

1622.8430, 1754.8619, 1770.9160, 1786.9052, 1895.9664, 1895.9664, 1943.0707, 1979.9825, 2099.9321, 2115.9241, 2453.2244, 2547.2544

9. gi|60547607 **Mass:** 9651 **Score:** 50 **Expect:** 6.2 **Queries matched:** 6

hypothetical protein At1g33450 [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1318.6300	1317.6227	1317.6598	-0.0371	30 -	40	1	---	NGKQMEEELIK
1318.6300	1317.6227	1317.6598	-0.0371	30 -	40	1	---	NGKQMEEELIK
1455.7562	1454.7489	1454.6567	0.0922	18 -	29	0	---	MNVMANMELLNK + 3 Oxidation (M)
1754.8619	1753.8546	1753.8160	0.0386	18 -	32	1	---	MNVMANMELLNKNGK + 3 Oxidation (M)
1770.9160	1769.9087	1769.8981	0.0106	51 -	66	1	---	ENVEELGHVMAKSALK + Oxidation (M)
2453.2244	2452.2171	2452.1759	0.0412	9 -	29	1	---	VAENISDLRMNVMANMELLNK + 3 Oxidation (M)

No match to: 713.3978, 768.5062, 830.4199, 846.4267, 989.4948, 1032.5616, 1092.5636, 1092.5636, 1155.5575, 1261.5885, 1344.7769, 1428.7333, 1448.9115, 1471.7473, 1570.7924, 1596.8088, 1596.8088, 1600.8933, 1619.7943, 1622.8430, 1630.8540, 1635.7867, 1766.8069, 1766.8069, 1786.9052, 1895.9664, 1895.9664, 1903.9036, 1943.0707, 1979.9825, 2099.9321, 2115.9241, 2547.2544

10. gi|147797914 **Mass:** 51075 **Score:** 48 **Expect:** 8.8 **Queries matched:** 9

hypothetical protein [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
846.4267	845.4194	845.4606	-0.0412	210 -	216	1	---	SLDREVK
1155.5575	1154.5502	1154.5719	-0.0217	2 -	11	0	---	EGSNGLLFYR
1318.6300	1317.6227	1317.5917	0.0310	273 -	283	1	---	KHNGVAEMMNR + 2 Oxidation (M)
1318.6300	1317.6227	1317.5917	0.0310	273 -	283	1	---	KHNGVAEMMNR + 2 Oxidation (M)
1471.7473	1470.7400	1470.7578	-0.0178	214 -	226	1	---	EVKVAHLGNSDFR
1754.8619	1753.8546	1753.8158	0.0388	339 -	353	0	---	DVVFQENQTLGDFDK
1770.9160	1769.9087	1769.8440	0.0647	235 -	249	1	---	DVCLAVYSKVCSDVR
1895.9664	1894.9591	1894.9458	0.0134	227 -	243	1	---	VEVDGVSRDVCLAVYSK
1895.9664	1894.9591	1894.9458	0.0134	227 -	243	1	---	VEVDGVSRDVCLAVYSK

No match to: 713.3978, 768.5062, 830.4199, 989.4948, 1032.5616, 1092.5636, 1092.5636, 1261.5885, 1344.7769, 1428.7333, 1448.9115, 1455.7562, 1570.7924, 1596.8088, 1596.8088, 1600.8933, 1619.7943, 1622.8430, 1630.8540, 1635.7867, 1766.8069, 1766.8069, 1786.9052, 1903.9036, 1943.0707, 1979.9825, 2099.9321, 2115.9241, 2453.2244, 2547.2544

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 39

Protein View

Match to: **gi|115434270** Score: **163** Expect: **3e-011**
Os01g0125800 [Oryza sativa (japonica cultivar-group)]

Nominal mass (M_r): **67097**; Calculated pI value: **6.48**
NCBI BLAST search of gi|115434270 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Oryza sativa Japonica Group
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|12328528 from Oryza sativa Japonica Group
gi|14090382 from Oryza sativa Japonica Group
gi|113531424 from Oryza sativa Japonica Group
gi|218187430 from Oryza sativa Indica Group
gi|222617661 from Oryza sativa Japonica Group

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **14%**

Matched peptides shown in **Bold Red**

```
   1 MAQLQETYAC SPATERGRGI LLAGDPKTET IAYCTGRSVI IRRLDAPLDC
  51 WAYPDHAYPT TVARFSPNGE WVASADASGC VRVWGRYGDR ALKAEFRPLS
 101 GRVDDLRWSP DGLRIVVSGD GKGKSFVRAF VWDSGSTVGE FDGHSKRVLS
 151 CDFKPTRPFR IVTCGEDFLA NYYEGPPFKF KHSIRDHSNF VNCIRYAPDG
 201 SKFISVSSDK KGLIYDGKTG DKIGELSSEG SHTGSIYAVS WSPDSKQVLT
 251 VSADKTAKVW DILEDASGKL NRTLACPGTG GVDDMLVGCL WQNDYLVTVS
 301 LGGTFNVFSA SNPDKEPVTF AGHLKTVSSL AFFPQSNPKT ILSTSYDGVI
 351 MRWIKGVGYG GRLMRKNNTQ IKCFTVAEEE LVTSGYDNKV FRIPLNGDQC
 401 GDAESVDVGG QPNALNLAIQ KPEFALVTTD SGIVLLHKST VISTTKVNYT
 451 ITSSAVSPDG TEAIVGAQDG KLRIYSINGD TVTEEALIEK HRGAITCIHY
 501 SPDVSMFASA DANREAVVWD RATREIKLKN MLFHSARINC LAWSPDNRLV
 551 ATGSLDTCAI VYEIDKPASS RITVKGAHLG GVHGLTFVDN DSLVTAGEDA
 601 CIRVWKLVPQ
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
91 - 102	1344.7769	1343.7696	1343.7673	0.0023	1	ALKAEFRPLSGR (No match)
94 - 102	1032.5616	1031.5543	1031.5512	0.0032	0	AEFRPLSGR (No match)
94 - 107	1630.8540	1629.8467	1629.8586	-0.0119	1	AEFRPLSGRVDDLR (No match)
103 - 114	1428.7333	1427.7260	1427.7157	0.0103	1	VDDLRWSPDGLR (No match)
108 - 114	830.4199	829.4126	829.4082	0.0044	0	WSPDGLR (No match)
148 - 160	1622.8430	1621.8357	1621.8398	-0.0041	0	VLSCDFKPTRPFR (No match)
182 - 195	1754.8619	1753.8546	1753.8430	0.0116	1	HSIRDHSNFVNCIR (No match)
186 - 195	1261.5885	1260.5812	1260.5669	0.0143	0	DHSNFVNCIR (No match)
186 - 202	1979.9825	1978.9752	1978.8955	0.0797	1	DHSNFVNCIRYAPDGSK (No match)
196 - 210	1600.8933	1599.8860	1599.7780	0.1080	1	YAPDGSKFISVSSDK (No match)
340 - 352	1455.7562	1454.7489	1454.7439	0.0050	0	TILSTSYDGVIMR (No match)
340 - 352	1471.7473	1470.7400	1470.7388	0.0012	0	TILSTSYDGVIMR Oxidation (M) (No match)
353 - 362	1092.5636	1091.5563	1091.5875	-0.0312	1	WIKGVGYGGR (No match)
353 - 362	1092.5636	1091.5563	1091.5875	-0.0312	1	WIKGVGYGGR (Ions score 66)

Spot 13

Index

	Accession	Mass	Score	Description
1.	gi|115434270	67097	230	Os01g0125800 [Oryza sativa (japonica cultivar-group)]
2.	gi|212723938	66930	120	hypothetical protein LOC100192950 [Zea mays]
3.	gi|223949659	66850	119	unknown [Zea mays]
4.	gi|147860511	162244	64	hypothetical protein [Vitis vinifera]
5.	gi|145332981	37885	60	SAPX (STROMAL ASCORBATE PEROXIDASE); L-ascorbate peroxidase [Arabidopsis thaliana]
6.	gi|15236483	40497	57	SAPX (STROMAL ASCORBATE PEROXIDASE); L-ascorbate peroxidase [Arabidopsis thaliana]
7.	gi|1419388	40560	57	stromal ascorbate peroxidase [Arabidopsis thaliana]
8.	gi|218188821	63046	56	hypothetical protein OsI_03217 [Oryza sativa Indica Group]
9.	gi|148909019	30076	56	unknown [Picea sitchensis]
10.	gi|46390022	13548	54	hypothetical protein [Oryza sativa Japonica Group]

Results List

1. gi|115434270 **Mass:** 67097 **Score:** 230 **Expect:** 6.1e-018 **Queries matched:** 17

Os01g0125800 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
830.4133	829.4060	829.4082	-0.0022	108	114	0	---	WSPDGLR
1032.5554	1031.5481	1031.5512	-0.0030	94	102	0	---	AEFRPLSGR
1092.5620	1091.5547	1091.5875	-0.0328	353	362	1	---	WIKGVGYGGR
1092.5620	1091.5547	1091.5875	-0.0328	353	362	1	100	WIKGVGYGGR
1261.5826	1260.5753	1260.5669	0.0084	186	195	0	---	DHSNFVNCIR
1344.7722	1343.7649	1343.7673	-0.0024	91	102	1	---	ALKAEFRPLSGR
1428.7200	1427.7127	1427.7157	-0.0030	103	114	1	---	VDDLRWSPDGLR
1455.7455	1454.7382	1454.7439	-0.0057	340	352	0	---	TILSTSYDGVIMR
1471.7314	1470.7241	1470.7388	-0.0147	340	352	0	---	TILSTSYDGVIMR + Oxidation (M)
1600.8947	1599.8874	1599.7780	0.1094	196	210	1	---	YAPDGSKFISVSSDK
1622.8429	1621.8356	1621.8398	-0.0042	148	160	0	---	VLSCDFKPTRPFR
1622.8429	1621.8356	1621.8398	-0.0042	148	160	0	32	VLSCDFKPTRPFR
1630.8572	1629.8499	1629.8586	-0.0087	94	107	1	---	AEFRPLSGRVDDLR
1754.8549	1753.8476	1753.8430	0.0046	182	195	1	---	HSIRDHSNFVNCIR
1778.9510	1777.9437	1777.9409	0.0028	147	160	1	---	RVLSCDFKPTRPFR
1979.9652	1978.9579	1978.8955	0.0624	186	202	1	---	DHSNFVNCIRYAPDGSK
1979.9652	1978.9579	1978.8955	0.0624	186	202	1	---	DHSNFVNCIRYAPDGSK

No match to: 713.3940, 768.5067, 782.4627, 989.4924, 1318.6219, 1448.8923, 1570.7941, 1596.8079, 1596.8079, 1616.8761, 1619.7915, 1635.7714, 1766.8065, 1766.8065, 1770.9066, 1786.9065, 1895.9662, 1903.9033, 1943.0767, 2031.0236, 2099.9319, 2115.9175, 2189.1223, 2193.1416, 2310.1057, 2392.1758, 2403.1780, 2438.2185, 2452.2402, 2547.2625, 2722.3962, 2853.3491

2. gi|212723938 **Mass:** 66930 **Score:** 120 **Expect:** 6.1e-007 **Queries matched:** 15

hypothetical protein LOC100192950 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
830.4133	829.4060	829.4082	-0.0022	108	-	114	0	---	WSPDGLR
1032.5554	1031.5481	1031.5512	-0.0030	94	-	102	0	---	AEFRPLSGR
1261.5826	1260.5753	1260.5669	0.0084	186	-	195	0	---	DHSNFVNCIR
1344.7722	1343.7649	1343.7673	-0.0024	91	-	102	1	---	ALKAEFRPLSGR
1428.7200	1427.7127	1427.7157	-0.0030	103	-	114	1	---	VDDLRWSPDGLR
1455.7455	1454.7382	1454.7439	-0.0057	340	-	352	0	---	TILSTSYDGVIMR
1471.7314	1470.7241	1470.7388	-0.0147	340	-	352	0	---	TILSTSYDGVIMR + Oxidation (M)
1622.8429	1621.8356	1621.8398	-0.0042	148	-	160	0	---	VLSCDFKPTRPFR
1622.8429	1621.8356	1621.8398	-0.0042	148	-	160	0	32	VLSCDFKPTRPFR
1630.8572	1629.8499	1629.8586	-0.0087	94	-	107	1	---	AEFRPLSGRVDDLR
1754.8549	1753.8476	1753.8430	0.0046	182	-	195	1	---	HSIRDHSNFVNCIR
1778.9510	1777.9437	1777.9409	0.0028	147	-	160	1	---	RVLSCDFKPTRPFR
1979.9652	1978.9579	1978.8955	0.0624	186	-	202	1	---	DHSNFVNCIRYAPDGSK
1979.9652	1978.9579	1978.8955	0.0624	186	-	202	1	---	DHSNFVNCIRYAPDGSK
2452.2402	2451.2329	2451.1764	0.0565	447	-	471	0	---	VNYAITSSSVSPDGTEAVVGAQDGK

No match to: 713.3940, 768.5067, 782.4627, 989.4924, 1092.5620, 1092.5620, 1318.6219, 1448.8923, 1570.7941, 1596.8079, 1596.8079, 1600.8947, 1616.8761, 1619.7915, 1635.7714, 1766.8065, 1766.8065, 1770.9066, 1786.9065, 1895.9662, 1903.9033, 1943.0767, 2031.0236, 2099.9319, 2115.9175, 2189.1223, 2193.1416, 2310.1057, 2392.1758, 2403.1780, 2438.2185, 2547.2625, 2722.3962, 2853.3491

3. gi|223949659 **Mass:** 66850 **Score:** 119 **Expect:** 7.6e-007 **Queries matched:** 15

unknown [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
830.4133	829.4060	829.4082	-0.0022	108	-	114	0	---	WSPDGLR
1032.5554	1031.5481	1031.5512	-0.0030	94	-	102	0	---	AEFRPLSGR
1261.5826	1260.5753	1260.5669	0.0084	186	-	195	0	---	DHSNFVNCIR
1344.7722	1343.7649	1343.7673	-0.0024	91	-	102	1	---	ALKAEFRPLSGR
1428.7200	1427.7127	1427.7157	-0.0030	103	-	114	1	---	VDDLRWSPDGLR
1455.7455	1454.7382	1454.7439	-0.0057	340	-	352	0	---	TILSTSYDGVIMR
1471.7314	1470.7241	1470.7388	-0.0147	340	-	352	0	---	TILSTSYDGVIMR + Oxidation (M)
1622.8429	1621.8356	1621.8398	-0.0042	148	-	160	0	---	VLSCDFKPTRPFR
1622.8429	1621.8356	1621.8398	-0.0042	148	-	160	0	32	VLSCDFKPTRPFR
1630.8572	1629.8499	1629.8586	-0.0087	94	-	107	1	---	AEFRPLSGRVDDLR
1754.8549	1753.8476	1753.8430	0.0046	182	-	195	1	---	HSIRDHSNFVNCIR
1778.9510	1777.9437	1777.9409	0.0028	147	-	160	1	---	RVLSCDFKPTRPFR
1979.9652	1978.9579	1978.8955	0.0624	186	-	202	1	---	DHSNFVNCIRYAPDGSK
1979.9652	1978.9579	1978.8955	0.0624	186	-	202	1	---	DHSNFVNCIRYAPDGSK

2310.1057	2309.0984	2309.0746	0.0238	493 - 514	0	---	GAITSIHYSPDVSMFASADANR

No match to: 713.3940, 768.5067, 782.4627, 989.4924, 1092.5620, 1092.5620, 1318.6219, 1448.8923, 1570.7941, 1596.8079, 1596.8079, 1600.8947, 1616.8761, 1619.7915, 1635.7714, 1766.8065, 1766.8065, 1770.9066, 1786.9065, 1895.9662, 1903.9033, 1943.0767, 2031.0236, 2099.9319, 2115.9175, 2189.1223, 2193.1416, 2392.1758, 2403.1780, 2438.2185, 2452.2402, 2547.2625, 2722.3962, 2853.3491

4. gi|147860511 **Mass:** 162244 **Score:** 64 **Expect:** 0.24 **Queries matched:** 15

hypothetical protein [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
768.5067	767.4994	767.5017	-0.0023	916 -	922	1	---	LKAALPR
1032.5554	1031.5481	1031.5247	0.0235	698 -	707	0	---	GNGSSIQELK
1092.5620	1091.5547	1091.5579	-0.0032	824 -	832	1	---	ALRIQGMCK + Oxidation (M)
1092.5620	1091.5547	1091.5512	0.0035	358 -	366	0	---	NFEAHPHLK
1261.5826	1260.5753	1260.6462	-0.0709	48 -	58	0	---	IHAVLHDAEEK
1318.6219	1317.6146	1317.6421	-0.0274	16 -	26	0	---	LVDMLACPDLR + Oxidation (M)
1596.8079	1595.8006	1595.7579	0.0427	392 -	404	0	---	NELNHEAWDDILK
1596.8079	1595.8006	1595.7579	0.0427	392 -	404	0	---	NELNHEAWDDILK
1616.8761	1615.8688	1615.8102	0.0586	1058 -	1071	0	---	LESFPEMGLPPMLR
1630.8572	1629.8499	1629.8685	-0.0186	941 -	955	0	---	NGVDLSSLTTLNIQR
1786.9065	1785.8992	1785.9182	-0.0190	1156 -	1172	0	---	CSSLPSLPTGELPSTLK
1895.9662	1894.9589	1894.9795	-0.0206	1028 -	1043	1	---	IENCANLQRLPNGLQR
1943.0767	1942.0694	1942.0193	0.0501	1156 -	1173	1	---	CSSLPSLPTGELPSTLKR
2310.1057	2309.0984	2309.2412	-0.1428	757 -	775	1	---	NELNEMLVLELLQPQRNLK + Oxidation (M)
2853.3491	2852.3418	2852.3796	-0.0378	322 -	346	1	---	NMGVATLTRTVSPYLLQELSNDDCR

No match to: 713.3940, 782.4627, 830.4133, 989.4924, 1344.7722, 1428.7200, 1448.8923, 1455.7455, 1471.7314, 1570.7941, 1600.8947, 1619.7915, 1622.8429, 1622.8429, 1635.7714, 1754.8549, 1766.8065, 1766.8065, 1770.9066, 1778.9510, 1903.9033, 1979.9652, 1979.9652, 2031.0236, 2099.9319, 2115.9175, 2189.1223, 2193.1416, 2392.1758, 2403.1780, 2438.2185, 2452.2402, 2547.2625, 2722.3962

5. gi|145332981 **Mass:** 37885 **Score:** 60 **Expect:** 0.61 **Queries matched:** 8

SAPX (STROMAL ASCORBATE PEROXIDASE); L-ascorbate peroxidase [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
713.3940	712.3867	712.3544	0.0324	218 -	222	0	---	EVFYR
989.4924	988.4851	988.4977	-0.0126	247 -	255	0	---	SGWGKPETK
1032.5554	1031.5481	1031.5975	-0.0493	7 -	16	0	---	STTAASLLLR
1261.5826	1260.5753	1260.5887	-0.0134	105 -	115	0	---	LGWHDAGTYNK
1428.7200	1427.7127	1427.7521	-0.0394	204 -	217	0	---	LPDAGPPSPATHLR
1616.8761	1615.8688	1615.8106	0.0582	105 -	118	1	---	LGWHDAGTYNKNIK
2031.0236	2030.0163	2029.9533	0.0630	314 -	331	1	---	YAADQDAFFKDYAVAHAK
2189.1223	2188.1150	2188.0588	0.0562	256 -	275	1	---	YTKEGPGAPGGQSWTPEWLK

No match to: 768.5067, 782.4627, 830.4133, 1092.5620, 1092.5620, 1318.6219, 1344.7722, 1448.8923, 1455.7455,

1471.7314, 1570.7941, 1596.8079, 1596.8079, 1600.8947, 1619.7915, 1622.8429, 1622.8429, 1630.8572, 1635.7714, 1754.8549, 1766.8065, 1766.8065, 1770.9066, 1778.9510, 1786.9065, 1895.9662, 1903.9033, 1943.0767, 1979.9652, 1979.9652, 2099.9319, 2115.9175, 2193.1416, 2310.1057, 2392.1758, 2403.1780, 2438.2185, 2452.2402, 2547.2625, 2722.3962, 2853.3491

6. gi|15236483 **Mass:** 40497 **Score:** 57 **Expect:** 1.2 **Queries matched:** 8

SAPX (STROMAL ASCORBATE PEROXIDASE); L-ascorbate peroxidase [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
713.3940	712.3867	712.3544	0.0324	243	247	0	---	EVFYR
989.4924	988.4851	988.4977	-0.0126	272	280	0	---	SGWGKPETK
1032.5554	1031.5481	1031.5975	-0.0493	31	40	0	---	STTAASLLLR
1261.5826	1260.5753	1260.5887	-0.0134	130	140	0	---	LGWHDAGTYNK
1428.7200	1427.7127	1427.7521	-0.0394	229	242	0	---	LPDAGPPSPATHLR
1616.8761	1615.8688	1615.8106	0.0582	130	143	1	---	LGWHDAGTYNKNIK
2031.0236	2030.0163	2029.9533	0.0630	339	356	1	---	YAADQDAFFKDYAVAHAK
2189.1223	2188.1150	2188.0588	0.0562	281	300	1	---	YTKEGPGAPGGQSWTPEWLK

No match to: 768.5067, 782.4627, 830.4133, 1092.5620, 1092.5620, 1318.6219, 1344.7722, 1448.8923, 1455.7455, 1471.7314, 1570.7941, 1596.8079, 1596.8079, 1600.8947, 1619.7915, 1622.8429, 1622.8429, 1630.8572, 1635.7714, 1754.8549, 1766.8065, 1766.8065, 1770.9066, 1778.9510, 1786.9065, 1895.9662, 1903.9033, 1943.0767, 1979.9652, 1979.9652, 2099.9319, 2115.9175, 2193.1416, 2310.1057, 2392.1758, 2403.1780, 2438.2185, 2452.2402, 2547.2625, 2722.3962, 2853.3491

7. gi|1419388 **Mass:** 40560 **Score:** 57 **Expect:** 1.2 **Queries matched:** 8

stromal ascorbate peroxidase [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
713.3940	712.3867	712.3544	0.0324	243	247	0	---	EVFYR
989.4924	988.4851	988.4977	-0.0126	272	280	0	---	SGWGKPETK
1032.5554	1031.5481	1031.5975	-0.0493	31	40	0	---	STTAASLLLR
1261.5826	1260.5753	1260.5887	-0.0134	130	140	0	---	LGWHDAGTYNK
1428.7200	1427.7127	1427.7521	-0.0394	229	242	0	---	LPDAGPPSPATHLR
1616.8761	1615.8688	1615.8106	0.0582	130	143	1	---	LGWHDAGTYNKNIK
2031.0236	2030.0163	2029.9533	0.0630	339	356	1	---	YAADQDAFFKDYAVAHAK
2189.1223	2188.1150	2188.0588	0.0562	281	300	1	---	YTKEGPGAPGGQSWTPEWLK

No match to: 768.5067, 782.4627, 830.4133, 1092.5620, 1092.5620, 1318.6219, 1344.7722, 1448.8923, 1455.7455, 1471.7314, 1570.7941, 1596.8079, 1596.8079, 1600.8947, 1619.7915, 1622.8429, 1622.8429, 1630.8572, 1635.7714, 1754.8549, 1766.8065, 1766.8065, 1770.9066, 1778.9510, 1786.9065, 1895.9662, 1903.9033, 1943.0767, 1979.9652, 1979.9652, 2099.9319, 2115.9175, 2193.1416, 2310.1057, 2392.1758, 2403.1780, 2438.2185, 2452.2402, 2547.2625, 2722.3962, 2853.3491

8. gi|218188821 **Mass:** 63046 **Score:** 56 **Expect:** 1.6 **Queries matched:** 11

hypothetical protein OsI_03217 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide

782.4627	781.4554	781.4122	0.0432	467 - 472	1	---	AYWSKK
830.4133	829.4060	829.4558	-0.0498	510 - 516	1	---	VGARNWK
1455.7455	1454.7382	1454.7340	0.0042	1 - 13	1	---	MPPATPSATRWPK + Oxidation (M)
1596.8079	1595.8006	1595.7362	0.0645	182 - 196	0	---	AHCSDAAVPIDDAVR
1596.8079	1595.8006	1595.7362	0.0645	182 - 196	0	---	AHCSDAAVPIDDAVR
1778.9510	1777.9437	1777.8273	0.1164	324 - 338	1	---	EGCLGQAMEILDRMR
1979.9652	1978.9579	1979.0952	-0.1372	140 - 158	0	---	SYTAVLAALVAHSHLSLAR
1979.9652	1978.9579	1979.0952	-0.1372	140 - 158	0	---	SYTAVLAALVAHSHLSLAR
2031.0236	2030.0163	2030.0870	-0.0707	418 - 435	0	---	GISTKPTTFHLLVECLSK
2193.1416	2192.1343	2192.0354	0.0990	200 - 218	0	---	NIPKPDACSYNTVIDGLCR
2438.2185	2437.2112	2437.2142	-0.0030	525 - 544	0	---	NLMFLCLGDCFLHGLMLLVR + Oxidation (M)

No match to: 713.3940, 768.5067, 989.4924, 1032.5554, 1092.5620, 1092.5620, 1261.5826, 1318.6219, 1344.7722, 1428.7200, 1448.8923, 1471.7314, 1570.7941, 1600.8947, 1616.8761, 1619.7915, 1622.8429, 1622.8429, 1630.8572, 1635.7714, 1754.8549, 1766.8065, 1766.8065, 1770.9066, 1786.9065, 1895.9662, 1903.9033, 1943.0767, 2099.9319, 2115.9175, 2189.1223, 2310.1057, 2392.1758, 2403.1780, 2452.2402, 2547.2625, 2722.3962, 2853.3491

9. gi|148909019 **Mass:** 30076 **Score:** 56 **Expect:** 1.6 **Queries matched:** 7

unknown [Picea sitchensis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
989.4924	988.4851	988.4470	0.0381	143 - 150	0	---	NHAEMLMK + Oxidation (M)
1455.7455	1454.7382	1454.7557	-0.0175	123 - 135	1	---	DNVGLPGFAKYFK
1635.7714	1634.7641	1634.7657	-0.0016	143 - 155	1	---	NHAEMLMKYQNTR
1754.8549	1753.8476	1753.9647	-0.1171	1 - 17	1	---	MLLKASATSFAAISSLK + Oxidation (M)
1778.9510	1777.9437	1777.8569	0.0868	24 - 38	1	---	DKVAGNNSLCWVPYR
1895.9662	1894.9589	1894.9875	-0.0286	241 - 256	1	---	IGKGHGIWHFDQMLLK + Oxidation (M)
2189.1223	2188.1150	2188.1060	0.0090	159 - 176	1	---	VKFQSILMPLMEFDHPEK

No match to: 713.3940, 768.5067, 782.4627, 830.4133, 1032.5554, 1092.5620, 1092.5620, 1261.5826, 1318.6219, 1344.7722, 1428.7200, 1448.8923, 1471.7314, 1570.7941, 1596.8079, 1596.8079, 1600.8947, 1616.8761, 1619.7915, 1622.8429, 1622.8429, 1630.8572, 1766.8065, 1766.8065, 1770.9066, 1786.9065, 1903.9033, 1943.0767, 1979.9652, 1979.9652, 2031.0236, 2099.9319, 2115.9175, 2193.1416, 2310.1057, 2392.1758, 2403.1780, 2438.2185, 2452.2402, 2547.2625, 2722.3962, 2853.3491

10. gi|46390022 **Mass:** 13548 **Score:** 54 **Expect:** 2.2 **Queries matched:** 6

hypothetical protein [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
989.4924	988.4851	988.4668	0.0184	41 - 46	0	---	QWWQWR
1619.7915	1618.7842	1618.7335	0.0508	101 - 118	0	---	WAAAGGDGALSSAGSGER
1622.8429	1621.8356	1621.7708	0.0648	47 - 64	0	---	AGAGGQWALAAHEGGGGR
1622.8429	1621.8356	1621.7708	0.0648	47 - 64	0	---	AGAGGQWALAAHEGGGGR
1778.9510	1777.9437	1777.8719	0.0718	47 - 65	1	---	AGAGGQWALAAHEGGGGRR
2189.1223	2188.1150	2188.0143	0.1007	66 - 90	0	---	WATGSGGALPSAGSGGGEEAGGVTR

No match to: 713.3940, 768.5067, 782.4627, 830.4133, 1032.5554, 1092.5620, 1092.5620, 1261.5826, 1318.6219, 1344.7722, 1428.7200, 1448.8923, 1455.7455, 1471.7314, 1570.7941, 1596.8079, 1596.8079, 1600.8947, 1616.8761, 1630.8572, 1635.7714, 1754.8549, 1766.8065, 1766.8065, 1770.9066, 1786.9065, 1895.9662, 1903.9033, 1943.0767, 1979.9652, 1979.9652, 2031.0236, 2099.9319, 2115.9175, 2193.1416, 2310.1057, 2392.1758, 2403.1780, 2438.2185, 2452.2402, 2547.2625, 2722.3962, 2853.3491

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 49

Protein View

Match to: **gi|115434270** Score: **230** Expect: **6.1e-018**
Os01g0125800 [Oryza sativa (japonica cultivar-group)]

Nominal mass (M_r): **67097**; Calculated pI value: **6.48**
NCBI BLAST search of gi|115434270 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Oryza sativa Japonica Group
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|12328528 from Oryza sativa Japonica Group
gi|14090382 from Oryza sativa Japonica Group
gi|113531424 from Oryza sativa Japonica Group
gi|218187430 from Oryza sativa Indica Group
gi|222617661 from Oryza sativa Japonica Group

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **14%**

Matched peptides shown in **Bold Red**

```
  1 MAQLQETYAC SPATERGRGI LLAGDPKTET IAYCTGRSVI IRRLDAPLDC
 51 WAYPDHAYPT TVARFSPNGE WVASADASGC VRVWGRYGDR ALKAEFRPLS
101 GRVDDLRWSP DGLRIVVSGD GKGKSFVRAF VWDSGSTVGE FDGHSKRVLS
151 CDFKPTRPFR IVTCGEDFLA NYYEGPPFKF KHSIRDHSNF VNCIRYAPDG
201 SKFISVSSDK KGLIYDGKTG DKIGELSSEG SHTGSIYAVS WSPDSKQVLT
251 VSADKTAKVW DILEDASGKL NRTLACPGTG GVDDMLVGCL WQNDYLVTVS
301 LGGTFNVFSA SNPDKEPVTF AGHLKTVSSL AFFPQSNPKT ILSTSYDGVI
351 MRWIKGVGYG GRLMRKNNTQ IKCFTVAEEE LVTSGYDNKV FRIPLNGDQC
401 GDAESVDVGG QPNALNLAIQ KPEFALVTTD SGIVLLHKST VISTTKVNYT
451 ITSSAVSPDG TEAIVGAQDG KLRIYSINGD TVTEEALIEK HRGAITCIHY
501 SPDVSMFASA DANREAVVWD RATREIKLKN MLFHSARINC LAWSPDNRLV
551 ATGSLDTCAI VYEIDKPASS RITVKGAHLG GVHGLTFVDN DSLVTAGEDA
601 CIRVWKLVPQ
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
91 - 102	1344.7722	1343.7649	1343.7673	-0.0024	1	**ALKAEFRPLSGR** (No match)
94 - 102	1032.5554	1031.5481	1031.5512	-0.0030	0	**AEFRPLSGR** (No match)
94 - 107	1630.8572	1629.8499	1629.8586	-0.0087	1	**AEFRPLSGRVDDLR** (No match)
103 - 114	1428.7200	1427.7127	1427.7157	-0.0030	1	**VDDLRWSPDGLR** (No match)
108 - 114	830.4133	829.4060	829.4082	-0.0022	0	**WSPDGLR** (No match)
147 - 160	1778.9510	1777.9437	1777.9409	0.0028	1	**RVLSCDFKPTRPFR** (No match)
148 - 160	1622.8429	1621.8356	1621.8398	-0.0042	0	**VLSCDFKPTRPFR** (No match)
148 - 160	1622.8429	1621.8356	1621.8398	-0.0042	0	**VLSCDFKPTRPFR** (Ions score 32)
182 - 195	1754.8549	1753.8476	1753.8430	0.0046	1	**HSIRDHSNFVNCIR** (No match)
186 - 195	1261.5826	1260.5753	1260.5669	0.0084	0	**DHSNFVNCIR** (No match)
186 - 202	1979.9652	1978.9579	1978.8955	0.0624	1	**DHSNFVNCIRYAPDGSK** (No match)
186 - 202	1979.9652	1978.9579	1978.8955	0.0624	1	**DHSNFVNCIRYAPDGSK** (No match)
196 - 210	1600.8947	1599.8874	1599.7780	0.1094	1	**YAPDGSKFISVSSDK** (No match)
340 - 352	1455.7455	1454.7382	1454.7439	-0.0057	0	**TILSTSYDGVIMR** (No match)
340 - 352	1471.7314	1470.7241	1470.7388	-0.0147	0	**TILSTSYDGVIMR** Oxidation (M) (No match)
353 - 362	1092.5620	1091.5547	1091.5875	-0.0328	1	**WIKGVGYGGR** (No match)
353 - 362	1092.5620	1091.5547	1091.5875	-0.0328	1	**WIKGVGYGGR** (Ions score 100)

Spot 14

Index

	Accession	Mass	Score	Description
1.	gi|115434270	67097	218	Os01g0125800 [Oryza sativa (japonica cultivar-group)]
2.	gi|212723938	66930	130	hypothetical protein LOC100192950 [Zea mays]
3.	gi|46390022	13548	50	hypothetical protein [Oryza sativa Japonica Group]
4.	gi|168000076	229933	49	predicted protein [Physcomitrella patens subsp. patens]
5.	gi|2702282	32975	47	unknown protein [Arabidopsis thaliana]
6.	gi|26451760	36906	47	unknown protein [Arabidopsis thaliana]
7.	gi|30685481	36933	47	meprin and TRAF homology domain-containing protein / MATH domain-containing protein [Arabidop
8.	gi|218201277	9559	46	hypothetical protein OsI_29525 [Oryza sativa Indica Group]
9.	gi|55296907	12065	44	BKRF1 encodes EBNA-1 protein-like [Oryza sativa Japonica Group]
10.	gi|115460926	133874	44	Os04g0645100 [Oryza sativa (japonica cultivar-group)]

Results List

1. gi|115434270 **Mass:** 67097 **Score:** 218 **Expect:** 9.6e-017 **Queries matched:** 18

Os01g0125800 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
765.4056	764.3983	764.4068	-0.0085	212	218	0	---	GLIYDGK
830.4145	829.4072	829.4082	-0.0010	108	114	0	---	WSPDGLR
1032.5569	1031.5496	1031.5512	-0.0015	94	102	0	---	AEFRPLSGR
1092.5607	1091.5534	1091.5875	-0.0341	353	362	1	97	WIKGVGYGGR
1092.5607	1091.5534	1091.5875	-0.0341	353	362	1	---	WIKGVGYGGR
1261.5842	1260.5769	1260.5669	0.0100	186	195	0	---	DHSNFVNCIR
1344.7756	1343.7683	1343.7673	0.0010	91	102	1	---	ALKAEFRPLSGR
1428.7228	1427.7155	1427.7157	-0.0002	103	114	1	---	VDDLRWSPDGLR
1455.7549	1454.7476	1454.7439	0.0037	340	352	0	---	TILSTSYDGVIMR
1471.7434	1470.7361	1470.7388	-0.0027	340	352	0	---	TILSTSYDGVIMR + Oxidation (M)
1622.8463	1621.8390	1621.8398	-0.0008	148	160	0	28	VLSCDFKPTRPFR
1622.8463	1621.8390	1621.8398	-0.0008	148	160	0	---	VLSCDFKPTRPFR
1630.8694	1629.8621	1629.8586	0.0035	94	107	1	---	AEFRPLSGRVDDLR
1754.8539	1753.8466	1753.8430	0.0036	182	195	1	---	HSIRDHSNFVNCIR
1778.9543	1777.9470	1777.9409	0.0061	147	160	1	---	RVLSCDFKPTRPFR
1979.9719	1978.9646	1978.8955	0.0691	186	202	1	---	DHSNFVNCIRYAPDGSK
1979.9719	1978.9646	1978.8955	0.0691	186	202	1	---	DHSNFVNCIRYAPDGSK
2495.1992	2494.1919	2494.1878	0.0041	161	181	1	---	IVTCGEDFLANYYEGPPFKFK

No match to: 713.4109, 768.5250, 811.4534, 825.4695, 846.4142, 960.4583, 989.4993, 1005.4875, 1075.5382, 1104.5651, 1108.5557, 1155.5475, 1230.6763, 1246.6680, 1274.6497, 1279.7650, 1318.6244, 1332.6399, 1334.8856, 1448.9194, 1570.7883, 1596.8063, 1596.8063, 1600.8882, 1616.8927, 1619.7892, 1635.7805, 1766.8049, 1766.8049,

1770.8932, 1780.8278, 1786.9048, 1895.9662, 1903.9036, 1943.0856, 1993.9714, 2030.0198, 2099.9307, 2115.9277, 2189.1230, 2193.1472, 2310.0911, 2452.2498, 2547.2830, 2564.2573, 2722.4028, 2853.3804

2. gi|212723938 **Mass:** 66930 **Score:** 130 **Expect:** 6e-008 **Queries matched:** 18

hypothetical protein LOC100192950 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
765.4056	764.3983	764.4068	-0.0085	212	218	0	---	GLIYDGK
830.4145	829.4072	829.4082	-0.0010	108	114	0	---	WSPDGLR
1005.4875	1004.4802	1004.4862	-0.0059	530	537	0	---	NMLYHTAR
1032.5569	1031.5496	1031.5512	-0.0015	94	102	0	---	AEFRPLSGR
1246.6680	1245.6607	1245.6652	-0.0045	528	537	1	---	LKNMLYHTAR
1261.5842	1260.5769	1260.5669	0.0100	186	195	0	---	DHSNFVNCIR
1344.7756	1343.7683	1343.7673	0.0010	91	102	1	---	ALKAEFRPLSGR
1428.7228	1427.7155	1427.7157	-0.0002	103	114	1	---	VDDLRWSPDGLR
1455.7549	1454.7476	1454.7439	0.0037	340	352	0	---	TILSTSYDGVIMR
1471.7434	1470.7361	1470.7388	-0.0027	340	352	0	---	TILSTSYDGVIMR + Oxidation (M)
1622.8463	1621.8390	1621.8398	-0.0008	148	160	0	28	VLSCDFKPTRPFR
1622.8463	1621.8390	1621.8398	-0.0008	148	160	0	---	VLSCDFKPTRPFR
1630.8694	1629.8621	1629.8586	0.0035	94	107	1	---	AEFRPLSGRVDDLR
1754.8539	1753.8466	1753.8430	0.0036	182	195	1	---	HSIRDHSNFVNCIR
1778.9543	1777.9470	1777.9409	0.0061	147	160	1	---	RVLSCDFKPTRPFR
1979.9719	1978.9646	1978.8955	0.0691	186	202	1	---	DHSNFVNCIRYAPDGSK
1979.9719	1978.9646	1978.8955	0.0691	186	202	1	---	DHSNFVNCIRYAPDGSK
2452.2498	2451.2425	2451.1764	0.0661	447	471	0	---	VNYAITSSSVSPDGTEAVVGAQDGK

No match to: 713.4109, 768.5250, 811.4534, 825.4695, 846.4142, 960.4583, 989.4993, 1075.5382, 1092.5607, 1092.5607, 1104.5651, 1108.5557, 1155.5475, 1230.6763, 1274.6497, 1279.7650, 1318.6244, 1332.6399, 1334.8856, 1448.9194, 1570.7883, 1596.8063, 1596.8063, 1600.8882, 1616.8927, 1619.7892, 1635.7805, 1766.8049, 1766.8049, 1770.8932, 1780.8278, 1786.9048, 1895.9662, 1903.9036, 1943.0856, 1993.9714, 2030.0198, 2099.9307, 2115.9277, 2189.1230, 2193.1472, 2310.0911, 2495.1992, 2547.2830, 2564.2573, 2722.4028, 2853.3804

3. gi|46390022 **Mass:** 13548 **Score:** 50 **Expect:** 6.5 **Queries matched:** 6

hypothetical protein [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
989.4993	988.4920	988.4668	0.0253	41	46	0	---	QWWQWR
1619.7892	1618.7819	1618.7335	0.0485	101	118	0	---	WAAAGGDGALSSAGSGER
1622.8463	1621.8390	1621.7708	0.0682	47	64	0	---	AGAGGQWALAAHEGGGGR
1622.8463	1621.8390	1621.7708	0.0682	47	64	0	---	AGAGGQWALAAHEGGGGR
1778.9543	1777.9470	1777.8719	0.0751	47	65	1	---	AGAGGQWALAAHEGGGGRR
2189.1230	2188.1157	2188.0143	0.1014	66	90	0	---	WATGSGGALPSAGSGGGEEAGGVTR

No match to: 713.4109, 765.4056, 768.5250, 811.4534, 825.4695, 830.4145, 846.4142, 960.4583, 1005.4875, 1032.5569, 1075.5382, 1092.5607, 1092.5607, 1104.5651, 1108.5557, 1155.5475, 1230.6763, 1246.6680, 1261.5842,

1274.6497, 1279.7650, 1318.6244, 1332.6399, 1334.8856, 1344.7756, 1428.7228, 1448.9194, 1455.7549, 1471.7434, 1570.7883, 1596.8063, 1596.8063, 1600.8882, 1616.8927, 1630.8694, 1635.7805, 1754.8539, 1766.8049, 1766.8049, 1770.8932, 1780.8278, 1786.9048, 1895.9662, 1903.9036, 1943.0856, 1979.9719, 1979.9719, 1993.9714, 2030.0198, 2099.9307, 2115.9277, 2193.1472, 2310.0911, 2452.2498, 2495.1992, 2547.2830, 2564.2573, 2722.4028, 2853.3804

4. gi|168000076 **Mass:** 229933 **Score:** 49 **Expect:** 8 **Queries matched:** 20

predicted protein [Physcomitrella patens subsp. patens]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
765.4056	764.3983	764.3704	0.0279	722 -	728	0	---	GDGFLEK
1104.5651	1103.5578	1103.5182	0.0397	844 -	852	0	---	NHCSQAFLK
1246.6680	1245.6607	1245.6750	-0.0143	956 -	967	0	---	ELTSLGIGMLGR
1274.6497	1273.6424	1273.6237	0.0187	1203 -	1212	0	---	EIWLNGNCIR
1600.8882	1599.8809	1599.8443	0.0367	1189 -	1202	0	---	LTELPTHFGSVMLR
1616.8927	1615.8854	1615.8392	0.0463	1189 -	1202	0	---	LTELPTHFGSVMLR + Oxidation (M)
1619.7892	1618.7819	1618.7508	0.0311	1734 -	1747	0	---	IQNEEMETPSQSVK
1622.8463	1621.8390	1621.8174	0.0217	252 -	264	0	---	QQIPNFMFVEELK
1622.8463	1621.8390	1621.8174	0.0217	252 -	264	0	---	QQIPNFMFVEELK
1630.8694	1629.8621	1629.8297	0.0325	844 -	857	1	---	NHCSQAFLKTLPSK
1635.7805	1634.7732	1634.7457	0.0275	1734 -	1747	0	---	IQNEEMETPSQSVK + Oxidation (M)
1766.8049	1765.7976	1765.8432	-0.0456	1818 -	1831	0	---	VWFCFTIQAHLCGK
1766.8049	1765.7976	1765.8432	-0.0456	1818 -	1831	0	---	VWFCFTIQAHLCGK
1786.9048	1785.8975	1785.9117	-0.0142	748 -	763	0	---	SLMQAIGCSVLLEHTK
1943.0856	1942.0783	1941.9941	0.0842	235 -	251	1	---	AQLLARLANVVDDCEQK
1993.9714	1992.9641	1992.8768	0.0873	1 -	18	0	---	MDPEEDTAGSGLQMLLDR + Oxidation (M)
2030.0198	2029.0125	2029.0699	-0.0574	748 -	765	1	---	SLMQAIGCSVLLEHTKVK + Oxidation (M)
2189.1230	2188.1157	2188.0066	0.1092	355 -	373	1	---	NQLQIEQEGKQGAMEQDDK
2193.1472	2192.1399	2192.0789	0.0610	816 -	834	1	---	FSGYVTIPSLDTYSKSWNK
2310.0911	2309.0838	2309.1070	-0.0231	1277 -	1296	1	---	LRTLQMNDNPISDQEDHVGK

No match to: 713.4109, 768.5250, 811.4534, 825.4695, 830.4145, 846.4142, 960.4583, 989.4993, 1005.4875, 1032.5569, 1075.5382, 1092.5607, 1092.5607, 1108.5557, 1155.5475, 1230.6763, 1261.5842, 1279.7650, 1318.6244, 1332.6399, 1334.8856, 1344.7756, 1428.7228, 1448.9194, 1455.7549, 1471.7434, 1570.7883, 1596.8063, 1596.8063, 1754.8539, 1770.8932, 1778.9543, 1780.8278, 1895.9662, 1903.9036, 1979.9719, 1979.9719, 2099.9307, 2115.9277, 2452.2498, 2495.1992, 2547.2830, 2564.2573, 2722.4028, 2853.3804

5. gi|2702282 **Mass:** 32975 **Score:** 47 **Expect:** 12 **Queries matched:** 3

unknown protein [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1092.5607	1091.5534	1091.5950	-0.0415	206 -	213	1	44	WKLVMYPR
1092.5607	1091.5534	1091.5950	-0.0415	206 -	213	1	---	WKLVMYPR
1108.5557	1107.5484	1107.5899	-0.0415	206 -	213	1	---	WKLVMYPR + Oxidation (M)

No match to: 713.4109, 765.4056, 768.5250, 811.4534, 825.4695, 830.4145, 846.4142, 960.4583, 989.4993, 1005.4875, 1032.5569, 1075.5382, 1104.5651, 1155.5475, 1230.6763, 1246.6680, 1261.5842, 1274.6497, 1279.7650, 1318.6244,

1332.6399, 1334.8856, 1344.7756, 1428.7228, 1448.9194, 1455.7549, 1471.7434, 1570.7883, 1596.8063, 1596.8063, 1600.8882, 1616.8927, 1619.7892, 1622.8463, 1622.8463, 1630.8694, 1635.7805, 1754.8539, 1766.8049, 1766.8049, 1770.8932, 1778.9543, 1780.8278, 1786.9048, 1895.9662, 1903.9036, 1943.0856, 1979.9719, 1979.9719, 1993.9714, 2030.0198, 2099.9307, 2115.9277, 2189.1230, 2193.1472, 2310.0911, 2452.2498, 2495.1992, 2547.2830, 2564.2573, 2722.4028, 2853.3804

6. gi|26451760 **Mass:** 36906 **Score:** 47 **Expect:** 12 **Queries matched:** 3

unknown protein [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1092.5607	1091.5534	1091.5950	-0.0415	206 -	213	1	44	WKLVMYPR
1092.5607	1091.5534	1091.5950	-0.0415	206 -	213	1	---	WKLVMYPR
1108.5557	1107.5484	1107.5899	-0.0415	206 -	213	1	---	WKLVMYPR + Oxidation (M)

No match to: 713.4109, 765.4056, 768.5250, 811.4534, 825.4695, 830.4145, 846.4142, 960.4583, 989.4993, 1005.4875, 1032.5569, 1075.5382, 1104.5651, 1155.5475, 1230.6763, 1246.6680, 1261.5842, 1274.6497, 1279.7650, 1318.6244, 1332.6399, 1334.8856, 1344.7756, 1428.7228, 1448.9194, 1455.7549, 1471.7434, 1570.7883, 1596.8063, 1596.8063, 1600.8882, 1616.8927, 1619.7892, 1622.8463, 1622.8463, 1630.8694, 1635.7805, 1754.8539, 1766.8049, 1766.8049, 1770.8932, 1778.9543, 1780.8278, 1786.9048, 1895.9662, 1903.9036, 1943.0856, 1979.9719, 1979.9719, 1993.9714, 2030.0198, 2099.9307, 2115.9277, 2189.1230, 2193.1472, 2310.0911, 2452.2498, 2495.1992, 2547.2830, 2564.2573, 2722.4028, 2853.3804

7. gi|30685481 **Mass:** 36933 **Score:** 47 **Expect:** 12 **Queries matched:** 3

meprin and TRAF homology domain-containing protein / MATH domain-containing protein [Arabidopsis th

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1092.5607	1091.5534	1091.5950	-0.0415	206 -	213	1	44	WKLVMYPR
1092.5607	1091.5534	1091.5950	-0.0415	206 -	213	1	---	WKLVMYPR
1108.5557	1107.5484	1107.5899	-0.0415	206 -	213	1	---	WKLVMYPR + Oxidation (M)

No match to: 713.4109, 765.4056, 768.5250, 811.4534, 825.4695, 830.4145, 846.4142, 960.4583, 989.4993, 1005.4875, 1032.5569, 1075.5382, 1104.5651, 1155.5475, 1230.6763, 1246.6680, 1261.5842, 1274.6497, 1279.7650, 1318.6244, 1332.6399, 1334.8856, 1344.7756, 1428.7228, 1448.9194, 1455.7549, 1471.7434, 1570.7883, 1596.8063, 1596.8063, 1600.8882, 1616.8927, 1619.7892, 1622.8463, 1622.8463, 1630.8694, 1635.7805, 1754.8539, 1766.8049, 1766.8049, 1770.8932, 1778.9543, 1780.8278, 1786.9048, 1895.9662, 1903.9036, 1943.0856, 1979.9719, 1979.9719, 1993.9714, 2030.0198, 2099.9307, 2115.9277, 2189.1230, 2193.1472, 2310.0911, 2452.2498, 2495.1992, 2547.2830, 2564.2573, 2722.4028, 2853.3804

8. gi|218201277 **Mass:** 9559 **Score:** 46 **Expect:** 14 **Queries matched:** 6

hypothetical protein OsI_29525 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
830.4145	829.4072	829.4116	-0.0044	74 -	81	0	---	GPDALMAR
846.4142	845.4069	845.4065	0.0004	74 -	81	0	---	GPDALMAR + Oxidation (M)
1075.5382	1074.5309	1074.5392	-0.0083	52 -	60	1	---	GLWRMEAGR
1092.5607	1091.5534	1091.5399	0.0135	65 -	73	0	13	EGLWEFVGR
1092.5607	1091.5534	1091.5399	0.0135	65 -	73	0	---	EGLWEFVGR
1903.9036	1902.8963	1902.9410	-0.0446	65 -	81	1	---	EGLWEFVGRGPDALMAR

No match to: 713.4109, 765.4056, 768.5250, 811.4534, 825.4695, 960.4583, 989.4993, 1005.4875, 1032.5569, 1104.5651, 1108.5557, 1155.5475, 1230.6763, 1246.6680, 1261.5842, 1274.6497, 1279.7650, 1318.6244, 1332.6399, 1334.8856, 1344.7756, 1428.7228, 1448.9194, 1455.7549, 1471.7434, 1570.7883, 1596.8063, 1596.8063, 1600.8882, 1616.8927, 1619.7892, 1622.8463, 1622.8463, 1630.8694, 1635.7805, 1754.8539, 1766.8049, 1766.8049, 1770.8932, 1778.9543, 1780.8278, 1786.9048, 1895.9662, 1943.0856, 1979.9719, 1979.9719, 1993.9714, 2030.0198, 2099.9307, 2115.9277, 2189.1230, 2193.1472, 2310.0911, 2452.2498, 2495.1992, 2547.2830, 2564.2573, 2722.4028, 2853.3804

9. gi|55296907 **Mass:** 12065 **Score:** 44 **Expect:** 24 **Queries matched:** 5

BKRF1 encodes EBNA-1 protein-like [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1230.6763	1229.6690	1229.6550	0.0141	4 -	14	0	---	MVVEVRPTGAR + Oxidation (M)
1274.6497	1273.6424	1273.6626	-0.0201	108 -	120	0	---	EVVATSTGVQAGR
1455.7549	1454.7476	1454.8027	-0.0551	2 -	14	1	---	PKMVVEVRPTGAR + Oxidation (M)
1570.7883	1569.7810	1569.8483	-0.0673	1 -	14	1	---	MPKMVVEVRPTGAR
1616.8927	1615.8854	1615.8430	0.0425	108 -	122	1	---	EVVATSTGVQAGRWR

No match to: 713.4109, 765.4056, 768.5250, 811.4534, 825.4695, 830.4145, 846.4142, 960.4583, 989.4993, 1005.4875, 1032.5569, 1075.5382, 1092.5607, 1092.5607, 1104.5651, 1108.5557, 1155.5475, 1246.6680, 1261.5842, 1279.7650, 1318.6244, 1332.6399, 1334.8856, 1344.7756, 1428.7228, 1448.9194, 1471.7434, 1596.8063, 1596.8063, 1600.8882, 1619.7892, 1622.8463, 1622.8463, 1630.8694, 1635.7805, 1754.8539, 1766.8049, 1766.8049, 1770.8932, 1778.9543, 1780.8278, 1786.9048, 1895.9662, 1903.9036, 1943.0856, 1979.9719, 1979.9719, 1993.9714, 2030.0198, 2099.9307, 2115.9277, 2189.1230, 2193.1472, 2310.0911, 2452.2498, 2495.1992, 2547.2830, 2564.2573, 2722.4028, 2853.3804

10. gi|115460926 **Mass:** 133874 **Score:** 44 **Expect:** 25 **Queries matched:** 13

Os04g0645100 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
830.4145	829.4072	829.4293	-0.0221	959 -	965	0	---	ALDINER
1092.5607	1091.5534	1091.5896	-0.0362	561 -	569	1	---	KILEDSLMK + Oxidation (M)
1092.5607	1091.5534	1091.5896	-0.0362	561 -	569	1	---	KILEDSLMK + Oxidation (M)
1155.5475	1154.5402	1154.5502	-0.0100	570 -	579	0	---	LENMPANNPR
1230.6763	1229.6690	1229.6727	-0.0037	50 -	60	1	---	GISTDRVLDVR
1332.6399	1331.6326	1331.6568	-0.0242	419 -	430	1	---	DQADASLKLEDK
1570.7883	1569.7810	1569.8449	-0.0639	917 -	930	1	---	ALSKIVAVCGPYHR
1630.8694	1629.8621	1629.8660	-0.0039	988 -	1000	1	---	LQHIEMALKYVNR + Oxidation (M)
1895.9662	1894.9589	1894.9478	0.0112	278 -	293	1	---	AFLDHNKFGNLPYGFR
1903.9036	1902.8963	1902.9799	-0.0835	883 -	899	1	---	HVVYSSIDGRNLLESSK
2030.0198	2029.0125	2028.9275	0.0850	211 -	228	1	---	KESNGASQEGDYFEIEVK
2189.1230	2188.1157	2188.1673	-0.0516	120 -	139	1	---	LLDIVACTTAFVNKPRDGAK
2547.2830	2546.2757	2546.1932	0.0826	534 -	556	0	---	IVNSDIASTQCPTPQSHVDNHAR

No match to: 713.4109, 765.4056, 768.5250, 811.4534, 825.4695, 846.4142, 960.4583, 989.4993, 1005.4875, 1032.5569, 1075.5382, 1104.5651, 1108.5557, 1246.6680, 1261.5842, 1274.6497, 1279.7650, 1318.6244, 1334.8856, 1344.7756, 1428.7228, 1448.9194, 1455.7549, 1471.7434, 1596.8063, 1596.8063, 1600.8882, 1616.8927, 1619.7892, 1622.8463, 1622.8463, 1635.7805, 1754.8539, 1766.8049, 1766.8049, 1770.8932, 1778.9543, 1780.8278, 1786.9048, 1943.0856, 1979.9719, 1979.9719, 1993.9714, 2099.9307, 2115.9277, 2193.1472, 2310.0911, 2452.2498, 2495.1992,

2564.2573, 2722.4028, 2853.3804

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 65

Protein View

Match to: **gi|115434270** Score: **218** Expect: **9.6e-017**
Os01g0125800 [Oryza sativa (japonica cultivar-group)]

Nominal mass (M_r): **67097**; Calculated pI value: **6.48**
NCBI BLAST search of gi|115434270 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Oryza sativa Japonica Group
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|12328528 from Oryza sativa Japonica Group
gi|14090382 from Oryza sativa Japonica Group
gi|113531424 from Oryza sativa Japonica Group
gi|218187430 from Oryza sativa Indica Group
gi|222617661 from Oryza sativa Japonica Group

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **18%**

Matched peptides shown in **Bold Red**

```
  1 MAQLQETYAC SPATERGRGI LLAGDPKTET IAYCTGRSVI IRRLDAPLDC
 51 WAYPDHAYPT TVARFSPNGE WVASADASGC VRVWGRYGDR ALKAEFRPLS
101 GRVDDLRWSP DGLRIVVSGD GKGKSFVRAF VWDSGSTVGE FDGHSKRVLS
151 CDFKPTRPFR IVTCGEDFLA NYYEGPPFKF KHSIRDHSNF VNCIRYAPDG
201 SKFISVSSDK KGLIYDGKTG DKIGELSSEG SHTGSIYAVS WSPDSKQVLT
251 VSADKTAKVW DILEDASGKL NRTLACPGTG GVDDMLVGCL WQNDYLVTVS
301 LGGTFNVFSA SNPDKEPVTF AGHLKTVSSL AFFPQSNPKT ILSTSYDGVI
351 MRWIKGVGYG GRLMRKNNTQ IKCFTVAEEE LVTSGYDNKV FRIPLNGDQC
401 GDAESVDVGG QPNALNLAIQ KPEFALVTTD SGIVLLHKST VISTTKVNYT
451 ITSSAVSPDG TEAIVGAQDG KLRIYSINGD TVTEEALIEK HRGAITCIHY
501 SPDVSMFASA DANREAVVWD RATREIKLKN MLFHSARINC LAWSPDNRLV
551 ATGSLDTCAI VYEIDKPASS RITVKGAHLG GVHGLTFVDN DSLVTAGEDA
601 CIRVWKLVPQ
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
91 - 102	1344.7756	1343.7683	1343.7673	0.0010	1	**ALKAEFRPLSGR** (No match)
94 - 102	1032.5569	1031.5496	1031.5512	-0.0015	0	**AEFRPLSGR** (No match)
94 - 107	1630.8694	1629.8621	1629.8586	0.0035	1	**AEFRPLSGRVDDLR** (No match)
103 - 114	1428.7228	1427.7155	1427.7157	-0.0002	1	**VDDLRWSPDGLR** (No match)
108 - 114	830.4145	829.4072	829.4082	-0.0010	0	**WSPDGLR** (No match)
147 - 160	1778.9543	1777.9470	1777.9409	0.0061	1	**RVLSCDFKPTRPFR** (No match)
148 - 160	1622.8463	1621.8390	1621.8398	-0.0008	0	**VLSCDFKPTRPFR** (Ions score 28)
148 - 160	1622.8463	1621.8390	1621.8398	-0.0008	0	**VLSCDFKPTRPFR** (No match)
161 - 181	2495.1992	2494.1919	2494.1878	0.0041	1	**IVTCGEDFLANYYEGPPFKFK** (No match)
182 - 195	1754.8539	1753.8466	1753.8430	0.0036	1	**HSIRDHSNFVNCIR** (No match)
186 - 195	1261.5842	1260.5769	1260.5669	0.0100	0	**DHSNFVNCIR** (No match)
186 - 202	1979.9719	1978.9646	1978.8955	0.0691	1	**DHSNFVNCIRYAPDGSK** (No match)
186 - 202	1979.9719	1978.9646	1978.8955	0.0691	1	**DHSNFVNCIRYAPDGSK** (No match)
212 - 218	765.4056	764.3983	764.4068	-0.0085	0	**GLIYDGK** (No match)
340 - 352	1455.7549	1454.7476	1454.7439	0.0037	0	**TILSTSYDGVIMR** (No match)
340 - 352	1471.7434	1470.7361	1470.7388	-0.0027	0	**TILSTSYDGVIMR** Oxidation (M) (No match)
353 - 362	1092.5607	1091.5534	1091.5875	-0.0341	1	**WIKGVGYGGR** (Ions score 97)
353 - 362	1092.5607	1091.5534	1091.5875	-0.0341	1	**WIKGVGYGGR** (No match)

Spot 15

Index

	Accession	Mass	Score	Description
1.	gi|209405432	63309	372	NADP-dependent malic enzyme [Hordeum vulgare]
2.	gi|158701881	63391	350	NADP-dependent malic enzyme [Triticum aestivum]
3.	gi|222630448	59086	164	hypothetical protein OsJ_17383 [Oryza sativa Japonica Group]
4.	gi|115462465	63294	160	Os05g0186300 [Oryza sativa (japonica cultivar-group)]
5.	gi|226510109	63197	142	NADP-dependent malic enzyme [Zea mays]
6.	gi|255546341	65487	107	malic enzyme, putative [Ricinus communis]
7.	gi|510876	65255	82	NADP dependent malic enzyme [Phaseolus vulgaris]
8.	gi|115420	65234	82	RecName: Full=NADP-dependent malic enzyme; Short=NADP-ME
9.	gi|1129068	21699	79	malate dehydrogenase [Lycopersicon esculentum]
10.	gi|118487388	54899	65	unknown [Populus trichocarpa]

Results List

1. gi|209405432 **Mass:** 63309 **Score:** 372 **Expect:** 3.8e-032 **Queries matched:** 32

NADP-dependent malic enzyme [Hordeum vulgare]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
758.3937	757.3864	757.3758	0.0106	129	134	0	---	YGSIYR
965.5033	964.4960	964.4977	-0.0017	538	546	0	---	AYDLGLASR
1004.5487	1003.5414	1003.5450	-0.0036	80	87	0	20	QYTVPLQR
1004.5487	1003.5414	1003.5450	-0.0036	80	87	0	---	QYTVPLQR
1052.6729	1051.6656	1051.6026	0.0631	547	555	0	---	LPRPDDLVK
1174.6976	1173.6903	1173.6869	0.0034	135	144	0	---	RPQGLYISLK
1274.7273	1273.7200	1273.7182	0.0018	514	524	0	---	GLIFPPFTNIR
1315.7260	1314.7187	1314.7143	0.0045	160	171	0	50	SIQVIVVTDGER
1315.7260	1314.7187	1314.7143	0.0045	160	171	0	---	SIQVIVVTDGER
1358.6957	1357.6884	1357.6738	0.0146	40	51	1	---	HNKGLAFSEAER
1382.7872	1381.7799	1381.7717	0.0082	149	159	1	---	VLEVLKNWPER
1382.7872	1381.7799	1381.7717	0.0082	149	159	1	48	VLEVLKNWPER
1402.8252	1401.8179	1401.8132	0.0047	514	525	1	---	GLIFPPFTNIRK
1417.8247	1416.8174	1416.8088	0.0086	135	146	1	---	RPQGLYISLKDK
1553.6864	1552.6791	1552.6690	0.0101	556	567	0	21	YAESCMYTPLYR
1553.6864	1552.6791	1552.6690	0.0101	556	567	0	---	YAESCMYTPLYR
1569.6699	1568.6626	1568.6639	-0.0013	556	567	0	---	YAESCMYTPLYR + Oxidation (M)
1614.9237	1613.9164	1613.9140	0.0024	348	361	1	---	IWLVDSKGLLVESR
1645.8865	1644.8792	1644.8835	-0.0042	58	72	0	---	GLLPPAIVSQEHQEK
1668.7946	1667.7873	1667.7759	0.0114	88	100	1	---	YIAMMDLQERNER

1684.7791	1683.7718	1683.7708	0.0010	88 - 100	1	---	YIAMMDLQERNER + Oxidation (M)
1700.7665	1699.7592	1699.7657	-0.0065	88 - 100	1	---	YIAMMDLQERNER + 2 Oxidation (M)
1734.8660	1733.8587	1733.8485	0.0103	43 - 57	1	---	GLAFSEAERDAHYLR
1734.8660	1733.8587	1733.8485	0.0103	43 - 57	1	14	GLAFSEAERDAHYLR
1768.9609	1767.9536	1767.9566	-0.0030	74 - 87	1	---	IMHNLRQYTVPLQR
1773.9893	1772.9820	1772.9784	0.0036	58 - 73	1	---	GLLPPAIVSQEHQEKK
1784.9565	1783.9492	1783.9515	-0.0023	74 - 87	1	---	IMHNLRQYTVPLQR + Oxidation (M)
1914.0616	1913.0543	1913.0522	0.0021	129 - 144	1	---	YGSIYRRPQGLYISLK
1957.9189	1956.9116	1956.9104	0.0012	444 - 462	0	---	GTAVFASGSPFDPVEYEGK
1999.0988	1998.0915	1998.0898	0.0018	538 - 555	1	---	AYDLGLASRLPRPDDLVK
2191.1169	2190.1096	2190.1109	-0.0012	256 - 274	0	---	VLVQFEDFANHNAFDLLAK
2783.4475	2782.4402	2782.4441	-0.0039	463 - 489	0	---	TYVPGQSNNAYVFPGFGLGVVISGAIR

No match to: 713.4050, 734.4852, 750.5104, 768.5143, 782.4734, 848.5323, 864.5402, 987.5311, 1092.5695, 1133.7024, 1279.7578, 1334.8503, 1448.9131, 1541.8282, 1562.9395, 1602.9470, 1628.8531, 1743.0243, 1897.0270, 2008.0580, 2114.0659, 2157.1868, 2230.2156, 2239.1404, 2284.1824, 2342.3025, 2368.3386, 2564.1897, 2663.3896, 2825.3171, 2921.3569, 3332.5649, 3349.6184

2. gi|158701881 **Mass:** 63391 **Score:** 350 **Expect:** 6.1e-030 **Queries matched:** 30

NADP-dependent malic enzyme [Triticum aestivum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
758.3937	757.3864	757.3758	0.0106	129 - 134	0	---	YGSIYR
965.5033	964.4960	964.4977	-0.0017	538 - 546	0	---	AYDLGLASR
1052.6729	1051.6656	1051.6026	0.0631	547 - 555	0	---	LPRPDDLVK
1174.6976	1173.6903	1173.6869	0.0034	135 - 144	0	---	RPQGLYISLK
1274.7273	1273.7200	1273.7182	0.0018	514 - 524	0	---	GLIFPPFTNIR
1315.7260	1314.7187	1314.7143	0.0045	160 - 171	0	50	SIQVIVVTDGER
1315.7260	1314.7187	1314.7143	0.0045	160 - 171	0	---	SIQVIVVTDGER
1358.6957	1357.6884	1357.6738	0.0146	40 - 51	1	---	HNKGLAFSEAER
1382.7872	1381.7799	1381.7717	0.0082	149 - 159	1	---	VLEVLKNWPER
1382.7872	1381.7799	1381.7717	0.0082	149 - 159	1	48	VLEVLKNWPER
1402.8252	1401.8179	1401.8132	0.0047	514 - 525	1	---	GLIFPPFTNIRK
1417.8247	1416.8174	1416.8088	0.0086	135 - 146	1	---	RPQGLYISLKDK
1553.6864	1552.6791	1552.6690	0.0101	556 - 567	0	21	YAESCMYTPLYR
1553.6864	1552.6791	1552.6690	0.0101	556 - 567	0	---	YAESCMYTPLYR
1569.6699	1568.6626	1568.6639	-0.0013	556 - 567	0	---	YAESCMYTPLYR + Oxidation (M)
1614.9237	1613.9164	1613.9140	0.0024	348 - 361	1	---	IWLVDSKGLLVESR
1645.8865	1644.8792	1644.8835	-0.0042	58 - 72	0	---	GLLPPAIVSQEHQEK
1668.7946	1667.7873	1667.7759	0.0114	88 - 100	1	---	YIAMMDLQERNER
1684.7791	1683.7718	1683.7708	0.0010	88 - 100	1	---	YIAMMDLQERNER + Oxidation (M)
1700.7665	1699.7592	1699.7657	-0.0065	88 - 100	1	---	YIAMMDLQERNER + 2 Oxidation (M)

1734.8660	1733.8587	1733.8485	0.0103	43 - 57	1	---	GLAFSEAERDAHYLR
1734.8660	1733.8587	1733.8485	0.0103	43 - 57	1	14	GLAFSEAERDAHYLR
1773.9893	1772.9820	1772.9784	0.0036	58 - 73	1	---	GLLPPAIVSQEHQEKK
1784.9565	1783.9492	1783.9324	0.0169	172 - 189	0	---	ILGLGDLGCQGMGIPVGK
1914.0616	1913.0543	1913.0522	0.0021	129 - 144	1	---	YGSIYRRPQGLYISLK
1957.9189	1956.9116	1956.9104	0.0012	444 - 462	0	---	GTAVFASGSPFDPVEYEGK
1999.0988	1998.0915	1998.0898	0.0018	538 - 555	1	---	AYDLGLASRLPRPDDLVK
2191.1169	2190.1096	2190.1109	-0.0012	256 - 274	0	---	VLVQFEDFANHNAFDLLAK
2239.1404	2238.1331	2238.0925	0.0406	80 - 97	1	---	SYTVPLHRYIAMMDLQER + Oxidation (M)
2663.3896	2662.3823	2662.2068	0.1756	490 - 513	0	---	VHDDMLLAASEALAEEATQENFDK + Oxidation (M)

No match to: 713.4050, 734.4852, 750.5104, 768.5143, 782.4734, 848.5323, 864.5402, 987.5311, 1004.5487, 1004.5487, 1092.5695, 1133.7024, 1279.7578, 1334.8503, 1448.9131, 1541.8282, 1562.9395, 1602.9470, 1628.8531, 1743.0243, 1768.9609, 1897.0270, 2008.0580, 2114.0659, 2157.1868, 2230.2156, 2284.1824, 2342.3025, 2368.3386, 2564.1897, 2783.4475, 2825.3171, 2921.3569, 3332.5649, 3349.6184

3. gi|222630448 **Mass:** 59086 **Score:** 164 **Expect:** 2.4e-011 **Queries matched:** 18

hypothetical protein OsJ_17383 [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start End	Miss	Ions	Peptide
758.3937	757.3864	757.3758	0.0106	129 - 134	0	---	YGSIYR
1052.6729	1051.6656	1051.6026	0.0631	506 - 514	0	---	LPRPDDLVK
1174.6976	1173.6903	1173.6869	0.0034	135 - 144	0	---	RPQGLYISLK
1274.7273	1273.7200	1273.7182	0.0018	473 - 483	0	---	GLIFPPFTNIR
1315.7260	1314.7187	1314.7143	0.0045	160 - 171	0	50	SIQVIVVTDGER
1315.7260	1314.7187	1314.7143	0.0045	160 - 171	0	---	SIQVIVVTDGER
1358.6957	1357.6884	1357.6738	0.0146	40 - 51	1	---	HNKGLAFSEAER
1402.8252	1401.8179	1401.8132	0.0047	473 - 484	1	---	GLIFPPFTNIRK
1417.8247	1416.8174	1416.8088	0.0086	135 - 146	1	---	RPQGLYISLKDK
1628.8531	1627.8458	1627.9045	-0.0587	348 - 361	1	---	VWLVDSRGLIVESR
1668.7946	1667.7873	1667.7759	0.0114	88 - 100	1	---	YIAMMDLQERNER
1684.7791	1683.7718	1683.7708	0.0010	88 - 100	1	---	YIAMMDLQERNER + Oxidation (M)
1700.7665	1699.7592	1699.7657	-0.0065	88 - 100	1	---	YIAMMDLQERNER + 2 Oxidation (M)
1734.8660	1733.8587	1733.8485	0.0103	43 - 57	1	---	GLAFSEAERDAHYLR
1734.8660	1733.8587	1733.8485	0.0103	43 - 57	1	14	GLAFSEAERDAHYLR
1784.9565	1783.9492	1783.9324	0.0169	172 - 189	0	---	ILGLGDLGCQGMGIPVGK
1914.0616	1913.0543	1913.0522	0.0021	129 - 144	1	---	YGSIYRRPQGLYISLK
2191.1169	2190.1096	2190.1109	-0.0012	256 - 274	0	---	VLVQFEDFANHNAFDLLAK

No match to: 713.4050, 734.4852, 750.5104, 768.5143, 782.4734, 848.5323, 864.5402, 965.5033, 987.5311, 1004.5487, 1004.5487, 1092.5695, 1133.7024, 1279.7578, 1334.8503, 1382.7872, 1382.7872, 1448.9131, 1541.8282, 1553.6864, 1553.6864, 1562.9395, 1569.6699, 1602.9470, 1614.9237, 1645.8865, 1743.0243, 1768.9609, 1773.9893, 1897.0270, 1957.9189, 1999.0988, 2008.0580, 2114.0659, 2157.1868, 2230.2156, 2239.1404, 2284.1824, 2342.3025, 2368.3386, 2564.1897, 2663.3896, 2783.4475, 2825.3171, 2921.3569, 3332.5649, 3349.6184

4. gi|115462465 **Mass:** 63294 **Score:** 160 **Expect:** 6.1e-011 **Queries matched:** 18

Os05g0186300 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
758.3937	757.3864	757.3758	0.0106	129	134	0	---	YGSIYR
1052.6729	1051.6656	1051.6026	0.0631	547	555	0	---	LPRPDDLVK
1174.6976	1173.6903	1173.6869	0.0034	135	144	0	---	RPQGLYISLK
1274.7273	1273.7200	1273.7182	0.0018	514	524	0	---	GLIFPPFTNIR
1315.7260	1314.7187	1314.7143	0.0045	160	171	0	50	SIQVIVVTDGER
1315.7260	1314.7187	1314.7143	0.0045	160	171	0	---	SIQVIVVTDGER
1358.6957	1357.6884	1357.6738	0.0146	40	51	1	---	HNKGLAFSEAER
1402.8252	1401.8179	1401.8132	0.0047	514	525	1	---	GLIFPPFTNIRK
1417.8247	1416.8174	1416.8088	0.0086	135	146	1	---	RPQGLYISLKDK
1628.8531	1627.8458	1627.9045	-0.0587	348	361	1	---	VWLVDSRGLIVESR
1668.7946	1667.7873	1667.7759	0.0114	88	100	1	---	YIAMMDLQERNER
1684.7791	1683.7718	1683.7708	0.0010	88	100	1	---	YIAMMDLQERNER + Oxidation (M)
1700.7665	1699.7592	1699.7657	-0.0065	88	100	1	---	YIAMMDLQERNER + 2 Oxidation (M)
1734.8660	1733.8587	1733.8485	0.0103	43	57	1	---	GLAFSEAERDAHYLR
1734.8660	1733.8587	1733.8485	0.0103	43	57	1	14	GLAFSEAERDAHYLR
1784.9565	1783.9492	1783.9324	0.0169	172	189	0	---	ILGLGDLGCQGMGIPVGK
1914.0616	1913.0543	1913.0522	0.0021	129	144	1	---	YGSIYRRPQGLYISLK
2191.1169	2190.1096	2190.1109	-0.0012	256	274	0	---	VLVQFEDFANHNAFDLLAK

No match to: 713.4050, 734.4852, 750.5104, 768.5143, 782.4734, 848.5323, 864.5402, 965.5033, 987.5311, 1004.5487, 1004.5487, 1092.5695, 1133.7024, 1279.7578, 1334.8503, 1382.7872, 1382.7872, 1448.9131, 1541.8282, 1553.6864, 1553.6864, 1562.9395, 1569.6699, 1602.9470, 1614.9237, 1645.8865, 1743.0243, 1768.9609, 1773.9893, 1897.0270, 1957.9189, 1999.0988, 2008.0580, 2114.0659, 2157.1868, 2230.2156, 2239.1404, 2284.1824, 2342.3025, 2368.3386, 2564.1897, 2663.3896, 2783.4475, 2825.3171, 2921.3569, 3332.5649, 3349.6184

5. gi|226510109 **Mass:** 63197 **Score:** 142 **Expect:** 3.8e-009 **Queries matched:** 16

NADP-dependent malic enzyme [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
758.3937	757.3864	757.3758	0.0106	129	134	0	---	YGSIYR
1052.6729	1051.6656	1051.6026	0.0631	547	555	0	---	LPRPDDLVK
1274.7273	1273.7200	1273.7182	0.0018	514	524	0	---	GLIFPPFTNIR
1315.7260	1314.7187	1314.7143	0.0045	160	171	0	50	SIQVIVVTDGER
1315.7260	1314.7187	1314.7143	0.0045	160	171	0	---	SIQVIVVTDGER
1358.6957	1357.6884	1357.6738	0.0146	40	51	1	---	HNKGLAFSEAER
1553.6864	1552.6791	1552.6690	0.0101	556	567	0	21	YAESCMYTPIYR
1553.6864	1552.6791	1552.6690	0.0101	556	567	0	---	YAESCMYTPIYR
1569.6699	1568.6626	1568.6639	-0.0013	556	567	0	---	YAESCMYTPIYR + Oxidation (M)
1668.7946	1667.7873	1667.7759	0.0114	88	100	1	---	YIAMMDLQERNER

1684.7791	1683.7718	1683.7708	0.0010	88 - 100	1	---	YIAMMDLQERNER + Oxidation (M)
1700.7665	1699.7592	1699.7657	-0.0065	88 - 100	1	---	YIAMMDLQERNER + 2 Oxidation (M)
1734.8660	1733.8587	1733.8485	0.0103	43 - 57	1	---	GLAFSEAERDAHYLR
1734.8660	1733.8587	1733.8485	0.0103	43 - 57	1	14	GLAFSEAERDAHYLR
1784.9565	1783.9492	1783.9324	0.0169	172 - 189	0	---	ILGLGDLGCQGMGIPVGK
2284.1824	2283.1751	2283.1140	0.0612	336 - 354	1	---	HTGSPIEECRPKIWLMDSK

No match to: 713.4050, 734.4852, 750.5104, 768.5143, 782.4734, 848.5323, 864.5402, 965.5033, 987.5311, 1004.5487, 1004.5487, 1092.5695, 1133.7024, 1174.6976, 1279.7578, 1334.8503, 1382.7872, 1382.7872, 1402.8252, 1417.8247, 1448.9131, 1541.8282, 1562.9395, 1602.9470, 1614.9237, 1628.8531, 1645.8865, 1743.0243, 1768.9609, 1773.9893, 1897.0270, 1914.0616, 1957.9189, 1999.0988, 2008.0580, 2114.0659, 2157.1868, 2191.1169, 2230.2156, 2239.1404, 2342.3025, 2368.3386, 2564.1897, 2663.3896, 2783.4475, 2825.3171, 2921.3569, 3332.5649, 3349.6184

6. gi|255546341 **Mass:** 65487 **Score:** 107 **Expect:** 1.2e-005 **Queries matched:** 7

malic enzyme, putative [Ricinus communis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1174.6976	1173.6903	1173.6869	0.0034	156 - 165		0	---	RPQGLYISLK
1315.7260	1314.7187	1314.7143	0.0045	181 - 192		0	50	SIQVIVVTDGER
1315.7260	1314.7187	1314.7143	0.0045	181 - 192		0	---	SIQVIVVTDGER
1382.7872	1381.7799	1381.7717	0.0082	170 - 180		1	---	ILDVLKNWPER
1382.7872	1381.7799	1381.7717	0.0082	170 - 180		1	40	ILDVLKNWPER
1768.9609	1767.9536	1767.9818	-0.0281	95 - 108		1	---	LMHTIRQYQLPLQK
1784.9565	1783.9492	1783.9324	0.0169	193 - 210		0	---	ILGLGDLGCQGMGIPVGK

No match to: 713.4050, 734.4852, 750.5104, 758.3937, 768.5143, 782.4734, 848.5323, 864.5402, 965.5033, 987.5311, 1004.5487, 1004.5487, 1052.6729, 1092.5695, 1133.7024, 1274.7273, 1279.7578, 1334.8503, 1358.6957, 1402.8252, 1417.8247, 1448.9131, 1541.8282, 1553.6864, 1553.6864, 1562.9395, 1569.6699, 1602.9470, 1614.9237, 1628.8531, 1645.8865, 1668.7946, 1684.7791, 1700.7665, 1734.8660, 1734.8660, 1743.0243, 1773.9893, 1897.0270, 1914.0616, 1957.9189, 1999.0988, 2008.0580, 2114.0659, 2157.1868, 2191.1169, 2230.2156, 2239.1404, 2284.1824, 2342.3025, 2368.3386, 2564.1897, 2663.3896, 2783.4475, 2825.3171, 2921.3569, 3332.5649, 3349.6184

7. gi|510876 **Mass:** 65255 **Score:** 82 **Expect:** 0.0041 **Queries matched:** 9

NADP dependent malic enzyme [Phaseolus vulgaris]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1174.6976	1173.6903	1173.6869	0.0034	154 - 163		0	---	RPQGLYISLK
1315.7260	1314.7187	1314.7143	0.0045	179 - 190		0	50	SIQVIVVTDGER
1315.7260	1314.7187	1314.7143	0.0045	179 - 190		0	---	SIQVIVVTDGER
1668.7946	1667.7873	1667.7759	0.0114	107 - 119		1	---	YMALMDLQERNER
1684.7791	1683.7718	1683.7708	0.0010	107 - 119		1	---	YMALMDLQERNER + Oxidation (M)
1700.7665	1699.7592	1699.7657	-0.0065	107 - 119		1	---	YMALMDLQERNER + 2 Oxidation (M)
1734.8660	1733.8587	1733.8485	0.0103	62 - 76		1	---	GLAFTEGERDAHYLR
1734.8660	1733.8587	1733.8485	0.0103	62 - 76		1	13	GLAFTEGERDAHYLR
1784.9565	1783.9492	1783.9324	0.0169	191 - 208		0	---	ILGLGDLGCQGMGIPVGK

No match to: 713.4050, 734.4852, 750.5104, 758.3937, 768.5143, 782.4734, 848.5323, 864.5402, 965.5033, 987.5311,

1004.5487, 1004.5487, 1052.6729, 1092.5695, 1133.7024, 1274.7273, 1279.7578, 1334.8503, 1358.6957, 1382.7872, 1382.7872, 1402.8252, 1417.8247, 1448.9131, 1541.8282, 1553.6864, 1553.6864, 1562.9395, 1569.6699, 1602.9470, 1614.9237, 1628.8531, 1645.8865, 1743.0243, 1768.9609, 1773.9893, 1897.0270, 1914.0616, 1957.9189, 1999.0988, 2008.0580, 2114.0659, 2157.1868, 2191.1169, 2230.2156, 2239.1404, 2284.1824, 2342.3025, 2368.3386, 2564.1897, 2663.3896, 2783.4475, 2825.3171, 2921.3569, 3332.5649, 3349.6184

8. gi|115420 **Mass:** 65234 **Score:** 82 **Expect:** 0.0041 **Queries matched:** 9

RecName: Full=NADP-dependent malic enzyme; Short=NADP-ME

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1174.6976	1173.6903	1173.6869	0.0034	154	163	0	---	RPQGLYISLK
1315.7260	1314.7187	1314.7143	0.0045	179	190	0	50	SIQVIVVTDGER
1315.7260	1314.7187	1314.7143	0.0045	179	190	0	---	SIQVIVVTDGER
1668.7946	1667.7873	1667.7759	0.0114	107	119	1	---	YMALMDLQERNER
1684.7791	1683.7718	1683.7708	0.0010	107	119	1	---	YMALMDLQERNER + Oxidation (M)
1700.7665	1699.7592	1699.7657	-0.0065	107	119	1	---	YMALMDLQERNER + 2 Oxidation (M)
1734.8660	1733.8587	1733.8485	0.0103	62	76	1	---	GLAFTEGERDAHYLR
1734.8660	1733.8587	1733.8485	0.0103	62	76	1	13	GLAFTEGERDAHYLR
1784.9565	1783.9492	1783.9324	0.0169	191	208	0	---	ILGLGDLGCQGMGIPVGK

No match to: 713.4050, 734.4852, 750.5104, 758.3937, 768.5143, 782.4734, 848.5323, 864.5402, 965.5033, 987.5311, 1004.5487, 1004.5487, 1052.6729, 1092.5695, 1133.7024, 1274.7273, 1279.7578, 1334.8503, 1358.6957, 1382.7872, 1382.7872, 1402.8252, 1417.8247, 1448.9131, 1541.8282, 1553.6864, 1553.6864, 1562.9395, 1569.6699, 1602.9470, 1614.9237, 1628.8531, 1645.8865, 1743.0243, 1768.9609, 1773.9893, 1897.0270, 1914.0616, 1957.9189, 1999.0988, 2008.0580, 2114.0659, 2157.1868, 2191.1169, 2230.2156, 2239.1404, 2284.1824, 2342.3025, 2368.3386, 2564.1897, 2663.3896, 2783.4475, 2825.3171, 2921.3569, 3332.5649, 3349.6184

9. gi|1129068 **Mass:** 21699 **Score:** 79 **Expect:** 0.0082 **Queries matched:** 7

malate dehydrogenase [Lycopersicon esculentum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1315.7260	1314.7187	1314.7143	0.0045	168	179	0	50	SIQVIVVTDGER
1315.7260	1314.7187	1314.7143	0.0045	168	179	0	---	SIQVIVVTDGER
1417.8247	1416.8174	1416.7724	0.0450	143	154	0	---	RPQGLYISLNEK
1668.7946	1667.7873	1667.7759	0.0114	96	108	1	---	YVAMMELQERNER
1684.7791	1683.7718	1683.7708	0.0010	96	108	1	---	YVAMMELQERNER + Oxidation (M)
1700.7665	1699.7592	1699.7657	-0.0065	96	108	1	---	YVAMMELQERNER + 2 Oxidation (M)
2342.3025	2341.2952	2341.2310	0.0642	168	189	1	---	SIQVIVVTDGERILGLGDLGCQ

No match to: 713.4050, 734.4852, 750.5104, 758.3937, 768.5143, 782.4734, 848.5323, 864.5402, 965.5033, 987.5311, 1004.5487, 1004.5487, 1052.6729, 1092.5695, 1133.7024, 1174.6976, 1274.7273, 1279.7578, 1334.8503, 1358.6957, 1382.7872, 1382.7872, 1402.8252, 1448.9131, 1541.8282, 1553.6864, 1553.6864, 1562.9395, 1569.6699, 1602.9470, 1614.9237, 1628.8531, 1645.8865, 1734.8660, 1734.8660, 1743.0243, 1768.9609, 1773.9893, 1784.9565, 1897.0270, 1914.0616, 1957.9189, 1999.0988, 2008.0580, 2114.0659, 2157.1868, 2191.1169, 2230.2156, 2239.1404, 2284.1824, 2368.3386, 2564.1897, 2663.3896, 2783.4475, 2825.3171, 2921.3569, 3332.5649, 3349.6184

10. gi|118487388 **Mass:** 54899 **Score:** 65 **Expect:** 0.19 **Queries matched:** 5

unknown [Populus trichocarpa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1174.6976	1173.6903	1173.6869	0.0034	61 -	70	0	---	RPQGLYISLK
1315.7260	1314.7187	1314.7143	0.0045	86 -	97	0	50	SIQVIVVTDGER
1315.7260	1314.7187	1314.7143	0.0045	86 -	97	0	---	SIQVIVVTDGER
1784.9565	1783.9492	1783.9324	0.0169	98 -	115	0	---	ILGLGDLGCQGMGIPVGK
1999.0988	1998.0915	1997.9733	0.1182	370 -	388	1	---	GKAIFASGSPFDPVEYEGK

No match to: 713.4050, 734.4852, 750.5104, 758.3937, 768.5143, 782.4734, 848.5323, 864.5402, 965.5033, 987.5311, 1004.5487, 1004.5487, 1052.6729, 1092.5695, 1133.7024, 1274.7273, 1279.7578, 1334.8503, 1358.6957, 1382.7872, 1382.7872, 1402.8252, 1417.8247, 1448.9131, 1541.8282, 1553.6864, 1553.6864, 1562.9395, 1569.6699, 1602.9470, 1614.9237, 1628.8531, 1645.8865, 1668.7946, 1684.7791, 1700.7665, 1734.8660, 1734.8660, 1743.0243, 1768.9609, 1773.9893, 1897.0270, 1914.0616, 1957.9189, 2008.0580, 2114.0659, 2157.1868, 2191.1169, 2230.2156, 2239.1404, 2284.1824, 2342.3025, 2368.3386, 2564.1897, 2663.3896, 2783.4475, 2825.3171, 2921.3569, 3332.5649, 3349.6184

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 65

Protein View

Match to: **gi|209405432** Score: **372** Expect: **3.8e-032**
NADP-dependent malic enzyme [Hordeum vulgare]

Nominal mass (M_r): **63309**; Calculated pI value: **5.57**
NCBI BLAST search of gi|209405432 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Hordeum vulgare

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **39%**

Matched peptides shown in **Bold Red**

```
    1 MAGGGVEDAY GEDRATEEQL VTPWSFSVAS GHSLLRDPRH NKGLAFSEAE
   51 RDAHYLRGLL PPAIVSQEHQ EKKIMHNLRQ YTVPLQRYIA MMDLQERNER
  101 LFYKLLIDNV EELLPVVYTP VVGEACQKYG SIYRRPQGLY ISLKDKGKVL
  151 EVLKNWPERS IQVIVVTDGE RILGLGDLGC QGMGIPVGKL SLYTALGGVR
  201 PSACLPITID VGTNNETLLN DEYYIGLRQR RATGDEYHEL LQEFMTAVKQ
  251 NYGEKVLVQF EDFANHNAFD LLAKYSKSHL VFNDDIQGTA SVVLAGLLAA
  301 LKVIGGGLVD QTYLFLGAGE AGTGIAELIA LEMSKHTDLP VDDCRKKIWL
  351 VDSKGLLVES RKESLQHFKK PFAHEHEELK TLLEAVQSIK PTVLIGTSGV
  401 GKTFTQEVIE AMASFNEKPV IFSLSNPTSH SECTAEEAYT WSKGTAVFAS
  451 GSPFDPVEYE GKTYVPGQSN NAYVFPGFGL GVVISGAIRV HDDMLLAASE
  501 ALAEQVTQEN FDKGLIFPPF TNIRKISANI AAKVAAKAYD LGLASRLPRP
  551 DDLVKYAESC MYTPLYRSYR
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
40 - 51	1358.6957	1357.6884	1357.6738	0.0146	1	HNKGLAFSEAER (No match)
43 - 57	1734.8660	1733.8587	1733.8485	0.0103	1	GLAFSEAERDAHYLR (No match)
43 - 57	1734.8660	1733.8587	1733.8485	0.0103	1	GLAFSEAERDAHYLR (Ions score 14)
58 - 72	1645.8865	1644.8792	1644.8835	-0.0042	0	GLLPPAIVSQEHQEK (No match)
58 - 73	1773.9893	1772.9820	1772.9784	0.0036	1	GLLPPAIVSQEHQEKK (No match)
74 - 87	1768.9609	1767.9536	1767.9566	-0.0030	1	IMHNLRQYTVPLQR (No match)
74 - 87	1784.9565	1783.9492	1783.9515	-0.0023	1	IMHNLRQYTVPLQR Oxidation (M) (No match)
80 - 87	1004.5487	1003.5414	1003.5450	-0.0036	0	QYTVPLQR (Ions score 20)
80 - 87	1004.5487	1003.5414	1003.5450	-0.0036	0	QYTVPLQR (No match)
88 - 100	1668.7946	1667.7873	1667.7759	0.0114	1	YIAMMDLQERNER (No match)
88 - 100	1684.7791	1683.7718	1683.7708	0.0010	1	YIAMMDLQERNER Oxidation (M) (No match)
88 - 100	1700.7665	1699.7592	1699.7657	-0.0065	1	YIAMMDLQERNER 2 Oxidation (M) (No match)
129 - 134	758.3937	757.3864	757.3758	0.0106	0	YGSIYR (No match)
129 - 144	1914.0616	1913.0543	1913.0522	0.0021	1	YGSIYRRPQGLYISLK (No match)
135 - 144	1174.6976	1173.6903	1173.6869	0.0034	0	RPQGLYISLK (No match)
135 - 146	1417.8247	1416.8174	1416.8088	0.0086	1	RPQGLYISLKDK (No match)
149 - 159	1382.7872	1381.7799	1381.7717	0.0082	1	VLEVLKNWPER (No match)
149 - 159	1382.7872	1381.7799	1381.7717	0.0082	1	VLEVLKNWPER (Ions score 48)
160 - 171	1315.7260	1314.7187	1314.7143	0.0045	0	SIQVIVVTDGER (Ions score 50)
160 - 171	1315.7260	1314.7187	1314.7143	0.0045	0	SIQVIVVTDGER (No match)
256 - 274	2191.1169	2190.1096	2190.1109	-0.0012	0	VLVQFEDFANHNAFDLLAK (No match)
348 - 361	1614.9237	1613.9164	1613.9140	0.0024	1	IWLVDSKGLLVESR (No match)
444 - 462	1957.9189	1956.9116	1956.9104	0.0012	0	GTAVFASGSPFDPVEYEGK (No match)
463 - 489	2783.4475	2782.4402	2782.4441	-0.0039	0	TYVPGQSNNAYVFPGFGLGVVISGAIR (No match)
514 - 524	1274.7273	1273.7200	1273.7182	0.0018	0	GLIFPPFTNIR (No match)
514 - 525	1402.8252	1401.8179	1401.8132	0.0047	1	GLIFPPFTNIRK (No match)
538 - 546	965.5033	964.4960	964.4977	-0.0017	0	AYDLGLASR (No match)
538 - 555	1999.0988	1998.0915	1998.0898	0.0018	1	AYDLGLASRLPRPDDLVK (No match)
547 - 555	1052.6729	1051.6656	1051.6026	0.0631	0	LPRPDDLVK (No match)
556 - 567	1553.6864	1552.6791	1552.6690	0.0101	0	YAESCMYTPLYR (Ions score 21)
556 - 567	1553.6864	1552.6791	1552.6690	0.0101	0	YAESCMYTPLYR (No match)
556 - 567	1569.6699	1568.6626	1568.6639	-0.0013	0	YAESCMYTPLYR Oxidation (M) (No match)

Spot 16

Index

	Accession	Mass	Score	Description
1.	gi|209405432	63309	245	NADP-dependent malic enzyme [Hordeum vulgare]
2.	gi|158701881	63391	220	NADP-dependent malic enzyme [Triticum aestivum]
3.	gi|222630448	59086	101	hypothetical protein OsJ_17383 [Oryza sativa Japonica Group]
4.	gi|115462465	63294	98	Os05g0186300 [Oryza sativa (japonica cultivar-group)]
5.	gi|226510109	63197	72	NADP-dependent malic enzyme [Zea mays]
6.	gi|115482368	13628	64	Os10g0462100 [Oryza sativa (japonica cultivar-group)]
7.	gi|1129068	21699	61	malate dehydrogenase [Lycopersicon esculentum]
8.	gi|255546341	65487	60	malic enzyme, putative [Ricinus communis]
9.	gi|226509306	34099	49	LOC100284730 [Zea mays]
10.	gi|115420	65234	49	RecName: Full=NADP-dependent malic enzyme; Short=NADP-ME

Results List

1. gi|209405432 **Mass:** 63309 **Score:** 245 **Expect:** 1.9e-019 **Queries matched:** 27

NADP-dependent malic enzyme [Hordeum vulgare]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
758.3827	757.3754	757.3758	-0.0004	129	134	0	---	YGSIYR
965.5171	964.5098	964.4977	0.0121	538	546	0	---	AYDLGLASR
1004.5593	1003.5520	1003.5450	0.0070	80	87	0	---	QYTVPLQR
1004.5593	1003.5520	1003.5450	0.0070	80	87	0	12	QYTVPLQR
1174.7028	1173.6955	1173.6869	0.0086	135	144	0	---	RPQGLYISLK
1274.7397	1273.7324	1273.7182	0.0142	514	524	0	---	GLIFPPFTNIR
1315.7297	1314.7224	1314.7143	0.0082	160	171	0	22	SIQVIVVTDGER
1315.7297	1314.7224	1314.7143	0.0082	160	171	0	---	SIQVIVVTDGER
1382.7910	1381.7837	1381.7717	0.0120	149	159	1	28	VLEVLKNWPER
1382.7910	1381.7837	1381.7717	0.0120	149	159	1	---	VLEVLKNWPER
1402.8331	1401.8258	1401.8132	0.0126	514	525	1	---	GLIFPPFTNIRK
1417.8306	1416.8233	1416.8088	0.0145	135	146	1	---	RPQGLYISLKDK
1553.6877	1552.6804	1552.6690	0.0114	556	567	0	---	YAESCMYTPLYR
1569.6729	1568.6656	1568.6639	0.0017	556	567	0	---	YAESCMYTPLYR + Oxidation (M)
1614.9288	1613.9215	1613.9140	0.0075	348	361	1	---	IWLVDSKGLLVESR
1645.8942	1644.8869	1644.8835	0.0035	58	72	0	---	GLLPPAIVSQEHQEK
1668.7953	1667.7880	1667.7759	0.0121	88	100	1	---	YIAMMDLQERNER
1684.7865	1683.7792	1683.7708	0.0084	88	100	1	---	YIAMMDLQERNER + Oxidation (M)
1700.7762	1699.7689	1699.7657	0.0032	88	100	1	---	YIAMMDLQERNER + 2 Oxidation (M)
1734.8629	1733.8556	1733.8485	0.0072	43	57	1	---	GLAFSEAERDAHYLR

1734.8629	1733.8556	1733.8485	0.0072	43 - 57	1	9	GLAFSEAERDAHYLR
1768.9689	1767.9616	1767.9566	0.0050	74 - 87	1	---	IMHNLRQYTVPLQR
1773.9861	1772.9788	1772.9784	0.0004	58 - 73	1	---	GLLPPAIVSQEHQEKK
1784.9476	1783.9403	1783.9324	0.0080	172 - 189	0	---	ILGLGDLGCQGMGIPVGK
1914.0668	1913.0595	1913.0522	0.0073	129 - 144	1	---	YGSIYRRPQGLYISLK
1957.9235	1956.9162	1956.9104	0.0058	444 - 462	0	---	GTAVFASGSPFDPVEYEGK
1999.1053	1998.0980	1998.0898	0.0083	538 - 555	1	---	AYDLGLASRLPRPDDLVK

No match to: 713.4003, 724.4890, 734.4842, 750.5093, 768.5125, 782.4767, 838.5190, 848.5302, 864.5245, 987.5303, 1088.5781, 1279.7574, 1334.8467, 1394.7542, 1448.9104, 1493.7441, 1602.9456, 1628.8588, 1628.8588, 1744.0348, 1878.0297, 2008.0549, 2114.0627, 2143.0491, 2158.1882, 2230.2224, 2239.1411, 2284.1982, 2342.3049, 2402.2727, 2564.1948, 2784.4617, 2825.3184, 2908.4287, 2921.3589, 3333.5569, 3349.5981

2. gi|158701881 **Mass:** 63391 **Score:** 220 **Expect:** 6.1e-017 **Queries matched:** 25

NADP-dependent malic enzyme [Triticum aestivum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
758.3827	757.3754	757.3758	-0.0004	129 - 134		0	---	YGSIYR
965.5171	964.5098	964.4977	0.0121	538 - 546		0	---	AYDLGLASR
1174.7028	1173.6955	1173.6869	0.0086	135 - 144		0	---	RPQGLYISLK
1274.7397	1273.7324	1273.7182	0.0142	514 - 524		0	---	GLIFPPFTNIR
1315.7297	1314.7224	1314.7143	0.0082	160 - 171		0	22	SIQVIVVTDGER
1315.7297	1314.7224	1314.7143	0.0082	160 - 171		0	---	SIQVIVVTDGER
1382.7910	1381.7837	1381.7717	0.0120	149 - 159		1	28	VLEVLKNWPER
1382.7910	1381.7837	1381.7717	0.0120	149 - 159		1	---	VLEVLKNWPER
1402.8331	1401.8258	1401.8132	0.0126	514 - 525		1	---	GLIFPPFTNIRK
1417.8306	1416.8233	1416.8088	0.0145	135 - 146		1	---	RPQGLYISLKDK
1553.6877	1552.6804	1552.6690	0.0114	556 - 567		0	---	YAESCMYTPLYR
1569.6729	1568.6656	1568.6639	0.0017	556 - 567		0	---	YAESCMYTPLYR + Oxidation (M)
1614.9288	1613.9215	1613.9140	0.0075	348 - 361		1	---	IWLVDSKGLLVESR
1645.8942	1644.8869	1644.8835	0.0035	58 - 72		0	---	GLLPPAIVSQEHQEK
1668.7953	1667.7880	1667.7759	0.0121	88 - 100		1	---	YIAMMDLQERNER
1684.7865	1683.7792	1683.7708	0.0084	88 - 100		1	---	YIAMMDLQERNER + Oxidation (M)
1700.7762	1699.7689	1699.7657	0.0032	88 - 100		1	---	YIAMMDLQERNER + 2 Oxidation (M)
1734.8629	1733.8556	1733.8485	0.0072	43 - 57		1	---	GLAFSEAERDAHYLR
1734.8629	1733.8556	1733.8485	0.0072	43 - 57		1	9	GLAFSEAERDAHYLR
1773.9861	1772.9788	1772.9784	0.0004	58 - 73		1	---	GLLPPAIVSQEHQEKK
1784.9476	1783.9403	1783.9324	0.0080	172 - 189		0	---	ILGLGDLGCQGMGIPVGK
1914.0668	1913.0595	1913.0522	0.0073	129 - 144		1	---	YGSIYRRPQGLYISLK
1957.9235	1956.9162	1956.9104	0.0058	444 - 462		0	---	GTAVFASGSPFDPVEYEGK
1999.1053	1998.0980	1998.0898	0.0083	538 - 555		1	---	AYDLGLASRLPRPDDLVK
2239.1411	2238.1338	2238.0925	0.0413	80 - 97		1	---	SYTVPLHRYIAMMDLQER + Oxidation (M)

No match to: 713.4003, 724.4890, 734.4842, 750.5093, 768.5125, 782.4767, 838.5190, 848.5302, 864.5245, 987.5303, 1004.5593, 1004.5593, 1088.5781, 1279.7574, 1334.8467, 1394.7542, 1448.9104, 1493.7441, 1602.9456, 1628.8588, 1628.8588, 1744.0348, 1768.9689, 1878.0297, 2008.0549, 2114.0627, 2143.0491, 2158.1882, 2230.2224, 2284.1982, 2342.3049, 2402.2727, 2564.1948, 2784.4617, 2825.3184, 2908.4287, 2921.3589, 3333.5569, 3349.5981

3. gi|222630448 **Mass:** 59086 **Score:** 101 **Expect:** 4.8e-005 **Queries matched:** 16

hypothetical protein OsJ_17383 [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
758.3827	757.3754	757.3758	-0.0004	129	134	0	---	YGSIYR
1174.7028	1173.6955	1173.6869	0.0086	135	144	0	---	RPQGLYISLK
1274.7397	1273.7324	1273.7182	0.0142	473	483	0	---	GLIFPPFTNIR
1315.7297	1314.7224	1314.7143	0.0082	160	171	0	22	SIQVIVVTDGER
1315.7297	1314.7224	1314.7143	0.0082	160	171	0	---	SIQVIVVTDGER
1402.8331	1401.8258	1401.8132	0.0126	473	484	1	---	GLIFPPFTNIRK
1417.8306	1416.8233	1416.8088	0.0145	135	146	1	---	RPQGLYISLKDK
1628.8588	1627.8515	1627.9045	-0.0530	348	361	1	---	VWLVDSRGLIVESR
1628.8588	1627.8515	1627.9045	-0.0530	348	361	1	---	VWLVDSRGLIVESR
1668.7953	1667.7880	1667.7759	0.0121	88	100	1	---	YIAMMDLQERNER
1684.7865	1683.7792	1683.7708	0.0084	88	100	1	---	YIAMMDLQERNER + Oxidation (M)
1700.7762	1699.7689	1699.7657	0.0032	88	100	1	---	YIAMMDLQERNER + 2 Oxidation (M)
1734.8629	1733.8556	1733.8485	0.0072	43	57	1	---	GLAFSEAERDAHYLR
1734.8629	1733.8556	1733.8485	0.0072	43	57	1	9	GLAFSEAERDAHYLR
1784.9476	1783.9403	1783.9324	0.0080	172	189	0	---	ILGLGDLGCQGMGIPVGK
1914.0668	1913.0595	1913.0522	0.0073	129	144	1	---	YGSIYRRPQGLYISLK

No match to: 713.4003, 724.4890, 734.4842, 750.5093, 768.5125, 782.4767, 838.5190, 848.5302, 864.5245, 965.5171, 987.5303, 1004.5593, 1004.5593, 1088.5781, 1279.7574, 1334.8467, 1382.7910, 1382.7910, 1394.7542, 1448.9104, 1493.7441, 1553.6877, 1569.6729, 1602.9456, 1614.9288, 1645.8942, 1744.0348, 1768.9689, 1773.9861, 1878.0297, 1957.9235, 1999.1053, 2008.0549, 2114.0627, 2143.0491, 2158.1882, 2230.2224, 2239.1411, 2284.1982, 2342.3049, 2402.2727, 2564.1948, 2784.4617, 2825.3184, 2908.4287, 2921.3589, 3333.5569, 3349.5981

4. gi|115462465 **Mass:** 63294 **Score:** 98 **Expect:** 0.0001 **Queries matched:** 16

Os05g0186300 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
758.3827	757.3754	757.3758	-0.0004	129	134	0	---	YGSIYR
1174.7028	1173.6955	1173.6869	0.0086	135	144	0	---	RPQGLYISLK
1274.7397	1273.7324	1273.7182	0.0142	514	524	0	---	GLIFPPFTNIR
1315.7297	1314.7224	1314.7143	0.0082	160	171	0	22	SIQVIVVTDGER
1315.7297	1314.7224	1314.7143	0.0082	160	171	0	---	SIQVIVVTDGER
1402.8331	1401.8258	1401.8132	0.0126	514	525	1	---	GLIFPPFTNIRK
1417.8306	1416.8233	1416.8088	0.0145	135	146	1	---	RPQGLYISLKDK
1628.8588	1627.8515	1627.9045	-0.0530	348	361	1	---	VWLVDSRGLIVESR

1628.8588	1627.8515	1627.9045	-0.0530	348 - 361	1	---	VWLVDSRGLIVESR
1668.7953	1667.7880	1667.7759	0.0121	88 - 100	1	---	YIAMMDLQERNER
1684.7865	1683.7792	1683.7708	0.0084	88 - 100	1	---	YIAMMDLQERNER + Oxidation (M)
1700.7762	1699.7689	1699.7657	0.0032	88 - 100	1	---	YIAMMDLQERNER + 2 Oxidation (M)
1734.8629	1733.8556	1733.8485	0.0072	43 - 57	1	---	GLAFSEAERDAHYLR
1734.8629	1733.8556	1733.8485	0.0072	43 - 57	1	9	GLAFSEAERDAHYLR
1784.9476	1783.9403	1783.9324	0.0080	172 - 189	0	---	ILGLGDLGCQGMGIPVGK
1914.0668	1913.0595	1913.0522	0.0073	129 - 144	1	---	YGSIYRRPQGLYISLK

No match to: 713.4003, 724.4890, 734.4842, 750.5093, 768.5125, 782.4767, 838.5190, 848.5302, 864.5245, 965.5171, 987.5303, 1004.5593, 1004.5593, 1088.5781, 1279.7574, 1334.8467, 1382.7910, 1382.7910, 1394.7542, 1448.9104, 1493.7441, 1553.6877, 1569.6729, 1602.9456, 1614.9288, 1645.8942, 1744.0348, 1768.9689, 1773.9861, 1878.0297, 1957.9235, 1999.1053, 2008.0549, 2114.0627, 2143.0491, 2158.1882, 2230.2224, 2239.1411, 2284.1982, 2342.3049, 2402.2727, 2564.1948, 2784.4617, 2825.3184, 2908.4287, 2921.3589, 3333.5569, 3349.5981

5. gi|226510109 **Mass:** 63197 **Score:** 72 **Expect:** 0.037 **Queries matched:** 13

NADP-dependent malic enzyme [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
758.3827	757.3754	757.3758	-0.0004	129 - 134	0	---	YGSIYR
1274.7397	1273.7324	1273.7182	0.0142	514 - 524	0	---	GLIFPPFTNIR
1315.7297	1314.7224	1314.7143	0.0082	160 - 171	0	22	SIQVIVVTDGER
1315.7297	1314.7224	1314.7143	0.0082	160 - 171	0	---	SIQVIVVTDGER
1553.6877	1552.6804	1552.6690	0.0114	556 - 567	0	---	YAESCMYTPIYR
1569.6729	1568.6656	1568.6639	0.0017	556 - 567	0	---	YAESCMYTPIYR + Oxidation (M)
1668.7953	1667.7880	1667.7759	0.0121	88 - 100	1	---	YIAMMDLQERNER
1684.7865	1683.7792	1683.7708	0.0084	88 - 100	1	---	YIAMMDLQERNER + Oxidation (M)
1700.7762	1699.7689	1699.7657	0.0032	88 - 100	1	---	YIAMMDLQERNER + 2 Oxidation (M)
1734.8629	1733.8556	1733.8485	0.0072	43 - 57	1	---	GLAFSEAERDAHYLR
1734.8629	1733.8556	1733.8485	0.0072	43 - 57	1	9	GLAFSEAERDAHYLR
1784.9476	1783.9403	1783.9324	0.0080	172 - 189	0	---	ILGLGDLGCQGMGIPVGK
2284.1982	2283.1909	2283.1140	0.0770	336 - 354	1	---	HTGSPIEECRPKIWLMDSK

No match to: 713.4003, 724.4890, 734.4842, 750.5093, 768.5125, 782.4767, 838.5190, 848.5302, 864.5245, 965.5171, 987.5303, 1004.5593, 1004.5593, 1088.5781, 1174.7028, 1279.7574, 1334.8467, 1382.7910, 1382.7910, 1394.7542, 1402.8331, 1417.8306, 1448.9104, 1493.7441, 1602.9456, 1614.9288, 1628.8588, 1628.8588, 1645.8942, 1744.0348, 1768.9689, 1773.9861, 1878.0297, 1914.0668, 1957.9235, 1999.1053, 2008.0549, 2114.0627, 2143.0491, 2158.1882, 2230.2224, 2239.1411, 2342.3049, 2402.2727, 2564.1948, 2784.4617, 2825.3184, 2908.4287, 2921.3589, 3333.5569, 3349.5981

6. gi|115482368 **Mass:** 13628 **Score:** 64 **Expect:** 0.27 **Queries matched:** 6

Os10g0462100 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
987.5303	986.5230	986.4893	0.0338	9 - 18	1	---	AAEEGAARGR
1700.7762	1699.7689	1699.7801	-0.0112	68 - 84	0	---	LASGFSSAAASSSWDTR

1878.0297	1877.0224	1876.9981	0.0243	96 - 112	0	---	MVLAEAALRPWPAAEPR
1999.1053	1998.0980	1998.0395	0.0586	34 - 53	1	---	SGAQVPHALRSASPPPPSSR
2230.2224	2229.2151	2229.1501	0.0650	44 - 67	1	---	SASPPPPSSRALGGVGDVAGTPPR
2784.4617	2783.4544	2783.4904	-0.0360	87 - 112	1	---	STSPLAPPRMVLAEAALRPWPAAEPR

No match to: 713.4003, 724.4890, 734.4842, 750.5093, 758.3827, 768.5125, 782.4767, 838.5190, 848.5302, 864.5245, 965.5171, 1004.5593, 1004.5593, 1088.5781, 1174.7028, 1274.7397, 1279.7574, 1315.7297, 1315.7297, 1334.8467, 1382.7910, 1382.7910, 1394.7542, 1402.8331, 1417.8306, 1448.9104, 1493.7441, 1553.6877, 1569.6729, 1602.9456, 1614.9288, 1628.8588, 1628.8588, 1645.8942, 1668.7953, 1684.7865, 1734.8629, 1734.8629, 1744.0348, 1768.9689, 1773.9861, 1784.9476, 1914.0668, 1957.9235, 2008.0549, 2114.0627, 2143.0491, 2158.1882, 2239.1411, 2284.1982, 2342.3049, 2402.2727, 2564.1948, 2825.3184, 2908.4287, 2921.3589, 3333.5569, 3349.5981

7. gi|1129068 **Mass:** 21699 **Score:** 61 **Expect:** 0.48 **Queries matched:** 8

malate dehydrogenase [Lycopersicon esculentum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1315.7297	1314.7224	1314.7143	0.0082	168 - 179	0	22	SIQVIVVTDGER
1315.7297	1314.7224	1314.7143	0.0082	168 - 179	0	---	SIQVIVVTDGER
1417.8306	1416.8233	1416.7724	0.0509	143 - 154	0	---	RPQGLYISLNEK
1668.7953	1667.7880	1667.7759	0.0121	96 - 108	1	---	YVAMMELQERNER
1684.7865	1683.7792	1683.7708	0.0084	96 - 108	1	---	YVAMMELQERNER + Oxidation (M)
1700.7762	1699.7689	1699.7657	0.0032	96 - 108	1	---	YVAMMELQERNER + 2 Oxidation (M)
1744.0348	1743.0275	1742.9137	0.1138	82 - 95	1	---	LMQSIRQYDVPLHK + Oxidation (M)
2342.3049	2341.2976	2341.2310	0.0666	168 - 189	1	---	SIQVIVVTDGERILGLGDLGCQ

No match to: 713.4003, 724.4890, 734.4842, 750.5093, 758.3827, 768.5125, 782.4767, 838.5190, 848.5302, 864.5245, 965.5171, 987.5303, 1004.5593, 1004.5593, 1088.5781, 1174.7028, 1274.7397, 1279.7574, 1334.8467, 1382.7910, 1382.7910, 1394.7542, 1402.8331, 1448.9104, 1493.7441, 1553.6877, 1569.6729, 1602.9456, 1614.9288, 1628.8588, 1628.8588, 1645.8942, 1734.8629, 1734.8629, 1768.9689, 1773.9861, 1784.9476, 1878.0297, 1914.0668, 1957.9235, 1999.1053, 2008.0549, 2114.0627, 2143.0491, 2158.1882, 2230.2224, 2239.1411, 2284.1982, 2402.2727, 2564.1948, 2784.4617, 2825.3184, 2908.4287, 2921.3589, 3333.5569, 3349.5981

8. gi|255546341 **Mass:** 65487 **Score:** 60 **Expect:** 0.57 **Queries matched:** 7

malic enzyme, putative [Ricinus communis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1174.7028	1173.6955	1173.6869	0.0086	156 - 165	0	---	RPQGLYISLK
1315.7297	1314.7224	1314.7143	0.0082	181 - 192	0	22	SIQVIVVTDGER
1315.7297	1314.7224	1314.7143	0.0082	181 - 192	0	---	SIQVIVVTDGER
1382.7910	1381.7837	1381.7717	0.0120	170 - 180	1	21	ILDVLKNWPER
1382.7910	1381.7837	1381.7717	0.0120	170 - 180	1	---	ILDVLKNWPER
1768.9689	1767.9616	1767.9818	-0.0201	95 - 108	1	---	LMHTIRQYQLPLQK
1784.9476	1783.9403	1783.9324	0.0080	193 - 210	0	---	ILGLGDLGCQGMGIPVGK

No match to: 713.4003, 724.4890, 734.4842, 750.5093, 758.3827, 768.5125, 782.4767, 838.5190, 848.5302, 864.5245, 965.5171, 987.5303, 1004.5593, 1004.5593, 1088.5781, 1274.7397, 1279.7574, 1334.8467, 1394.7542, 1402.8331, 1417.8306, 1448.9104, 1493.7441, 1553.6877, 1569.6729, 1602.9456, 1614.9288, 1628.8588, 1628.8588, 1645.8942,

1668.7953, 1684.7865, 1700.7762, 1734.8629, 1734.8629, 1744.0348, 1773.9861, 1878.0297, 1914.0668, 1957.9235, 1999.1053, 2008.0549, 2114.0627, 2143.0491, 2158.1882, 2230.2224, 2239.1411, 2284.1982, 2342.3049, 2402.2727, 2564.1948, 2784.4617, 2825.3184, 2908.4287, 2921.3589, 3333.5569, 3349.5981

9. gi|226509306 **Mass:** 34099 **Score:** 49 **Expect:** 7.1 **Queries matched:** 7

LOC100284730 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1088.5781	1087.5708	1087.6237	-0.0528	25	34	1	---	ATNETIALKK
1402.8331	1401.8258	1401.7728	0.0531	139	151	1	---	NNALKLADFGLAR
1553.6877	1552.6804	1552.7732	-0.0928	37	50	0	---	LEQEDEGVPPTAIR
1602.9456	1601.9383	1601.9041	0.0342	144	158	1	---	LADFGLARAFGIPVR
1768.9689	1767.9616	1767.9301	0.0316	51	65	1	---	EISLLKEMNHGNIVR + Oxidation (M)
2114.0627	2113.0554	2113.0486	0.0068	57	74	1	---	EMNHGNIVRLHDVVHSEK
2908.4287	2907.4214	2907.5527	-0.1313	244	269	1	---	WQAQDLATIVPNLEPAGLDLLSKMLR + Oxidation (M)

No match to: 713.4003, 724.4890, 734.4842, 750.5093, 758.3827, 768.5125, 782.4767, 838.5190, 848.5302, 864.5245, 965.5171, 987.5303, 1004.5593, 1004.5593, 1174.7028, 1274.7397, 1279.7574, 1315.7297, 1315.7297, 1334.8467, 1382.7910, 1382.7910, 1394.7542, 1417.8306, 1448.9104, 1493.7441, 1569.6729, 1614.9288, 1628.8588, 1628.8588, 1645.8942, 1668.7953, 1684.7865, 1700.7762, 1734.8629, 1734.8629, 1744.0348, 1773.9861, 1784.9476, 1878.0297, 1914.0668, 1957.9235, 1999.1053, 2008.0549, 2143.0491, 2158.1882, 2230.2224, 2239.1411, 2284.1982, 2342.3049, 2402.2727, 2564.1948, 2784.4617, 2825.3184, 2921.3589, 3333.5569, 3349.5981

10. gi|115420 **Mass:** 65234 **Score:** 49 **Expect:** 7.6 **Queries matched:** 9

RecName: Full=NADP-dependent malic enzyme; Short=NADP-ME

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1174.7028	1173.6955	1173.6869	0.0086	154	163	0	---	RPQGLYISLK
1315.7297	1314.7224	1314.7143	0.0082	179	190	0	22	SIQVIVVTDGER
1315.7297	1314.7224	1314.7143	0.0082	179	190	0	---	SIQVIVVTDGER
1668.7953	1667.7880	1667.7759	0.0121	107	119	1	---	YMALMDLQERNER
1684.7865	1683.7792	1683.7708	0.0084	107	119	1	---	YMALMDLQERNER + Oxidation (M)
1700.7762	1699.7689	1699.7657	0.0032	107	119	1	---	YMALMDLQERNER + 2 Oxidation (M)
1734.8629	1733.8556	1733.8485	0.0072	62	76	1	---	GLAFTEGERDAHYLR
1734.8629	1733.8556	1733.8485	0.0072	62	76	1	8	GLAFTEGERDAHYLR
1784.9476	1783.9403	1783.9324	0.0080	191	208	0	---	ILGLGDLGCQGMGIPVGK

No match to: 713.4003, 724.4890, 734.4842, 750.5093, 758.3827, 768.5125, 782.4767, 838.5190, 848.5302, 864.5245, 965.5171, 987.5303, 1004.5593, 1004.5593, 1088.5781, 1274.7397, 1279.7574, 1334.8467, 1382.7910, 1382.7910, 1394.7542, 1402.8331, 1417.8306, 1448.9104, 1493.7441, 1553.6877, 1569.6729, 1602.9456, 1614.9288, 1628.8588, 1628.8588, 1645.8942, 1744.0348, 1768.9689, 1773.9861, 1878.0297, 1914.0668, 1957.9235, 1999.1053, 2008.0549, 2114.0627, 2143.0491, 2158.1882, 2230.2224, 2239.1411, 2284.1982, 2342.3049, 2402.2727, 2564.1948, 2784.4617, 2825.3184, 2908.4287, 2921.3589, 3333.5569, 3349.5981

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 64

Protein View

Match to: **gi|209405432** Score: **245** Expect: **1.9e-019**
NADP-dependent malic enzyme [Hordeum vulgare]

Nominal mass (M_r): **63309**; Calculated pI value: **5.57**
NCBI BLAST search of gi|209405432 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Hordeum vulgare

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **33%**

Matched peptides shown in **Bold Red**

```
     1 MAGGGVEDAY GEDRATEEQL VTPWSFSVAS GHSLLRDPRH NKGLAFSEAE
    51 RDAHYLRGLL PPAIVSQEHQ EKKIMHNLRQ YTVPLQRYIA MMDLQERNER
   101 LFYKLLIDNV EELLPVVYTP VVGEACQKYG SIYRRPQGLY ISLKDKGKVL
   151 EVLKNWPERS IQVIVVTDGE RILGLGDLGC QGMGIPVGKL SLYTALGGVR
   201 PSACLPITID VGTNNETLLN DEYYIGLRQR RATGDEYHEL LQEFMTAVKQ
   251 NYGEKVLVQF EDFANHNAFD LLAKYSKSHL VFNDDIQGTA SVVLAGLLAA
   301 LKVIGGGLVD QTYLFLGAGE AGTGIAELIA LEMSKHTDLP VDDCRKKIWL
   351 VDSKGLLVES RKESLQHFKK PFAHEHEELK TLLEAVQSIK PTVLIGTSGV
   401 GKTFTQEVIE AMASFNEKPV IFSLSNPTSH SECTAEEAYT WSKGTAVFAS
   451 GSPFDPVEYE GKTYVPGQSN NAYVFPGFGL GVVISGAIRV HDDMLLAASE
   501 ALAEQVTQEN FDKGLIFPPF TNIRKISANI AAKVAAKAYD LGLASRLPRP
   551 DDLVKYAESC MYTPLYRSYR
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
43 - 57	1734.8629	1733.8556	1733.8485	0.0072	1	GLAFSEAERDAHYLR (No match)
43 - 57	1734.8629	1733.8556	1733.8485	0.0072	1	GLAFSEAERDAHYLR (Ions score 9)
58 - 72	1645.8942	1644.8869	1644.8835	0.0035	0	GLLPPAIVSQEHQEK (No match)
58 - 73	1773.9861	1772.9788	1772.9784	0.0004	1	GLLPPAIVSQEHQEKK (No match)
74 - 87	1768.9689	1767.9616	1767.9566	0.0050	1	IMHNLRQYTVPLQR (No match)
80 - 87	1004.5593	1003.5520	1003.5450	0.0070	0	QYTVPLQR (No match)
80 - 87	1004.5593	1003.5520	1003.5450	0.0070	0	QYTVPLQR (Ions score 12)
88 - 100	1668.7953	1667.7880	1667.7759	0.0121	1	YIAMMDLQERNER (No match)
88 - 100	1684.7865	1683.7792	1683.7708	0.0084	1	YIAMMDLQERNER Oxidation (M) (No match)
88 - 100	1700.7762	1699.7689	1699.7657	0.0032	1	YIAMMDLQERNER 2 Oxidation (M) (No match)
129 - 134	758.3827	757.3754	757.3758	-0.0004	0	YGSIYR (No match)
129 - 144	1914.0668	1913.0595	1913.0522	0.0073	1	YGSIYRRPQGLYISLK (No match)
135 - 144	1174.7028	1173.6955	1173.6869	0.0086	0	RPQGLYISLK (No match)
135 - 146	1417.8306	1416.8233	1416.8088	0.0145	1	RPQGLYISLKDK (No match)
149 - 159	1382.7910	1381.7837	1381.7717	0.0120	1	VLEVLKNWPER (Ions score 28)
149 - 159	1382.7910	1381.7837	1381.7717	0.0120	1	VLEVLKNWPER (No match)
160 - 171	1315.7297	1314.7224	1314.7143	0.0082	0	SIQVIVVTDGER (Ions score 22)
160 - 171	1315.7297	1314.7224	1314.7143	0.0082	0	SIQVIVVTDGER (No match)
172 - 189	1784.9476	1783.9403	1783.9324	0.0080	0	ILGLGDLGCQGMGIPVGK (No match)
348 - 361	1614.9288	1613.9215	1613.9140	0.0075	1	IWLVDSKGLLVESR (No match)
444 - 462	1957.9235	1956.9162	1956.9104	0.0058	0	GTAVFASGSPFDPVEYEGK (No match)
514 - 524	1274.7397	1273.7324	1273.7182	0.0142	0	GLIFPPFTNIR (No match)
514 - 525	1402.8331	1401.8258	1401.8132	0.0126	1	GLIFPPFTNIRK (No match)
538 - 546	965.5171	964.5098	964.4977	0.0121	0	AYDLGLASR (No match)
538 - 555	1999.1053	1998.0980	1998.0898	0.0083	1	AYDLGLASRLPRPDDLVK (No match)
556 - 567	1553.6877	1552.6804	1552.6690	0.0114	0	YAESCMYTPLYR (No match)
556 - 567	1569.6729	1568.6656	1568.6639	0.0017	0	YAESCMYTPLYR Oxidation (M) (No match)

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	Accession	Mass	Score	Description
1.	gi|224140653	61371	89	predicted protein [Populus trichocarpa]
2.	gi|118487061	29578	80	unknown [Populus trichocarpa]
3.	gi|133872436	25759	79	Bp2A protein [Triticum turgidum subsp. dicoccoides]
4.	gi|133872396	25821	79	Bp2A protein [Triticum turgidum subsp. dicoccoides]
5.	gi|133872360	25773	79	Bp2A protein [Triticum turgidum subsp. dicoccon]
6.	gi|115440691	60980	75	Os01g0817700 [Oryza sativa (japonica cultivar-group)]
7.	gi|218189276	60952	75	hypothetical protein OsI_04213 [Oryza sativa Indica Group]
8.	gi|224069046	61146	75	predicted protein [Populus trichocarpa]
9.	gi|551288	60763	75	phosphoglycerate mutase [Zea mays]
10.	gi|162461400	60753	75	2,3-bisphosphoglycerate-independent phosphoglycerate mutase [Zea mays]

Results List

1. gi|224140653 **Mass:** 61371 **Score:** 89 **Expect:** 0.00082 **Queries matched:** 5

predicted protein [Populus trichocarpa]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1348.7036	1347.6963	1347.7146	-0.0183	413	-	424	1	58	DAILSGKFDQVR
1348.7036	1347.6963	1347.7146	-0.0183	413	-	424	1	---	DAILSGKFDQVR
1481.7040	1480.6967	1480.6999	-0.0032	363	-	374	0	---	FGHVTFFWNGNR
1605.8422	1604.8349	1604.8059	0.0290	2	-	16	1	---	GSPGQNAWKLADHPK
1605.8422	1604.8349	1604.8059	0.0290	2	-	16	1	---	GSPGQNAWKLADHPK

No match to: 768.5225, 1170.6766, 1473.6885, 1473.6885, 2706.2393

2. gi|118487061 **Mass:** 29578 **Score:** 80 **Expect:** 0.0058 **Queries matched:** 3

unknown [Populus trichocarpa]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1348.7036	1347.6963	1347.7146	-0.0183	123	-	134	1	58	DAILSGKFDQVR
1348.7036	1347.6963	1347.7146	-0.0183	123	-	134	1	---	DAILSGKFDQVR
1481.7040	1480.6967	1480.6999	-0.0032	73	-	84	0	---	FGHVTFFWNGNR

No match to: 768.5225, 1170.6766, 1473.6885, 1473.6885, 1605.8422, 1605.8422, 2706.2393

3. gi|133872436 **Mass:** 25759 **Score:** 79 **Expect:** 0.0078 **Queries matched:** 3

Bp2A protein [Triticum turgidum subsp. dicoccoides]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1348.7036	1347.6963	1347.7146	-0.0183	210	-	221	1	58	DAILSGKFDQVR
1348.7036	1347.6963	1347.7146	-0.0183	210	-	221	1	---	DAILSGKFDQVR
1481.7040	1480.6967	1480.6999	-0.0032	160	-	171	0	---	FGHVTFFWNGNR

No match to: 768.5225, 1170.6766, 1473.6885, 1473.6885, 1605.8422, 1605.8422, 2706.2393

4. gi|133872396 **Mass:** 25821 **Score:** 79 **Expect:** 0.0078 **Queries matched:** 3

Bp2A protein [Triticum turgidum subsp. dicoccoides]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1348.7036	1347.6963	1347.7146	-0.0183	210	221	1	58	DAILSGKFDQVR
1348.7036	1347.6963	1347.7146	-0.0183	210	221	1	---	DAILSGKFDQVR
1481.7040	1480.6967	1480.6999	-0.0032	160	171	0	---	FGHVTFFWNGNR

No match to: 768.5225, 1170.6766, 1473.6885, 1473.6885, 1605.8422, 1605.8422, 2706.2393

5. gi|133872360 **Mass:** 25773 **Score:** 79 **Expect:** 0.0078 **Queries matched:** 3

Bp2A protein [Triticum turgidum subsp. dicoccon]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1348.7036	1347.6963	1347.7146	-0.0183	210	221	1	58	DAILSGKFDQVR
1348.7036	1347.6963	1347.7146	-0.0183	210	221	1	---	DAILSGKFDQVR
1481.7040	1480.6967	1480.6999	-0.0032	160	171	0	---	FGHVTFFWNGNR

No match to: 768.5225, 1170.6766, 1473.6885, 1473.6885, 1605.8422, 1605.8422, 2706.2393

6. gi|115440691 **Mass:** 60980 **Score:** 75 **Expect:** 0.022 **Queries matched:** 3

Os01g0817700 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1348.7036	1347.6963	1347.7146	-0.0183	412	423	1	58	DAILSGKFDQVR
1348.7036	1347.6963	1347.7146	-0.0183	412	423	1	---	DAILSGKFDQVR
1481.7040	1480.6967	1480.6999	-0.0032	362	373	0	---	FGHVTFFWNGNR

No match to: 768.5225, 1170.6766, 1473.6885, 1473.6885, 1605.8422, 1605.8422, 2706.2393

7. gi|218189276 **Mass:** 60952 **Score:** 75 **Expect:** 0.022 **Queries matched:** 3

hypothetical protein OsI_04213 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1348.7036	1347.6963	1347.7146	-0.0183	412	423	1	58	DAILSGKFDQVR
1348.7036	1347.6963	1347.7146	-0.0183	412	423	1	---	DAILSGKFDQVR
1481.7040	1480.6967	1480.6999	-0.0032	362	373	0	---	FGHVTFFWNGNR

No match to: 768.5225, 1170.6766, 1473.6885, 1473.6885, 1605.8422, 1605.8422, 2706.2393

8. gi|224069046 **Mass:** 61146 **Score:** 75 **Expect:** 0.022 **Queries matched:** 3

predicted protein [Populus trichocarpa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1348.7036	1347.6963	1347.7146	-0.0183	413	424	1	58	DAILSGKFDQVR
1348.7036	1347.6963	1347.7146	-0.0183	413	424	1	---	DAILSGKFDQVR
1481.7040	1480.6967	1480.6999	-0.0032	363	374	0	---	FGHVTFFWNGNR

No match to: 768.5225, 1170.6766, 1473.6885, 1473.6885, 1605.8422, 1605.8422, 2706.2393

9. gi|551288 **Mass:** 60763 **Score:** 75 **Expect:** 0.022 **Queries matched:** 3

phosphoglycerate mutase [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1348.7036	1347.6963	1347.7146	-0.0183	412	423	1	58	DALLSGKFDQVR
1348.7036	1347.6963	1347.7146	-0.0183	412	423	1	---	DALLSGKFDQVR
1481.7040	1480.6967	1480.6999	-0.0032	362	373	0	---	FGHVTFFWNGNR

No match to: 768.5225, 1170.6766, 1473.6885, 1473.6885, 1605.8422, 1605.8422, 2706.2393

10. gi|162461400 **Mass:** 60753 **Score:** 75 **Expect:** 0.022 **Queries matched:** 3

2,3-bisphosphoglycerate-independent phosphoglycerate mutase [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1348.7036	1347.6963	1347.7146	-0.0183	412	423	1	58	DALLSGKFDQVR
1348.7036	1347.6963	1347.7146	-0.0183	412	423	1	---	DALLSGKFDQVR
1481.7040	1480.6967	1480.6999	-0.0032	362	373	0	---	FGHVTFFWNGNR

No match to: 768.5225, 1170.6766, 1473.6885, 1473.6885, 1605.8422, 1605.8422, 2706.2393

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 10

Protein View

Match to: **gi|224140653** Score: **89** Expect: **0.00082**
predicted protein [Populus trichocarpa]

Nominal mass (M_r): **61371**; Calculated pI value: **5.40**
NCBI BLAST search of gi|224140653 against nr
Unformatted sequence string for pasting into other applications
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|222868326 from Populus trichocarpa

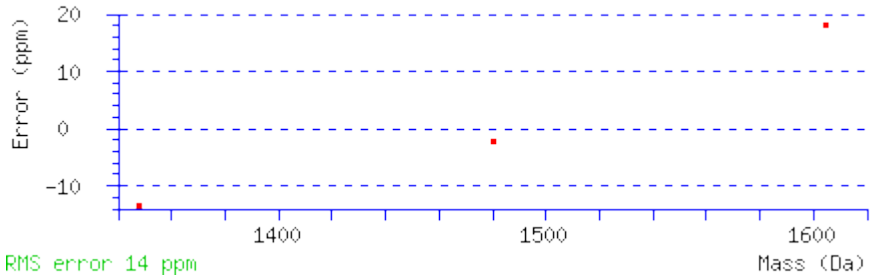
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **6%**

Matched peptides shown in **Bold Red**

```
   1 MGSPGQNAWK LADHPKLPKG KTIAMVVLDG WGEAKPDQYN CIHVAHTPTM
  51 DSFKTTAPEK WRLIKAHGTA VGLPSEDDMG NSEVGHNALG AGRIFAQGAK
 101 LVDLALASGK IYDGEGFKYI KECFDNGTLH LIGLLSDGGV HSRLDQLQLL
 151 LKGAVENGAK RIRVHILTDG RDVLDGSSIG FVETLEKDLS NLREKGIDAQ
 201 IASGGGRMYV TMDRYENDWD VVKRGWDAQV LGEAPYKFRN AVEAVKKLRE
 251 EPKANDQYLP PFVIVDESGN PVGPIKDGDA VVTFNFRADR MAMLAKALEY
 301 EDFDKFDRVR VPKIHYAGML QYDGELKLPS HYLVSPPEID RTSGEYLVHN
 351 GIRTFACSET VKFGHVTFFW NGNRSGYFNQ EMEEYVEIPS DVGITFNVQP
 401 KMKAIEIAEK ARDAILSGKF DQVRVNLPNG DMVGHTGDIE ATVVACKVAD
 451 DAVKMIIDAI EQVGGIFVIT ADHGNAEDMV KRDKSGKPLL DKNGNLQILT
 501 SHTLQPVPIA IGGPGLAPGA RFRNDVPTGG LANVAATVMN LHGFEAPSDY
 551 EPTLIEVVDN
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
2 - 16	1605.8422	1604.8349	1604.8059	0.0290	1	GSPGQNAWKLADHPK	(No match)
2 - 16	1605.8422	1604.8349	1604.8059	0.0290	1	GSPGQNAWKLADHPK	(No match)
363 - 374	1481.7040	1480.6967	1480.6999	-0.0032	0	FGHVTFFWNGNR	(No match)
413 - 424	1348.7036	1347.6963	1347.7146	-0.0183	1	DAILSGKFDQVR	(Ions score 58)
413 - 424	1348.7036	1347.6963	1347.7146	-0.0183	1	DAILSGKFDQVR	(No match)



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	Accession	Mass	Score	Description
1.	gi|223945023	60423	250	unknown [Zea mays]
2.	gi|551288	60763	250	phosphoglycerate mutase [Zea mays]
3.	gi|162461400	60753	250	2,3-bisphosphoglycerate-independent phosphoglycerate mutase [Zea mays]
4.	gi|195628730	60811	250	2,3-bisphosphoglycerate-independent phosphoglycerate mutase [Zea mays]
5.	gi|115464537	61003	249	Os05g0482700 [Oryza sativa (japonica cultivar-group)]
6.	gi|218196991	63374	248	hypothetical protein OsI_20375 [Oryza sativa Indica Group]
7.	gi|224140653	61371	151	predicted protein [Populus trichocarpa]
8.	gi|3914394	61316	149	RecName: Full=2,3-bisphosphoglycerate-independent phosphoglycerate mutase; Short=BPG-independe
9.	gi|118487061	29578	147	unknown [Populus trichocarpa]
10.	gi|133872436	25759	146	Bp2A protein [Triticum turgidum subsp. dicoccoides]

Results List

1. gi|223945023 **Mass:** 60423 **Score:** 250 **Expect:** 6.1e-020 **Queries matched:** 8

unknown [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1348.7531	1347.7458	1347.7146	0.0312	409	420	1	---	DALLSGKFDQVR
1348.7531	1347.7458	1347.7146	0.0312	409	420	1	88	DALLSGKFDQVR
1481.7399	1480.7326	1480.6999	0.0327	359	370	0	27	FGHVTFFWNGNR
1481.7399	1480.7326	1480.6999	0.0327	359	370	0	---	FGHVTFFWNGNR
2505.2217	2504.2144	2504.1694	0.0450	350	370	1	---	TFACSETVKFGHVTFFWNGNR
2705.2661	2704.2588	2704.2258	0.0330	62	89	0	---	AHGTAVGLPSDDDMGNSEVGHNALGAGR
2705.2661	2704.2588	2704.2258	0.0330	62	89	0	95	AHGTAVGLPSDDDMGNSEVGHNALGAGR
2721.2905	2720.2832	2720.2207	0.0625	62	89	0	---	AHGTAVGLPSDDDMGNSEVGHNALGAGR + Oxidation (M)

No match to: 768.5547, 1170.7155, 1473.7354, 1473.7354, 1605.8743, 1605.8743, 1728.9044, 1790.9740, 2053.1257, 2360.3315

2. gi|551288 **Mass:** 60763 **Score:** 250 **Expect:** 6.1e-020 **Queries matched:** 8

phosphoglycerate mutase [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1348.7531	1347.7458	1347.7146	0.0312	412	423	1	---	DALLSGKFDQVR
1348.7531	1347.7458	1347.7146	0.0312	412	423	1	88	DALLSGKFDQVR
1481.7399	1480.7326	1480.6999	0.0327	362	373	0	27	FGHVTFFWNGNR
1481.7399	1480.7326	1480.6999	0.0327	362	373	0	---	FGHVTFFWNGNR
2505.2217	2504.2144	2504.1694	0.0450	353	373	1	---	TFACSETVKFGHVTFFWNGNR
2705.2661	2704.2588	2704.2258	0.0330	65	92	0	---	AHGTAVGLPSDDDMGNSEVGHNALGAGR
2705.2661	2704.2588	2704.2258	0.0330	65	92	0	95	AHGTAVGLPSDDDMGNSEVGHNALGAGR
2721.2905	2720.2832	2720.2207	0.0625	65	92	0	---	AHGTAVGLPSDDDMGNSEVGHNALGAGR + Oxidation (M)

No match to: 768.5547, 1170.7155, 1473.7354, 1473.7354, 1605.8743, 1605.8743, 1728.9044, 1790.9740, 2053.1257, 2360.3315

3. gi|162461400 **Mass:** 60753 **Score:** 250 **Expect:** 6.1e-020 **Queries matched:** 8

2,3-bisphosphoglycerate-independent phosphoglycerate mutase [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1348.7531	1347.7458	1347.7146	0.0312	412	423	1	---	DALLSGKFDQVR
1348.7531	1347.7458	1347.7146	0.0312	412	423	1	88	DALLSGKFDQVR
1481.7399	1480.7326	1480.6999	0.0327	362	373	0	27	FGHVTFFWNGNR
1481.7399	1480.7326	1480.6999	0.0327	362	373	0	---	FGHVTFFWNGNR
2505.2217	2504.2144	2504.1694	0.0450	353	373	1	---	TFACSETVKFGHVTFFWNGNR
2705.2661	2704.2588	2704.2258	0.0330	65	92	0	---	AHGTAVGLPSDDDMGNSEVGHNALGAGR
2705.2661	2704.2588	2704.2258	0.0330	65	92	0	95	AHGTAVGLPSDDDMGNSEVGHNALGAGR
2721.2905	2720.2832	2720.2207	0.0625	65	92	0	---	AHGTAVGLPSDDDMGNSEVGHNALGAGR + Oxidation (M)

No match to: 768.5547, 1170.7155, 1473.7354, 1473.7354, 1605.8743, 1605.8743, 1728.9044, 1790.9740, 2053.1257, 2360.3315

4. gi|195628730 **Mass:** 60811 **Score:** 250 **Expect:** 6.1e-020 **Queries matched:** 8

2,3-bisphosphoglycerate-independent phosphoglycerate mutase [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1348.7531	1347.7458	1347.7146	0.0312	412	423	1	---	DALLSGKFDQVR
1348.7531	1347.7458	1347.7146	0.0312	412	423	1	88	DALLSGKFDQVR
1481.7399	1480.7326	1480.6999	0.0327	362	373	0	27	FGHVTFFWNGNR
1481.7399	1480.7326	1480.6999	0.0327	362	373	0	---	FGHVTFFWNGNR
2505.2217	2504.2144	2504.1694	0.0450	353	373	1	---	TFACSETVKFGHVTFFWNGNR
2705.2661	2704.2588	2704.2258	0.0330	65	92	0	---	AHGTAVGLPSDDDMGNSEVGHNALGAGR
2705.2661	2704.2588	2704.2258	0.0330	65	92	0	95	AHGTAVGLPSDDDMGNSEVGHNALGAGR
2721.2905	2720.2832	2720.2207	0.0625	65	92	0	---	AHGTAVGLPSDDDMGNSEVGHNALGAGR + Oxidation (M)

No match to: 768.5547, 1170.7155, 1473.7354, 1473.7354, 1605.8743, 1605.8743, 1728.9044, 1790.9740, 2053.1257, 2360.3315

5. gi|115464537 **Mass:** 61003 **Score:** 249 **Expect:** 7.6e-020 **Queries matched:** 8

Os05g0482700 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1348.7531	1347.7458	1347.7146	0.0312	412	423	1	---	DAILSGKFDQVR
1348.7531	1347.7458	1347.7146	0.0312	412	423	1	88	DAILSGKFDQVR
1481.7399	1480.7326	1480.6999	0.0327	362	373	0	27	FGHVTFFWNGNR
1481.7399	1480.7326	1480.6999	0.0327	362	373	0	---	FGHVTFFWNGNR
2505.2217	2504.2144	2504.1694	0.0450	353	373	1	---	TFACSETVKFGHVTFFWNGNR
2705.2661	2704.2588	2704.2258	0.0330	65	92	0	---	AHGTAVGLPSDDDMGNSEVGHNALGAGR
2705.2661	2704.2588	2704.2258	0.0330	65	92	0	95	AHGTAVGLPSDDDMGNSEVGHNALGAGR
2721.2905	2720.2832	2720.2207	0.0625	65	92	0	---	AHGTAVGLPSDDDMGNSEVGHNALGAGR + Oxidation (M)

No match to: 768.5547, 1170.7155, 1473.7354, 1473.7354, 1605.8743, 1605.8743, 1728.9044, 1790.9740, 2053.1257, 2360.3315

6. gi|218196991 **Mass:** 63374 **Score:** 248 **Expect:** 9.6e-020 **Queries matched:** 8

hypothetical protein OsI_20375 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1348.7531	1347.7458	1347.7146	0.0312	430	441	1	---	DAILSGKFDQVR
1348.7531	1347.7458	1347.7146	0.0312	430	441	1	88	DAILSGKFDQVR
1481.7399	1480.7326	1480.6999	0.0327	380	391	0	27	FGHVTFFWNGNR
1481.7399	1480.7326	1480.6999	0.0327	380	391	0	---	FGHVTFFWNGNR
2505.2217	2504.2144	2504.1694	0.0450	371	391	1	---	TFACSETVKFGHVTFFWNGNR
2705.2661	2704.2588	2704.2258	0.0330	88	115	0	---	AHGTAVGLPSDDDMGNSEVGHNALGAGR
2705.2661	2704.2588	2704.2258	0.0330	88	115	0	95	AHGTAVGLPSDDDMGNSEVGHNALGAGR
2721.2905	2720.2832	2720.2207	0.0625	88	115	0	---	AHGTAVGLPSDDDMGNSEVGHNALGAGR + Oxidation (M)

No match to: 768.5547, 1170.7155, 1473.7354, 1473.7354, 1605.8743, 1605.8743, 1728.9044, 1790.9740, 2053.1257, 2360.3315

7. gi|224140653 **Mass:** 61371 **Score:** 151 **Expect:** 4.8e-010 **Queries matched:** 7

predicted protein [Populus trichocarpa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1348.7531	1347.7458	1347.7146	0.0312	413	424	1	---	DAILSGKFDQVR
1348.7531	1347.7458	1347.7146	0.0312	413	424	1	88	DAILSGKFDQVR
1481.7399	1480.7326	1480.6999	0.0327	363	374	0	27	FGHVTFFWNGNR
1481.7399	1480.7326	1480.6999	0.0327	363	374	0	---	FGHVTFFWNGNR
1605.8743	1604.8670	1604.8059	0.0611	2	16	1	---	GSPGQNAWKLADHPK
1605.8743	1604.8670	1604.8059	0.0611	2	16	1	---	GSPGQNAWKLADHPK
2505.2217	2504.2144	2504.1694	0.0450	354	374	1	---	TFACSETVKFGHVTFFWNGNR

No match to: 768.5547, 1170.7155, 1473.7354, 1473.7354, 1728.9044, 1790.9740, 2053.1257, 2360.3315, 2705.2661, 2705.2661, 2721.2905

8. gi|3914394 **Mass:** 61316 **Score:** 149 **Expect:** 7.6e-010 **Queries matched:** 6

RecName: Full=2,3-bisphosphoglycerate-independent phosphoglycerate mutase; Short=BPG-independent PG

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1348.7531	1347.7458	1347.7146	0.0312	412	423	1	---	DAILSGKFDQVR
1348.7531	1347.7458	1347.7146	0.0312	412	423	1	88	DAILSGKFDQVR
1481.7399	1480.7326	1480.6999	0.0327	362	373	0	27	FGHVTFFWNGNR
1481.7399	1480.7326	1480.6999	0.0327	362	373	0	---	FGHVTFFWNGNR
2360.3315	2359.3242	2359.1695	0.1547	249	269	1	---	QEPKANDQYLPPFVVVDESGK
2505.2217	2504.2144	2504.1694	0.0450	353	373	1	---	TFACSETVKFGHVTFFWNGNR

No match to: 768.5547, 1170.7155, 1473.7354, 1473.7354, 1605.8743, 1605.8743, 1728.9044, 1790.9740, 2053.1257, 2705.2661, 2705.2661, 2721.2905

9. gi|118487061 **Mass:** 29578 **Score:** 147 **Expect:** 1.2e-009 **Queries matched:** 5

unknown [Populus trichocarpa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1348.7531	1347.7458	1347.7146	0.0312	123	134	1	---	DAILSGKFDQVR
1348.7531	1347.7458	1347.7146	0.0312	123	134	1	88	DAILSGKFDQVR
1481.7399	1480.7326	1480.6999	0.0327	73	84	0	27	FGHVTFFWNGNR
1481.7399	1480.7326	1480.6999	0.0327	73	84	0	---	FGHVTFFWNGNR
2505.2217	2504.2144	2504.1694	0.0450	64	84	1	---	TFACSETVKFGHVTFFWNGNR

No match to: 768.5547, 1170.7155, 1473.7354, 1473.7354, 1605.8743, 1605.8743, 1728.9044, 1790.9740, 2053.1257, 2360.3315, 2705.2661, 2705.2661, 2721.2905

10. gi|133872436 **Mass:** 25759 **Score:** 146 **Expect:** 1.5e-009 **Queries matched:** 5

Bp2A protein [Triticum turgidum subsp. dicoccoides]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1348.7531	1347.7458	1347.7146	0.0312	210	221	1	---	DAILSGKFDQVR
1348.7531	1347.7458	1347.7146	0.0312	210	221	1	88	DAILSGKFDQVR
1481.7399	1480.7326	1480.6999	0.0327	160	171	0	27	FGHVTFFWNGNR
1481.7399	1480.7326	1480.6999	0.0327	160	171	0	---	FGHVTFFWNGNR
2505.2217	2504.2144	2504.1694	0.0450	151	171	1	---	TFACSETVKFGHVTFFWNGNR

No match to: 768.5547, 1170.7155, 1473.7354, 1473.7354, 1605.8743, 1605.8743, 1728.9044, 1790.9740, 2053.1257, 2360.3315, 2705.2661, 2705.2661, 2721.2905

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 18

Protein View

Match to: **gi|551288** Score: **250** Expect: **6.1e-020**
phosphoglycerate mutase [Zea mays]

Nominal mass (M_r): **60763**; Calculated pI value: **5.29**
NCBI BLAST search of gi|551288 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Zea mays
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|219888361 from Zea mays

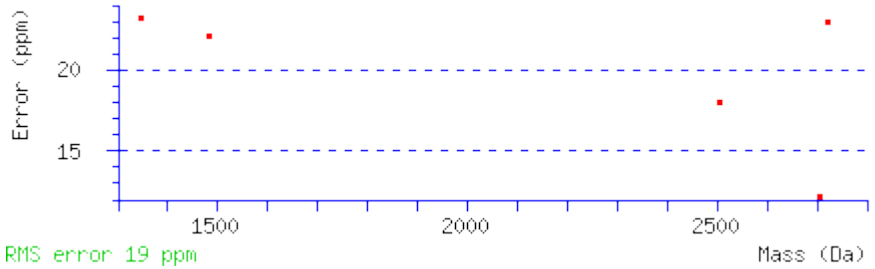
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **10%**

Matched peptides shown in **Bold Red**

```
     1 MGSSGFSWTL PDHPKLPKGK PVAVVVLDGW GEANPDQYNC IHVAQTPVMD
    51 SLKNGAPEKW RLVKAHGTAV GLPSDDDMGN SEVGHNALGA GRIFAQGAKL
   101 VDQALASGKI YDGDGFNYIK ESFESGTLHL IGLLSDGGVH SRLDQLQLLL
   151 KGVSERGAKK IRVHILTDGR DVLDGSSIGF VETLENDLLE LRAKGVDAQI
   201 ASGGGRMYVT MDRYENDWDV VKRGWDAQVL GEAPYKFKSA LEAVKTLRAQ
   251 PKANDQYLPP FVIVDDSGNA VGPVLDGDAV VTINFRADRM VMLAKALEYA
   301 DFDNFDRVRV PKIRYAGMLQ YDGELKLPSR YLVSPPEIDR TSGEYLVKNG
   351 IRTFACSETV KFGHVTFFWN GNRSGYFDAT KEEYVEVPSD SGITFNVAPN
   401 MKALEIAEKA RDALLSGKFD QVRVNLPNGD MVGHTGDIEA TVVACKAADE
   451 AVKIILDAVE QVGGIYLVTA DHGNAEDMVK RNKSGKPLLD KNDRIQILTS
   501 HTLQPVPVAI GGPGLHPGVK FRNDIQTPGL ANVAATVMNL HGFEAPADYE
   551 QTLIEVADN
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
65 - 92	2705.2661	2704.2588	2704.2258	0.0330	0	**AHGTAVGLPSDDDMGNSEVGHNALGAGR**	(No match)
65 - 92	2705.2661	2704.2588	2704.2258	0.0330	0	**AHGTAVGLPSDDDMGNSEVGHNALGAGR**	(Ions score 95)
65 - 92	2721.2905	2720.2832	2720.2207	0.0625	0	**AHGTAVGLPSDDDMGNSEVGHNALGAGR**	Oxidation (M) (No match)
353 - 373	2505.2217	2504.2144	2504.1694	0.0450	1	**TFACSETVKFGHVTFFWNGNR**	(No match)
362 - 373	1481.7399	1480.7326	1480.6999	0.0327	0	**FGHVTFFWNGNR**	(Ions score 27)
362 - 373	1481.7399	1480.7326	1480.6999	0.0327	0	**FGHVTFFWNGNR**	(No match)
412 - 423	1348.7531	1347.7458	1347.7146	0.0312	1	**DALLSGKFDQVR**	(No match)
412 - 423	1348.7531	1347.7458	1347.7146	0.0312	1	**DALLSGKFDQVR**	(Ions score 88)



Spot 19

Index

	Accession	Mass	Score	Description
1.	gi|133872436	25759	174	Bp2A protein [Triticum turgidum subsp. dicoccoides]
2.	gi|133872360	25773	174	Bp2A protein [Triticum turgidum subsp. dicoccon]
3.	gi|133872396	25821	158	Bp2A protein [Triticum turgidum subsp. dicoccoides]
4.	gi|223945023	60423	152	unknown [Zea mays]
5.	gi|551288	60763	152	phosphoglycerate mutase [Zea mays]
6.	gi|162461400	60753	152	2,3-bisphosphoglycerate-independent phosphoglycerate mutase [Zea mays]
7.	gi|195628730	60811	152	2,3-bisphosphoglycerate-independent phosphoglycerate mutase [Zea mays]
8.	gi|115464537	61003	151	Os05g0482700 [Oryza sativa (japonica cultivar-group)]
9.	gi|224140653	61371	150	predicted protein [Populus trichocarpa]
10.	gi|218196991	63374	150	hypothetical protein OsI_20375 [Oryza sativa Indica Group]

Results List

1. gi|133872436 **Mass:** 25759 **Score:** 174 **Expect:** 2.4e-012 **Queries matched:** 7

Bp2A protein [Triticum turgidum subsp. dicoccoides]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1186.6906	1185.6833	1185.6757	0.0076	129	138	0	---	YLVSPPLIER
1348.7264	1347.7191	1347.7146	0.0045	210	221	1	82	DAILSGKFDQVR
1348.7264	1347.7191	1347.7146	0.0045	210	221	1	---	DAILSGKFDQVR
1481.7129	1480.7056	1480.6999	0.0057	160	171	0	---	FGHVTFFWNGNR
1481.7129	1480.7056	1480.6999	0.0057	160	171	0	34	FGHVTFFWNGNR
1792.9333	1791.9260	1791.9155	0.0106	68	84	0	---	SVGPIVDGDAVVTFNFR
2505.1848	2504.1775	2504.1694	0.0081	151	171	1	---	TFACSETVKFGHVTFFWNGNR

No match to: 1073.5490, 1170.6891, 1473.7054, 1473.7054, 1605.8489, 1605.8489, 1728.8738, 1728.8738, 1865.9591, 2053.0981, 2360.3066, 2705.2498

2. gi|133872360 **Mass:** 25773 **Score:** 174 **Expect:** 2.4e-012 **Queries matched:** 7

Bp2A protein [Triticum turgidum subsp. dicoccon]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1186.6906	1185.6833	1185.6757	0.0076	129	138	0	---	YLVSPPLIER
1348.7264	1347.7191	1347.7146	0.0045	210	221	1	82	DAILSGKFDQVR
1348.7264	1347.7191	1347.7146	0.0045	210	221	1	---	DAILSGKFDQVR
1481.7129	1480.7056	1480.6999	0.0057	160	171	0	---	FGHVTFFWNGNR
1481.7129	1480.7056	1480.6999	0.0057	160	171	0	34	FGHVTFFWNGNR
1792.9333	1791.9260	1791.9155	0.0106	68	84	0	---	SVGPIVDGDAVVTFNFR
2505.1848	2504.1775	2504.1694	0.0081	151	171	1	---	TFACSETVKFGHVTFFWNGNR

No match to: 1073.5490, 1170.6891, 1473.7054, 1473.7054, 1605.8489, 1605.8489, 1728.8738, 1728.8738, 1865.9591, 2053.0981, 2360.3066, 2705.2498

3. gi|133872396 **Mass:** 25821 **Score:** 158 **Expect:** 9.6e-011 **Queries matched:** 6

Bp2A protein [Triticum turgidum subsp. dicoccoides]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1186.6906	1185.6833	1185.6757	0.0076	129	-	138	0	---	YLVSPPLIER
1348.7264	1347.7191	1347.7146	0.0045	210	-	221	1	82	DAILSGKFDQVR
1348.7264	1347.7191	1347.7146	0.0045	210	-	221	1	---	DAILSGKFDQVR
1481.7129	1480.7056	1480.6999	0.0057	160	-	171	0	---	FGHVTFFWNGNR
1481.7129	1480.7056	1480.6999	0.0057	160	-	171	0	34	FGHVTFFWNGNR
2505.1848	2504.1775	2504.1694	0.0081	151	-	171	1	---	TFACSETVKFGHVTFFWNGNR

No match to: 1073.5490, 1170.6891, 1473.7054, 1473.7054, 1605.8489, 1605.8489, 1728.8738, 1728.8738, 1792.9333, 1865.9591, 2053.0981, 2360.3066, 2705.2498

4. gi|223945023 **Mass:** 60423 **Score:** 152 **Expect:** 3.8e-010 **Queries matched:** 6

unknown [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1348.7264	1347.7191	1347.7146	0.0045	409	-	420	1	82	DALLSGKFDQVR
1348.7264	1347.7191	1347.7146	0.0045	409	-	420	1	---	DALLSGKFDQVR
1481.7129	1480.7056	1480.6999	0.0057	359	-	370	0	---	FGHVTFFWNGNR
1481.7129	1480.7056	1480.6999	0.0057	359	-	370	0	34	FGHVTFFWNGNR
2505.1848	2504.1775	2504.1694	0.0081	350	-	370	1	---	TFACSETVKFGHVTFFWNGNR
2705.2498	2704.2425	2704.2258	0.0167	62	-	89	0	---	AHGTAVGLPSDDDMGNSEVGHNALGAGR

No match to: 1073.5490, 1170.6891, 1186.6906, 1473.7054, 1473.7054, 1605.8489, 1605.8489, 1728.8738, 1728.8738, 1792.9333, 1865.9591, 2053.0981, 2360.3066

5. gi|551288 **Mass:** 60763 **Score:** 152 **Expect:** 3.8e-010 **Queries matched:** 6

phosphoglycerate mutase [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1348.7264	1347.7191	1347.7146	0.0045	412	-	423	1	82	DALLSGKFDQVR
1348.7264	1347.7191	1347.7146	0.0045	412	-	423	1	---	DALLSGKFDQVR
1481.7129	1480.7056	1480.6999	0.0057	362	-	373	0	---	FGHVTFFWNGNR
1481.7129	1480.7056	1480.6999	0.0057	362	-	373	0	34	FGHVTFFWNGNR
2505.1848	2504.1775	2504.1694	0.0081	353	-	373	1	---	TFACSETVKFGHVTFFWNGNR
2705.2498	2704.2425	2704.2258	0.0167	65	-	92	0	---	AHGTAVGLPSDDDMGNSEVGHNALGAGR

No match to: 1073.5490, 1170.6891, 1186.6906, 1473.7054, 1473.7054, 1605.8489, 1605.8489, 1728.8738, 1728.8738, 1792.9333, 1865.9591, 2053.0981, 2360.3066

6. gi|162461400 **Mass:** 60753 **Score:** 152 **Expect:** 3.8e-010 **Queries matched:** 6

2,3-bisphosphoglycerate-independent phosphoglycerate mutase [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1348.7264	1347.7191	1347.7146	0.0045	412	-	423	1	82	DALLSGKFDQVR
1348.7264	1347.7191	1347.7146	0.0045	412	-	423	1	---	DALLSGKFDQVR

1481.7129	1480.7056	1480.6999	0.0057	362 - 373	0	---	FGHVTFFWNGNR
1481.7129	1480.7056	1480.6999	0.0057	362 - 373	0	34	FGHVTFFWNGNR
2505.1848	2504.1775	2504.1694	0.0081	353 - 373	1	---	TFACSETVKFGHVTFFWNGNR
2705.2498	2704.2425	2704.2258	0.0167	65 - 92	0	---	AHGTAVGLPSDDDMGNSEVGHNALGAGR

No match to: 1073.5490, 1170.6891, 1186.6906, 1473.7054, 1473.7054, 1605.8489, 1605.8489, 1728.8738, 1728.8738, 1792.9333, 1865.9591, 2053.0981, 2360.3066

7. gi|195628730 **Mass:** 60811 **Score:** 152 **Expect:** 3.8e-010 **Queries matched:** 6

2,3-bisphosphoglycerate-independent phosphoglycerate mutase [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start - End	Miss	Ions	Peptide
1348.7264	1347.7191	1347.7146	0.0045	412 - 423	1	82	DALLSGKFDQVR
1348.7264	1347.7191	1347.7146	0.0045	412 - 423	1	---	DALLSGKFDQVR
1481.7129	1480.7056	1480.6999	0.0057	362 - 373	0	---	FGHVTFFWNGNR
1481.7129	1480.7056	1480.6999	0.0057	362 - 373	0	34	FGHVTFFWNGNR
2505.1848	2504.1775	2504.1694	0.0081	353 - 373	1	---	TFACSETVKFGHVTFFWNGNR
2705.2498	2704.2425	2704.2258	0.0167	65 - 92	0	---	AHGTAVGLPSDDDMGNSEVGHNALGAGR

No match to: 1073.5490, 1170.6891, 1186.6906, 1473.7054, 1473.7054, 1605.8489, 1605.8489, 1728.8738, 1728.8738, 1792.9333, 1865.9591, 2053.0981, 2360.3066

8. gi|115464537 **Mass:** 61003 **Score:** 151 **Expect:** 4.8e-010 **Queries matched:** 6

Os05g0482700 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start - End	Miss	Ions	Peptide
1348.7264	1347.7191	1347.7146	0.0045	412 - 423	1	82	DAILSGKFDQVR
1348.7264	1347.7191	1347.7146	0.0045	412 - 423	1	---	DAILSGKFDQVR
1481.7129	1480.7056	1480.6999	0.0057	362 - 373	0	---	FGHVTFFWNGNR
1481.7129	1480.7056	1480.6999	0.0057	362 - 373	0	34	FGHVTFFWNGNR
2505.1848	2504.1775	2504.1694	0.0081	353 - 373	1	---	TFACSETVKFGHVTFFWNGNR
2705.2498	2704.2425	2704.2258	0.0167	65 - 92	0	---	AHGTAVGLPSDDDMGNSEVGHNALGAGR

No match to: 1073.5490, 1170.6891, 1186.6906, 1473.7054, 1473.7054, 1605.8489, 1605.8489, 1728.8738, 1728.8738, 1792.9333, 1865.9591, 2053.0981, 2360.3066

9. gi|224140653 **Mass:** 61371 **Score:** 150 **Expect:** 6.1e-010 **Queries matched:** 7

predicted protein [Populus trichocarpa]

Observed	Mr(expt)	Mr(calc)	Delta	Start - End	Miss	Ions	Peptide
1348.7264	1347.7191	1347.7146	0.0045	413 - 424	1	82	DAILSGKFDQVR
1348.7264	1347.7191	1347.7146	0.0045	413 - 424	1	---	DAILSGKFDQVR
1481.7129	1480.7056	1480.6999	0.0057	363 - 374	0	---	FGHVTFFWNGNR
1481.7129	1480.7056	1480.6999	0.0057	363 - 374	0	34	FGHVTFFWNGNR
1605.8489	1604.8416	1604.8059	0.0357	2 - 16	1	---	GSPGQNAWKLADHPK
1605.8489	1604.8416	1604.8059	0.0357	2 - 16	1	---	GSPGQNAWKLADHPK
2505.1848	2504.1775	2504.1694	0.0081	354 - 374	1	---	TFACSETVKFGHVTFFWNGNR

No match to: 1073.5490, 1170.6891, 1186.6906, 1473.7054, 1473.7054, 1728.8738, 1728.8738, 1792.9333, 1865.9591,

2053.0981, 2360.3066, 2705.2498

10. gi|218196991 **Mass:** 63374 **Score:** 150 **Expect:** 6.1e-010 **Queries matched:** 6
hypothetical protein OsI_20375 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1348.7264	1347.7191	1347.7146	0.0045	430	441	1	82	DAILSGKFDQVR
1348.7264	1347.7191	1347.7146	0.0045	430	441	1	---	DAILSGKFDQVR
1481.7129	1480.7056	1480.6999	0.0057	380	391	0	---	FGHVTFFWNGNR
1481.7129	1480.7056	1480.6999	0.0057	380	391	0	34	FGHVTFFWNGNR
2505.1848	2504.1775	2504.1694	0.0081	371	391	1	---	TFACSETVKFGHVTFFWNGNR
2705.2498	2704.2425	2704.2258	0.0167	88	115	0	---	AHGTAVGLPSDDDMGNSEVGHNALGAGR

No match to: 1073.5490, 1170.6891, 1186.6906, 1473.7054, 1473.7054, 1605.8489, 1605.8489, 1728.8738, 1728.8738, 1792.9333, 1865.9591, 2053.0981, 2360.3066

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 19

Protein View

Match to: **gi|133872360** Score: **174** Expect: **2.4e-012**
Bp2A protein [Triticum turgidum subsp. dicoccon]

Nominal mass (M_r): **25773**; Calculated pI value: **5.86**
NCBI BLAST search of gi|133872360 against nr
Unformatted sequence string for pasting into other applications

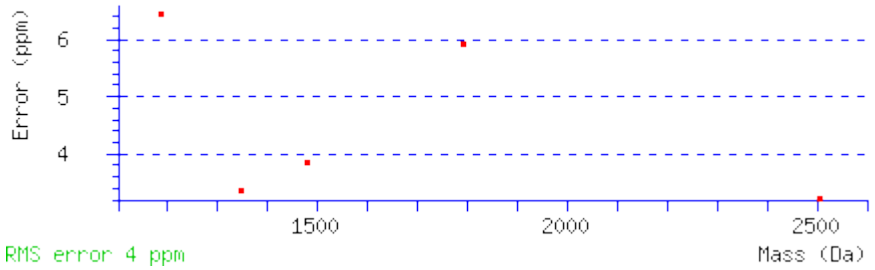
Taxonomy: Triticum turgidum subsp. dicoccon
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **26%**

Matched peptides shown in **Bold Red**

```
   1 GGGRMYVTMD RYENDWSVVK RGWDAQVLGE APHKFQNALE AVKTLRAEPK
  51 ANDQYLPPFV IVDESGKSVG PIVDGDAVVT FNFRADRMVM LAKALEFPDF
 101 DKFDRVRVPK IKYAGMLQYD GELKLPSKYL VSPPLIERTS GEYLVKNGVR
 151 TFACSETVKF GHVTFFWNGN RSGYFDETRE EYVEIPSDSG ITFNEQPKMK
 201 ALEIAERTRD AILSGKFDQV RINLPNG
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
68 - 84	1792.9333	1791.9260	1791.9155	0.0106	0	SVGPIVDGDAVVTFNFR	(No match)
129 - 138	1186.6906	1185.6833	1185.6757	0.0076	0	YLVSPPLIER	(No match)
151 - 171	2505.1848	2504.1775	2504.1694	0.0081	1	TFACSETVKFGHVTFFWNGNR	(No match)
160 - 171	1481.7129	1480.7056	1480.6999	0.0057	0	FGHVTFFWNGNR	(No match)
160 - 171	1481.7129	1480.7056	1480.6999	0.0057	0	FGHVTFFWNGNR	(Ions score 34)
210 - 221	1348.7264	1347.7191	1347.7146	0.0045	1	DAILSGKFDQVR	(Ions score 82)
210 - 221	1348.7264	1347.7191	1347.7146	0.0045	1	DAILSGKFDQVR	(No match)



Spot 20

Index

	Accession	Mass	Score	Description
1.	gi|6136111	51783	459	RecName: Full=UTP--glucose-1-phosphate uridylyltransferase; AltName: Full=UDP-glucose pyrophos
2.	gi|194688950	52227	339	unknown [Zea mays]
3.	gi|212275097	52227	339	hypothetical protein LOC100191463 [Zea mays]
4.	gi|158705664	51965	338	UDP-glucose pyrophosphorylase [Dendrocalamus sinicus]
5.	gi|212275438	52317	324	hypothetical protein LOC100191846 [Zea mays]
6.	gi|220682974	52431	306	UDP-glucose pyrophosphorylase [Saccharum officinarum]
7.	gi|37729658	52131	297	UDP-glucose pyrophosphorylase [Bambusa oldhamii]
8.	gi|115480571	51821	297	Os09g0553200 [Oryza sativa (japonica cultivar-group)]
9.	gi|88866516	51791	297	UDP-glucose pyrophosphorylase [Oryza sativa (indica cultivar-group)]
10.	gi|114848914	51813	297	UDP-glucose pyrophosphorylase [Oryza sativa (indica cultivar-group)]

Results List

1. gi|6136111 **Mass:** 51783 **Score:** 459 **Expect:** 7.6e-041 **Queries matched:** 26

RecName: Full=UTP--glucose-1-phosphate uridylyltransferase; AltName: Full=UDP-glucose pyrophosphory

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
702.4088	701.4015	701.4071	-0.0056	104	109	0	---	SVIEVR
790.4575	789.4502	789.4497	0.0006	407	413	0	---	VANFLAR
846.5212	845.5139	845.5123	0.0017	358	364	1	---	SRFLPVK
918.5548	917.5475	917.5446	0.0029	406	413	1	---	KVANFLAR
1052.5386	1051.5313	1051.5298	0.0016	261	270	0	---	GGTLISYEGR
1111.7338	1110.7265	1110.7376	-0.0110	79	88	1	---	ALLDKLVVLK
1300.7242	1299.7169	1299.7285	-0.0116	416	427	0	---	SIPSIVELDSLK
1312.7596	1311.7523	1311.7510	0.0013	333	345	0	72	VLQLETAAGAAIR
1312.7596	1311.7523	1311.7510	0.0013	333	345	0	---	VLQLETAAGAAIR
1358.7452	1357.7379	1357.7493	-0.0113	172	183	0	---	IVTEDFLPLPSK
1463.6866	1462.6793	1462.6908	-0.0115	89	103	0	---	LNGGLGTTMGCTGPK
1475.7909	1474.7836	1474.7932	-0.0096	295	306	0	---	IFNTNNLWVNLK
1479.6849	1478.6776	1478.6857	-0.0081	89	103	0	---	LNGGLGTTMGCTGPK + Oxidation (M)
1539.7246	1538.7173	1538.7252	-0.0079	40	52	0	108	YLSGEAEQIEWSK
1539.7246	1538.7173	1538.7252	-0.0079	40	52	0	---	YLSGEAEQIEWSK
1575.8867	1574.8794	1574.8919	-0.0125	414	427	1	---	FKSIPSIVELDSLK
1641.8766	1640.8693	1640.8773	-0.0080	391	405	0	---	VKPSNPSIELGPEFK
1679.8929	1678.8856	1678.8889	-0.0033	255	270	1	---	TLADVKGGTLISYEGR
1750.9441	1749.9368	1749.9565	-0.0197	293	306	1	---	FKIFNTNNLWVNLK
1769.9738	1768.9665	1768.9722	-0.0057	391	406	1	---	VKPSNPSIELGPEFKK
1769.9738	1768.9665	1768.9722	-0.0057	391	406	1	78	VKPSNPSIELGPEFKK

1780.9775	1779.9702	1779.9804	-0.0102	311 - 326	1	---	LVDAEALKMEIIPNPK
1796.9771	1795.9698	1795.9753	-0.0055	311 - 326	1	---	LVDAEALKMEIIPNPK + Oxidation (M)
1863.9628	1862.9555	1863.0253	-0.0698	333 - 349	1	---	VLQLETAAGAAIRFFEK
1940.0712	1939.0639	1939.0737	-0.0098	327 - 345	1	---	EVDGVKVLQLETAAGAAIR
2892.5303	2891.5230	2891.5392	-0.0162	365 - 390	1	---	ATSDLLLVQSDLYTLVDGYVIRNPAR

No match to: 713.4095, 734.4982, 736.4973, 750.5197, 765.3887, 768.5233, 797.4609, 806.4505, 917.2792, 978.5045, 1077.1870, 1101.5369, 1117.5294, 1279.7675, 1334.8816, 1348.7349, 1385.7344, 1390.6862, 1438.7821, 1446.6938, 1448.9131, 1572.8069, 1671.9220, 1671.9220, 1739.9232, 1790.9253, 1825.8942, 1983.8425, 2019.9862, 2108.0935, 2140.9988, 2157.0015, 2183.9958, 2183.9958, 2303.0859, 2319.0955, 2504.2456, 2522.2813, 2653.2776

2. gi|194688950 **Mass:** 52227 **Score:** 339 **Expect:** 7.6e-029 **Queries matched:** 21

unknown [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
702.4088	701.4015	701.4071	-0.0056	104 - 109		0	---	SVIEVR
790.4575	789.4502	789.4497	0.0006	407 - 413		0	---	VANFLAR
846.5212	845.5139	845.5123	0.0017	358 - 364		1	---	SRFLPVK
918.5548	917.5475	917.5446	0.0029	406 - 413		1	---	KVANFLAR
1052.5386	1051.5313	1051.5298	0.0016	261 - 270		0	---	GGTLISYEGR
1300.7242	1299.7169	1299.7285	-0.0116	416 - 427		0	---	SIPSIVELDSLK
1312.7596	1311.7523	1311.7510	0.0013	333 - 345		0	72	VLQLETAAGAAIR
1312.7596	1311.7523	1311.7510	0.0013	333 - 345		0	---	VLQLETAAGAAIR
1358.7452	1357.7379	1357.7493	-0.0113	172 - 183		0	---	IVTEDFLPLPSK
1463.6866	1462.6793	1462.6908	-0.0115	89 - 103		0	---	LNGGLGTTMGCTGPK
1475.7909	1474.7836	1474.7932	-0.0096	295 - 306		0	---	IFNTNNLWVNLK
1479.6849	1478.6776	1478.6857	-0.0081	89 - 103		0	---	LNGGLGTTMGCTGPK + Oxidation (M)
1539.7246	1538.7173	1538.7252	-0.0079	40 - 52		0	108	YLSGEAEQIEWSK
1539.7246	1538.7173	1538.7252	-0.0079	40 - 52		0	---	YLSGEAEQIEWSK
1575.8867	1574.8794	1574.8919	-0.0125	414 - 427		1	---	FKSIPSIVELDSLK
1679.8929	1678.8856	1678.8889	-0.0033	255 - 270		1	---	TLADVKGGTLISYEGR
1750.9441	1749.9368	1749.9565	-0.0197	293 - 306		1	---	FKIFNTNNLWVNLK
1940.0712	1939.0639	1939.0737	-0.0098	327 - 345		1	---	EVDGVKVLQLETAAGAAIR
2108.0935	2107.0862	2107.0949	-0.0087	271 - 288		0	---	VQLLEIAQVPDEHVNEFK
2157.0015	2155.9942	2156.0272	-0.0330	454 - 473		1	---	LEVPDGAVFENKDVNGPEDL
2892.5303	2891.5230	2891.5392	-0.0162	365 - 390		1	---	ATSDLLLVQSDLYTLVDGFVIRNPSR

No match to: 713.4095, 734.4982, 736.4973, 750.5197, 765.3887, 768.5233, 797.4609, 806.4505, 917.2792, 978.5045, 1077.1870, 1101.5369, 1111.7338, 1117.5294, 1279.7675, 1334.8816, 1348.7349, 1385.7344, 1390.6862, 1438.7821, 1446.6938, 1448.9131, 1572.8069, 1641.8766, 1671.9220, 1671.9220, 1739.9232, 1769.9738, 1769.9738, 1780.9775, 1790.9253, 1796.9771, 1825.8942, 1863.9628, 1983.8425, 2019.9862, 2140.9988, 2183.9958, 2183.9958, 2303.0859, 2319.0955, 2504.2456, 2522.2813, 2653.2776

3. gi|212275097 **Mass:** 52227 **Score:** 339 **Expect:** 7.6e-029 **Queries matched:** 21

hypothetical protein LOC100191463 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
702.4088	701.4015	701.4071	-0.0056	104	109	0	---	SVIEVR
790.4575	789.4502	789.4497	0.0006	407	413	0	---	VANFLAR
846.5212	845.5139	845.5123	0.0017	358	364	1	---	SRFLPVK
918.5548	917.5475	917.5446	0.0029	406	413	1	---	KVANFLAR
1052.5386	1051.5313	1051.5298	0.0016	261	270	0	---	GGTLISYEGR
1300.7242	1299.7169	1299.7285	-0.0116	416	427	0	---	SIPSIVELDSLK
1312.7596	1311.7523	1311.7510	0.0013	333	345	0	72	VLQLETAAGAAIR
1312.7596	1311.7523	1311.7510	0.0013	333	345	0	---	VLQLETAAGAAIR
1358.7452	1357.7379	1357.7493	-0.0113	172	183	0	---	IVTEDFLPLPSK
1463.6866	1462.6793	1462.6908	-0.0115	89	103	0	---	LNGGLGTTMGCTGPK
1475.7909	1474.7836	1474.7932	-0.0096	295	306	0	---	IFNTNNLWVNLK
1479.6849	1478.6776	1478.6857	-0.0081	89	103	0	---	LNGGLGTTMGCTGPK + Oxidation (M)
1539.7246	1538.7173	1538.7252	-0.0079	40	52	0	108	YLSGEAEQIEWSK
1539.7246	1538.7173	1538.7252	-0.0079	40	52	0	---	YLSGEAEQIEWSK
1575.8867	1574.8794	1574.8919	-0.0125	414	427	1	---	FKSIPSIVELDSLK
1679.8929	1678.8856	1678.8889	-0.0033	255	270	1	---	TLADVKGGTLISYEGR
1750.9441	1749.9368	1749.9565	-0.0197	293	306	1	---	FKIFNTNNLWVNLK
1940.0712	1939.0639	1939.0737	-0.0098	327	345	1	---	EVDGVKVLQLETAAGAAIR
2108.0935	2107.0862	2107.0949	-0.0087	271	288	0	---	VQLLEIAQVPDEHVNEFK
2157.0015	2155.9942	2156.0272	-0.0330	454	473	1	---	LEVPDGAVFENKDVNGPEDL
2892.5303	2891.5230	2891.5392	-0.0162	365	390	1	---	ATSDLLLVQSDLYTLVDGFVIRNPSR

No match to: 713.4095, 734.4982, 736.4973, 750.5197, 765.3887, 768.5233, 797.4609, 806.4505, 917.2792, 978.5045, 1077.1870, 1101.5369, 1111.7338, 1117.5294, 1279.7675, 1334.8816, 1348.7349, 1385.7344, 1390.6862, 1438.7821, 1446.6938, 1448.9131, 1572.8069, 1641.8766, 1671.9220, 1671.9220, 1739.9232, 1769.9738, 1769.9738, 1780.9775, 1790.9253, 1796.9771, 1825.8942, 1863.9628, 1983.8425, 2019.9862, 2140.9988, 2183.9958, 2183.9958, 2303.0859, 2319.0955, 2504.2456, 2522.2813, 2653.2776

4. gi|158705664 **Mass:** 51965 **Score:** 338 **Expect:** 9.6e-029 **Queries matched:** 22

UDP-glucose pyrophosphorylase [Dendrocalamus sinicus]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
702.4088	701.4015	701.4071	-0.0056	104	109	0	---	SVIEVR
790.4575	789.4502	789.4497	0.0006	407	413	0	---	VANFLAR
846.5212	845.5139	845.5123	0.0017	358	364	1	---	SRFLPVK
918.5548	917.5475	917.5446	0.0029	406	413	1	---	KVANFLAR
1052.5386	1051.5313	1051.5298	0.0016	261	270	0	---	GGTLISYEGR
1300.7242	1299.7169	1299.7285	-0.0116	416	427	0	---	SIPSIVELDSLK
1312.7596	1311.7523	1311.7510	0.0013	333	345	0	72	VLQLETAAGAAIR
1312.7596	1311.7523	1311.7510	0.0013	333	345	0	---	VLQLETAAGAAIR
1358.7452	1357.7379	1357.7493	-0.0113	172	183	0	---	IVTEDFLPLPSK
1463.6866	1462.6793	1462.6908	-0.0115	89	103	0	---	LNGGLGTTMGCTGPK
1475.7909	1474.7836	1474.7932	-0.0096	295	306	0	---	IFNTNNLWVNLK

1479.6849	1478.6776	1478.6857	-0.0081	89 - 103	0	---	LNGGLGTTMGCTGPK + Oxidation (M)
1539.7246	1538.7173	1538.7252	-0.0079	40 - 52	0	108	YLSGEAEQIEWSK
1539.7246	1538.7173	1538.7252	-0.0079	40 - 52	0	---	YLSGEAEQIEWSK
1575.8867	1574.8794	1574.8919	-0.0125	414 - 427	1	---	FKSIPSIVELDSLK
1679.8929	1678.8856	1678.8889	-0.0033	255 - 270	1	---	TLADVKGGTLISYEGR
1750.9441	1749.9368	1749.9565	-0.0197	293 - 306	1	---	FKIFNTNNLWVNLK
1780.9775	1779.9702	1779.9804	-0.0102	311 - 326	1	---	LVEGEALKMEIIPNPK
1796.9771	1795.9698	1795.9753	-0.0055	311 - 326	1	---	LVEGEALKMEIIPNPK + Oxidation (M)
1940.0712	1939.0639	1939.0737	-0.0098	327 - 345	1	---	EVDGVKVLQLETAAGAAIR
2108.0935	2107.0862	2107.0949	-0.0087	271 - 288	0	---	VQLLEIAQVPDEHVNEFK
2140.9988	2139.9915	2140.0535	-0.0619	454 - 473	1	---	LEISDGAVLENKDINGPEDL

No match to: 713.4095, 734.4982, 736.4973, 750.5197, 765.3887, 768.5233, 797.4609, 806.4505, 917.2792, 978.5045, 1077.1870, 1101.5369, 1111.7338, 1117.5294, 1279.7675, 1334.8816, 1348.7349, 1385.7344, 1390.6862, 1438.7821, 1446.6938, 1448.9131, 1572.8069, 1641.8766, 1671.9220, 1671.9220, 1739.9232, 1769.9738, 1769.9738, 1790.9253, 1825.8942, 1863.9628, 1983.8425, 2019.9862, 2157.0015, 2183.9958, 2183.9958, 2303.0859, 2319.0955, 2504.2456, 2522.2813, 2653.2776, 2892.5303

5. gi|212275438 **Mass:** 52317 **Score:** 324 **Expect:** 2.4e-027 **Queries matched:** 20

hypothetical protein LOC100191846 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
702.4088	701.4015	701.4071	-0.0056	104 - 109	0	---	SVIEVR
790.4575	789.4502	789.4497	0.0006	407 - 413	0	---	VANFLAR
846.5212	845.5139	845.5123	0.0017	358 - 364	1	---	SRFLPVK
918.5548	917.5475	917.5446	0.0029	406 - 413	1	---	KVANFLAR
1052.5386	1051.5313	1051.5298	0.0016	261 - 270	0	---	GGTLISYEGR
1300.7242	1299.7169	1299.7285	-0.0116	416 - 427	0	---	SIPSIVELDSLK
1312.7596	1311.7523	1311.7510	0.0013	333 - 345	0	72	VLQLETAAGAAIR
1312.7596	1311.7523	1311.7510	0.0013	333 - 345	0	---	VLQLETAAGAAIR
1358.7452	1357.7379	1357.7493	-0.0113	172 - 183	0	---	IVTEDFLPLPSK
1463.6866	1462.6793	1462.6908	-0.0115	89 - 103	0	---	LNGGLGTTMGCTGPK
1475.7909	1474.7836	1474.7932	-0.0096	295 - 306	0	---	IFNTNNLWVNLK
1479.6849	1478.6776	1478.6857	-0.0081	89 - 103	0	---	LNGGLGTTMGCTGPK + Oxidation (M)
1539.7246	1538.7173	1538.7252	-0.0079	40 - 52	0	108	YLSGEAEQIEWSK
1539.7246	1538.7173	1538.7252	-0.0079	40 - 52	0	---	YLSGEAEQIEWSK
1575.8867	1574.8794	1574.8919	-0.0125	414 - 427	1	---	FKSIPSIVELDSLK
1679.8929	1678.8856	1678.8889	-0.0033	255 - 270	1	---	TLADVKGGTLISYEGR
1750.9441	1749.9368	1749.9565	-0.0197	293 - 306	1	---	FKIFNTNNLWVNLK
1940.0712	1939.0639	1939.0737	-0.0098	327 - 345	1	---	EVDGVKVLQLETAAGAAIR
2108.0935	2107.0862	2107.0949	-0.0087	271 - 288	0	---	VQLLEIAQVPDEHVNEFK
2892.5303	2891.5230	2891.5392	-0.0162	365 - 390	1	---	ATSDLLLVQSDLYTLVDGFVIRNPSR

No match to: 713.4095, 734.4982, 736.4973, 750.5197, 765.3887, 768.5233, 797.4609, 806.4505, 917.2792, 978.5045, 1077.1870, 1101.5369, 1111.7338, 1117.5294, 1279.7675, 1334.8816, 1348.7349, 1385.7344, 1390.6862, 1438.7821,

1446.6938, 1448.9131, 1572.8069, 1641.8766, 1671.9220, 1671.9220, 1739.9232, 1769.9738, 1769.9738, 1780.9775, 1790.9253, 1796.9771, 1825.8942, 1863.9628, 1983.8425, 2019.9862, 2140.9988, 2157.0015, 2183.9958, 2183.9958, 2303.0859, 2319.0955, 2504.2456, 2522.2813, 2653.2776

6. gi|220682974 **Mass:** 52431 **Score:** 306 **Expect:** 1.5e-025 **Queries matched:** 19

UDP-glucose pyrophosphorylase [Saccharum officinarum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
702.4088	701.4015	701.4071	-0.0056	107	112	0	---	SVIEVR
790.4575	789.4502	789.4497	0.0006	410	416	0	---	VANFLAR
846.5212	845.5139	845.5123	0.0017	361	367	1	---	SRFLPVK
918.5548	917.5475	917.5446	0.0029	409	416	1	---	KVANFLAR
1052.5386	1051.5313	1051.5298	0.0016	264	273	0	---	GGTLISYEGR
1300.7242	1299.7169	1299.7285	-0.0116	419	430	0	---	SIPSIVELDSLK
1312.7596	1311.7523	1311.7510	0.0013	336	348	0	72	VLQLETAAGAAIR
1312.7596	1311.7523	1311.7510	0.0013	336	348	0	---	VLQLETAAGAAIR
1358.7452	1357.7379	1357.7493	-0.0113	175	186	0	---	IVTEDFLPLPSK
1463.6866	1462.6793	1462.6908	-0.0115	92	106	0	---	LNGGLGTTMGCTGPK
1475.7909	1474.7836	1474.7932	-0.0096	298	309	0	---	IFNTNNLWVNLK
1479.6849	1478.6776	1478.6857	-0.0081	92	106	0	---	LNGGLGTTMGCTGPK + Oxidation (M)
1539.7246	1538.7173	1538.7252	-0.0079	43	55	0	108	YLSGEAEQIEWSK
1539.7246	1538.7173	1538.7252	-0.0079	43	55	0	---	YLSGEAEQIEWSK
1575.8867	1574.8794	1574.8919	-0.0125	417	430	1	---	FKSIPSIVELDSLK
1679.8929	1678.8856	1678.8889	-0.0033	258	273	1	---	TLADVKGGTLISYEGR
1750.9441	1749.9368	1749.9565	-0.0197	296	309	1	---	FKIFNTNNLWVNLK
1940.0712	1939.0639	1939.0737	-0.0098	330	348	1	---	EVDGVKVLQLETAAGAAIR
2108.0935	2107.0862	2107.0949	-0.0087	274	291	0	---	VQLLEIAQVPDEHVNEFK

No match to: 713.4095, 734.4982, 736.4973, 750.5197, 765.3887, 768.5233, 797.4609, 806.4505, 917.2792, 978.5045, 1077.1870, 1101.5369, 1111.7338, 1117.5294, 1279.7675, 1334.8816, 1348.7349, 1385.7344, 1390.6862, 1438.7821, 1446.6938, 1448.9131, 1572.8069, 1641.8766, 1671.9220, 1671.9220, 1739.9232, 1769.9738, 1769.9738, 1780.9775, 1790.9253, 1796.9771, 1825.8942, 1863.9628, 1983.8425, 2019.9862, 2140.9988, 2157.0015, 2183.9958, 2183.9958, 2303.0859, 2319.0955, 2504.2456, 2522.2813, 2653.2776, 2892.5303

7. gi|37729658 **Mass:** 52131 **Score:** 297 **Expect:** 1.2e-024 **Queries matched:** 18

UDP-glucose pyrophosphorylase [Bambusa oldhamii]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
702.4088	701.4015	701.4071	-0.0056	104	109	0	---	SVIEVR
790.4575	789.4502	789.4497	0.0006	407	413	0	---	VANFLAR
846.5212	845.5139	845.5123	0.0017	358	364	1	---	SRFLPVK
918.5548	917.5475	917.5446	0.0029	406	413	1	---	KVANFLAR
1052.5386	1051.5313	1051.5298	0.0016	261	270	0	---	GGTLISYEGR
1312.7596	1311.7523	1311.7510	0.0013	333	345	0	72	VLQLETAAGAAIR
1312.7596	1311.7523	1311.7510	0.0013	333	345	0	---	VLQLETAAGAAIR

1358.7452	1357.7379	1357.7493	-0.0113	172 - 183	0	---	IVTEDFLPLPSK
1463.6866	1462.6793	1462.6908	-0.0115	89 - 103	0	---	LNGGLGTTMGCTGPK
1475.7909	1474.7836	1474.7932	-0.0096	295 - 306	0	---	IFNTNNLWVNLK
1479.6849	1478.6776	1478.6857	-0.0081	89 - 103	0	---	LNGGLGTTMGCTGPK + Oxidation (M)
1539.7246	1538.7173	1538.7252	-0.0079	40 - 52	0	108	YLSGEAEQIEWSK
1539.7246	1538.7173	1538.7252	-0.0079	40 - 52	0	---	YLSGEAEQIEWSK
1679.8929	1678.8856	1678.8889	-0.0033	255 - 270	1	---	TLADVKGGTLISYEGR
1750.9441	1749.9368	1749.9565	-0.0197	293 - 306	1	---	FKIFNTNNLWVNLK
1863.9628	1862.9555	1863.0253	-0.0698	333 - 349	1	---	VLQLETAAGAAIRFFEK
1940.0712	1939.0639	1939.0737	-0.0098	327 - 345	1	---	EVDGVKVLQLETAAGAAIR
2108.0935	2107.0862	2107.0949	-0.0087	271 - 288	0	---	VQLLEIAQVPDEHVNEFK

No match to: 713.4095, 734.4982, 736.4973, 750.5197, 765.3887, 768.5233, 797.4609, 806.4505, 917.2792, 978.5045, 1077.1870, 1101.5369, 1111.7338, 1117.5294, 1279.7675, 1300.7242, 1334.8816, 1348.7349, 1385.7344, 1390.6862, 1438.7821, 1446.6938, 1448.9131, 1572.8069, 1575.8867, 1641.8766, 1671.9220, 1671.9220, 1739.9232, 1769.9738, 1769.9738, 1780.9775, 1790.9253, 1796.9771, 1825.8942, 1983.8425, 2019.9862, 2140.9988, 2157.0015, 2183.9958, 2183.9958, 2303.0859, 2319.0955, 2504.2456, 2522.2813, 2653.2776, 2892.5303

8. gi|115480571 **Mass:** 51821 **Score:** 297 **Expect:** 1.2e-024 **Queries matched:** 18

Os09g0553200 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
702.4088	701.4015	701.4071	-0.0056	101 - 106	0	---	SVIEVR
790.4575	789.4502	789.4497	0.0006	404 - 410	0	---	VANFLAR
846.5212	845.5139	845.5123	0.0017	355 - 361	1	---	SRFLPVK
918.5548	917.5475	917.5446	0.0029	403 - 410	1	---	KVANFLAR
1052.5386	1051.5313	1051.5298	0.0016	258 - 267	0	---	GGTLISYEGR
1312.7596	1311.7523	1311.7510	0.0013	330 - 342	0	72	VLQLETAAGAAIR
1312.7596	1311.7523	1311.7510	0.0013	330 - 342	0	---	VLQLETAAGAAIR
1358.7452	1357.7379	1357.7493	-0.0113	169 - 180	0	---	IVTEDFLPLPSK
1463.6866	1462.6793	1462.6908	-0.0115	86 - 100	0	---	LNGGLGTTMGCTGPK
1475.7909	1474.7836	1474.7932	-0.0096	292 - 303	0	---	IFNTNNLWVNLK
1479.6849	1478.6776	1478.6857	-0.0081	86 - 100	0	---	LNGGLGTTMGCTGPK + Oxidation (M)
1539.7246	1538.7173	1538.7252	-0.0079	37 - 49	0	108	YLSGEAEQIEWSK
1539.7246	1538.7173	1538.7252	-0.0079	37 - 49	0	---	YLSGEAEQIEWSK
1679.8929	1678.8856	1678.8889	-0.0033	252 - 267	1	---	TLADVKGGTLISYEGR
1750.9441	1749.9368	1749.9565	-0.0197	290 - 303	1	---	FKIFNTNNLWVNLK
1863.9628	1862.9555	1863.0253	-0.0698	330 - 346	1	---	VLQLETAAGAAIRFFEK
1940.0712	1939.0639	1939.0737	-0.0098	324 - 342	1	---	EVDGVKVLQLETAAGAAIR
2108.0935	2107.0862	2107.0949	-0.0087	268 - 285	0	---	VQLLEIAQVPDEHVNEFK

No match to: 713.4095, 734.4982, 736.4973, 750.5197, 765.3887, 768.5233, 797.4609, 806.4505, 917.2792, 978.5045, 1077.1870, 1101.5369, 1111.7338, 1117.5294, 1279.7675, 1300.7242, 1334.8816, 1348.7349, 1385.7344, 1390.6862, 1438.7821, 1446.6938, 1448.9131, 1572.8069, 1575.8867, 1641.8766, 1671.9220, 1671.9220, 1739.9232, 1769.9738, 1769.9738, 1780.9775, 1790.9253, 1796.9771, 1825.8942, 1983.8425, 2019.9862, 2140.9988, 2157.0015, 2183.9958,

2183.9958, 2303.0859, 2319.0955, 2504.2456, 2522.2813, 2653.2776, 2892.5303

9. gi|88866516 **Mass:** 51791 **Score:** 297 **Expect:** 1.2e-024 **Queries matched:** 18

UDP-glucose pyrophosphorylase [Oryza sativa (indica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
702.4088	701.4015	701.4071	-0.0056	101	106	0	---	SVIEVR
790.4575	789.4502	789.4497	0.0006	404	410	0	---	VANFLAR
846.5212	845.5139	845.5123	0.0017	355	361	1	---	SRFLPVK
918.5548	917.5475	917.5446	0.0029	403	410	1	---	KVANFLAR
1052.5386	1051.5313	1051.5298	0.0016	258	267	0	---	GGTLISYEGR
1312.7596	1311.7523	1311.7510	0.0013	330	342	0	72	VLQLETAAGAAIR
1312.7596	1311.7523	1311.7510	0.0013	330	342	0	---	VLQLETAAGAAIR
1358.7452	1357.7379	1357.7493	-0.0113	169	180	0	---	IVTEDFLPLPSK
1463.6866	1462.6793	1462.6908	-0.0115	86	100	0	---	LNGGLGTTMGCTGPK
1475.7909	1474.7836	1474.7932	-0.0096	292	303	0	---	IFNTNNLWVNLK
1479.6849	1478.6776	1478.6857	-0.0081	86	100	0	---	LNGGLGTTMGCTGPK + Oxidation (M)
1539.7246	1538.7173	1538.7252	-0.0079	37	49	0	108	YLSGEAEQIEWSK
1539.7246	1538.7173	1538.7252	-0.0079	37	49	0	---	YLSGEAEQIEWSK
1679.8929	1678.8856	1678.8889	-0.0033	252	267	1	---	TLADVKGGTLISYEGR
1750.9441	1749.9368	1749.9565	-0.0197	290	303	1	---	FKIFNTNNLWVNLK
1863.9628	1862.9555	1863.0253	-0.0698	330	346	1	---	VLQLETAAGAAIRFFEK
1940.0712	1939.0639	1939.0737	-0.0098	324	342	1	---	EVDGVKVLQLETAAGAAIR
2108.0935	2107.0862	2107.0949	-0.0087	268	285	0	---	VQLLEIAQVPDEHVNEFK

No match to: 713.4095, 734.4982, 736.4973, 750.5197, 765.3887, 768.5233, 797.4609, 806.4505, 917.2792, 978.5045, 1077.1870, 1101.5369, 1111.7338, 1117.5294, 1279.7675, 1300.7242, 1334.8816, 1348.7349, 1385.7344, 1390.6862, 1438.7821, 1446.6938, 1448.9131, 1572.8069, 1575.8867, 1641.8766, 1671.9220, 1671.9220, 1739.9232, 1769.9738, 1769.9738, 1780.9775, 1790.9253, 1796.9771, 1825.8942, 1983.8425, 2019.9862, 2140.9988, 2157.0015, 2183.9958, 2183.9958, 2303.0859, 2319.0955, 2504.2456, 2522.2813, 2653.2776, 2892.5303

10. gi|114848914 **Mass:** 51813 **Score:** 297 **Expect:** 1.2e-024 **Queries matched:** 18

UDP-glucose pyrophosphorylase [Oryza sativa (indica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
702.4088	701.4015	701.4071	-0.0056	101	106	0	---	SVIEVR
790.4575	789.4502	789.4497	0.0006	404	410	0	---	VANFLAR
846.5212	845.5139	845.5123	0.0017	355	361	1	---	SRFLPVK
918.5548	917.5475	917.5446	0.0029	403	410	1	---	KVANFLAR
1052.5386	1051.5313	1051.5298	0.0016	258	267	0	---	GGTLISYEGR
1312.7596	1311.7523	1311.7510	0.0013	330	342	0	72	VLQLETAAGAAIR
1312.7596	1311.7523	1311.7510	0.0013	330	342	0	---	VLQLETAAGAAIR
1358.7452	1357.7379	1357.7493	-0.0113	169	180	0	---	IVTEDFLPLPSK
1463.6866	1462.6793	1462.6908	-0.0115	86	100	0	---	LNGGLGTTMGCTGPK
1475.7909	1474.7836	1474.7932	-0.0096	292	303	0	---	IFNTNNLWVNLK

1479.6849	1478.6776	1478.6857	-0.0081	86 - 100	0	---	LNGGLGTTMGCTGPK + Oxidation (M)
1539.7246	1538.7173	1538.7252	-0.0079	37 - 49	0	108	YLSGEAEQIEWSK
1539.7246	1538.7173	1538.7252	-0.0079	37 - 49	0	---	YLSGEAEQIEWSK
1679.8929	1678.8856	1678.8889	-0.0033	252 - 267	1	---	TLADVKGGTLISYEGR
1750.9441	1749.9368	1749.9565	-0.0197	290 - 303	1	---	FKIFNTNNLWVNLK
1863.9628	1862.9555	1863.0253	-0.0698	330 - 346	1	---	VLQLETAAGAAIRFFEK
1940.0712	1939.0639	1939.0737	-0.0098	324 - 342	1	---	EVDGVKVLQLETAAGAAIR
2108.0935	2107.0862	2107.0949	-0.0087	268 - 285	0	---	VQLLEIAQVPDEHVNEFK

No match to: 713.4095, 734.4982, 736.4973, 750.5197, 765.3887, 768.5233, 797.4609, 806.4505, 917.2792, 978.5045, 1077.1870, 1101.5369, 1111.7338, 1117.5294, 1279.7675, 1300.7242, 1334.8816, 1348.7349, 1385.7344, 1390.6862, 1438.7821, 1446.6938, 1448.9131, 1572.8069, 1575.8867, 1641.8766, 1671.9220, 1671.9220, 1739.9232, 1769.9738, 1769.9738, 1780.9775, 1790.9253, 1796.9771, 1825.8942, 1983.8425, 2019.9862, 2140.9988, 2157.0015, 2183.9958, 2183.9958, 2303.0859, 2319.0955, 2504.2456, 2522.2813, 2653.2776, 2892.5303

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 65

Protein View

Match to: **gi|6136111** Score: **459** Expect: **7.6e-041**
RecName: Full=UTP--glucose-1-phosphate uridylyltransferase; AltName: Full=UDP-glucose pyrophosphory

Nominal mass (M_r): **51783**; Calculated pI value: **5.20**
NCBI BLAST search of gi|6136111 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Hordeum vulgare
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|1212996 from Hordeum vulgare subsp. vulgare

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **41%**

Matched peptides shown in **Bold Red**

```
   1 MAAAAVAADS KIDGLRDAVA KLGEISENEK AGFISLVSRY LSGEAEQIEW
  51 SKIQTPTDEV VVPYDTLAPP PEDLDAMKAL LDKLVVLKLN GGLGTTMGCT
 101 GPKSVIEVRN GFTFLDLIVI QIESLNKKYG CSVPLLLMNS FNTHDDTQKI
 151 VEKYSNSNIE IHTFNQSQYP RIVTEDFLPL PSKGQTGKDG WYPPGHGDVF
 201 PSLNNSGKLD TLLSQGKEYV FVANSDNLGA IVDIKILNHL IHNQNEYCME
 251 VTPKTLADVK GGTLISYEGR VQLLEIAQVP DEHVDEFKSI EKFKIFNTNN
 301 LWVNLKAIKR LVDAEALKME IIPNPKEVDG VKVLQLETAA GAAIRFFEKA
 351 IGINVPRSRF LPVKATSDLL LVQSDLYTLV DGYVIRNPAR VKPSNPSIEL
 401 GPEFKKVANF LARFKSIPSI VELDSLKVSG DVSFGSGVVL KGNVTIAAKA
 451 GVKLEIPDGA VLENKDINGP EDI
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
40 - 52	1539.7246	1538.7173	1538.7252	-0.0079	0	**YLSGEAEQIEWSK** (Ions score 108)
40 - 52	1539.7246	1538.7173	1538.7252	-0.0079	0	**YLSGEAEQIEWSK** (No match)
79 - 88	1111.7338	1110.7265	1110.7376	-0.0110	1	**ALLDKLVVLK** (No match)
89 - 103	1463.6866	1462.6793	1462.6908	-0.0115	0	**LNGGLGTTMGCTGPK** (No match)
89 - 103	1479.6849	1478.6776	1478.6857	-0.0081	0	**LNGGLGTTMGCTGPK** Oxidation (M) (No match)
104 - 109	702.4088	701.4015	701.4071	-0.0056	0	**SVIEVR** (No match)
172 - 183	1358.7452	1357.7379	1357.7493	-0.0113	0	**IVTEDFLPLPSK** (No match)
255 - 270	1679.8929	1678.8856	1678.8889	-0.0033	1	**TLADVKGGTLISYEGR** (No match)
261 - 270	1052.5386	1051.5313	1051.5298	0.0016	0	**GGTLISYEGR** (No match)
293 - 306	1750.9441	1749.9368	1749.9565	-0.0197	1	**FKIFNTNNLWVNLK** (No match)
295 - 306	1475.7909	1474.7836	1474.7932	-0.0096	0	**IFNTNNLWVNLK** (No match)
311 - 326	1780.9775	1779.9702	1779.9804	-0.0102	1	**LVDAEALKMEIIPNPK** (No match)
311 - 326	1796.9771	1795.9698	1795.9753	-0.0055	1	**LVDAEALKMEIIPNPK** Oxidation (M) (No match)
327 - 345	1940.0712	1939.0639	1939.0737	-0.0098	1	**EVDGVKVLQLETAAGAAIR** (No match)
333 - 345	1312.7596	1311.7523	1311.7510	0.0013	0	**VLQLETAAGAAIR** (Ions score 72)
333 - 345	1312.7596	1311.7523	1311.7510	0.0013	0	**VLQLETAAGAAIR** (No match)
333 - 349	1863.9628	1862.9555	1863.0253	-0.0698	1	**VLQLETAAGAAIRFFEK** (No match)
358 - 364	846.5212	845.5139	845.5123	0.0017	1	**SRFLPVK** (No match)
365 - 390	2892.5303	2891.5230	2891.5392	-0.0162	1	**ATSDLLLVQSDLYTLVDGYVIRNPAR** (No match)
391 - 405	1641.8766	1640.8693	1640.8773	-0.0080	0	**VKPSNPSIELGPEFK** (No match)
391 - 406	1769.9738	1768.9665	1768.9722	-0.0057	1	**VKPSNPSIELGPEFKK** (No match)
391 - 406	1769.9738	1768.9665	1768.9722	-0.0057	1	**VKPSNPSIELGPEFKK** (Ions score 78)
406 - 413	918.5548	917.5475	917.5446	0.0029	1	**KVANFLAR** (No match)
407 - 413	790.4575	789.4502	789.4497	0.0006	0	**VANFLAR** (No match)
414 - 427	1575.8867	1574.8794	1574.8919	-0.0125	1	**FKSIPSIVELDSLK** (No match)
416 - 427	1300.7242	1299.7169	1299.7285	-0.0116	0	**SIPSIVELDSLK** (No match)

Spot 21

Index

	Accession	Mass	Score	Description
1.	gi|218184182	48356	286	hypothetical protein OsI_32842 [Oryza sativa Indica Group]
2.	gi|780372	48299	285	enolase
3.	gi|90110845	48285	285	RecName: Full=Enolase; AltName: Full=2-phosphoglycerate dehydratase; AltName: Full=2-phospho-D
4.	gi|115481260	48227	285	Os10g0167300 [Oryza sativa (japonica cultivar-group)]
5.	gi|110288667	51892	284	Enolase, putative, expressed [Oryza sativa (japonica cultivar-group)]
6.	gi|110288669	51834	284	Enolase, putative, expressed [Oryza sativa (japonica cultivar-group)]
7.	gi|22655764	46197	273	Putative enolase (2-phospho-D-glycerate hydroylase) [Oryza sativa (japonica cultivar-group)]
8.	gi|115451911	48285	270	Os03g0248600 [Oryza sativa (japonica cultivar-group)]
9.	gi|218192440	48299	270	hypothetical protein OsI_10758 [Oryza sativa Indica Group]
10.	gi|162460735	48418	217	enolase 2 [Zea mays]

Results List

1. gi|218184182 **Mass:** 48356 **Score:** 286 **Expect:** 1.5e-023 **Queries matched:** 15

hypothetical protein OsI_32842 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
765.3979	764.3906	764.3817	0.0090	12	17	0	---	QIFDSR
978.5164	977.5091	977.4970	0.0121	440	447	1	45	FRAPVEPY
978.5164	977.5091	977.4970	0.0121	440	447	1	---	FRAPVEPY
1101.5448	1100.5375	1100.5185	0.0190	375	384	0	46	AGWGVMTSHR
1101.5448	1100.5375	1100.5185	0.0190	375	384	0	---	AGWGVMTSHR
1117.5380	1116.5307	1116.5134	0.0173	375	384	0	---	AGWGVMTSHR + Oxidation (M)
1118.6465	1117.6392	1117.6607	-0.0215	416	424	1	---	LAKYNQLLR
1257.6488	1256.6415	1256.6196	0.0219	374	384	1	---	RAGWGVMTSHR
1273.6510	1272.6437	1272.6145	0.0292	374	384	1	---	RAGWGVMTSHR + Oxidation (M)
1573.8627	1572.8554	1572.8358	0.0196	356	370	0	---	VNQIGSVTESIEAVK
1679.9424	1678.9351	1678.9518	-0.0167	133	147	1	35	KIPLYQHIANLAGNK
1679.9424	1678.9351	1678.9518	-0.0167	133	147	1	---	KIPLYQHIANLAGNK
1790.9595	1789.9522	1789.9209	0.0313	36	53	0	60	AAVPSGASTGVYEALELR
1790.9595	1789.9522	1789.9209	0.0313	36	53	0	---	AAVPSGASTGVYEALELR
1983.9110	1982.9037	1982.8462	0.0576	18	35	0	---	GNPTVEVDVCCSDGTFAR

No match to: 768.5382, 1312.7831, 1385.7532, 1385.7532, 1390.7145, 1409.8273, 1572.8689, 1739.9482, 2141.0427, 2442.2825, 2558.3259

2. gi|780372 **Mass:** 48299 **Score:** 285 **Expect:** 1.9e-023 **Queries matched:** 15

enolase

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
765.3979	764.3906	764.3817	0.0090	12	17	0	---	QIFDSR

978.5164	977.5091	977.4970	0.0121	439 - 446	1	45	FRAPVEPY
978.5164	977.5091	977.4970	0.0121	439 - 446	1	---	FRAPVEPY
1101.5448	1100.5375	1100.5185	0.0190	374 - 383	0	46	AGWGVMTSHR
1101.5448	1100.5375	1100.5185	0.0190	374 - 383	0	---	AGWGVMTSHR
1117.5380	1116.5307	1116.5134	0.0173	374 - 383	0	---	AGWGVMTSHR + Oxidation (M)
1118.6465	1117.6392	1117.6607	-0.0215	415 - 423	1	---	LAKYNQLLR
1257.6488	1256.6415	1256.6196	0.0219	373 - 383	1	---	RAGWGVMTSHR
1273.6510	1272.6437	1272.6145	0.0292	373 - 383	1	---	RAGWGVMTSHR + Oxidation (M)
1573.8627	1572.8554	1572.8358	0.0196	355 - 369	0	---	VNQIGSVTESIEAVK
1679.9424	1678.9351	1678.9518	-0.0167	133 - 147	1	35	KIPLYQHIANLAGNK
1679.9424	1678.9351	1678.9518	-0.0167	133 - 147	1	---	KIPLYQHIANLAGNK
1790.9595	1789.9522	1789.9209	0.0313	36 - 53	0	60	AAVPSGASTGVYEALELR
1790.9595	1789.9522	1789.9209	0.0313	36 - 53	0	---	AAVPSGASTGVYEALELR
1983.9110	1982.9037	1982.8462	0.0576	18 - 35	0	---	GNPTVEVDVCCSDGTFAR

No match to: 768.5382, 1312.7831, 1385.7532, 1385.7532, 1390.7145, 1409.8273, 1572.8689, 1739.9482, 2141.0427, 2442.2825, 2558.3259

3. gi|90110845 **Mass:** 48285 **Score:** 285 **Expect:** 1.9e-023 **Queries matched:** 15

RecName: Full=Enolase; AltName: Full=2-phosphoglycerate dehydratase; AltName: Full=2-phospho-D-glyc

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
765.3979	764.3906	764.3817	0.0090	12 - 17		0	---	QIFDSR
978.5164	977.5091	977.4970	0.0121	439 - 446		1	45	FRAPVEPY
978.5164	977.5091	977.4970	0.0121	439 - 446		1	---	FRAPVEPY
1101.5448	1100.5375	1100.5185	0.0190	374 - 383		0	46	AGWGVMTSHR
1101.5448	1100.5375	1100.5185	0.0190	374 - 383		0	---	AGWGVMTSHR
1117.5380	1116.5307	1116.5134	0.0173	374 - 383		0	---	AGWGVMTSHR + Oxidation (M)
1118.6465	1117.6392	1117.6607	-0.0215	415 - 423		1	---	LAKYNQLLR
1257.6488	1256.6415	1256.6196	0.0219	373 - 383		1	---	RAGWGVMTSHR
1273.6510	1272.6437	1272.6145	0.0292	373 - 383		1	---	RAGWGVMTSHR + Oxidation (M)
1573.8627	1572.8554	1572.8358	0.0196	355 - 369		0	---	VNQIGSVTESIEAVK
1679.9424	1678.9351	1678.9518	-0.0167	133 - 147		1	35	KIPLYQHIANLAGNK
1679.9424	1678.9351	1678.9518	-0.0167	133 - 147		1	---	KIPLYQHIANLAGNK
1790.9595	1789.9522	1789.9209	0.0313	36 - 53		0	60	AAVPSGASTGVYEALELR
1790.9595	1789.9522	1789.9209	0.0313	36 - 53		0	---	AAVPSGASTGVYEALELR
1983.9110	1982.9037	1982.8462	0.0576	18 - 35		0	---	GNPTVEVDVCCSDGTFAR

No match to: 768.5382, 1312.7831, 1385.7532, 1385.7532, 1390.7145, 1409.8273, 1572.8689, 1739.9482, 2141.0427, 2442.2825, 2558.3259

4. gi|115481260 **Mass:** 48227 **Score:** 285 **Expect:** 1.9e-023 **Queries matched:** 15

Os10g0167300 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide

765.3979	764.3906	764.3817	0.0090	12 - 17	0	---	QIFDSR
978.5164	977.5091	977.4970	0.0121	439 - 446	1	45	FRAPVEPY
978.5164	977.5091	977.4970	0.0121	439 - 446	1	---	FRAPVEPY
1101.5448	1100.5375	1100.5185	0.0190	374 - 383	0	46	AGWGVMTSHR
1101.5448	1100.5375	1100.5185	0.0190	374 - 383	0	---	AGWGVMTSHR
1117.5380	1116.5307	1116.5134	0.0173	374 - 383	0	---	AGWGVMTSHR + Oxidation (M)
1118.6465	1117.6392	1117.6607	-0.0215	415 - 423	1	---	LAKYNQLLR
1257.6488	1256.6415	1256.6196	0.0219	373 - 383	1	---	RAGWGVMTSHR
1273.6510	1272.6437	1272.6145	0.0292	373 - 383	1	---	RAGWGVMTSHR + Oxidation (M)
1573.8627	1572.8554	1572.8358	0.0196	355 - 369	0	---	VNQIGSVTESIEAVK
1679.9424	1678.9351	1678.9518	-0.0167	133 - 147	1	35	KIPLYQHIANLAGNK
1679.9424	1678.9351	1678.9518	-0.0167	133 - 147	1	---	KIPLYQHIANLAGNK
1790.9595	1789.9522	1789.9209	0.0313	36 - 53	0	60	AAVPSGASTGVYEALELR
1790.9595	1789.9522	1789.9209	0.0313	36 - 53	0	---	AAVPSGASTGVYEALELR
1983.9110	1982.9037	1982.8462	0.0576	18 - 35	0	---	GNPTVEVDVCCSDGTFAR

No match to: 768.5382, 1312.7831, 1385.7532, 1385.7532, 1390.7145, 1409.8273, 1572.8689, 1739.9482, 2141.0427, 2442.2825, 2558.3259

5. gi|110288667 **Mass:** 51892 **Score:** 284 **Expect:** 2.4e-023 **Queries matched:** 15

Enolase, putative, expressed [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start End	Miss	Ions	Peptide
765.3979	764.3906	764.3817	0.0090	46 - 51	0	---	QIFDSR
978.5164	977.5091	977.4970	0.0121	473 - 480	1	45	FRAPVEPY
978.5164	977.5091	977.4970	0.0121	473 - 480	1	---	FRAPVEPY
1101.5448	1100.5375	1100.5185	0.0190	408 - 417	0	46	AGWGVMTSHR
1101.5448	1100.5375	1100.5185	0.0190	408 - 417	0	---	AGWGVMTSHR
1117.5380	1116.5307	1116.5134	0.0173	408 - 417	0	---	AGWGVMTSHR + Oxidation (M)
1118.6465	1117.6392	1117.6607	-0.0215	449 - 457	1	---	LAKYNQLLR
1257.6488	1256.6415	1256.6196	0.0219	407 - 417	1	---	RAGWGVMTSHR
1273.6510	1272.6437	1272.6145	0.0292	407 - 417	1	---	RAGWGVMTSHR + Oxidation (M)
1573.8627	1572.8554	1572.8358	0.0196	389 - 403	0	---	VNQIGSVTESIEAVK
1679.9424	1678.9351	1678.9518	-0.0167	167 - 181	1	35	KIPLYQHIANLAGNK
1679.9424	1678.9351	1678.9518	-0.0167	167 - 181	1	---	KIPLYQHIANLAGNK
1790.9595	1789.9522	1789.9209	0.0313	70 - 87	0	60	AAVPSGASTGVYEALELR
1790.9595	1789.9522	1789.9209	0.0313	70 - 87	0	---	AAVPSGASTGVYEALELR
1983.9110	1982.9037	1982.8462	0.0576	52 - 69	0	---	GNPTVEVDVCCSDGTFAR

No match to: 768.5382, 1312.7831, 1385.7532, 1385.7532, 1390.7145, 1409.8273, 1572.8689, 1739.9482, 2141.0427, 2442.2825, 2558.3259

6. gi|110288669 **Mass:** 51834 **Score:** 284 **Expect:** 2.4e-023 **Queries matched:** 15

Enolase, putative, expressed [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
765.3979	764.3906	764.3817	0.0090	46	51	0	---	QIFDSR
978.5164	977.5091	977.4970	0.0121	473	480	1	45	FRAPVEPY
978.5164	977.5091	977.4970	0.0121	473	480	1	---	FRAPVEPY
1101.5448	1100.5375	1100.5185	0.0190	408	417	0	46	AGWGVMTSHR
1101.5448	1100.5375	1100.5185	0.0190	408	417	0	---	AGWGVMTSHR
1117.5380	1116.5307	1116.5134	0.0173	408	417	0	---	AGWGVMTSHR + Oxidation (M)
1118.6465	1117.6392	1117.6607	-0.0215	449	457	1	---	LAKYNQLLR
1257.6488	1256.6415	1256.6196	0.0219	407	417	1	---	RAGWGVMTSHR
1273.6510	1272.6437	1272.6145	0.0292	407	417	1	---	RAGWGVMTSHR + Oxidation (M)
1573.8627	1572.8554	1572.8358	0.0196	389	403	0	---	VNQIGSVTESIEAVK
1679.9424	1678.9351	1678.9518	-0.0167	167	181	1	35	KIPLYQHIANLAGNK
1679.9424	1678.9351	1678.9518	-0.0167	167	181	1	---	KIPLYQHIANLAGNK
1790.9595	1789.9522	1789.9209	0.0313	70	87	0	60	AAVPSGASTGVYEALELR
1790.9595	1789.9522	1789.9209	0.0313	70	87	0	---	AAVPSGASTGVYEALELR
1983.9110	1982.9037	1982.8462	0.0576	52	69	0	---	GNPTVEVDVCCSDGTFAR

No match to: 768.5382, 1312.7831, 1385.7532, 1385.7532, 1390.7145, 1409.8273, 1572.8689, 1739.9482, 2141.0427, 2442.2825, 2558.3259

7. gi|22655764 **Mass:** 46197 **Score:** 273 **Expect:** 3e-022 **Queries matched:** 14

Putative enolase (2-phospho-D-glycerate hydroylase) [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
765.3979	764.3906	764.3817	0.0090	12	17	0	---	QIFDSR
978.5164	977.5091	977.4970	0.0121	421	428	1	45	FRAPVEPY
978.5164	977.5091	977.4970	0.0121	421	428	1	---	FRAPVEPY
1101.5448	1100.5375	1100.5185	0.0190	375	384	0	46	AGWGVMTSHR
1101.5448	1100.5375	1100.5185	0.0190	375	384	0	---	AGWGVMTSHR
1117.5380	1116.5307	1116.5134	0.0173	375	384	0	---	AGWGVMTSHR + Oxidation (M)
1257.6488	1256.6415	1256.6196	0.0219	374	384	1	---	RAGWGVMTSHR
1273.6510	1272.6437	1272.6145	0.0292	374	384	1	---	RAGWGVMTSHR + Oxidation (M)
1573.8627	1572.8554	1572.8358	0.0196	356	370	0	---	VNQIGSVTESIEAVK
1679.9424	1678.9351	1678.9518	-0.0167	133	147	1	35	KIPLYQHIANLAGNK
1679.9424	1678.9351	1678.9518	-0.0167	133	147	1	---	KIPLYQHIANLAGNK
1790.9595	1789.9522	1789.9209	0.0313	36	53	0	60	AAVPSGASTGVYEALELR
1790.9595	1789.9522	1789.9209	0.0313	36	53	0	---	AAVPSGASTGVYEALELR
1983.9110	1982.9037	1982.8462	0.0576	18	35	0	---	GNPTVEVDVCCSDGTFAR

No match to: 768.5382, 1118.6465, 1312.7831, 1385.7532, 1385.7532, 1390.7145, 1409.8273, 1572.8689, 1739.9482, 2141.0427, 2442.2825, 2558.3259

8. gi|115451911 **Mass:** 48285 **Score:** 270 **Expect:** 6.1e-022 **Queries matched:** 14

Os03g0248600 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide

765.3979	764.3906	764.3817	0.0090	12 - 17	0	---	QIFDSR
978.5164	977.5091	977.4970	0.0121	438 - 445	1	45	FRAPVEPY
978.5164	977.5091	977.4970	0.0121	438 - 445	1	---	FRAPVEPY
1101.5448	1100.5375	1100.5185	0.0190	373 - 382	0	46	AGWGVMTSHR
1101.5448	1100.5375	1100.5185	0.0190	373 - 382	0	---	AGWGVMTSHR
1117.5380	1116.5307	1116.5134	0.0173	373 - 382	0	---	AGWGVMTSHR + Oxidation (M)
1118.6465	1117.6392	1117.6607	-0.0215	414 - 422	1	---	LAKYNQLLR
1257.6488	1256.6415	1256.6196	0.0219	372 - 382	1	---	RAGWGVMTSHR
1273.6510	1272.6437	1272.6145	0.0292	372 - 382	1	---	RAGWGVMTSHR + Oxidation (M)
1573.8627	1572.8554	1572.8358	0.0196	354 - 368	0	---	VNQIGSVTESIEAVK
1679.9424	1678.9351	1678.9518	-0.0167	133 - 147	1	35	KIPLYQHIANLAGNK
1679.9424	1678.9351	1678.9518	-0.0167	133 - 147	1	---	KIPLYQHIANLAGNK
1790.9595	1789.9522	1789.9209	0.0313	36 - 53	0	60	AAVPSGASTGVYEALELR
1790.9595	1789.9522	1789.9209	0.0313	36 - 53	0	---	AAVPSGASTGVYEALELR

No match to: 768.5382, 1312.7831, 1385.7532, 1385.7532, 1390.7145, 1409.8273, 1572.8689, 1739.9482, 1983.9110, 2141.0427, 2442.2825, 2558.3259

9. gi|218192440 **Mass:** 48299 **Score:** 270 **Expect:** 6.1e-022 **Queries matched:** 14

hypothetical protein OsI_10758 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
765.3979	764.3906	764.3817	0.0090	12 - 17	0	---	QIFDSR
978.5164	977.5091	977.4970	0.0121	438 - 445	1	45	FRAPVEPY
978.5164	977.5091	977.4970	0.0121	438 - 445	1	---	FRAPVEPY
1101.5448	1100.5375	1100.5185	0.0190	373 - 382	0	46	AGWGVMTSHR
1101.5448	1100.5375	1100.5185	0.0190	373 - 382	0	---	AGWGVMTSHR
1117.5380	1116.5307	1116.5134	0.0173	373 - 382	0	---	AGWGVMTSHR + Oxidation (M)
1118.6465	1117.6392	1117.6607	-0.0215	414 - 422	1	---	LAKYNQLLR
1257.6488	1256.6415	1256.6196	0.0219	372 - 382	1	---	RAGWGVMTSHR
1273.6510	1272.6437	1272.6145	0.0292	372 - 382	1	---	RAGWGVMTSHR + Oxidation (M)
1573.8627	1572.8554	1572.8358	0.0196	354 - 368	0	---	VNQIGSVTESIEAVK
1679.9424	1678.9351	1678.9518	-0.0167	133 - 147	1	35	KIPLYQHIANLAGNK
1679.9424	1678.9351	1678.9518	-0.0167	133 - 147	1	---	KIPLYQHIANLAGNK
1790.9595	1789.9522	1789.9209	0.0313	36 - 53	0	60	AAVPSGASTGVYEALELR
1790.9595	1789.9522	1789.9209	0.0313	36 - 53	0	---	AAVPSGASTGVYEALELR

No match to: 768.5382, 1312.7831, 1385.7532, 1385.7532, 1390.7145, 1409.8273, 1572.8689, 1739.9482, 1983.9110, 2141.0427, 2442.2825, 2558.3259

10. gi|162460735 **Mass:** 48418 **Score:** 217 **Expect:** 1.2e-016 **Queries matched:** 12

enolase 2 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
765.3979	764.3906	764.3817	0.0090	12 - 17	0	---	QIFDSR

978.5164	977.5091	977.4970	0.0121	439 - 446	1	45	FRAPVEPY
978.5164	977.5091	977.4970	0.0121	439 - 446	1	---	FRAPVEPY
1101.5448	1100.5375	1100.5185	0.0190	374 - 383	0	46	AGWGVMTSHR
1101.5448	1100.5375	1100.5185	0.0190	374 - 383	0	---	AGWGVMTSHR
1117.5380	1116.5307	1116.5134	0.0173	374 - 383	0	---	AGWGVMTSHR + Oxidation (M)
1118.6465	1117.6392	1117.6607	-0.0215	415 - 423	1	---	LAKYNQLLR
1257.6488	1256.6415	1256.6196	0.0219	373 - 383	1	---	RAGWGVMTSHR
1273.6510	1272.6437	1272.6145	0.0292	373 - 383	1	---	RAGWGVMTSHR + Oxidation (M)
1573.8627	1572.8554	1572.8358	0.0196	355 - 369	0	---	VNQIGSVTESIEAVK
1790.9595	1789.9522	1789.9209	0.0313	36 - 53	0	60	AAVPSGASTGVYEALELR
1790.9595	1789.9522	1789.9209	0.0313	36 - 53	0	---	AAVPSGASTGVYEALELR

No match to: 768.5382, 1312.7831, 1385.7532, 1385.7532, 1390.7145, 1409.8273, 1572.8689, 1679.9424, 1679.9424, 1739.9482, 1983.9110, 2141.0427, 2442.2825, 2558.3259

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 26

Protein View

Match to: **gi|218184182** Score: **286** Expect: **1.5e-023**
hypothetical protein OsI_32842 [Oryza sativa Indica Group]

Nominal mass (M_r): **48356**; Calculated pI value: **5.41**
NCBI BLAST search of gi|218184182 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Oryza sativa Indica Group
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|222612493 from Oryza sativa Japonica Group

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **22%**

Matched peptides shown in **Bold Red**

```
   1 MAATIVSVKA RQIFDSRGNP TVEVDVCCSD GTFARAAVPS GASTGVYEAL
  51 ELRDGGSDYL GKGVSKAVDN VNSVIAPALI GKDPTSQAEL DNFMVQQLDG
 101 TKNEWGWCKQ KLGANAILAV SLAICKAGAI IKKIPLYQHI ANLAGNKQLV
 151 LPVPAFNVIN GGSHAGNKLA MQAEFMILPT GAASFKEAMK MGVEVYHNLK
 201 SVIKKKYGQD ATNVGDEGGF APNIQENKEG LELLKTAIEK AGYTGKVVIG
 251 MDVAASEFYN DKDKTYDLNF KEENNDGSQK ISGDSLKNVY KSFVSEYPIV
 301 SIEDPFDQDD WEHYAKMTAE IGEQVQIVGD DLLVTNPTRV AKAIQEKSCN
 351 ALLLKVNQIG SVTESIEAVK MSKRAGWGVM TSHRSGETED TFIADLAVGL
 401 ATGQIKTGAP CRSERLAKYN QLLRIEEELG AAAVYAGAKF RAPVEPY
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
12 - 17	765.3979	764.3906	764.3817	0.0090	0	QIFDSR	(No match)
18 - 35	1983.9110	1982.9037	1982.8462	0.0576	0	GNPTVEVDVCCSDGTFAR	(No match)
36 - 53	1790.9595	1789.9522	1789.9209	0.0313	0	AAVPSGASTGVYEALELR	(Ions score 60)
36 - 53	1790.9595	1789.9522	1789.9209	0.0313	0	AAVPSGASTGVYEALELR	(No match)
133 - 147	1679.9424	1678.9351	1678.9518	-0.0167	1	KIPLYQHIANLAGNK	(Ions score 35)
133 - 147	1679.9424	1678.9351	1678.9518	-0.0167	1	KIPLYQHIANLAGNK	(No match)
356 - 370	1573.8627	1572.8554	1572.8358	0.0196	0	VNQIGSVTESIEAVK	(No match)
374 - 384	1257.6488	1256.6415	1256.6196	0.0219	1	RAGWGVMTSHR	(No match)
374 - 384	1273.6510	1272.6437	1272.6145	0.0292	1	RAGWGVMTSHR	Oxidation (M) (No match)
375 - 384	1101.5448	1100.5375	1100.5185	0.0190	0	AGWGVMTSHR	(Ions score 46)
375 - 384	1101.5448	1100.5375	1100.5185	0.0190	0	AGWGVMTSHR	(No match)
375 - 384	1117.5380	1116.5307	1116.5134	0.0173	0	AGWGVMTSHR	Oxidation (M) (No match)
416 - 424	1118.6465	1117.6392	1117.6607	-0.0215	1	LAKYNQLLR	(No match)
440 - 447	978.5164	977.5091	977.4970	0.0121	1	FRAPVEPY	(Ions score 45)
440 - 447	978.5164	977.5091	977.4970	0.0121	1	FRAPVEPY	(No match)

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Index

	Accession	Mass	Score	Description
1.	gi|162460735	48418	334	enolase 2 [Zea mays]
2.	gi|195619804	48386	334	enolase [Zea mays]
3.	gi|223944349	48370	334	unknown [Zea mays]
4.	gi|192910834	48127	275	enolase [Elaeis guineensis]
5.	gi|223947323	51441	127	unknown [Zea mays]
6.	gi|222622048	46847	118	hypothetical protein OsJ_05131 [Oryza sativa Japonica Group]
7.	gi|218189925	49849	117	hypothetical protein OsI_05593 [Oryza sativa Indica Group]
8.	gi|115443819	51808	117	Os02g0117700 [Oryza sativa (japonica cultivar-group)]
9.	gi|7417426	51866	117	UDP-glucose pyrophosphorylase [Oryza sativa subsp. indica]
10.	gi|12585489	51501	115	RecName: Full=UTP--glucose-1-phosphate uridylyltransferase; AltName: Full=UDP-glucose pyrophos

Results List

1. gi|162460735 **Mass:** 48418 **Score:** 334 **Expect:** 2.4e-028 **Queries matched:** 8

enolase 2 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
765.3914	764.3841	764.3817	0.0025	12	17	0	---	QIFDSR
978.5112	977.5039	977.4970	0.0069	439	446	1	51	FRAPVEPY
978.5112	977.5039	977.4970	0.0069	439	446	1	---	FRAPVEPY
1790.9568	1789.9495	1789.9209	0.0286	36	53	0	---	AAVPSGASTGVYEALELR
2321.2874	2320.2801	2320.2426	0.0376	418	438	1	---	YNQLLRIEEELGAIAVYAGAK
2321.2874	2320.2801	2320.2426	0.0376	418	438	1	41	YNQLLRIEEELGAIAVYAGAK
2557.3188	2556.3115	2556.2741	0.0375	316	338	0	186	MTEEIGEQVQIVGDDLLVTNPTR
2557.3188	2556.3115	2556.2741	0.0375	316	338	0	---	MTEEIGEQVQIVGDDLLVTNPTR

No match to: 1385.7476, 1385.7476, 1679.9282, 1983.8876, 2141.0374, 2141.0374, 2441.3003, 2634.5115, 2687.5034

2. gi|195619804 **Mass:** 48386 **Score:** 334 **Expect:** 2.4e-028 **Queries matched:** 8

enolase [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
765.3914	764.3841	764.3817	0.0025	12	17	0	---	QIFDSR
978.5112	977.5039	977.4970	0.0069	439	446	1	51	FRAPVEPY
978.5112	977.5039	977.4970	0.0069	439	446	1	---	FRAPVEPY
1790.9568	1789.9495	1789.9209	0.0286	36	53	0	---	AAVPSGASTGVYEALELR
2321.2874	2320.2801	2320.2426	0.0376	418	438	1	---	YNQLLRIEEELGAIAVYAGAK
2321.2874	2320.2801	2320.2426	0.0376	418	438	1	41	YNQLLRIEEELGAIAVYAGAK
2557.3188	2556.3115	2556.2741	0.0375	316	338	0	186	MTEEIGEQVQIVGDDLLVTNPTR
2557.3188	2556.3115	2556.2741	0.0375	316	338	0	---	MTEEIGEQVQIVGDDLLVTNPTR

No match to: 1385.7476, 1385.7476, 1679.9282, 1983.8876, 2141.0374, 2141.0374, 2441.3003, 2634.5115, 2687.5034

3. gi|223944349 **Mass:** 48370 **Score:** 334 **Expect:** 2.4e-028 **Queries matched:** 8

unknown [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
765.3914	764.3841	764.3817	0.0025	12	17	0	---	QIFDSR
978.5112	977.5039	977.4970	0.0069	439	446	1	51	FRAPVEPY
978.5112	977.5039	977.4970	0.0069	439	446	1	---	FRAPVEPY
1790.9568	1789.9495	1789.9209	0.0286	36	53	0	---	AAVPSGASTGVYEALELR
2321.2874	2320.2801	2320.2426	0.0376	418	438	1	---	YNQLLRIEEELGAIAVYAGAK
2321.2874	2320.2801	2320.2426	0.0376	418	438	1	41	YNQLLRIEEELGAIAVYAGAK
2557.3188	2556.3115	2556.2741	0.0375	316	338	0	186	MTEEIGEQVQIVGDDLLVTNPTR
2557.3188	2556.3115	2556.2741	0.0375	316	338	0	---	MTEEIGEQVQIVGDDLLVTNPTR

No match to: 1385.7476, 1385.7476, 1679.9282, 1983.8876, 2141.0374, 2141.0374, 2441.3003, 2634.5115, 2687.5034

4. gi|192910834 **Mass:** 48127 **Score:** 275 **Expect:** 1.9e-022 **Queries matched:** 6

enolase [Elaeis guineensis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
765.3914	764.3841	764.3817	0.0025	11	16	0	---	QIFDSR
978.5112	977.5039	977.4970	0.0069	438	445	1	51	FRAPVEPY
978.5112	977.5039	977.4970	0.0069	438	445	1	---	FRAPVEPY
1679.9282	1678.9209	1678.9518	-0.0309	132	146	1	---	KIPLYQHIANLAGNK
2557.3188	2556.3115	2556.2741	0.0375	315	337	0	186	MTEEIGEQVQIVGDDLLVTNPTR
2557.3188	2556.3115	2556.2741	0.0375	315	337	0	---	MTEEIGEQVQIVGDDLLVTNPTR

No match to: 1385.7476, 1385.7476, 1790.9568, 1983.8876, 2141.0374, 2141.0374, 2321.2874, 2321.2874, 2441.3003, 2634.5115, 2687.5034

5. gi|223947323 **Mass:** 51441 **Score:** 127 **Expect:** 1.2e-007 **Queries matched:** 4

unknown [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1385.7476	1384.7403	1384.7251	0.0152	340	351	0	---	FFDHAIGINVPR
1385.7476	1384.7403	1384.7251	0.0152	340	351	0	101	FFDHAIGINVPR
1679.9282	1678.9209	1678.8889	0.0320	249	264	1	---	TLADVKGGTLISYEGR
2441.3003	2440.2930	2440.2485	0.0445	359	380	0	---	ATSDLQLVQSDLYTLVDGFVTR

No match to: 765.3914, 978.5112, 978.5112, 1790.9568, 1983.8876, 2141.0374, 2141.0374, 2321.2874, 2321.2874, 2557.3188, 2557.3188, 2634.5115, 2687.5034

6. gi|222622048 **Mass:** 46847 **Score:** 118 **Expect:** 9.6e-007 **Queries matched:** 3

hypothetical protein OsJ_05131 [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1385.7476	1384.7403	1384.7251	0.0152	297	308	0	---	FFDHAIGINVPR
1385.7476	1384.7403	1384.7251	0.0152	297	308	0	101	FFDHAIGINVPR

2441.3003 2440.2930 2440.2485 0.0445 316 - 337 0 --- ATSDLQLVQSDLYTLVDGFVTR

No match to: 765.3914, 978.5112, 978.5112, 1679.9282, 1790.9568, 1983.8876, 2141.0374, 2141.0374, 2321.2874, 2321.2874, 2557.3188, 2557.3188, 2634.5115, 2687.5034

7. gi|218189925 **Mass:** 49849 **Score:** 117 **Expect:** 1.2e-006 **Queries matched:** 3

hypothetical protein OsI_05593 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1385.7476	1384.7403	1384.7251	0.0152	323	334	0	---	FFDHAIGINVPR
1385.7476	1384.7403	1384.7251	0.0152	323	334	0	101	FFDHAIGINVPR
2441.3003	2440.2930	2440.2485	0.0445	342	363	0	---	ATSDLQLVQSDLYTLVDGFVTR

No match to: 765.3914, 978.5112, 978.5112, 1679.9282, 1790.9568, 1983.8876, 2141.0374, 2141.0374, 2321.2874, 2321.2874, 2557.3188, 2557.3188, 2634.5115, 2687.5034

8. gi|115443819 **Mass:** 51808 **Score:** 117 **Expect:** 1.2e-006 **Queries matched:** 3

Os02g0117700 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1385.7476	1384.7403	1384.7251	0.0152	340	351	0	---	FFDHAIGINVPR
1385.7476	1384.7403	1384.7251	0.0152	340	351	0	101	FFDHAIGINVPR
2441.3003	2440.2930	2440.2485	0.0445	359	380	0	---	ATSDLQLVQSDLYTLVDGFVTR

No match to: 765.3914, 978.5112, 978.5112, 1679.9282, 1790.9568, 1983.8876, 2141.0374, 2141.0374, 2321.2874, 2321.2874, 2557.3188, 2557.3188, 2634.5115, 2687.5034

9. gi|7417426 **Mass:** 51866 **Score:** 117 **Expect:** 1.2e-006 **Queries matched:** 3

UDP-glucose pyrophosphorylase [Oryza sativa subsp. indica]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1385.7476	1384.7403	1384.7251	0.0152	340	351	0	---	FFDHAIGINVPR
1385.7476	1384.7403	1384.7251	0.0152	340	351	0	101	FFDHAIGINVPR
2441.3003	2440.2930	2440.2485	0.0445	359	380	0	---	ATSDLQLVQSDLYTLVDGFVTR

No match to: 765.3914, 978.5112, 978.5112, 1679.9282, 1790.9568, 1983.8876, 2141.0374, 2141.0374, 2321.2874, 2321.2874, 2557.3188, 2557.3188, 2634.5115, 2687.5034

10. gi|12585489 **Mass:** 51501 **Score:** 115 **Expect:** 1.9e-006 **Queries matched:** 3

RecName: Full=UTP--glucose-1-phosphate uridylyltransferase; AltName: Full=UDP-glucose pyrophosphory

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1385.7476	1384.7403	1384.7251	0.0152	340	351	0	---	FFDHAIGINVPR
1385.7476	1384.7403	1384.7251	0.0152	340	351	0	101	FFDHAIGINVPR
1679.9282	1678.9209	1678.8889	0.0320	249	264	1	---	TLADVKGGTLISYEGR

No match to: 765.3914, 978.5112, 978.5112, 1790.9568, 1983.8876, 2141.0374, 2141.0374, 2321.2874, 2321.2874, 2441.3003, 2557.3188, 2557.3188, 2634.5115, 2687.5034

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Query1 (765.3914,1+) : 17

Protein View

Match to: **gi|195619804** Score: **334** Expect: **2.4e-028**
enolase [Zea mays]

Nominal mass (M_r): **48386**; Calculated pI value: **5.59**
NCBI BLAST search of gi|195619804 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Zea mays

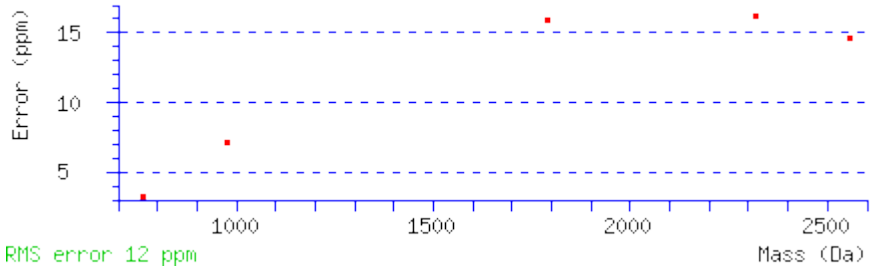
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **17%**

Matched peptides shown in **Bold Red**

```
     1 MAATIQSVKA RQIFDSRGNP TVEVDVFCSD GTFARAAVPS GASTGVYEAL
    51 ELRDGGSDYL GKGVSKAVNN VNSVIGPALI GKDPTAQTEI DNFMVQQLDG
   101 TKNEWGWCKQ KLGANAILAV SLAVCKAGAS IKRIPLYQHI ANLAGNKQLV
   151 LPVPAFNVIN GGSHAGNKLA MQEFMILPTG AASFKEAMKM GVEVYHHLKS
   201 VIKKKYGQDA TNVGDEGGFA PNIQENKEGL ELLKTAIEKA GYTGKVVIGM
   251 DVASSEFYSD KDQTYDLNFK EENNDGSQKI SGDSLKNVYK SFVSEYPIVS
   301 IEDPFDQDDW VHYAKMTEEI GEQVQIVGDD LLVTNPTRVA KAIKEKSCNA
   351 LLLKVNQIGS VTESIEAVKM SKRAGWGVMT SHRSGETEDT FIADLAVGLS
   401 TGQIKTGAPC RSERLAKYNQ LLRIEEELGA IAVYAGAKFR APVEPY
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
12 - 17	765.3914	764.3841	764.3817	0.0025	0	QIFDSR (No match)
36 - 53	1790.9568	1789.9495	1789.9209	0.0286	0	AAVPSGASTGVYEALELR (No match)
316 - 338	2557.3188	2556.3115	2556.2741	0.0375	0	MTEEIGEQVQIVGDDLLVTNPTR (Ions score 186)
316 - 338	2557.3188	2556.3115	2556.2741	0.0375	0	MTEEIGEQVQIVGDDLLVTNPTR (No match)
418 - 438	2321.2874	2320.2801	2320.2426	0.0376	1	YNQLLRIEEELGAIAVYAGAK (No match)
418 - 438	2321.2874	2320.2801	2320.2426	0.0376	1	YNQLLRIEEELGAIAVYAGAK (Ions score 41)
439 - 446	978.5112	977.5039	977.4970	0.0069	1	FRAPVEPY (Ions score 51)
439 - 446	978.5112	977.5039	977.4970	0.0069	1	FRAPVEPY (No match)



Spot 23

Index

	Accession	Mass	Score	Description
1.	gi|223947323	51441	295	unknown [Zea mays]
2.	gi|222622048	46847	254	hypothetical protein OsJ_05131 [Oryza sativa Japonica Group]
3.	gi|218189925	49849	249	hypothetical protein OsI_05593 [Oryza sativa Indica Group]
4.	gi|115443819	51808	247	Os02g0117700 [Oryza sativa (japonica cultivar-group)]
5.	gi|7417426	51866	247	UDP-glucose pyrophosphorylase [Oryza sativa subsp. indica]
6.	gi|12585489	51501	191	RecName: Full=UTP--glucose-1-phosphate uridylyltransferase; AltName: Full=UDP-glucose pyrophos
7.	gi|116787113	53356	133	unknown [Picea sitchensis]
8.	gi|32527831	51949	128	UDP-glucose pyrophosphorylase [Populus tremula x Populus tremuloides]
9.	gi|148908315	53349	121	unknown [Picea sitchensis]
10.	gi|12585472	51632	116	RecName: Full=UTP--glucose-1-phosphate uridylyltransferase; AltName: Full=UDP-glucose pyrophos

Results List

1. gi|223947323 **Mass:** 51441 **Score:** 295 **Expect:** 1.9e-024 **Queries matched:** 23

unknown [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
702.4168	701.4095	701.4071	0.0024	98	103	0	---	SVIEVR
735.4225	734.4152	734.4075	0.0078	401	407	0	---	VGSFLGR
846.5223	845.5150	845.5123	0.0028	352	358	1	---	SRFLPVK
863.5111	862.5038	862.5024	0.0014	400	407	1	---	KVGSFLGR
1052.5995	1051.5922	1051.5298	0.0625	255	264	0	---	GGTLISYEGR
1312.7654	1311.7581	1311.7510	0.0071	327	339	0	---	VLQLETAAGAAIR
1385.7407	1384.7334	1384.7251	0.0083	340	351	0	54	FFDHAIGINVPR
1385.7407	1384.7334	1384.7251	0.0083	340	351	0	---	FFDHAIGINVPR
1463.7178	1462.7105	1462.6908	0.0197	83	97	0	---	LNGGLGTTMGCTGPK
1475.7997	1474.7924	1474.7932	-0.0008	289	300	0	---	IFNTNNLWVNLK
1572.8427	1571.8354	1571.8347	0.0007	166	179	1	---	VVADEFLPWPSKGK
1575.8730	1574.8657	1574.8919	-0.0262	408	421	1	---	FKSIPSIVELDSLK
1679.9081	1678.9008	1678.8889	0.0119	249	264	1	---	TLADVKGGTLISYEGR
1679.9081	1678.9008	1678.8889	0.0119	249	264	1	23	TLADVKGGTLISYEGR
1750.9662	1749.9589	1749.9565	0.0024	287	300	1	---	FKIFNTNNLWVNLK
1796.9681	1795.9608	1795.9753	-0.0145	305	320	1	---	LVEADALKMEIIPNPK + Oxidation (M)
1940.0924	1939.0851	1939.0737	0.0114	321	339	1	---	EVDGVKVLQLETAAGAAIR
2367.2087	2366.2014	2366.1875	0.0140	230	248	1	---	ILNHLIHKQNEYCMEVTPK
2383.2034	2382.1961	2382.1824	0.0138	230	248	1	---	ILNHLIHKQNEYCMEVTPK + Oxidation (M)
2441.2605	2440.2532	2440.2485	0.0047	359	380	0	---	ATSDLQLVQSDLYTLVDGFVTR

2441.2605	2440.2532	2440.2485	0.0047	359 - 380	0	44	ATSDLQLVQSDLYTLVDGFVTR
2679.4780	2678.4707	2678.4655	0.0052	327 - 351	1	---	VLQLETAAGAAIRFFDHAIGINVPR
3025.6294	3024.6221	3024.6171	0.0050	354 - 380	1	---	FLPVKATSDLQLVQSDLYTLVDGFVTR

No match to: 713.3992, 724.4901, 734.4889, 768.5152, 782.4811, 808.4171, 848.5247, 936.5123, 965.5440, 978.5097, 1279.7625, 1447.6781, 1602.7478, 1616.7609, 1739.9388, 1758.8915, 1774.9303, 1790.9382, 1944.1184, 1983.8634, 2051.0874, 2130.0352, 2141.0176, 2141.0176, 2187.1150, 2230.2236, 2240.1489, 2270.1167, 2284.1921, 2417.2715, 2417.2715, 2508.3423, 2545.3208, 2564.1929, 2610.2991, 2663.3713, 2670.8943, 2686.4612, 2824.3235, 2921.3699, 3332.5684, 3349.6060

2. gi|222622048 **Mass:** 46847 **Score:** 254 **Expect:** 2.4e-020 **Queries matched:** 20

hypothetical protein OsJ_05131 [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
702.4168	701.4095	701.4071	0.0024	98 - 103		0	---	SVIEVR
808.4171	807.4098	807.4061	0.0037	358 - 364		0	---	VGCFLGR
846.5223	845.5150	845.5123	0.0028	309 - 315		1	---	SRFLPVK
936.5123	935.5050	935.5010	0.0040	357 - 364		1	---	KVGCFLGR
1312.7654	1311.7581	1311.7510	0.0071	284 - 296		0	---	VLQLETAAGAAIR
1385.7407	1384.7334	1384.7251	0.0083	297 - 308		0	54	FFDHAIGINVPR
1385.7407	1384.7334	1384.7251	0.0083	297 - 308		0	---	FFDHAIGINVPR
1463.7178	1462.7105	1462.6908	0.0197	83 - 97		0	---	LNGGLGTTMGCTGPK
1475.7997	1474.7924	1474.7932	-0.0008	246 - 257		0	---	IFNTNNLWVNLK
1572.8427	1571.8354	1571.8347	0.0007	123 - 136		1	---	VVADEFLPWPSKGK
1750.9662	1749.9589	1749.9565	0.0024	244 - 257		1	---	FKIFNTNNLWVNLK
1796.9681	1795.9608	1795.9753	-0.0145	262 - 277		1	---	LVEADALKMEIIPNPK + Oxidation (M)
1940.0924	1939.0851	1939.0737	0.0114	278 - 296		1	---	EVDGVKVLQLETAAGAAIR
2367.2087	2366.2014	2366.1875	0.0140	187 - 205		1	---	ILNHLIHKQNEYCMEVTPK
2383.2034	2382.1961	2382.1824	0.0138	187 - 205		1	---	ILNHLIHKQNEYCMEVTPK + Oxidation (M)
2441.2605	2440.2532	2440.2485	0.0047	316 - 337		0	---	ATSDLQLVQSDLYTLVDGFVTR
2441.2605	2440.2532	2440.2485	0.0047	316 - 337		0	44	ATSDLQLVQSDLYTLVDGFVTR
2564.1929	2563.1856	2563.1624	0.0233	137 - 159		1	---	TCKDGWYPPGHGDIFPSLMNSGK
2679.4780	2678.4707	2678.4655	0.0052	284 - 308		1	---	VLQLETAAGAAIRFFDHAIGINVPR
3025.6294	3024.6221	3024.6171	0.0050	311 - 337		1	---	FLPVKATSDLQLVQSDLYTLVDGFVTR

No match to: 713.3992, 724.4901, 734.4889, 735.4225, 768.5152, 782.4811, 848.5247, 863.5111, 965.5440, 978.5097, 1052.5995, 1279.7625, 1447.6781, 1575.8730, 1602.7478, 1616.7609, 1679.9081, 1679.9081, 1739.9388, 1758.8915, 1774.9303, 1790.9382, 1944.1184, 1983.8634, 2051.0874, 2130.0352, 2141.0176, 2141.0176, 2187.1150, 2230.2236, 2240.1489, 2270.1167, 2284.1921, 2417.2715, 2417.2715, 2508.3423, 2545.3208, 2610.2991, 2663.3713, 2670.8943, 2686.4612, 2824.3235, 2921.3699, 3332.5684, 3349.6060

3. gi|218189925 **Mass:** 49849 **Score:** 249 **Expect:** 7.6e-020 **Queries matched:** 20

hypothetical protein OsI_05593 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
702.4168	701.4095	701.4071	0.0024	98 - 103		0	---	SVIEVR

808.4171	807.4098	807.4061	0.0037	384 - 390	0	---	VGCFLGR
846.5223	845.5150	845.5123	0.0028	335 - 341	1	---	SRFLPVK
936.5123	935.5050	935.5010	0.0040	383 - 390	1	---	KVGCFLGR
1312.7654	1311.7581	1311.7510	0.0071	310 - 322	0	---	VLQLETAAGAAIR
1385.7407	1384.7334	1384.7251	0.0083	323 - 334	0	54	FFDHAIGINVPR
1385.7407	1384.7334	1384.7251	0.0083	323 - 334	0	---	FFDHAIGINVPR
1463.7178	1462.7105	1462.6908	0.0197	83 - 97	0	---	LNGGLGTTMGCTGPK
1475.7997	1474.7924	1474.7932	-0.0008	272 - 283	0	---	IFNTNNLWVNLK
1572.8427	1571.8354	1571.8347	0.0007	149 - 162	1	---	VVADEFLPWPSKGK
1750.9662	1749.9589	1749.9565	0.0024	270 - 283	1	---	FKIFNTNNLWVNLK
1796.9681	1795.9608	1795.9753	-0.0145	288 - 303	1	---	LVEADALKMEIIPNPK + Oxidation (M)
1940.0924	1939.0851	1939.0737	0.0114	304 - 322	1	---	EVDGVKVLQLETAAGAAIR
2367.2087	2366.2014	2366.1875	0.0140	213 - 231	1	---	ILNHLIHKQNEYCMEVTPK
2383.2034	2382.1961	2382.1824	0.0138	213 - 231	1	---	ILNHLIHKQNEYCMEVTPK + Oxidation (M)
2441.2605	2440.2532	2440.2485	0.0047	342 - 363	0	---	ATSDLQLVQSDLYTLVDGFVTR
2441.2605	2440.2532	2440.2485	0.0047	342 - 363	0	44	ATSDLQLVQSDLYTLVDGFVTR
2564.1929	2563.1856	2563.1624	0.0233	163 - 185	1	---	TCKDGWYPPGHGDIFPSLMNSGK
2679.4780	2678.4707	2678.4655	0.0052	310 - 334	1	---	VLQLETAAGAAIRFFDHAIGINVPR
3025.6294	3024.6221	3024.6171	0.0050	337 - 363	1	---	FLPVKATSDLQLVQSDLYTLVDGFVTR

No match to: 713.3992, 724.4901, 734.4889, 735.4225, 768.5152, 782.4811, 848.5247, 863.5111, 965.5440, 978.5097, 1052.5995, 1279.7625, 1447.6781, 1575.8730, 1602.7478, 1616.7609, 1679.9081, 1679.9081, 1739.9388, 1758.8915, 1774.9303, 1790.9382, 1944.1184, 1983.8634, 2051.0874, 2130.0352, 2141.0176, 2141.0176, 2187.1150, 2230.2236, 2240.1489, 2270.1167, 2284.1921, 2417.2715, 2417.2715, 2508.3423, 2545.3208, 2610.2991, 2663.3713, 2670.8943, 2686.4612, 2824.3235, 2921.3699, 3332.5684, 3349.6060

4. gi|115443819 **Mass:** 51808 **Score:** 247 **Expect:** 1.2e-019 **Queries matched:** 20

Os02g0117700 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start - End	Miss	Ions	Peptide
702.4168	701.4095	701.4071	0.0024	98 - 103	0	---	SVIEVR
808.4171	807.4098	807.4061	0.0037	401 - 407	0	---	VGCFLGR
846.5223	845.5150	845.5123	0.0028	352 - 358	1	---	SRFLPVK
936.5123	935.5050	935.5010	0.0040	400 - 407	1	---	KVGCFLGR
1312.7654	1311.7581	1311.7510	0.0071	327 - 339	0	---	VLQLETAAGAAIR
1385.7407	1384.7334	1384.7251	0.0083	340 - 351	0	54	FFDHAIGINVPR
1385.7407	1384.7334	1384.7251	0.0083	340 - 351	0	---	FFDHAIGINVPR
1463.7178	1462.7105	1462.6908	0.0197	83 - 97	0	---	LNGGLGTTMGCTGPK
1475.7997	1474.7924	1474.7932	-0.0008	289 - 300	0	---	IFNTNNLWVNLK
1572.8427	1571.8354	1571.8347	0.0007	166 - 179	1	---	VVADEFLPWPSKGK
1750.9662	1749.9589	1749.9565	0.0024	287 - 300	1	---	FKIFNTNNLWVNLK
1796.9681	1795.9608	1795.9753	-0.0145	305 - 320	1	---	LVEADALKMEIIPNPK + Oxidation (M)
1940.0924	1939.0851	1939.0737	0.0114	321 - 339	1	---	EVDGVKVLQLETAAGAAIR

2367.2087	2366.2014	2366.1875	0.0140	230 - 248	1	---	ILNHLIHKQNEYCMEVTPK
2383.2034	2382.1961	2382.1824	0.0138	230 - 248	1	---	ILNHLIHKQNEYCMEVTPK + Oxidation (M)
2441.2605	2440.2532	2440.2485	0.0047	359 - 380	0	---	ATSDLQLVQSDLYTLVDGFVTR
2441.2605	2440.2532	2440.2485	0.0047	359 - 380	0	44	ATSDLQLVQSDLYTLVDGFVTR
2564.1929	2563.1856	2563.1624	0.0233	180 - 202	1	---	TCKDGWYPPGHGDIFPSLMNSGK
2679.4780	2678.4707	2678.4655	0.0052	327 - 351	1	---	VLQLETAAGAAIRFFDHAIGINVPR
3025.6294	3024.6221	3024.6171	0.0050	354 - 380	1	---	FLPVKATSDLQLVQSDLYTLVDGFVTR

No match to: 713.3992, 724.4901, 734.4889, 735.4225, 768.5152, 782.4811, 848.5247, 863.5111, 965.5440, 978.5097, 1052.5995, 1279.7625, 1447.6781, 1575.8730, 1602.7478, 1616.7609, 1679.9081, 1679.9081, 1739.9388, 1758.8915, 1774.9303, 1790.9382, 1944.1184, 1983.8634, 2051.0874, 2130.0352, 2141.0176, 2141.0176, 2187.1150, 2230.2236, 2240.1489, 2270.1167, 2284.1921, 2417.2715, 2417.2715, 2508.3423, 2545.3208, 2610.2991, 2663.3713, 2670.8943, 2686.4612, 2824.3235, 2921.3699, 3332.5684, 3349.6060

5. gi|7417426 **Mass:** 51866 **Score:** 247 **Expect:** 1.2e-019 **Queries matched:** 20

UDP-glucose pyrophosphorylase [Oryza sativa subsp. indica]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
702.4168	701.4095	701.4071	0.0024	98 - 103		0	---	SVIEVR
808.4171	807.4098	807.4061	0.0037	401 - 407		0	---	VGCFLGR
846.5223	845.5150	845.5123	0.0028	352 - 358		1	---	SRFLPVK
936.5123	935.5050	935.5010	0.0040	400 - 407		1	---	KVGCFLGR
1312.7654	1311.7581	1311.7510	0.0071	327 - 339		0	---	VLQLETAAGAAIR
1385.7407	1384.7334	1384.7251	0.0083	340 - 351		0	54	FFDHAIGINVPR
1385.7407	1384.7334	1384.7251	0.0083	340 - 351		0	---	FFDHAIGINVPR
1463.7178	1462.7105	1462.6908	0.0197	83 - 97		0	---	LNGGLGTTMGCTGPK
1475.7997	1474.7924	1474.7932	-0.0008	289 - 300		0	---	IFNTNNLWVNLK
1572.8427	1571.8354	1571.8347	0.0007	166 - 179		1	---	VVADEFLPWPSKGK
1750.9662	1749.9589	1749.9565	0.0024	287 - 300		1	---	FKIFNTNNLWVNLK
1796.9681	1795.9608	1795.9753	-0.0145	305 - 320		1	---	LVEADALKMEIIPNPK + Oxidation (M)
1940.0924	1939.0851	1939.0737	0.0114	321 - 339		1	---	EVDGVKVLQLETAAGAAIR
2367.2087	2366.2014	2366.1875	0.0140	230 - 248		1	---	ILNHLIHKQNEYCMEVTPK
2383.2034	2382.1961	2382.1824	0.0138	230 - 248		1	---	ILNHLIHKQNEYCMEVTPK + Oxidation (M)
2441.2605	2440.2532	2440.2485	0.0047	359 - 380		0	---	ATSDLQLVQSDLYTLVDGFVTR
2441.2605	2440.2532	2440.2485	0.0047	359 - 380		0	44	ATSDLQLVQSDLYTLVDGFVTR
2564.1929	2563.1856	2563.1624	0.0233	180 - 202		1	---	TCKDGWYPPGHGDIFPSLMNSGK
2679.4780	2678.4707	2678.4655	0.0052	327 - 351		1	---	VLQLETAAGAAIRFFDHAIGINVPR
3025.6294	3024.6221	3024.6171	0.0050	354 - 380		1	---	FLPVKATSDLQLVQSDLYTLVDGFVTR

No match to: 713.3992, 724.4901, 734.4889, 735.4225, 768.5152, 782.4811, 848.5247, 863.5111, 965.5440, 978.5097, 1052.5995, 1279.7625, 1447.6781, 1575.8730, 1602.7478, 1616.7609, 1679.9081, 1679.9081, 1739.9388, 1758.8915, 1774.9303, 1790.9382, 1944.1184, 1983.8634, 2051.0874, 2130.0352, 2141.0176, 2141.0176, 2187.1150, 2230.2236, 2240.1489, 2270.1167, 2284.1921, 2417.2715, 2417.2715, 2508.3423, 2545.3208, 2610.2991, 2663.3713, 2670.8943, 2686.4612, 2824.3235, 2921.3699, 3332.5684, 3349.6060

6. gi|12585489 **Mass:** 51501 **Score:** 191 **Expect:** 4.8e-014 **Queries matched:** 17

RecName: Full=UTP--glucose-1-phosphate uridylyltransferase; AltName: Full=UDP-glucose pyrophosphory

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
702.4168	701.4095	701.4071	0.0024	98	103	0	---	SVIEVR
846.5223	845.5150	845.5123	0.0028	352	358	1	---	SRFLPVK
863.5111	862.5038	862.4582	0.0456	1	8	1	---	MADAKIAK + Oxidation (M)
965.5440	964.5367	964.5341	0.0026	25	33	0	---	SGFISLVSR
1052.5995	1051.5922	1051.5298	0.0625	255	264	0	---	GGTLISYEGR
1312.7654	1311.7581	1311.7510	0.0071	327	339	0	---	VLQLETAAGAAIR
1385.7407	1384.7334	1384.7251	0.0083	340	351	0	54	FFDHAIGINVPR
1385.7407	1384.7334	1384.7251	0.0083	340	351	0	---	FFDHAIGINVPR
1463.7178	1462.7105	1462.6908	0.0197	83	97	0	---	LNGGLGTTMGCTGPK
1475.7997	1474.7924	1474.7932	-0.0008	289	300	0	---	IFNTNNLWVNLK
1575.8730	1574.8657	1574.8919	-0.0262	408	421	1	---	FKSIPSIVELDSLK
1679.9081	1678.9008	1678.8889	0.0119	249	264	1	---	TLADVKGGTLISYEGR
1679.9081	1678.9008	1678.8889	0.0119	249	264	1	23	TLADVKGGTLISYEGR
1750.9662	1749.9589	1749.9565	0.0024	287	300	1	---	FKIFNTNNLWVNLK
1796.9681	1795.9608	1795.9753	-0.0145	305	320	1	---	LVEADALKMEIIPNPK + Oxidation (M)
1940.0924	1939.0851	1939.0737	0.0114	321	339	1	---	EVDGVKVLQLETAAGAAIR
2679.4780	2678.4707	2678.4655	0.0052	327	351	1	---	VLQLETAAGAAIRFFDHAIGINVPR

No match to: 713.3992, 724.4901, 734.4889, 735.4225, 768.5152, 782.4811, 808.4171, 848.5247, 936.5123, 978.5097, 1279.7625, 1447.6781, 1572.8427, 1602.7478, 1616.7609, 1739.9388, 1758.8915, 1774.9303, 1790.9382, 1944.1184, 1983.8634, 2051.0874, 2130.0352, 2141.0176, 2141.0176, 2187.1150, 2230.2236, 2240.1489, 2270.1167, 2284.1921, 2367.2087, 2383.2034, 2417.2715, 2417.2715, 2441.2605, 2441.2605, 2508.3423, 2545.3208, 2564.1929, 2610.2991, 2663.3713, 2670.8943, 2686.4612, 2824.3235, 2921.3699, 3025.6294, 3332.5684, 3349.6060

7. gi|116787113 **Mass:** 53356 **Score:** 133 **Expect:** 3e-008 **Queries matched:** 18

unknown [Picea sitchensis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
702.4168	701.4095	701.4071	0.0024	109	114	0	---	SVIEVR
846.5223	845.5150	845.5123	0.0028	363	369	1	---	SRFLPVK
1052.5995	1051.5922	1051.5298	0.0625	266	275	0	---	GGTLISYEGR
1312.7654	1311.7581	1311.7510	0.0071	338	350	0	---	VLQLETAAGAAIR
1385.7407	1384.7334	1384.7085	0.0249	459	470	0	---	LEIPDESVIENK
1385.7407	1384.7334	1384.7085	0.0249	459	470	0	---	LEIPDESVIENK
1463.7178	1462.7105	1462.6908	0.0197	94	108	0	---	LNGGLGTTMGCTGPK
1475.7997	1474.7924	1474.7932	-0.0008	300	311	0	---	IFNTNNLWVNLK
1575.8730	1574.8657	1574.8919	-0.0262	419	432	1	---	FKSIPSIIDLDSLK
1679.9081	1678.9008	1678.8889	0.0119	260	275	1	---	TLADVKGGTLISYEGR
1679.9081	1678.9008	1678.8889	0.0119	260	275	1	23	TLADVKGGTLISYEGR

1739.9388	1738.9315	1738.9253	0.0062	396 - 411	1	---	VNPANPSIELGPEFKK
1750.9662	1749.9589	1749.9565	0.0024	298 - 311	1	---	FKIFNTNNLWVNLK
1796.9681	1795.9608	1795.9753	-0.0145	316 - 331	1	---	LVEADALKMEIIPNPK + Oxidation (M)
1940.0924	1939.0851	1939.0737	0.0114	332 - 350	1	---	EVDGVKVLQLETAAGAAIR
1944.1184	1943.1111	1942.9822	0.1289	138 - 154	0	---	VPLVLMNSFNTHDDTIK
2141.0176	2140.0103	2140.0377	-0.0274	194 - 213	0	---	EGWYPPGHGDVFPALLNSGK
2141.0176	2140.0103	2140.0377	-0.0274	194 - 213	0	---	EGWYPPGHGDVFPALLNSGK

No match to: 713.3992, 724.4901, 734.4889, 735.4225, 768.5152, 782.4811, 808.4171, 848.5247, 863.5111, 936.5123, 965.5440, 978.5097, 1279.7625, 1447.6781, 1572.8427, 1602.7478, 1616.7609, 1758.8915, 1774.9303, 1790.9382, 1983.8634, 2051.0874, 2130.0352, 2187.1150, 2230.2236, 2240.1489, 2270.1167, 2284.1921, 2367.2087, 2383.2034, 2417.2715, 2417.2715, 2441.2605, 2441.2605, 2508.3423, 2545.3208, 2564.1929, 2610.2991, 2663.3713, 2670.8943, 2679.4780, 2686.4612, 2824.3235, 2921.3699, 3025.6294, 3332.5684, 3349.6060

8. gi|32527831 **Mass:** 51949 **Score:** 128 **Expect:** 9.6e-008 **Queries matched:** 12

UDP-glucose pyrophosphorylase [Populus tremula x Populus tremuloides]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
702.4168	701.4095	701.4071	0.0024	100 - 105	0	---	SVIEVR
846.5223	845.5150	845.5123	0.0028	354 - 360	1	---	SRFLPVK
1312.7654	1311.7581	1311.7510	0.0071	329 - 341	0	---	VLQLETAAGAAIR
1385.7407	1384.7334	1384.7251	0.0083	342 - 353	0	54	FFDHAIGINVPR
1385.7407	1384.7334	1384.7251	0.0083	342 - 353	0	---	FFDHAIGINVPR
1463.7178	1462.7105	1462.6908	0.0197	85 - 99	0	---	LNGGLGTTMGCTGPK
1475.7997	1474.7924	1474.7932	-0.0008	291 - 302	0	---	IFNTNNLWVNLK
1750.9662	1749.9589	1749.9565	0.0024	289 - 302	1	---	FKIFNTNNLWVNLK
1796.9681	1795.9608	1795.9753	-0.0145	307 - 322	1	---	LVEADALKMEIIPNPK + Oxidation (M)
1940.0924	1939.0851	1939.0737	0.0114	323 - 341	1	---	EVDGVKVLQLETAAGAAIR
2564.1929	2563.1856	2563.3645	-0.1789	267 - 288	1	---	VQLLEIAQVPDQHVNEFKSIEK
2679.4780	2678.4707	2678.4655	0.0052	329 - 353	1	---	VLQLETAAGAAIRFFDHAIGINVPR

No match to: 713.3992, 724.4901, 734.4889, 735.4225, 768.5152, 782.4811, 808.4171, 848.5247, 863.5111, 936.5123, 965.5440, 978.5097, 1052.5995, 1279.7625, 1447.6781, 1572.8427, 1575.8730, 1602.7478, 1616.7609, 1679.9081, 1679.9081, 1739.9388, 1758.8915, 1774.9303, 1790.9382, 1944.1184, 1983.8634, 2051.0874, 2130.0352, 2141.0176, 2141.0176, 2187.1150, 2230.2236, 2240.1489, 2270.1167, 2284.1921, 2367.2087, 2383.2034, 2417.2715, 2417.2715, 2441.2605, 2441.2605, 2508.3423, 2545.3208, 2610.2991, 2663.3713, 2670.8943, 2686.4612, 2824.3235, 2921.3699, 3025.6294, 3332.5684, 3349.6060

9. gi|148908315 **Mass:** 53349 **Score:** 121 **Expect:** 4.8e-007 **Queries matched:** 17

unknown [Picea sitchensis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
702.4168	701.4095	701.4071	0.0024	109 - 114	0	---	SVIEVR
846.5223	845.5150	845.5123	0.0028	363 - 369	1	---	SRFLPVK
1052.5995	1051.5922	1051.5298	0.0625	266 - 275	0	---	GGTLISYEGR
1312.7654	1311.7581	1311.7510	0.0071	338 - 350	0	---	VLQLETAAGAAIR

1385.7407	1384.7334	1384.7085	0.0249	459 - 470	0	---	LEIPDESVIENK
1385.7407	1384.7334	1384.7085	0.0249	459 - 470	0	---	LEIPDESVIENK
1463.7178	1462.7105	1462.6908	0.0197	94 - 108	0	---	LNGGLGTTMGCTGPK
1475.7997	1474.7924	1474.7932	-0.0008	300 - 311	0	---	IFNTNNLWVNLK
1679.9081	1678.9008	1678.8889	0.0119	260 - 275	1	---	TLADVKGGTLISYEGR
1679.9081	1678.9008	1678.8889	0.0119	260 - 275	1	23	TLADVKGGTLISYEGR
1739.9388	1738.9315	1738.9253	0.0062	396 - 411	1	---	VNPANPSIELGPEFKK
1750.9662	1749.9589	1749.9565	0.0024	298 - 311	1	---	FKIFNTNNLWVNLK
1796.9681	1795.9608	1795.9753	-0.0145	316 - 331	1	---	LVEADALKMEIIPNPK + Oxidation (M)
1940.0924	1939.0851	1939.0737	0.0114	332 - 350	1	---	EVDGVKVLQLETAAGAAIR
1944.1184	1943.1111	1942.9822	0.1289	138 - 154	0	---	VPLVLMNSFNTHDDTIK
2141.0176	2140.0103	2140.0377	-0.0274	194 - 213	0	---	EGWYPPGHGDVFPALLNSGK
2141.0176	2140.0103	2140.0377	-0.0274	194 - 213	0	---	EGWYPPGHGDVFPALLNSGK

No match to: 713.3992, 724.4901, 734.4889, 735.4225, 768.5152, 782.4811, 808.4171, 848.5247, 863.5111, 936.5123, 965.5440, 978.5097, 1279.7625, 1447.6781, 1572.8427, 1575.8730, 1602.7478, 1616.7609, 1758.8915, 1774.9303, 1790.9382, 1983.8634, 2051.0874, 2130.0352, 2187.1150, 2230.2236, 2240.1489, 2270.1167, 2284.1921, 2367.2087, 2383.2034, 2417.2715, 2417.2715, 2441.2605, 2441.2605, 2508.3423, 2545.3208, 2564.1929, 2610.2991, 2663.3713, 2670.8943, 2679.4780, 2686.4612, 2824.3235, 2921.3699, 3025.6294, 3332.5684, 3349.6060

10. gi|12585472 **Mass:** 51632 **Score:** 116 **Expect:** 1.5e-006 **Queries matched:** 14

RecName: Full=UTP--glucose-1-phosphate uridylyltransferase; AltName: Full=UDP-glucose pyrophosphory

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
702.4168	701.4095	701.4071	0.0024	102 - 107	0	---	SVIEVR
846.5223	845.5150	845.5123	0.0028	356 - 362	1	---	SRFLPVK
1052.5995	1051.5922	1051.5298	0.0625	259 - 268	0	---	GGTLISYEGR
1312.7654	1311.7581	1311.7510	0.0071	331 - 343	0	---	VLQLETAAGAAIR
1463.7178	1462.7105	1462.6908	0.0197	87 - 101	0	---	LNGGLGTTMGCTGPK
1475.7997	1474.7924	1474.7932	-0.0008	293 - 304	0	---	IFNTNNLWVNLK
1575.8730	1574.8657	1574.8919	-0.0262	412 - 425	1	---	FKSIPSIVELDSLK
1679.9081	1678.9008	1678.8889	0.0119	253 - 268	1	---	TLADVKGGTLISYEGR
1679.9081	1678.9008	1678.8889	0.0119	253 - 268	1	23	TLADVKGGTLISYEGR
1750.9662	1749.9589	1749.9565	0.0024	291 - 304	1	---	FKIFNTNNLWVNLK
1796.9681	1795.9608	1795.9753	-0.0145	309 - 324	1	---	LVEADALKMEIIPNPK + Oxidation (M)
1940.0924	1939.0851	1939.0737	0.0114	325 - 343	1	---	EVDGVKVLQLETAAGAAIR
2051.0874	2050.0801	2050.0734	0.0067	269 - 286	0	---	VQLLEIAQVPDEHVGEFK
2508.3423	2507.3350	2507.3270	0.0080	269 - 290	1	---	VQLLEIAQVPDEHVGEFKSIEK

No match to: 713.3992, 724.4901, 734.4889, 735.4225, 768.5152, 782.4811, 808.4171, 848.5247, 863.5111, 936.5123, 965.5440, 978.5097, 1279.7625, 1385.7407, 1385.7407, 1447.6781, 1572.8427, 1602.7478, 1616.7609, 1739.9388, 1758.8915, 1774.9303, 1790.9382, 1944.1184, 1983.8634, 2130.0352, 2141.0176, 2141.0176, 2187.1150, 2230.2236, 2240.1489, 2270.1167, 2284.1921, 2367.2087, 2383.2034, 2417.2715, 2417.2715, 2441.2605, 2441.2605, 2545.3208, 2564.1929, 2610.2991, 2663.3713, 2670.8943, 2679.4780, 2686.4612, 2824.3235, 2921.3699, 3025.6294, 3332.5684, 3349.6060

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 65

Protein View

Match to: **gi|223947323** Score: **295** Expect: **1.9e-024**
unknown [Zea mays]

Nominal mass (M_r): **51441**; Calculated pI value: **5.72**
NCBI BLAST search of gi|223947323 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Zea mays

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **38%**

Matched peptides shown in **Bold Red**

```
     1 MADEKLAKLR EATAGLTQIS ENEKSGFLSL VGRYLSGDEE HIEWAKIHTP
    51 TDEVVVPYDT LESPPEGTEA TKKLLDKLAV LKLNGGLGTT MGCTGPKSVI
   101 EVRNGFTFLD LIVIQIESLN KKYGSNVPLL LMNSFNTHDD TLKIVEKYTN
   151 SSIEIHTFNQ SQYPRVVADE FLPWPSKGKT DKDGWYPPGH GDIFPSLMNS
   201 GKLDLLLSQG KEYVFIANSD NLGAIVDMKI LNHLIHKQNE YCMEVTPKTL
   251 ADVKGGTLIS YEGRVQLLEI AQVPDAHVNE FKSIEKFKIF NTNNLWVNLK
   301 AIKRLVEADA LKMEIIPNPK EVDGVKVLQL ETAAGAAIRF FDHAIGINVP
   351 RSRFLPVKAT SDLQLVQSDL YTLVDGFVTR NSARTNPSNP SIELGPEFKK
   401 VGSFLGRFKS IPSIVELDSL KVSGDVWFGS GIVLKGKVTI TAKPGVKLEI
   451 PDGAVIGNKD ISGPEDL
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
83 - 97	1463.7178	1462.7105	1462.6908	0.0197	0	LNGGLGTTMGCTGPK (No match)
98 - 103	702.4168	701.4095	701.4071	0.0024	0	SVIEVR (No match)
166 - 179	1572.8427	1571.8354	1571.8347	0.0007	1	VVADEFLPWPSKGK (No match)
230 - 248	2367.2087	2366.2014	2366.1875	0.0140	1	ILNHLIHKQNEYCMEVTPK (No match)
230 - 248	2383.2034	2382.1961	2382.1824	0.0138	1	ILNHLIHKQNEYCMEVTPK Oxidation (M) (No match)
249 - 264	1679.9081	1678.9008	1678.8889	0.0119	1	TLADVKGGTLISYEGR (No match)
249 - 264	1679.9081	1678.9008	1678.8889	0.0119	1	TLADVKGGTLISYEGR (Ions score 23)
255 - 264	1052.5995	1051.5922	1051.5298	0.0625	0	GGTLISYEGR (No match)
287 - 300	1750.9662	1749.9589	1749.9565	0.0024	1	FKIFNTNNLWVNLK (No match)
289 - 300	1475.7997	1474.7924	1474.7932	-0.0008	0	IFNTNNLWVNLK (No match)
305 - 320	1796.9681	1795.9608	1795.9753	-0.0145	1	LVEADALKMEIIPNPK Oxidation (M) (No match)
321 - 339	1940.0924	1939.0851	1939.0737	0.0114	1	EVDGVKVLQLETAAGAAIR (No match)
327 - 339	1312.7654	1311.7581	1311.7510	0.0071	0	VLQLETAAGAAIR (No match)
327 - 351	2679.4780	2678.4707	2678.4655	0.0052	1	VLQLETAAGAAIRFFDHAIGINVPR (No match)
340 - 351	1385.7407	1384.7334	1384.7251	0.0083	0	FFDHAIGINVPR (Ions score 54)
340 - 351	1385.7407	1384.7334	1384.7251	0.0083	0	FFDHAIGINVPR (No match)
352 - 358	846.5223	845.5150	845.5123	0.0028	1	SRFLPVK (No match)
354 - 380	3025.6294	3024.6221	3024.6171	0.0050	1	FLPVKATSDLQLVQSDLYTLVDGFVTR (No match)
359 - 380	2441.2605	2440.2532	2440.2485	0.0047	0	ATSDLQLVQSDLYTLVDGFVTR (No match)
359 - 380	2441.2605	2440.2532	2440.2485	0.0047	0	ATSDLQLVQSDLYTLVDGFVTR (Ions score 44)
400 - 407	863.5111	862.5038	862.5024	0.0014	1	KVGSFLGR (No match)
401 - 407	735.4225	734.4152	734.4075	0.0078	0	VGSFLGR (No match)
408 - 421	1575.8730	1574.8657	1574.8919	-0.0262	1	FKSIPSIVELDSLK (No match)

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	Accession	Mass	Score	Description
1.	gi|226502766	50634	133	rab GDP dissociation inhibitor alpha [Zea mays]
2.	gi|219888133	50692	133	unknown [Zea mays]
3.	gi|115452233	50469	85	Os03g0277000 [Oryza sativa (japonica cultivar-group)]
4.	gi|147833953	50309	78	hypothetical protein [Vitis vinifera]
5.	gi|225467971	50301	77	PREDICTED: hypothetical protein [Vitis vinifera]
6.	gi|255586034	50384	75	protein with unknown function [Ricinus communis]
7.	gi|2501850	50127	74	GDP dissociation inhibitor [Nicotiana tabacum]
8.	gi|157890964	49978	74	GDP dissociation inhibitor [Brassica rapa]
9.	gi|82623395	50114	74	GDP dissociation inhibitor 1-like [Solanum tuberosum]
10.	gi|226503165	50236	67	LOC100284832 [Zea mays]

Results List

1. gi|226502766 **Mass:** 50634 **Score:** 133 **Expect:** 3e-008 **Queries matched:** 17

rab GDP dissociation inhibitor alpha [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
922.5003	921.4930	921.4919	0.0011	210	217	0	---	LYAESLAR
1109.5663	1108.5590	1108.5521	0.0069	79	88	0	---	FMMANGALVR
1109.5663	1108.5590	1108.5521	0.0069	79	88	0	14	FMMANGALVR
1125.5432	1124.5359	1124.5470	-0.0111	79	88	0	---	FMMANGALVR + Oxidation (M)
1141.5344	1140.5271	1140.5419	-0.0148	79	88	0	---	FMMANGALVR + 2 Oxidation (M)
1181.6381	1180.6308	1180.6274	0.0034	208	217	1	4	MKLYAESLAR
1181.6381	1180.6308	1180.6274	0.0034	208	217	1	---	MKLYAESLAR
1197.6172	1196.6099	1196.6223	-0.0124	208	217	1	---	MKLYAESLAR + Oxidation (M)
1270.6021	1269.5948	1269.5989	-0.0041	103	114	0	---	AVDGSFVYNNGK
1523.7933	1522.7860	1522.8000	-0.0139	301	313	1	---	AICIMKHPIPDTK
2048.8748	2047.8675	2047.8590	0.0085	331	347	0	---	SDMYVFCCSYAHNVAPK
2142.0344	2141.0271	2141.0541	-0.0270	174	192	0	---	YGLEDDTVDFIGHALALHR
2176.9666	2175.9593	2175.9539	0.0054	330	347	1	---	KSDMYVFCCSYAHNVAPK
2192.9607	2191.9534	2191.9489	0.0046	330	347	1	---	KSDMYVFCCSYAHNVAPK + Oxidation (M)
2544.2952	2543.2879	2543.2848	0.0031	218	240	0	---	FQGGSPYIYPLYGLGELPQAFAR
2544.2952	2543.2879	2543.2848	0.0031	218	240	0	48	FQGGSPYIYPLYGLGELPQAFAR
2838.3293	2837.3220	2837.3251	-0.0030	241	265	1	---	LSAVYGGTYMLNKPECKVEFDESGK + Oxidation (M)

No match to: 713.3995, 734.4913, 746.3563, 750.5146, 768.5093, 782.4819, 848.5242, 864.5309, 1259.5885, 1279.7584, 1334.8693, 1385.7383, 1421.7358, 1448.9049, 1475.7944, 1562.9410, 1572.8119, 1620.8257, 1620.8257, 1679.9114, 1681.9984, 1732.0881, 1748.9181, 1758.7611, 1931.9637, 1933.0092, 1959.0741, 2087.9829, 2127.0898, 2178.9749, 2262.1211, 2333.0762, 2349.0635, 2390.1704, 2413.1523, 2413.1523, 2429.1433, 2564.1882, 2648.3120,

2664.3220, 2741.4807, 2758.4880, 2825.3223, 2921.3674, 2966.4207, 3296.5911, 3349.6021, 3423.6685

2. gi|219888133 **Mass:** 50692 **Score:** 133 **Expect:** 3e-008 **Queries matched:** 17

unknown [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
922.5003	921.4930	921.4919	0.0011	210	217	0	---	LYAESLAR
1109.5663	1108.5590	1108.5521	0.0069	79	88	0	---	FMMANGALVR
1109.5663	1108.5590	1108.5521	0.0069	79	88	0	14	FMMANGALVR
1125.5432	1124.5359	1124.5470	-0.0111	79	88	0	---	FMMANGALVR + Oxidation (M)
1141.5344	1140.5271	1140.5419	-0.0148	79	88	0	---	FMMANGALVR + 2 Oxidation (M)
1181.6381	1180.6308	1180.6274	0.0034	208	217	1	4	MKLYAESLAR
1181.6381	1180.6308	1180.6274	0.0034	208	217	1	---	MKLYAESLAR
1197.6172	1196.6099	1196.6223	-0.0124	208	217	1	---	MKLYAESLAR + Oxidation (M)
1270.6021	1269.5948	1269.5989	-0.0041	103	114	0	---	AVDGSFVYNNGK
1523.7933	1522.7860	1522.8000	-0.0139	301	313	1	---	AICIMKHPIPDTK
2048.8748	2047.8675	2047.8590	0.0085	331	347	0	---	SDMYVFCCSYAHNVAPK
2142.0344	2141.0271	2141.0541	-0.0270	174	192	0	---	YGLEDDTVDFIGHALALHR
2176.9666	2175.9593	2175.9539	0.0054	330	347	1	---	KSDMYVFCCSYAHNVAPK
2192.9607	2191.9534	2191.9489	0.0046	330	347	1	---	KSDMYVFCCSYAHNVAPK + Oxidation (M)
2544.2952	2543.2879	2543.2848	0.0031	218	240	0	---	FQGGSPYIYPLYGLGELPQAFAR
2544.2952	2543.2879	2543.2848	0.0031	218	240	0	48	FQGGSPYIYPLYGLGELPQAFAR
2838.3293	2837.3220	2837.3251	-0.0030	241	265	1	---	LSAVYGGTYMLNKPECKVEFDESGK + Oxidation (M)

No match to: 713.3995, 734.4913, 746.3563, 750.5146, 768.5093, 782.4819, 848.5242, 864.5309, 1259.5885, 1279.7584, 1334.8693, 1385.7383, 1421.7358, 1448.9049, 1475.7944, 1562.9410, 1572.8119, 1620.8257, 1620.8257, 1679.9114, 1681.9984, 1732.0881, 1748.9181, 1758.7611, 1931.9637, 1933.0092, 1959.0741, 2087.9829, 2127.0898, 2178.9749, 2262.1211, 2333.0762, 2349.0635, 2390.1704, 2413.1523, 2413.1523, 2429.1433, 2564.1882, 2648.3120, 2664.3220, 2741.4807, 2758.4880, 2825.3223, 2921.3674, 2966.4207, 3296.5911, 3349.6021, 3423.6685

3. gi|115452233 **Mass:** 50469 **Score:** 85 **Expect:** 0.0021 **Queries matched:** 17

Os03g0277000 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
922.5003	921.4930	921.4919	0.0011	210	217	0	---	LYAESLAR
1109.5663	1108.5590	1108.5521	0.0069	79	88	0	---	FMMANGALVR
1109.5663	1108.5590	1108.5521	0.0069	79	88	0	14	FMMANGALVR
1125.5432	1124.5359	1124.5470	-0.0111	79	88	0	---	FMMANGALVR + Oxidation (M)
1141.5344	1140.5271	1140.5419	-0.0148	79	88	0	---	FMMANGALVR + 2 Oxidation (M)
1181.6381	1180.6308	1180.6274	0.0034	208	217	1	4	MKLYAESLAR
1181.6381	1180.6308	1180.6274	0.0034	208	217	1	---	MKLYAESLAR
1197.6172	1196.6099	1196.6223	-0.0124	208	217	1	---	MKLYAESLAR + Oxidation (M)
1270.6021	1269.5948	1269.5989	-0.0041	103	114	0	---	AVDGSFVYNNGK
1523.7933	1522.7860	1522.8000	-0.0139	301	313	1	---	AICIMKHPIPDTK

2048.8748	2047.8675	2047.8590	0.0085	331 - 347	0	---	SDMYVFCCSYAHNVAPK
2142.0344	2141.0271	2141.0541	-0.0270	174 - 192	0	---	YGLEDDTVDFIGHALALHR
2176.9666	2175.9593	2175.9539	0.0054	330 - 347	1	---	KSDMYVFCCSYAHNVAPK
2192.9607	2191.9534	2191.9489	0.0046	330 - 347	1	---	KSDMYVFCCSYAHNVAPK + Oxidation (M)
2413.1523	2412.1450	2412.1379	0.0071	30 - 50	1	---	VLHMDRNDYYGGESTSLNLTK
2413.1523	2412.1450	2412.1379	0.0071	30 - 50	1	14	VLHMDRNDYYGGESTSLNLTK
2429.1433	2428.1360	2428.1328	0.0032	30 - 50	1	---	VLHMDRNDYYGGESTSLNLTK + Oxidation (M)

No match to: 713.3995, 734.4913, 746.3563, 750.5146, 768.5093, 782.4819, 848.5242, 864.5309, 1259.5885, 1279.7584, 1334.8693, 1385.7383, 1421.7358, 1448.9049, 1475.7944, 1562.9410, 1572.8119, 1620.8257, 1620.8257, 1679.9114, 1681.9984, 1732.0881, 1748.9181, 1758.7611, 1931.9637, 1933.0092, 1959.0741, 2087.9829, 2127.0898, 2178.9749, 2262.1211, 2333.0762, 2349.0635, 2390.1704, 2544.2952, 2544.2952, 2564.1882, 2648.3120, 2664.3220, 2741.4807, 2758.4880, 2825.3223, 2838.3293, 2921.3674, 2966.4207, 3296.5911, 3349.6021, 3423.6685

4. gi|147833953 **Mass:** 50309 **Score:** 78 **Expect:** 0.01 **Queries matched:** 10

hypothetical protein [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
922.5003	921.4930	921.4919	0.0011	210 - 217		0	---	LYAESLAR
1109.5663	1108.5590	1108.5521	0.0069	79 - 88		0	---	FMMANGALVR
1109.5663	1108.5590	1108.5521	0.0069	79 - 88		0	14	FMMANGALVR
1125.5432	1124.5359	1124.5470	-0.0111	79 - 88		0	---	FMMANGALVR + Oxidation (M)
1141.5344	1140.5271	1140.5419	-0.0148	79 - 88		0	---	FMMANGALVR + 2 Oxidation (M)
1181.6381	1180.6308	1180.6274	0.0034	208 - 217		1	4	MKLYAESLAR
1181.6381	1180.6308	1180.6274	0.0034	208 - 217		1	---	MKLYAESLAR
1197.6172	1196.6099	1196.6223	-0.0124	208 - 217		1	---	MKLYAESLAR + Oxidation (M)
2544.2952	2543.2879	2543.2848	0.0031	218 - 240		0	---	FQGGSPYIYPLYGLGELPQAFAR
2544.2952	2543.2879	2543.2848	0.0031	218 - 240		0	48	FQGGSPYIYPLYGLGELPQAFAR

No match to: 713.3995, 734.4913, 746.3563, 750.5146, 768.5093, 782.4819, 848.5242, 864.5309, 1259.5885, 1270.6021, 1279.7584, 1334.8693, 1385.7383, 1421.7358, 1448.9049, 1475.7944, 1523.7933, 1562.9410, 1572.8119, 1620.8257, 1620.8257, 1679.9114, 1681.9984, 1732.0881, 1748.9181, 1758.7611, 1931.9637, 1933.0092, 1959.0741, 2048.8748, 2087.9829, 2127.0898, 2142.0344, 2176.9666, 2178.9749, 2192.9607, 2262.1211, 2333.0762, 2349.0635, 2390.1704, 2413.1523, 2413.1523, 2429.1433, 2564.1882, 2648.3120, 2664.3220, 2741.4807, 2758.4880, 2825.3223, 2838.3293, 2921.3674, 2966.4207, 3296.5911, 3349.6021, 3423.6685

5. gi|225467971 **Mass:** 50301 **Score:** 77 **Expect:** 0.011 **Queries matched:** 10

PREDICTED: hypothetical protein [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
922.5003	921.4930	921.4919	0.0011	210 - 217		0	---	LYAESLAR
1109.5663	1108.5590	1108.5521	0.0069	79 - 88		0	---	FMMANGALVR
1109.5663	1108.5590	1108.5521	0.0069	79 - 88		0	14	FMMANGALVR
1125.5432	1124.5359	1124.5470	-0.0111	79 - 88		0	---	FMMANGALVR + Oxidation (M)
1141.5344	1140.5271	1140.5419	-0.0148	79 - 88		0	---	FMMANGALVR + 2 Oxidation (M)
1181.6381	1180.6308	1180.6274	0.0034	208 - 217		1	4	MKLYAESLAR

1181.6381	1180.6308	1180.6274	0.0034	208 - 217	1	---	MKLYAESLAR
1197.6172	1196.6099	1196.6223	-0.0124	208 - 217	1	---	MKLYAESLAR + Oxidation (M)
2544.2952	2543.2879	2543.2848	0.0031	218 - 240	0	---	FQGGSPYIYPLYGLGELPQAFAR
2544.2952	2543.2879	2543.2848	0.0031	218 - 240	0	48	FQGGSPYIYPLYGLGELPQAFAR

No match to: 713.3995, 734.4913, 746.3563, 750.5146, 768.5093, 782.4819, 848.5242, 864.5309, 1259.5885, 1270.6021, 1279.7584, 1334.8693, 1385.7383, 1421.7358, 1448.9049, 1475.7944, 1523.7933, 1562.9410, 1572.8119, 1620.8257, 1620.8257, 1679.9114, 1681.9984, 1732.0881, 1748.9181, 1758.7611, 1931.9637, 1933.0092, 1959.0741, 2048.8748, 2087.9829, 2127.0898, 2142.0344, 2176.9666, 2178.9749, 2192.9607, 2262.1211, 2333.0762, 2349.0635, 2390.1704, 2413.1523, 2413.1523, 2429.1433, 2564.1882, 2648.3120, 2664.3220, 2741.4807, 2758.4880, 2825.3223, 2838.3293, 2921.3674, 2966.4207, 3296.5911, 3349.6021, 3423.6685

6. gi|255586034 **Mass:** 50384 **Score:** 75 **Expect:** 0.022 **Queries matched:** 7

protein with unknown function [Ricinus communis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1109.5663	1108.5590	1108.5521	0.0069	79 -	88	0	---	FMMANGALVR
1109.5663	1108.5590	1108.5521	0.0069	79 -	88	0	14	FMMANGALVR
1125.5432	1124.5359	1124.5470	-0.0111	79 -	88	0	---	FMMANGALVR + Oxidation (M)
1141.5344	1140.5271	1140.5419	-0.0148	79 -	88	0	---	FMMANGALVR + 2 Oxidation (M)
2544.2952	2543.2879	2543.2848	0.0031	218 -	240	0	---	FQGGSPYIYPLYGLGELPQAFAR
2544.2952	2543.2879	2543.2848	0.0031	218 -	240	0	48	FQGGSPYIYPLYGLGELPQAFAR
2838.3293	2837.3220	2837.4316	-0.1096	301 -	325	0	---	AICIMSHPIPNTHDSHSVQVILPQK + Oxidation (M)

No match to: 713.3995, 734.4913, 746.3563, 750.5146, 768.5093, 782.4819, 848.5242, 864.5309, 922.5003, 1181.6381, 1181.6381, 1197.6172, 1259.5885, 1270.6021, 1279.7584, 1334.8693, 1385.7383, 1421.7358, 1448.9049, 1475.7944, 1523.7933, 1562.9410, 1572.8119, 1620.8257, 1620.8257, 1679.9114, 1681.9984, 1732.0881, 1748.9181, 1758.7611, 1931.9637, 1933.0092, 1959.0741, 2048.8748, 2087.9829, 2127.0898, 2142.0344, 2176.9666, 2178.9749, 2192.9607, 2262.1211, 2333.0762, 2349.0635, 2390.1704, 2413.1523, 2413.1523, 2429.1433, 2564.1882, 2648.3120, 2664.3220, 2741.4807, 2758.4880, 2825.3223, 2921.3674, 2966.4207, 3296.5911, 3349.6021, 3423.6685

7. gi|2501850 **Mass:** 50127 **Score:** 74 **Expect:** 0.022 **Queries matched:** 8

GDP dissociation inhibitor [Nicotiana tabacum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
922.5003	921.4930	921.4919	0.0011	210 -	217	0	---	LYAESLAR
1181.6381	1180.6308	1180.6274	0.0034	208 -	217	1	4	MKLYAESLAR
1181.6381	1180.6308	1180.6274	0.0034	208 -	217	1	---	MKLYAESLAR
1197.6172	1196.6099	1196.6223	-0.0124	208 -	217	1	---	MKLYAESLAR + Oxidation (M)
2127.0898	2126.0825	2126.0544	0.0281	174 -	192	0	---	YGLDDNTVDFIGHALALHR
2544.2952	2543.2879	2543.2848	0.0031	218 -	240	0	---	FQGGSPYIYPLYGLGELPQAFAR
2544.2952	2543.2879	2543.2848	0.0031	218 -	240	0	48	FQGGSPYIYPLYGLGELPQAFAR
2838.3293	2837.3220	2837.3806	-0.0586	30 -	53	1	---	VLHMDRNDYYGGESTSLNLVQLWK

No match to: 713.3995, 734.4913, 746.3563, 750.5146, 768.5093, 782.4819, 848.5242, 864.5309, 1109.5663, 1109.5663, 1125.5432, 1141.5344, 1259.5885, 1270.6021, 1279.7584, 1334.8693, 1385.7383, 1421.7358, 1448.9049, 1475.7944, 1523.7933, 1562.9410, 1572.8119, 1620.8257, 1620.8257, 1679.9114, 1681.9984, 1732.0881, 1748.9181,

1758.7611, 1931.9637, 1933.0092, 1959.0741, 2048.8748, 2087.9829, 2142.0344, 2176.9666, 2178.9749, 2192.9607, 2262.1211, 2333.0762, 2349.0635, 2390.1704, 2413.1523, 2413.1523, 2429.1433, 2564.1882, 2648.3120, 2664.3220, 2741.4807, 2758.4880, 2825.3223, 2921.3674, 2966.4207, 3296.5911, 3349.6021, 3423.6685

8. gi|157890964 **Mass:** 49978 **Score:** 74 **Expect:** 0.023 **Queries matched:** 8

GDP dissociation inhibitor [Brassica rapa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
922.5003	921.4930	921.4919	0.0011	210	217	0	---	LYAESLAR
1181.6381	1180.6308	1180.6274	0.0034	208	217	1	4	MKLYAESLAR
1181.6381	1180.6308	1180.6274	0.0034	208	217	1	---	MKLYAESLAR
1197.6172	1196.6099	1196.6223	-0.0124	208	217	1	---	MKLYAESLAR + Oxidation (M)
2142.0344	2141.0271	2140.9833	0.0438	258	277	1	---	VEFDEEGKVMGVTSEGETAK
2192.9607	2191.9534	2191.9489	0.0046	330	347	1	---	KSDMYVFCCSYSHNVAPK
2544.2952	2543.2879	2543.2848	0.0031	218	240	0	---	FQGGSPYIYPLYGLGELPQAFAR
2544.2952	2543.2879	2543.2848	0.0031	218	240	0	48	FQGGSPYIYPLYGLGELPQAFAR

No match to: 713.3995, 734.4913, 746.3563, 750.5146, 768.5093, 782.4819, 848.5242, 864.5309, 1109.5663, 1109.5663, 1125.5432, 1141.5344, 1259.5885, 1270.6021, 1279.7584, 1334.8693, 1385.7383, 1421.7358, 1448.9049, 1475.7944, 1523.7933, 1562.9410, 1572.8119, 1620.8257, 1620.8257, 1679.9114, 1681.9984, 1732.0881, 1748.9181, 1758.7611, 1931.9637, 1933.0092, 1959.0741, 2048.8748, 2087.9829, 2127.0898, 2176.9666, 2178.9749, 2262.1211, 2333.0762, 2349.0635, 2390.1704, 2413.1523, 2413.1523, 2429.1433, 2564.1882, 2648.3120, 2664.3220, 2741.4807, 2758.4880, 2825.3223, 2838.3293, 2921.3674, 2966.4207, 3296.5911, 3349.6021, 3423.6685

9. gi|82623395 **Mass:** 50114 **Score:** 74 **Expect:** 0.026 **Queries matched:** 8

GDP dissociation inhibitor 1-like [Solanum tuberosum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
922.5003	921.4930	921.4919	0.0011	210	217	0	---	LYAESLAR
1181.6381	1180.6308	1180.6274	0.0034	208	217	1	4	MKLYAESLAR
1181.6381	1180.6308	1180.6274	0.0034	208	217	1	---	MKLYAESLAR
1197.6172	1196.6099	1196.6223	-0.0124	208	217	1	---	MKLYAESLAR + Oxidation (M)
2127.0898	2126.0825	2126.0544	0.0281	174	192	0	---	YGLDDNTVDFIGHALALHR
2544.2952	2543.2879	2543.2848	0.0031	218	240	0	---	FQGGSPYIYPLYGLGELPQAFAR
2544.2952	2543.2879	2543.2848	0.0031	218	240	0	48	FQGGSPYIYPLYGLGELPQAFAR
2838.3293	2837.3220	2837.3806	-0.0586	30	53	1	---	VLHMDRNDYYGGESTSLNLVQLWK

No match to: 713.3995, 734.4913, 746.3563, 750.5146, 768.5093, 782.4819, 848.5242, 864.5309, 1109.5663, 1109.5663, 1125.5432, 1141.5344, 1259.5885, 1270.6021, 1279.7584, 1334.8693, 1385.7383, 1421.7358, 1448.9049, 1475.7944, 1523.7933, 1562.9410, 1572.8119, 1620.8257, 1620.8257, 1679.9114, 1681.9984, 1732.0881, 1748.9181, 1758.7611, 1931.9637, 1933.0092, 1959.0741, 2048.8748, 2087.9829, 2142.0344, 2176.9666, 2178.9749, 2192.9607, 2262.1211, 2333.0762, 2349.0635, 2390.1704, 2413.1523, 2413.1523, 2429.1433, 2564.1882, 2648.3120, 2664.3220, 2741.4807, 2758.4880, 2825.3223, 2921.3674, 2966.4207, 3296.5911, 3349.6021, 3423.6685

10. gi|226503165 **Mass:** 50236 **Score:** 67 **Expect:** 0.13 **Queries matched:** 7

LOC100284832 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
922.5003	921.4930	921.4919	0.0011	210 -	217	0	---	LYAESLAR
1181.6381	1180.6308	1180.6274	0.0034	208 -	217	1	4	MKLYAESLAR
1181.6381	1180.6308	1180.6274	0.0034	208 -	217	1	---	MKLYAESLAR
1197.6172	1196.6099	1196.6223	-0.0124	208 -	217	1	---	MKLYAESLAR + Oxidation (M)
2087.9829	2086.9756	2086.9595	0.0161	36 -	53	0	---	NDYYGGDSTSLNLNQLWK
2544.2952	2543.2879	2543.2848	0.0031	218 -	240	0	---	FQGGSPYIYPLYGLGELPQAFAR
2544.2952	2543.2879	2543.2848	0.0031	218 -	240	0	48	FQGGSPYIYPLYGLGELPQAFAR

No match to: 713.3995, 734.4913, 746.3563, 750.5146, 768.5093, 782.4819, 848.5242, 864.5309, 1109.5663, 1109.5663, 1125.5432, 1141.5344, 1259.5885, 1270.6021, 1279.7584, 1334.8693, 1385.7383, 1421.7358, 1448.9049, 1475.7944, 1523.7933, 1562.9410, 1572.8119, 1620.8257, 1620.8257, 1679.9114, 1681.9984, 1732.0881, 1748.9181, 1758.7611, 1931.9637, 1933.0092, 1959.0741, 2048.8748, 2127.0898, 2142.0344, 2176.9666, 2178.9749, 2192.9607, 2262.1211, 2333.0762, 2349.0635, 2390.1704, 2413.1523, 2413.1523, 2429.1433, 2564.1882, 2648.3120, 2664.3220, 2741.4807, 2758.4880, 2825.3223, 2838.3293, 2921.3674, 2966.4207, 3296.5911, 3349.6021, 3423.6685

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 65

Protein View

Match to: **gi|226502766** Score: **133** Expect: **3e-008**
rab GDP dissociation inhibitor alpha [Zea mays]

Nominal mass (M_r): **50634**; Calculated pI value: **5.38**
NCBI BLAST search of gi|226502766 against nr
Unformatted sequence string for pasting into other applications
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|195637100 from Zea mays
gi|224028293 (no taxonomy information for this entry)

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **29%**

Matched peptides shown in **Bold Red**

```
    1 MDEEYDVIVL GTGLKECIIS GLLSVDGLKV LHMDRNDYYG GESSSLNLTK
   51 LWNRFKGNDS PPEHLGVSKE YNVDMVPKFM MANGALVRVL IRTSVTKYLN
  101 FKAVDGSFVY NNGKIHKVPA TDVEALKSNL MGLFEKRRAR KFFIYVQDYE
  151 EDDPKSHEGL DLNKVTTREV ISKYGLEDDT VDFIGHALAL HRDDSYLDEP
  201 AIDTVKRMKL YAESLARFQG GSPYIYPLYG LGELPQAFAR LSAVYGGTYM
  251 LNKPECKVEF DESGKAYGVT SEGETAKCKK IVCDPSYLPD KVKKVGRVAR
  301 AICIMKHPIP DTKDSHSVQI ILPKKQLKRK SDMYVFCCSY AHNVAPKGKF
  351 IAFVSTEAET DKPEIELKPG IDLLGPVEET FFDIYDRYEP VNNPDDDCCF
  401 LTNSYDSTTH FETTVKDVLA LYNKITGKEL DLSVDLNAAS ATEQEAA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
79 - 88	1109.5663	1108.5590	1108.5521	0.0069	0	**FMMANGALVR** (No match)
79 - 88	1109.5663	1108.5590	1108.5521	0.0069	0	**FMMANGALVR** (Ions score 14)
79 - 88	1125.5432	1124.5359	1124.5470	-0.0111	0	**FMMANGALVR** Oxidation (M) (No match)
79 - 88	1141.5344	1140.5271	1140.5419	-0.0148	0	**FMMANGALVR** 2 Oxidation (M) (No match)
103 - 114	1270.6021	1269.5948	1269.5989	-0.0041	0	**AVDGSFVYNNGK** (No match)
174 - 192	2142.0344	2141.0271	2141.0541	-0.0270	0	**YGLEDDTVDFIGHALALHR** (No match)
208 - 217	1181.6381	1180.6308	1180.6274	0.0034	1	**MKLYAESLAR** (Ions score 4)
208 - 217	1181.6381	1180.6308	1180.6274	0.0034	1	**MKLYAESLAR** (No match)
208 - 217	1197.6172	1196.6099	1196.6223	-0.0124	1	**MKLYAESLAR** Oxidation (M) (No match)
210 - 217	922.5003	921.4930	921.4919	0.0011	0	**LYAESLAR** (No match)
218 - 240	2544.2952	2543.2879	2543.2848	0.0031	0	**FQGGSPYIYPLYGLGELPQAFAR** (No match)
218 - 240	2544.2952	2543.2879	2543.2848	0.0031	0	**FQGGSPYIYPLYGLGELPQAFAR** (Ions score 48)
241 - 265	2838.3293	2837.3220	2837.3251	-0.0030	1	**LSAVYGGTYMLNKPECKVEFDESGK** Oxidation (M) (No match)
301 - 313	1523.7933	1522.7860	1522.8000	-0.0139	1	**AICIMKHPIPDTK** (No match)
330 - 347	2176.9666	2175.9593	2175.9539	0.0054	1	**KSDMYVFCCSYAHNVAPK** (No match)
330 - 347	2192.9607	2191.9534	2191.9489	0.0046	1	**KSDMYVFCCSYAHNVAPK** Oxidation (M) (No match)
331 - 347	2048.8748	2047.8675	2047.8590	0.0085	0	**SDMYVFCCSYAHNVAPK** (No match)

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	Accession	Mass	Score	Description
1.	gi|195637100	50634	176	rab GDP dissociation inhibitor alpha [Zea mays]
2.	gi|219888133	50692	176	unknown [Zea mays]
3.	gi|147833953	50309	145	hypothetical protein [Vitis vinifera]
4.	gi|157330628	50301	136	unnamed protein product [Vitis vinifera]
5.	gi|157890964	49978	108	GDP dissociation inhibitor [Brassica rapa]

Results List

1. gi|195637100 **Mass:** 50634 **Score:** 176 **Expect:** 1.5e-012 **Queries matched:** 17

rab GDP dissociation inhibitor alpha [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
922.5048	921.4975	921.4919	0.0056	210	217	0	---	LYAESLAR
1109.5621	1108.5548	1108.5521	0.0027	79	88	0	---	FMMANGALVR
1109.5621	1108.5548	1108.5521	0.0027	79	88	0	31	FMMANGALVR
1125.5470	1124.5397	1124.5470	-0.0073	79	88	0	---	FMMANGALVR + Oxidation (M)
1141.5459	1140.5386	1140.5419	-0.0033	79	88	0	---	FMMANGALVR + 2 Oxidation (M)
1181.6360	1180.6287	1180.6274	0.0013	208	217	1	25	MKLYAESLAR
1181.6360	1180.6287	1180.6274	0.0013	208	217	1	---	MKLYAESLAR
1197.6224	1196.6151	1196.6223	-0.0072	208	217	1	---	MKLYAESLAR + Oxidation (M)
1270.6044	1269.5971	1269.5989	-0.0018	103	114	0	---	AVDGSFVYNNGK
1523.8047	1522.7974	1522.8000	-0.0025	301	313	1	---	AICIMKHPIPDTK
1539.7997	1538.7924	1538.7949	-0.0025	301	313	1	---	AICIMKHPIPDTK + Oxidation (M)
1930.9442	1929.9369	1929.9328	0.0041	241	257	0	---	LSAVYGGTYMLNKPECK
2048.8672	2047.8599	2047.8590	0.0009	331	347	0	---	SDMYVFCCSYAHNVAPK
2176.9785	2175.9712	2175.9539	0.0173	330	347	1	---	KSDMYVFCCSYAHNVAPK
2192.9656	2191.9583	2191.9489	0.0095	330	347	1	---	KSDMYVFCCSYAHNVAPK + Oxidation (M)
2544.2932	2543.2859	2543.2848	0.0011	218	240	0	57	FQGGSPYIYPLYGLGELPQAFAR
2544.2932	2543.2859	2543.2848	0.0011	218	240	0	---	FQGGSPYIYPLYGLGELPQAFAR

No match to: 713.4116, 724.4903, 734.4911, 768.5233, 864.5253, 917.2755, 978.5028, 1259.5913, 1279.7672, 1334.8765, 1350.7323, 1366.7249, 1385.7383, 1421.7333, 1448.9141, 1572.8074, 1619.0718, 1620.8315, 1620.8315, 1679.8951, 1681.9961, 1696.8533, 1732.1002, 1734.0526, 1748.9216, 1791.9175, 1890.1270, 1933.0131, 1933.0131, 2061.1106, 2087.9700, 2261.1506, 2333.0640, 2349.0698, 2413.1523, 2453.2651, 2648.3140, 2664.3325, 2741.4968

2. gi|219888133 **Mass:** 50692 **Score:** 176 **Expect:** 1.5e-012 **Queries matched:** 17

unknown [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
922.5048	921.4975	921.4919	0.0056	210	217	0	---	LYAESLAR

1109.5621	1108.5548	1108.5521	0.0027	79 - 88	0	---	FMMANGALVR
1109.5621	1108.5548	1108.5521	0.0027	79 - 88	0	31	FMMANGALVR
1125.5470	1124.5397	1124.5470	-0.0073	79 - 88	0	---	FMMANGALVR + Oxidation (M)
1141.5459	1140.5386	1140.5419	-0.0033	79 - 88	0	---	FMMANGALVR + 2 Oxidation (M)
1181.6360	1180.6287	1180.6274	0.0013	208 - 217	1	25	MKLYAESLAR
1181.6360	1180.6287	1180.6274	0.0013	208 - 217	1	---	MKLYAESLAR
1197.6224	1196.6151	1196.6223	-0.0072	208 - 217	1	---	MKLYAESLAR + Oxidation (M)
1270.6044	1269.5971	1269.5989	-0.0018	103 - 114	0	---	AVDGSFVYNNGK
1523.8047	1522.7974	1522.8000	-0.0025	301 - 313	1	---	AICIMKHPIPDTK
1539.7997	1538.7924	1538.7949	-0.0025	301 - 313	1	---	AICIMKHPIPDTK + Oxidation (M)
1930.9442	1929.9369	1929.9328	0.0041	241 - 257	0	---	LSAVYGGTYMLNKPECK
2048.8672	2047.8599	2047.8590	0.0009	331 - 347	0	---	SDMYVFCCSYAHNVAPK
2176.9785	2175.9712	2175.9539	0.0173	330 - 347	1	---	KSDMYVFCCSYAHNVAPK
2192.9656	2191.9583	2191.9489	0.0095	330 - 347	1	---	KSDMYVFCCSYAHNVAPK + Oxidation (M)
2544.2932	2543.2859	2543.2848	0.0011	218 - 240	0	57	FQGGSPYIYPLYGLGELPQAFAR
2544.2932	2543.2859	2543.2848	0.0011	218 - 240	0	---	FQGGSPYIYPLYGLGELPQAFAR

No match to: 713.4116, 724.4903, 734.4911, 768.5233, 864.5253, 917.2755, 978.5028, 1259.5913, 1279.7672, 1334.8765, 1350.7323, 1366.7249, 1385.7383, 1421.7333, 1448.9141, 1572.8074, 1619.0718, 1620.8315, 1620.8315, 1679.8951, 1681.9961, 1696.8533, 1732.1002, 1734.0526, 1748.9216, 1791.9175, 1890.1270, 1933.0131, 1933.0131, 2061.1106, 2087.9700, 2261.1506, 2333.0640, 2349.0698, 2413.1523, 2453.2651, 2648.3140, 2664.3325, 2741.4968

3. gi|147833953 **Mass:** 50309 **Score:** 145 **Expect:** 1.9e-009 **Queries matched:** 12

hypothetical protein [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
922.5048	921.4975	921.4919	0.0056	210 - 217	0	---	LYAESLAR
1109.5621	1108.5548	1108.5521	0.0027	79 - 88	0	---	FMMANGALVR
1109.5621	1108.5548	1108.5521	0.0027	79 - 88	0	31	FMMANGALVR
1125.5470	1124.5397	1124.5470	-0.0073	79 - 88	0	---	FMMANGALVR + Oxidation (M)
1141.5459	1140.5386	1140.5419	-0.0033	79 - 88	0	---	FMMANGALVR + 2 Oxidation (M)
1181.6360	1180.6287	1180.6274	0.0013	208 - 217	1	25	MKLYAESLAR
1181.6360	1180.6287	1180.6274	0.0013	208 - 217	1	---	MKLYAESLAR
1197.6224	1196.6151	1196.6223	-0.0072	208 - 217	1	---	MKLYAESLAR + Oxidation (M)
1930.9442	1929.9369	1929.9328	0.0041	241 - 257	0	---	LSAVYGGTYMLNKPECK
2061.1106	2060.1033	2060.0863	0.0170	118 - 136	1	---	VPATDVEALKSPLMGLFEK + Oxidation (M)
2544.2932	2543.2859	2543.2848	0.0011	218 - 240	0	57	FQGGSPYIYPLYGLGELPQAFAR
2544.2932	2543.2859	2543.2848	0.0011	218 - 240	0	---	FQGGSPYIYPLYGLGELPQAFAR

No match to: 713.4116, 724.4903, 734.4911, 768.5233, 864.5253, 917.2755, 978.5028, 1259.5913, 1270.6044, 1279.7672, 1334.8765, 1350.7323, 1366.7249, 1385.7383, 1421.7333, 1448.9141, 1523.8047, 1539.7997, 1572.8074, 1619.0718, 1620.8315, 1620.8315, 1679.8951, 1681.9961, 1696.8533, 1732.1002, 1734.0526, 1748.9216, 1791.9175, 1890.1270, 1933.0131, 1933.0131, 2048.8672, 2087.9700, 2176.9785, 2192.9656, 2261.1506, 2333.0640, 2349.0698, 2413.1523, 2453.2651, 2648.3140, 2664.3325, 2741.4968

4. gi|157330628 **Mass:** 50301 **Score:** 136 **Expect:** 1.5e-008 **Queries matched:** 11

unnamed protein product [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
922.5048	921.4975	921.4919	0.0056	210	217	0	---	LYAESLAR
1109.5621	1108.5548	1108.5521	0.0027	79	88	0	---	FMMANGALVR
1109.5621	1108.5548	1108.5521	0.0027	79	88	0	31	FMMANGALVR
1125.5470	1124.5397	1124.5470	-0.0073	79	88	0	---	FMMANGALVR + Oxidation (M)
1141.5459	1140.5386	1140.5419	-0.0033	79	88	0	---	FMMANGALVR + 2 Oxidation (M)
1181.6360	1180.6287	1180.6274	0.0013	208	217	1	25	MKLYAESLAR
1181.6360	1180.6287	1180.6274	0.0013	208	217	1	---	MKLYAESLAR
1197.6224	1196.6151	1196.6223	-0.0072	208	217	1	---	MKLYAESLAR + Oxidation (M)
2061.1106	2060.1033	2060.0863	0.0170	118	136	1	---	VPATDVEALKSPLMGLFEK + Oxidation (M)
2544.2932	2543.2859	2543.2848	0.0011	218	240	0	57	FQGGSPYIYPLYGLGELPQAFAR
2544.2932	2543.2859	2543.2848	0.0011	218	240	0	---	FQGGSPYIYPLYGLGELPQAFAR

No match to: 713.4116, 724.4903, 734.4911, 768.5233, 864.5253, 917.2755, 978.5028, 1259.5913, 1270.6044, 1279.7672, 1334.8765, 1350.7323, 1366.7249, 1385.7383, 1421.7333, 1448.9141, 1523.8047, 1539.7997, 1572.8074, 1619.0718, 1620.8315, 1620.8315, 1679.8951, 1681.9961, 1696.8533, 1732.1002, 1734.0526, 1748.9216, 1791.9175, 1890.1270, 1930.9442, 1933.0131, 1933.0131, 2048.8672, 2087.9700, 2176.9785, 2192.9656, 2261.1506, 2333.0640, 2349.0698, 2413.1523, 2453.2651, 2648.3140, 2664.3325, 2741.4968

5. gi|157890964 **Mass:** 49978 **Score:** 108 **Expect:** 9.6e-006 **Queries matched:** 8

GDP dissociation inhibitor [Brassica rapa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
922.5048	921.4975	921.4919	0.0056	210	217	0	---	LYAESLAR
1181.6360	1180.6287	1180.6274	0.0013	208	217	1	25	MKLYAESLAR
1181.6360	1180.6287	1180.6274	0.0013	208	217	1	---	MKLYAESLAR
1197.6224	1196.6151	1196.6223	-0.0072	208	217	1	---	MKLYAESLAR + Oxidation (M)
1930.9442	1929.9369	1929.9328	0.0041	241	257	0	---	LSAVYGGTYMLNKPECK
2192.9656	2191.9583	2191.9489	0.0095	330	347	1	---	KSDMYVFCCSYSHNVAPK
2544.2932	2543.2859	2543.2848	0.0011	218	240	0	57	FQGGSPYIYPLYGLGELPQAFAR
2544.2932	2543.2859	2543.2848	0.0011	218	240	0	---	FQGGSPYIYPLYGLGELPQAFAR

No match to: 713.4116, 724.4903, 734.4911, 768.5233, 864.5253, 917.2755, 978.5028, 1109.5621, 1109.5621, 1125.5470, 1141.5459, 1259.5913, 1270.6044, 1279.7672, 1334.8765, 1350.7323, 1366.7249, 1385.7383, 1421.7333, 1448.9141, 1523.8047, 1539.7997, 1572.8074, 1619.0718, 1620.8315, 1620.8315, 1679.8951, 1681.9961, 1696.8533, 1732.1002, 1734.0526, 1748.9216, 1791.9175, 1890.1270, 1933.0131, 1933.0131, 2048.8672, 2061.1106, 2087.9700, 2176.9785, 2261.1506, 2333.0640, 2349.0698, 2413.1523, 2453.2651, 2648.3140, 2664.3325, 2741.4968

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 56

Protein View

Match to: **gi|195637100** Score: **176** Expect: **1.5e-012**
rab GDP dissociation inhibitor alpha [Zea mays]

Nominal mass (M_r): **50634**; Calculated pI value: **5.38**
NCBI BLAST search of gi|195637100 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Zea mays

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **23%**

Matched peptides shown in **Bold Red**

```
     1 MDEEYDVIVL GTGLKECIIS GLLSVDGLKV LHMDRNDYYG GESSSLNLTK
    51 LWNRFKGNDS PPEHLGVSKE YNVDMVPKFM MANGALVRVL IRTSVTKYLN
   101 FKAVDGSFVY NNGKIHKVPA TDVEALKSNL MGLFEKRRAR KFFIYVQDYE
   151 EDDPKSHEGL DLNKVTTREV ISKYGLEDDT VDFIGHALAL HRDDSYLDEP
   201 AIDTVKRMKL YAESLARFQG GSPYIYPLYG LGELPQAFAR LSAVYGGTYM
   251 LNKPECKVEF DESGKAYGVT SEGETAKCKK IVCDPSYLPD KVKKVGRVAR
   301 AICIMKHPIP DTKDSHSVQI ILPKKQLKRK SDMYVFCCSY AHNVAPKGKF
   351 IAFVSTEAET DKPEIELKPG IDLLGPVEET FFDIYDRYEP VNNPDDDCCF
   401 LTNSYDSTTH FETTVKDVLA LYNKITGKEL DLSVDLNAAS ATEQEAA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
79 - 88	1109.5621	1108.5548	1108.5521	0.0027	0	**FMMANGALVR** (No match)
79 - 88	1109.5621	1108.5548	1108.5521	0.0027	0	**FMMANGALVR** (Ions score 31)
79 - 88	1125.5470	1124.5397	1124.5470	-0.0073	0	**FMMANGALVR** Oxidation (M) (No match)
79 - 88	1141.5459	1140.5386	1140.5419	-0.0033	0	**FMMANGALVR** 2 Oxidation (M) (No match)
103 - 114	1270.6044	1269.5971	1269.5989	-0.0018	0	**AVDGSFVYNNGK** (No match)
208 - 217	1181.6360	1180.6287	1180.6274	0.0013	1	**MKLYAESLAR** (Ions score 25)
208 - 217	1181.6360	1180.6287	1180.6274	0.0013	1	**MKLYAESLAR** (No match)
208 - 217	1197.6224	1196.6151	1196.6223	-0.0072	1	**MKLYAESLAR** Oxidation (M) (No match)
210 - 217	922.5048	921.4975	921.4919	0.0056	0	**LYAESLAR** (No match)
218 - 240	2544.2932	2543.2859	2543.2848	0.0011	0	**FQGGSPYIYPLYGLGELPQAFAR** (Ions score 57)
218 - 240	2544.2932	2543.2859	2543.2848	0.0011	0	**FQGGSPYIYPLYGLGELPQAFAR** (No match)
241 - 257	1930.9442	1929.9369	1929.9328	0.0041	0	**LSAVYGGTYMLNKPECK** (No match)
301 - 313	1523.8047	1522.7974	1522.8000	-0.0025	1	**AICIMKHPIPDTK** (No match)
301 - 313	1539.7997	1538.7924	1538.7949	-0.0025	1	**AICIMKHPIPDTK** Oxidation (M) (No match)
330 - 347	2176.9785	2175.9712	2175.9539	0.0173	1	**KSDMYVFCCSYAHNVAPK** (No match)
330 - 347	2192.9656	2191.9583	2191.9489	0.0095	1	**KSDMYVFCCSYAHNVAPK** Oxidation (M) (No match)
331 - 347	2048.8672	2047.8599	2047.8590	0.0009	0	**SDMYVFCCSYAHNVAPK** (No match)

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	Accession	Mass	Score	Description
1.	gi|125525704	48512	81	hypothetical protein OsI_01694 [Oryza sativa Indica Group]
2.	gi|115436320	53009	81	Os01g0328700 [Oryza sativa (japonica cultivar-group)]
3.	gi|68052018	1201	69	RecName: Full=Dihydrolipoyl dehydrogenase; AltName: Full=Dihydrolipoamide dehydrogenase
4.	gi|168022120	83802	44	predicted protein [Physcomitrella patens subsp. patens]
5.	gi|82582805	71525	41	resistance-related receptor-like kinase [Triticum aestivum]
6.	gi|154756868	13710	39	mitogen-activated protein kinase [Olea europaea]
7.	gi|223545018	14598	37	conserved hypothetical protein [Ricinus communis]
8.	gi|168034841	40262	36	predicted protein [Physcomitrella patens subsp. patens]
9.	gi|75107094	26178	36	RecName: Full=50S ribosomal protein L19, chloroplastic; AltName: Full=CL19; Flags: Precursor
10.	gi|22122902	117956	35	putative transposon protein [Oryza sativa (japonica cultivar-group)]

Results List

1. gi|125525704 **Mass:** 48512 **Score:** 81 **Expect:** 0.0047 **Queries matched:** 4

hypothetical protein OsI_01694 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1201.7047	1200.6974	1200.6978	-0.0004	377	387	1	58	VGKFPLLANSR
1201.7047	1200.6974	1200.6978	-0.0004	377	387	1	---	VGKFPLLANSR
2119.1072	2118.0999	2118.0956	0.0043	275	295	1	9	VPYTAGIGLESVGVETDKAGR
2119.1072	2118.0999	2118.0956	0.0043	275	295	1	---	VPYTAGIGLESVGVETDKAGR

No match to: 713.4109, 744.3872, 750.5163, 768.5253, 886.9869, 1092.6147, 1174.5985, 1334.8787, 1551.7416, 1567.7390, 1716.7621, 1732.7230, 1732.7230, 1773.8732, 1773.8732, 1921.0808, 2825.3286, 3810.8547

2. gi|115436320 **Mass:** 53009 **Score:** 81 **Expect:** 0.0054 **Queries matched:** 4

Os01g0328700 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1201.7047	1200.6974	1200.6978	-0.0004	413	423	1	58	VGKFPLLANSR
1201.7047	1200.6974	1200.6978	-0.0004	413	423	1	---	VGKFPLLANSR
2119.1072	2118.0999	2118.0956	0.0043	311	331	1	9	VPYTAGIGLESVGVETDKAGR
2119.1072	2118.0999	2118.0956	0.0043	311	331	1	---	VPYTAGIGLESVGVETDKAGR

No match to: 713.4109, 744.3872, 750.5163, 768.5253, 886.9869, 1092.6147, 1174.5985, 1334.8787, 1551.7416, 1567.7390, 1716.7621, 1732.7230, 1732.7230, 1773.8732, 1773.8732, 1921.0808, 2825.3286, 3810.8547

3. gi|68052018 **Mass:** 1201 **Score:** 69 **Expect:** 0.073 **Queries matched:** 2

RecName: Full=Dihydrolipoyl dehydrogenase; AltName: Full=Dihydrolipoamide dehydrogenase

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1201.7047	1200.6974	1200.6978	-0.0004	1	11	1	58	VGKFPLLANSR
1201.7047	1200.6974	1200.6978	-0.0004	1	11	1	---	VGKFPLLANSR

No match to: 713.4109, 744.3872, 750.5163, 768.5253, 886.9869, 1092.6147, 1174.5985, 1334.8787, 1551.7416, 1567.7390, 1716.7621, 1732.7230, 1732.7230, 1773.8732, 1773.8732, 1921.0808, 2119.1072, 2119.1072, 2825.3286, 3810.8547

4. gi|168022120 **Mass:** 83802 **Score:** 44 **Expect:** 27 **Queries matched:** 6

predicted protein [Physcomitrella patens subsp. patens]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1174.5985	1173.5912	1173.5989	-0.0077	625 -	634	1	---	KIGTLQDDER
1201.7047	1200.6974	1200.6462	0.0512	719 -	729	0	20	IQALTVEANSR
1201.7047	1200.6974	1200.6462	0.0512	719 -	729	0	---	IQALTVEANSR
1551.7416	1550.7343	1550.7517	-0.0174	148 -	160	0	---	YGNSWEIFSHALK
1773.8732	1772.8659	1772.9057	-0.0397	226 -	240	1	---	ALVQDYLKEHETTAR
1773.8732	1772.8659	1772.9057	-0.0397	226 -	240	1	---	ALVQDYLKEHETTAR

No match to: 713.4109, 744.3872, 750.5163, 768.5253, 886.9869, 1092.6147, 1334.8787, 1567.7390, 1716.7621, 1732.7230, 1732.7230, 1921.0808, 2119.1072, 2119.1072, 2825.3286, 3810.8547

5. gi|82582805 **Mass:** 71525 **Score:** 41 **Expect:** 50 **Queries matched:** 7

resistance-related receptor-like kinase [Triticum aestivum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
744.3872	743.3799	743.3674	0.0125	539 -	544	1	---	RNSDPR
1174.5985	1173.5912	1173.6353	-0.0441	490 -	500	0	---	DQSIVTLTAAR
1773.8732	1772.8659	1772.9130	-0.0471	310 -	324	1	---	VEMFLKTYGTSKPTR + Oxidation (M)
1773.8732	1772.8659	1772.9130	-0.0471	310 -	324	1	---	VEMFLKTYGTSKPTR + Oxidation (M)
2119.1072	2118.0999	2118.1217	-0.0217	102 -	119	1	---	SSMKLIPLVDPCFVLQQK + Oxidation (M)
2119.1072	2118.0999	2118.1217	-0.0217	102 -	119	1	---	SSMKLIPLVDPCFVLQQK + Oxidation (M)
2825.3286	2824.3213	2824.4429	-0.1215	120 -	144	1	---	LVISRSSSSPQADVINYEMPSLYLR

No match to: 713.4109, 750.5163, 768.5253, 886.9869, 1092.6147, 1201.7047, 1201.7047, 1334.8787, 1551.7416, 1567.7390, 1716.7621, 1732.7230, 1732.7230, 1921.0808, 3810.8547

6. gi|154756868 **Mass:** 13710 **Score:** 39 **Expect:** 85 **Queries matched:** 4

mitogen-activated protein kinase [Olea europaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1092.6147	1091.6074	1091.5797	0.0277	51 -	59	1	---	MLVFDPSKR
1921.0808	1920.0735	1919.9815	0.0920	103 -	118	1	---	ELIWMESVKLNPDPLH
2119.1072	2118.0999	2118.1044	-0.0044	59 -	76	1	---	RISVDEALCHPYLAPLHK
2119.1072	2118.0999	2118.1044	-0.0044	59 -	76	1	---	RISVDEALCHPYLAPLHK

No match to: 713.4109, 744.3872, 750.5163, 768.5253, 886.9869, 1174.5985, 1201.7047, 1201.7047, 1334.8787, 1551.7416, 1567.7390, 1716.7621, 1732.7230, 1732.7230, 1773.8732, 1773.8732, 2825.3286, 3810.8547

7. gi|223545018 **Mass:** 14598 **Score:** 37 **Expect:** 1.2e+002 **Queries matched:** 3

conserved hypothetical protein [Ricinus communis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide

768.5253	767.5180	767.5129	0.0051	22 - 27	1	---	VRKPLR
1174.5985	1173.5912	1173.5349	0.0563	115 - 123	0	---	WMPNSRPDR + Oxidation (M)
3810.8547	3809.8474	3809.9041	-0.0567	77 - 110	1	---	CKCSGEQPNGEIEEQVLPANLIAPALMPYLEVIK

No match to: 713.4109, 744.3872, 750.5163, 886.9869, 1092.6147, 1201.7047, 1201.7047, 1334.8787, 1551.7416, 1567.7390, 1716.7621, 1732.7230, 1732.7230, 1773.8732, 1773.8732, 1921.0808, 2119.1072, 2119.1072, 2825.3286

8. gi|168034841 **Mass:** 40262 **Score:** 36 **Expect:** 1.5e+002 **Queries matched:** 5

predicted protein [Physcomitrella patens subsp. patens]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
744.3872	743.3799	743.4078	-0.0279	351 - 356	0	---	WVGVQR
1201.7047	1200.6974	1200.6462	0.0513	357 - 368	1	---	SRGAEEAVAAIK
1201.7047	1200.6974	1200.6462	0.0513	357 - 368	1	---	SRGAEEAVAAIK
1773.8732	1772.8659	1772.9090	-0.0431	149 - 164	1	---	VAIECGLQSAAELEKR
1773.8732	1772.8659	1772.9090	-0.0431	149 - 164	1	12	VAIECGLQSAAELEKR

No match to: 713.4109, 750.5163, 768.5253, 886.9869, 1092.6147, 1174.5985, 1334.8787, 1551.7416, 1567.7390, 1716.7621, 1732.7230, 1732.7230, 1921.0808, 2119.1072, 2119.1072, 2825.3286, 3810.8547

9. gi|75107094 **Mass:** 26178 **Score:** 36 **Expect:** 1.6e+002 **Queries matched:** 5

RecName: Full=50S ribosomal protein L19, chloroplastic; AltName: Full=CL19; Flags: Precursor

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1201.7047	1200.6974	1200.6900	0.0075	119 - 129	1	---	LGDIMGILNKK
1201.7047	1200.6974	1200.6900	0.0075	119 - 129	1	---	LGDIMGILNKK
1773.8732	1772.8659	1772.8297	0.0362	38 - 52	1	---	FSLSSNCRSNLMVSR + Oxidation (M)
1773.8732	1772.8659	1772.8297	0.0362	38 - 52	1	---	FSLSSNCRSNLMVSR + Oxidation (M)
3810.8547	3809.8474	3809.7238	0.1237	78 - 113	0	---	SEAEDSSDAPAESVAVVAEEELPVESEAEAEERPPR

No match to: 713.4109, 744.3872, 750.5163, 768.5253, 886.9869, 1092.6147, 1174.5985, 1334.8787, 1551.7416, 1567.7390, 1716.7621, 1732.7230, 1732.7230, 1921.0808, 2119.1072, 2119.1072, 2825.3286

10. gi|22122902 **Mass:** 117956 **Score:** 35 **Expect:** 2e+002 **Queries matched:** 6

putative transposon protein [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
744.3872	743.3799	743.4038	-0.0239	283 - 288	1	---	DARNIR
1174.5985	1173.5912	1173.5989	-0.0077	493 - 502	1	---	DTLEARNDLK
1551.7416	1550.7343	1550.7338	0.0005	263 - 275	1	---	HPADGSQWRNIDR
1716.7621	1715.7548	1715.7746	-0.0197	532 - 545	1	---	AEKESMFECLESIK + Oxidation (M)
2825.3286	2824.3213	2824.3193	0.0020	881 - 905	1	---	CQWVRLTGEGVMIDDSGMTTVDLNK
3810.8547	3809.8474	3809.8762	-0.0288	847 - 880	1	---	VNAMGHDGTIGTYYGAIEDIWELDYGPLKVPLFR

No match to: 713.4109, 750.5163, 768.5253, 886.9869, 1092.6147, 1201.7047, 1201.7047, 1334.8787, 1567.7390, 1732.7230, 1732.7230, 1773.8732, 1773.8732, 1921.0808, 2119.1072, 2119.1072

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 22

Protein View

Match to: **gi|125525704** Score: **81** Expect: **0.0047**
hypothetical protein OsI_01694 [Oryza sativa Indica Group]

Nominal mass (M_r): **48512**; Calculated pI value: **6.26**
NCBI BLAST search of gi|125525704 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Oryza sativa Indica Group

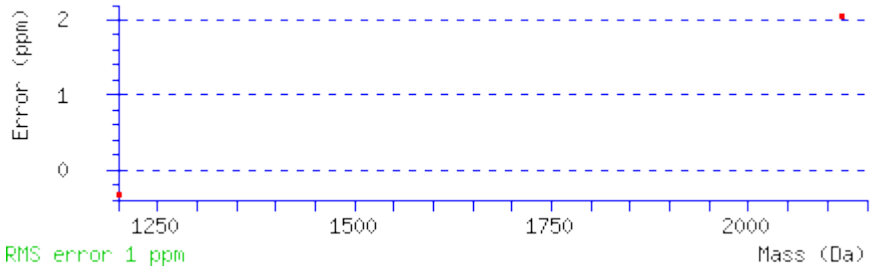
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **6%**

Matched peptides shown in **Bold Red**

```
     1 MALASPGEEA GGGGAAAAAA GGGGGVGAEG VVRGGGGGGE RRGGGGRRAG
    51 RALLHSSHMY HEAKSSFAHH GVKFSNLEVD LPAMMAQKDK AVAGLTKGIE
   101 GLFKKNKVTY VKGFGKLASP SEVSVDLSDG GSTVVKGKNI IIATGSDVKS
   151 LPGVTIDEKK IVSSTGALCL SEIPKKLVVI GAGYIGLEMG SVWNRLGSEV
   201 TVVEFAPDIV PSMDGEVRKQ FQRMLEKQKM KFMLKTKVVG DDTSGDGVKL
   251 TLEPAAGGEQ SVIEADIVLV SAGRVPYTAG IGLESVGVET DKAGRILVDK
   301 RFMTNVNGVY AIGDAIPGPM LAHKAEEDGV ACVEFIAGKE GHVDYDTVPG
   351 VVYTHPEVAS VGKTEEQVKA LGIPYRVGKF PLLANSRAKA IDDAEGLVKV
   401 VAEKETDKIL GVHIMAPGAG EIIHEAVLAL QYGASSEDIA RTCHAHPTVS
   451 EALKEACLQT FTKAIHI
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
275 - 295	2119.1072	2118.0999	2118.0956	0.0043	1	**VPYTAGIGLESVGVETDKAGR**	(Ions score 9)
275 - 295	2119.1072	2118.0999	2118.0956	0.0043	1	**VPYTAGIGLESVGVETDKAGR**	(No match)
377 - 387	1201.7047	1200.6974	1200.6978	-0.0004	1	**VGKFPLLANSR**	(Ions score 58)
377 - 387	1201.7047	1200.6974	1200.6978	-0.0004	1	**VGKFPLLANSR**	(No match)



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	Accession	Mass	Score	Description
1.	gi|54144332	56979	117	pollen allergen Phl p 4 [Phleum pratense]
2.	gi|189014266	56147	116	pollen allergen Phl p 4.0102 [Phleum pratense]
3.	gi|82492267	58590	113	major pollen allergen Phl p 4 precursor [Phleum pratense]
4.	gi|54144334	56741	113	pollen allergen Phl p 4 [Phleum pratense]
5.	gi|189014268	55889	113	pollen allergen Phl p 4.0202 [Phleum pratense]
6.	gi|189014270	55917	113	pollen allergen Phl p 4.0203 [Phleum pratense]
7.	gi|189014272	55931	113	pollen allergen Phl p 4.0204 [Phleum pratense]
8.	gi|116787119	27168	57	unknown [Picea sitchensis]
9.	gi|115470567	18837	52	Os07g0144900 [Oryza sativa (japonica cultivar-group)]
10.	gi|28372694	74935	50	hypothetical protein [Oryza sativa (japonica cultivar-group)]

Results List

1. gi|54144332 **Mass:** 56979 **Score:** 117 **Expect:** 1.2e-006 **Queries matched:** 5

pollen allergen Phl p 4 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1199.7201	1198.7128	1198.7073	0.0055	26	35	1	---	EIPPRLLYAK
1475.8005	1474.7932	1474.7779	0.0153	36	49	0	94	SSPAYPSVLGQTIR
1475.8005	1474.7932	1474.7779	0.0153	36	49	0	---	SSPAYPSVLGQTIR
1832.9749	1831.9676	1831.9540	0.0136	36	52	1	---	SSPAYPSVLGQTIRNSR
3310.6594	3309.6521	3309.5269	0.1252	300	327	0	---	FPELGMNASHCNEMSWIQSIPFVHLGHR + Oxidation (M)

No match to: 713.3990, 734.4868, 768.5148, 864.5477, 1060.5394, 1076.5686, 1107.6002, 1279.7476, 1305.6923, 1315.7266, 1337.6707, 1364.6824, 1404.7780, 1415.7965, 1443.8228, 1448.8972, 1520.7657, 1520.7657, 1541.8318, 1541.8318, 1682.9670, 1693.8003, 1709.8025, 1900.0239, 1900.0239, 1958.9545, 1972.0267, 2123.0430, 2187.1218, 2231.2273, 2248.2366, 2342.2061, 2453.1401, 2453.1401, 2826.3247

2. gi|189014266 **Mass:** 56147 **Score:** 116 **Expect:** 1.5e-006 **Queries matched:** 5

pollen allergen Phl p 4.0102 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1199.7201	1198.7128	1198.7073	0.0055	18	27	1	---	EIPPRLLYAK
1475.8005	1474.7932	1474.7779	0.0153	28	41	0	94	SSPAYPSVLGQTIR
1475.8005	1474.7932	1474.7779	0.0153	28	41	0	---	SSPAYPSVLGQTIR
1832.9749	1831.9676	1831.9540	0.0136	28	44	1	---	SSPAYPSVLGQTIRNSR
3310.6594	3309.6521	3309.5269	0.1252	292	319	0	---	FPELGMNASHCNEMSWIQSIPFVHLGHR + Oxidation (M)

No match to: 713.3990, 734.4868, 768.5148, 864.5477, 1060.5394, 1076.5686, 1107.6002, 1279.7476, 1305.6923, 1315.7266, 1337.6707, 1364.6824, 1404.7780, 1415.7965, 1443.8228, 1448.8972, 1520.7657, 1520.7657, 1541.8318, 1541.8318, 1682.9670, 1693.8003, 1709.8025, 1900.0239, 1900.0239, 1958.9545, 1972.0267, 2123.0430, 2187.1218,

2231.2273, 2248.2366, 2342.2061, 2453.1401, 2453.1401, 2826.3247

3. gi|82492267 **Mass:** 58590 **Score:** 113 **Expect:** 3e-006 **Queries matched:** 5

major pollen allergen Phl p 4 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1060.5394	1059.5321	1059.5137	0.0184	491 -	498	1	---	YFKGNFER
1199.7201	1198.7128	1198.7073	0.0055	43 -	52	1	---	EIPPRLLYAK
1475.8005	1474.7932	1474.7779	0.0153	53 -	66	0	94	SSPAYPSVLGQTIR
1475.8005	1474.7932	1474.7779	0.0153	53 -	66	0	---	SSPAYPSVLGQTIR
1832.9749	1831.9676	1831.9540	0.0136	53 -	69	1	---	SSPAYPSVLGQTIRNSR

No match to: 713.3990, 734.4868, 768.5148, 864.5477, 1076.5686, 1107.6002, 1279.7476, 1305.6923, 1315.7266, 1337.6707, 1364.6824, 1404.7780, 1415.7965, 1443.8228, 1448.8972, 1520.7657, 1520.7657, 1541.8318, 1541.8318, 1682.9670, 1693.8003, 1709.8025, 1900.0239, 1900.0239, 1958.9545, 1972.0267, 2123.0430, 2187.1218, 2231.2273, 2248.2366, 2342.2061, 2453.1401, 2453.1401, 2826.3247, 3310.6594

4. gi|54144334 **Mass:** 56741 **Score:** 113 **Expect:** 3e-006 **Queries matched:** 5

pollen allergen Phl p 4 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1060.5394	1059.5321	1059.5137	0.0184	474 -	481	1	---	YFKGNFER
1199.7201	1198.7128	1198.7073	0.0055	26 -	35	1	---	EIPPRLLYAK
1475.8005	1474.7932	1474.7779	0.0153	36 -	49	0	94	SSPAYPSVLGQTIR
1475.8005	1474.7932	1474.7779	0.0153	36 -	49	0	---	SSPAYPSVLGQTIR
1832.9749	1831.9676	1831.9540	0.0136	36 -	52	1	---	SSPAYPSVLGQTIRNSR

No match to: 713.3990, 734.4868, 768.5148, 864.5477, 1076.5686, 1107.6002, 1279.7476, 1305.6923, 1315.7266, 1337.6707, 1364.6824, 1404.7780, 1415.7965, 1443.8228, 1448.8972, 1520.7657, 1520.7657, 1541.8318, 1541.8318, 1682.9670, 1693.8003, 1709.8025, 1900.0239, 1900.0239, 1958.9545, 1972.0267, 2123.0430, 2187.1218, 2231.2273, 2248.2366, 2342.2061, 2453.1401, 2453.1401, 2826.3247, 3310.6594

5. gi|189014268 **Mass:** 55889 **Score:** 113 **Expect:** 3e-006 **Queries matched:** 5

pollen allergen Phl p 4.0202 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1060.5394	1059.5321	1059.5137	0.0184	466 -	473	1	---	YFKGNFER
1199.7201	1198.7128	1198.7073	0.0055	18 -	27	1	---	EIPPRLLYAK
1475.8005	1474.7932	1474.7779	0.0153	28 -	41	0	94	SSPAYPSVLGQTIR
1475.8005	1474.7932	1474.7779	0.0153	28 -	41	0	---	SSPAYPSVLGQTIR
1832.9749	1831.9676	1831.9540	0.0136	28 -	44	1	---	SSPAYPSVLGQTIRNSR

No match to: 713.3990, 734.4868, 768.5148, 864.5477, 1076.5686, 1107.6002, 1279.7476, 1305.6923, 1315.7266, 1337.6707, 1364.6824, 1404.7780, 1415.7965, 1443.8228, 1448.8972, 1520.7657, 1520.7657, 1541.8318, 1541.8318, 1682.9670, 1693.8003, 1709.8025, 1900.0239, 1900.0239, 1958.9545, 1972.0267, 2123.0430, 2187.1218, 2231.2273, 2248.2366, 2342.2061, 2453.1401, 2453.1401, 2826.3247, 3310.6594

6. gi|189014270 **Mass:** 55917 **Score:** 113 **Expect:** 3e-006 **Queries matched:** 5

pollen allergen Phl p 4.0203 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1060.5394	1059.5321	1059.5137	0.0184	466 -	473	1	---	YFKGNFER
1199.7201	1198.7128	1198.7073	0.0055	18 -	27	1	---	EIPPRLLYAK
1475.8005	1474.7932	1474.7779	0.0153	28 -	41	0	94	SSPAYPSVLGQTIR
1475.8005	1474.7932	1474.7779	0.0153	28 -	41	0	---	SSPAYPSVLGQTIR
1832.9749	1831.9676	1831.9540	0.0136	28 -	44	1	---	SSPAYPSVLGQTIRNSR

No match to: 713.3990, 734.4868, 768.5148, 864.5477, 1076.5686, 1107.6002, 1279.7476, 1305.6923, 1315.7266, 1337.6707, 1364.6824, 1404.7780, 1415.7965, 1443.8228, 1448.8972, 1520.7657, 1520.7657, 1541.8318, 1541.8318, 1682.9670, 1693.8003, 1709.8025, 1900.0239, 1900.0239, 1958.9545, 1972.0267, 2123.0430, 2187.1218, 2231.2273, 2248.2366, 2342.2061, 2453.1401, 2453.1401, 2826.3247, 3310.6594

7. gi|189014272 **Mass:** 55931 **Score:** 113 **Expect:** 3e-006 **Queries matched:** 5

pollen allergen Phl p 4.0204 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1060.5394	1059.5321	1059.5137	0.0184	466 -	473	1	---	YFKGNFER
1199.7201	1198.7128	1198.7073	0.0055	18 -	27	1	---	EIPPRLLYAK
1475.8005	1474.7932	1474.7779	0.0153	28 -	41	0	94	SSPAYPSVLGQTIR
1475.8005	1474.7932	1474.7779	0.0153	28 -	41	0	---	SSPAYPSVLGQTIR
1832.9749	1831.9676	1831.9540	0.0136	28 -	44	1	---	SSPAYPSVLGQTIRNSR

No match to: 713.3990, 734.4868, 768.5148, 864.5477, 1076.5686, 1107.6002, 1279.7476, 1305.6923, 1315.7266, 1337.6707, 1364.6824, 1404.7780, 1415.7965, 1443.8228, 1448.8972, 1520.7657, 1520.7657, 1541.8318, 1541.8318, 1682.9670, 1693.8003, 1709.8025, 1900.0239, 1900.0239, 1958.9545, 1972.0267, 2123.0430, 2187.1218, 2231.2273, 2248.2366, 2342.2061, 2453.1401, 2453.1401, 2826.3247, 3310.6594

8. gi|116787119 **Mass:** 27168 **Score:** 57 **Expect:** 1.1 **Queries matched:** 7

unknown [Picea sitchensis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1404.7780	1403.7707	1403.7992	-0.0285	68 -	79	1	---	MSMQIVARILVK + Oxidation (M)
1520.7657	1519.7584	1519.8106	-0.0522	215 -	228	1	---	KNTADGIPLEHVAR
1520.7657	1519.7584	1519.8106	-0.0522	215 -	228	1	---	KNTADGIPLEHVAR
1693.8003	1692.7930	1692.9046	-0.1115	163 -	178	0	---	HVLAEAVNVEGLSLDK
1972.0267	1971.0194	1970.9706	0.0489	60 -	75	1	---	LYQFEPARMSMQIVAR + 2 Oxidation (M)
2123.0430	2122.0357	2122.1210	-0.0853	198 -	215	1	---	GQLIVFPPNEYNHPELKK
2826.3247	2825.3174	2825.4608	-0.1433	100 -	122	1	---	LQMMEPFITLITLSHYLETARFR + Oxidation (M)

No match to: 713.3990, 734.4868, 768.5148, 864.5477, 1060.5394, 1076.5686, 1107.6002, 1199.7201, 1279.7476, 1305.6923, 1315.7266, 1337.6707, 1364.6824, 1415.7965, 1443.8228, 1448.8972, 1475.8005, 1475.8005, 1541.8318, 1541.8318, 1682.9670, 1709.8025, 1832.9749, 1900.0239, 1900.0239, 1958.9545, 2187.1218, 2231.2273, 2248.2366, 2342.2061, 2453.1401, 2453.1401, 3310.6594

9. gi|115470567 **Mass:** 18837 **Score:** 52 **Expect:** 3.7 **Queries matched:** 6

Os07g0144900 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1060.5394	1059.5321	1059.5998	-0.0677	16	25	0	---	MIILISADGK
1076.5686	1075.5613	1075.5947	-0.0334	16	25	0	---	MIILISADGK + Oxidation (M)
1337.6707	1336.6634	1336.5928	0.0706	1	15	0	---	MAAAAAEATTDGGGK + Oxidation (M)
1832.9749	1831.9676	1831.9719	-0.0043	96	111	0	---	FDAELVQALENPVLFK
1958.9545	1957.9472	1957.8730	0.0743	123	139	1	---	SLLDMTCQRVADMMSGK + Oxidation (M)
2248.2366	2247.2293	2247.1416	0.0878	2	25	1	---	AAAAAEATTDGGGKMIILISADGK + Oxidation (M)

No match to: 713.3990, 734.4868, 768.5148, 864.5477, 1107.6002, 1199.7201, 1279.7476, 1305.6923, 1315.7266, 1364.6824, 1404.7780, 1415.7965, 1443.8228, 1448.8972, 1475.8005, 1475.8005, 1520.7657, 1520.7657, 1541.8318, 1541.8318, 1682.9670, 1693.8003, 1709.8025, 1900.0239, 1900.0239, 1972.0267, 2123.0430, 2187.1218, 2231.2273, 2342.2061, 2453.1401, 2453.1401, 2826.3247, 3310.6594

10. gi|28372694 **Mass:** 74935 **Score:** 50 **Expect:** 6.2 **Queries matched:** 9

hypothetical protein [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1060.5394	1059.5321	1059.5560	-0.0238	505	513	1	---	VSELEAREK
1076.5686	1075.5613	1075.5444	0.0169	350	358	1	---	TMALEAERR
1279.7476	1278.7403	1278.6792	0.0611	327	338	1	---	GILDAAAAHERR
1364.6824	1363.6751	1363.7571	-0.0820	628	640	0	---	AAVELVLASHQAR
1443.8228	1442.8155	1442.7728	0.0427	291	304	0	---	QAALIASSVLDEAR
2187.1218	2186.1145	2186.0814	0.0331	285	304	1	---	EAEEERQAALIASSVLDEAR
2342.2061	2341.1988	2341.0473	0.1515	641	660	0	---	DPEFMPWHALEDFPPGTEAR
2453.1401	2452.1328	2452.2379	-0.1051	1	27	0	---	MPGGGGVSSSPQSGPSTALPVGSLVAR
2453.1401	2452.1328	2452.2379	-0.1051	1	27	0	---	MPGGGGVSSSPQSGPSTALPVGSLVAR

No match to: 713.3990, 734.4868, 768.5148, 864.5477, 1107.6002, 1199.7201, 1305.6923, 1315.7266, 1337.6707, 1404.7780, 1415.7965, 1448.8972, 1475.8005, 1475.8005, 1520.7657, 1520.7657, 1541.8318, 1541.8318, 1682.9670, 1693.8003, 1709.8025, 1832.9749, 1900.0239, 1900.0239, 1958.9545, 1972.0267, 2123.0430, 2231.2273, 2248.2366, 2826.3247, 3310.6594

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 40

Protein View

Match to: **gi|54144332** Score: **117** Expect: **1.2e-006**
pollen allergen Phl p 4 [Phleum pratense]

Nominal mass (M_r): **56979**; Calculated pI value: **8.75**
NCBI BLAST search of gi|54144332 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

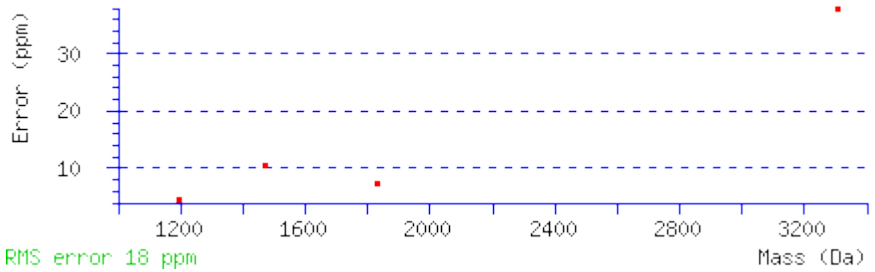
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **10%**

Matched peptides shown in **Bold Red**

```
   1 SSCEVALSYY PTPLAKEDFL RCLVKEIPPR LLYAKSSPAY PSVLGQTIRN
  51 SRWSSPDNVK PIYIVTPTNA SHIQSAVVCG RRHGVRIRVR SGGHDYEGLS
 101 YRSLQPEEFA VVDLSKMRAV WVDGKARTAW VDSGAQLGEL YYAIHKASPV
 151 LAFPAGVCPT IGVGGNFAGG GFGMLLRKYG IAAENVIDVK LVDANGTLHD
 201 KKSMGDDHFW AVRGGGGESF GIVVAWKVRL LPVPPTVTVF KIPKKASEGA
 251 VDIINRWQVV APQLPDDLMI RVIAQGPTAT FEAMYLGTCQ TLTPMMSSKF
 301 PELGMNASHC NEMSWIQSIP FVHLGHRDNI EDDLLNRNNT FKPFAEYKSD
 351 YVYEPFPKEV WEQIFSTWLL KPGAGIMIFD PYGATISATP EWATPFPHRK
 401 GVLFNIQYVN YWFAPGAGAA PLSWSKEIYN YMEPYVSKNP RQAYANYRDI
 451 DLGRNEVVND VSTFSSGLVW GQKYFKGNFQ RLAITKGKVD PTDYFRNEQS
 501 IPPLIQKY
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
26 - 35	1199.7201	1198.7128	1198.7073	0.0055	1	**EIPPRLLYAK**	(No match)
36 - 49	1475.8005	1474.7932	1474.7779	0.0153	0	**SSPAYPSVLGQTIR**	(Ions score 94)
36 - 49	1475.8005	1474.7932	1474.7779	0.0153	0	**SSPAYPSVLGQTIR**	(No match)
36 - 52	1832.9749	1831.9676	1831.9540	0.0136	1	**SSPAYPSVLGQTIRNSR**	(No match)
300 - 327	3310.6594	3309.6521	3309.5269	0.1252	0	**FPELGMNASHCNEMSWIQSIPFVHLGHR**	Oxidation (M) (No match)



Peptide View

MS/MS Fragmentation of **SSPAYPSVLGQTIR**
Found in **gi|54144332**, pollen allergen Phl p 4 [Phleum pratense]

Match to Query 18: 1474.793224 from(1475.800500,1+)
MaldiWellID: 81947, SpectrumID: 214102,

Click mouse within plot area to zoom in by factor of two about that point
Or, to Da

MONOISOTOPIC mass of neutral peptide Mr(calc): 1474.7779
Fixed modifications: Carbamidomethyl (C)
Ions Score: 94 **Expect:** 3e-007
Matches (Bold Red): 39/218 fragment ions using 27 most intense peaks

#	Immon.	a	a*	a^0	b	b*	b^0	Seq.	v	y	y*	y^0	#
1	60.0444	60.0444		42.0338	88.0393		**70.0287**	S					14
2	60.0444	147.0764		129.0659	**175.0713**		157.0608	S	1356.7270	1388.7532	1371.7267	1370.7427	13
3	**70.0651**	244.1292		226.1186	**272.1241**		**254.1135**	P	1259.6742	**1301.7212**	1284.6946	1283.7106	12
4	44.0495	315.1663		297.1557	**343.1612**		325.1506	A	1188.6371	1204.6684	1187.6419	1186.6579	11
5	136.0757	478.2296		460.2191	**506.2245**		488.2140	Y	1025.5738	1133.6313	1116.6048	1115.6208	10
6	**70.0651**	575.2824		557.2718	603.2773		585.2667	P	928.5210	**970.5680**	**953.5414**	952.5574	9
7	60.0444	662.3144		644.3039	690.3093		672.2988	S	841.4890	873.5152	856.4887	855.5047	8
8	**72.0808**	761.3828		743.3723	789.3777		771.3672	V	742.4206	**786.4832**	769.4567	768.4726	7
9	**86.0964**	874.4669		856.4563	902.4618		884.4512	L	629.3365	**687.4148**	**670.3882**	669.4042	6

10	30.0338	931.4883		913.4778	959.4833		941.4727	G		574.3307	557.3042	556.3202	5
11	101.0709	1059.5469	1042.5204	1041.5364	1087.5418	1070.5153	1069.5313	Q	444.2565	517.3093	500.2827	499.2987	4
12	74.0600	1160.5946	1143.5681	1142.5840	1188.5895	1171.5630	1170.5790	T	343.2088	389.2507	372.2241	371.2401	3
13	86.0964	1273.6787	1256.6521	1255.6681	1301.6736	1284.6470	1283.6630	I	230.1248	288.2030	271.1765		2
14	129.1135							R	74.0236	175.1189	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
SP	157.0972	185.0921	SPA	228.1343	256.1292	SPAY	391.1976	419.1925
SPAYP	488.2504	516.2453	SPAYPS	575.2824	603.2773	SPAYPSV	674.3508	702.3457
PA	141.1022	169.0971	PAY	304.1656	332.1605	PAYP	401.2183	429.2132
PAYPS	488.2504	516.2453	PAYPSV	587.3188	615.3137	AY	207.1128	235.1077
AYP	304.1656	332.1605	AYPS	391.1976	419.1925	AYPSV	490.2660	518.2609
AYPSVL	603.3501	631.3450	AYPSVLG	660.3715	688.3664	YP	233.1285	261.1234
YPS	320.1605	348.1554	YPSV	419.2289	447.2238	YPSVL	532.3130	560.3079
YPSVLG	589.3344	617.3293	PS	157.0972	185.0921	PSV	256.1656	284.1605
PSVL	369.2496	397.2445	PSVLG	426.2711	454.2660	PSVLGQ	554.3297	582.3246
PSVLGQT	655.3773	683.3723	SV	159.1128	187.1077	SVL	272.1969	300.1918
SVLG	329.2183	357.2132	SVLGQ	457.2769	485.2718	SVLGQT	558.3246	586.3195
SVLGQTI	671.4086	699.4036	VL	185.1648	213.1597	VLG	242.1863	270.1812
VLGQ	370.2449	398.2398	VLGQT	471.2926	499.2875	VLGQTI	584.3766	612.3715
LG	143.1179	171.1128	LGQ	271.1765	299.1714	LGQT	372.2241	400.2191
LGQTI	485.3082	513.3031	GQ	158.0924	186.0873	GQT	259.1401	287.1350
GQTI	372.2241	400.2191	QT	202.1186	230.1135	QTI	315.2027	343.1976
TI	187.1441	215.1390						

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Index

	Accession	Mass	Score	Description
1.	gi|82492267	58590	71	major pollen allergen Phl p 4 precursor [Phleum pratense]
2.	gi|189014268	55889	70	pollen allergen Phl p 4.0202 [Phleum pratense]
3.	gi|189014270	55917	70	pollen allergen Phl p 4.0203 [Phleum pratense]
4.	gi|189014272	55931	70	pollen allergen Phl p 4.0204 [Phleum pratense]
5.	gi|54144334	56741	70	pollen allergen Phl p 4 [Phleum pratense]
6.	gi|189014266	56147	70	pollen allergen Phl p 4.0102 [Phleum pratense]
7.	gi|54144332	56979	70	pollen allergen Phl p 4 [Phleum pratense]
8.	gi|20563358	35284	58	granule-bound starch synthase [Frangula alnus]
9.	gi|115442427	37713	56	Os01g0965400 [Oryza sativa (japonica cultivar-group)]
10.	gi|218189798	38940	56	hypothetical protein OsI_05332 [Oryza sativa Indica Group]

Results List

1. gi|82492267 **Mass:** 58590 **Score:** 71 **Expect:** 0.053 **Queries matched:** 3

major pollen allergen Phl p 4 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1475.7838	1474.7765	1474.7779	-0.0014	53	-	66	0	56	SSPAYPSVLGQTIR
1475.7838	1474.7765	1474.7779	-0.0014	53	-	66	0	---	SSPAYPSVLGQTIR
1832.9517	1831.9444	1831.9540	-0.0096	53	-	69	1	---	SSPAYPSVLGQTIRNSR

No match to: 713.3809, 768.5023, 1076.5908, 1364.6908, 1404.7953, 1520.7590, 1520.7590, 1541.8372, 1541.8372, 1900.0295, 1900.0295, 2453.1521, 2453.1521

2. gi|189014268 **Mass:** 55889 **Score:** 70 **Expect:** 0.059 **Queries matched:** 3

pollen allergen Phl p 4.0202 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1475.7838	1474.7765	1474.7779	-0.0014	28	-	41	0	56	SSPAYPSVLGQTIR
1475.7838	1474.7765	1474.7779	-0.0014	28	-	41	0	---	SSPAYPSVLGQTIR
1832.9517	1831.9444	1831.9540	-0.0096	28	-	44	1	---	SSPAYPSVLGQTIRNSR

No match to: 713.3809, 768.5023, 1076.5908, 1364.6908, 1404.7953, 1520.7590, 1520.7590, 1541.8372, 1541.8372, 1900.0295, 1900.0295, 2453.1521, 2453.1521

3. gi|189014270 **Mass:** 55917 **Score:** 70 **Expect:** 0.059 **Queries matched:** 3

pollen allergen Phl p 4.0203 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1475.7838	1474.7765	1474.7779	-0.0014	28	-	41	0	56	SSPAYPSVLGQTIR
1475.7838	1474.7765	1474.7779	-0.0014	28	-	41	0	---	SSPAYPSVLGQTIR
1832.9517	1831.9444	1831.9540	-0.0096	28	-	44	1	---	SSPAYPSVLGQTIRNSR

No match to: 713.3809, 768.5023, 1076.5908, 1364.6908, 1404.7953, 1520.7590, 1520.7590, 1541.8372, 1541.8372, 1900.0295, 1900.0295, 2453.1521, 2453.1521

4. gi|189014272 **Mass:** 55931 **Score:** 70 **Expect:** 0.059 **Queries matched:** 3

pollen allergen Phl p 4.0204 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1475.7838	1474.7765	1474.7779	-0.0014	28	-	41	0	56	SSPAYPSVLGQTIR
1475.7838	1474.7765	1474.7779	-0.0014	28	-	41	0	---	SSPAYPSVLGQTIR
1832.9517	1831.9444	1831.9540	-0.0096	28	-	44	1	---	SSPAYPSVLGQTIRNSR

No match to: 713.3809, 768.5023, 1076.5908, 1364.6908, 1404.7953, 1520.7590, 1520.7590, 1541.8372, 1541.8372, 1900.0295, 1900.0295, 2453.1521, 2453.1521

5. gi|54144334 **Mass:** 56741 **Score:** 70 **Expect:** 0.061 **Queries matched:** 3

pollen allergen Phl p 4 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1475.7838	1474.7765	1474.7779	-0.0014	36	-	49	0	56	SSPAYPSVLGQTIR
1475.7838	1474.7765	1474.7779	-0.0014	36	-	49	0	---	SSPAYPSVLGQTIR
1832.9517	1831.9444	1831.9540	-0.0096	36	-	52	1	---	SSPAYPSVLGQTIRNSR

No match to: 713.3809, 768.5023, 1076.5908, 1364.6908, 1404.7953, 1520.7590, 1520.7590, 1541.8372, 1541.8372, 1900.0295, 1900.0295, 2453.1521, 2453.1521

6. gi|189014266 **Mass:** 56147 **Score:** 70 **Expect:** 0.067 **Queries matched:** 3

pollen allergen Phl p 4.0102 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1475.7838	1474.7765	1474.7779	-0.0014	28	-	41	0	56	SSPAYPSVLGQTIR
1475.7838	1474.7765	1474.7779	-0.0014	28	-	41	0	---	SSPAYPSVLGQTIR
1832.9517	1831.9444	1831.9540	-0.0096	28	-	44	1	---	SSPAYPSVLGQTIRNSR

No match to: 713.3809, 768.5023, 1076.5908, 1364.6908, 1404.7953, 1520.7590, 1520.7590, 1541.8372, 1541.8372, 1900.0295, 1900.0295, 2453.1521, 2453.1521

7. gi|54144332 **Mass:** 56979 **Score:** 70 **Expect:** 0.068 **Queries matched:** 3

pollen allergen Phl p 4 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1475.7838	1474.7765	1474.7779	-0.0014	36	-	49	0	56	SSPAYPSVLGQTIR
1475.7838	1474.7765	1474.7779	-0.0014	36	-	49	0	---	SSPAYPSVLGQTIR
1832.9517	1831.9444	1831.9540	-0.0096	36	-	52	1	---	SSPAYPSVLGQTIRNSR

No match to: 713.3809, 768.5023, 1076.5908, 1364.6908, 1404.7953, 1520.7590, 1520.7590, 1541.8372, 1541.8372, 1900.0295, 1900.0295, 2453.1521, 2453.1521

8. gi|20563358 **Mass:** 35284 **Score:** 58 **Expect:** 1 **Queries matched:** 7

granule-bound starch synthase [Frangula alnus]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide

1475.7838	1474.7765	1474.7602	0.0163	100 - 112	0	11	FSLLCQAALEAPR
1475.7838	1474.7765	1474.7602	0.0163	100 - 112	0	---	FSLLCQAALEAPR
1520.7590	1519.7517	1519.7605	-0.0088	161 - 173	0	---	VAFCIHNIAYQGK
1520.7590	1519.7517	1519.7605	-0.0088	161 - 173	0	---	VAFCIHNIAYQGK
1832.9517	1831.9444	1831.9203	0.0241	33 - 48	1	---	DAWDTEVTIELKVGEK
1900.0295	1899.0222	1899.0312	-0.0090	230 - 246	1	---	ELVSSVEKGVELDNILR
1900.0295	1899.0222	1899.0312	-0.0090	230 - 246	1	---	ELVSSVEKGVELDNILR

No match to: 713.3809, 768.5023, 1076.5908, 1364.6908, 1404.7953, 1541.8372, 1541.8372, 2453.1521, 2453.1521

9. gi|115442427 **Mass:** 37713 **Score:** 56 **Expect:** 1.4 **Queries matched:** 7

Os01g0965400 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1364.6908	1363.6835	1363.6255	0.0580	252 - 264		0	---	ATNVDGVYDADPK
1520.7590	1519.7517	1519.7266	0.0251	252 - 265		1	5	ATNVDGVYDADPKR
1520.7590	1519.7517	1519.7266	0.0251	252 - 265		1	---	ATNVDGVYDADPKR
1541.8372	1540.8299	1540.8361	-0.0062	21 - 35		0	---	LSPSPPASSHVPLPR
1541.8372	1540.8299	1540.8361	-0.0062	21 - 35		0	5	LSPSPPASSHVPLPR
2453.1521	2452.1448	2452.2862	-0.1414	217 - 240		1	---	GRVVIFAAGTGNPFFTTDTAAALR
2453.1521	2452.1448	2452.2862	-0.1414	217 - 240		1	---	GRVVIFAAGTGNPFFTTDTAAALR

No match to: 713.3809, 768.5023, 1076.5908, 1404.7953, 1475.7838, 1475.7838, 1832.9517, 1900.0295, 1900.0295

10. gi|218189798 **Mass:** 38940 **Score:** 56 **Expect:** 1.5 **Queries matched:** 7

hypothetical protein OsI_05332 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1364.6908	1363.6835	1363.6255	0.0580	264 - 276		0	---	ATNVDGVYDADPK
1520.7590	1519.7517	1519.7266	0.0251	264 - 277		1	5	ATNVDGVYDADPKR
1520.7590	1519.7517	1519.7266	0.0251	264 - 277		1	---	ATNVDGVYDADPKR
1541.8372	1540.8299	1540.8361	-0.0062	21 - 35		0	---	LSPSPPASSHVPLPR
1541.8372	1540.8299	1540.8361	-0.0062	21 - 35		0	5	LSPSPPASSHVPLPR
2453.1521	2452.1448	2452.2862	-0.1414	229 - 252		1	---	GRVVIFAAGTGNPFFTTDTAAALR
2453.1521	2452.1448	2452.2862	-0.1414	229 - 252		1	---	GRVVIFAAGTGNPFFTTDTAAALR

No match to: 713.3809, 768.5023, 1076.5908, 1404.7953, 1475.7838, 1475.7838, 1832.9517, 1900.0295, 1900.0295

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 16

Protein View

Match to: **gi|82492267** Score: **71** Expect: **0.053**
major pollen allergen Phl p 4 precursor [Phleum pratense]

Nominal mass (M_r): **58590**; Calculated pI value: **9.18**
NCBI BLAST search of gi|82492267 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

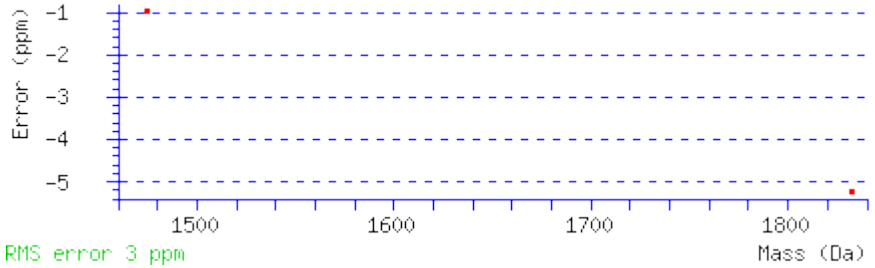
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **3%**

Matched peptides shown in **Bold Red**

```
     1 MANSRAFALV LLFCALASSC QVAFSYFPPP AAKEDFLGCL VKEIPPRLLY
    51 AK**SSPAYPSV LGQTIRNSR**W SSPDNVKPLY IITPTNVSHI QSAVVCGRRH
   101 SVRIRVRSGG HDYEGLSYRS LQPETFAVVD LNKMRAVWVD GKARTAWVDS
   151 GAQLGELYYA IYKASPTLAF PAGVCPTIGV GGNFAGGGFG MLLRKYGIAA
   201 ENVIDVKLVD ANGKLHDKKS MGDDHFWAVR GGGGESFGIV VAWQVKLLPV
   251 PPTVTIFKIS KTVSEGAVDI INKWQVVAPQ LPADLMIRII AQGPKATFEA
   301 MYLGTCKTLT PLMSSKFPEL GMNPSHCNEM SWIQSIPFVH LGHRDALEDD
   351 LLNRNNSFKP FAEYKSDYVY QPFPKTVWEQ ILNTWLVKPG AGIMIFDPYG
   401 ATISATPESA TPFPHRKGVL FNIQYVNYWF APGAAAAPLS WSKDIYNYME
   451 PYVSKNPRQA YANYRDIDLG RNEVVNDVST YASGKVWGQK YFKGNFERLA
   501 ITKGKVDPTD YFRNEQSIPP LIKKY
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
53 - 66	1475.7838	1474.7765	1474.7779	-0.0014	0	SSPAYPSVLGQTIR	(Ions score 56)
53 - 66	1475.7838	1474.7765	1474.7779	-0.0014	0	SSPAYPSVLGQTIR	(No match)
53 - 69	1832.9517	1831.9444	1831.9540	-0.0096	1	SSPAYPSVLGQTIRNSR	(No match)



Peptide View

MS/MS Fragmentation of **SSPAYPSVLGQTIR**
Found in **gi|82492267**, major pollen allergen Phl p 4 precursor [Phleum pratense]

Match to Query 6: 1474.776524 from(1475.783800,1+)
MaldiWellID: 81949, SpectrumID: 214114,

Click mouse within plot area to zoom in by factor of two about that point
Or, to Da
MONOISOTOPIC mass of neutral peptide Mr(calc): 1474.7779
Fixed modifications: Carbamidomethyl (C)
Ions Score: 56 **Expect:** 0.0021
Matches (Bold Red): 28/218 fragment ions using 21 most intense peaks

#	Immon.	a	a*	a^0	b	b*	b^0	Seq.	v	y	y*	y^0	#
1	60.0444	60.0444		42.0338	88.0393		**70.0287**	S					14
2	60.0444	147.0764		129.0659	**175.0713**		157.0608	S	1356.7270	1388.7532	1371.7267	1370.7427	13
3	**70.0651**	244.1292		226.1186	**272.1241**		254.1135	P	1259.6742	1301.7212	1284.6946	1283.7106	12
4	44.0495	315.1663		297.1557	**343.1612**		325.1506	A	1188.6371	1204.6684	1187.6419	1186.6579	11
5	**136.0757**	**478.2296**		460.2191	**506.2245**		488.2140	Y	1025.5738	1133.6313	1116.6048	1115.6208	10

6	70.0651	575.2824		557.2718	603.2773		585.2667	P	928.5210	970.5680	953.5414	952.5574	9
7	60.0444	662.3144		644.3039	690.3093		672.2988	S	841.4890	873.5152	856.4887	855.5047	8
8	72.0808	761.3828		743.3723	789.3777		771.3672	V	742.4206	786.4832	769.4567	768.4726	7
9	86.0964	874.4669		856.4563	902.4618		884.4512	L	629.3365	687.4148	670.3882	669.4042	6
10	30.0338	931.4883		913.4778	959.4833		941.4727	G		574.3307	557.3042	556.3202	5
11	101.0709	1059.5469	1042.5204	1041.5364	1087.5418	1070.5153	1069.5313	Q	444.2565	517.3093	500.2827	499.2987	4
12	74.0600	1160.5946	1143.5681	1142.5840	1188.5895	1171.5630	1170.5790	T	343.2088	389.2507	372.2241	371.2401	3
13	86.0964	1273.6787	1256.6521	1255.6681	1301.6736	1284.6470	1283.6630	I	230.1248	288.2030	271.1765		2
14	129.1135							R	74.0236	175.1189	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
SP	157.0972	185.0921	SPA	228.1343	256.1292	SPAY	391.1976	419.1925
SPAYP	488.2504	516.2453	SPAYPS	575.2824	603.2773	SPAYPSV	674.3508	702.3457
PA	141.1022	169.0971	PAY	304.1656	332.1605	PAYP	401.2183	429.2132
PAYPS	488.2504	516.2453	PAYPSV	587.3188	615.3137	AY	207.1128	235.1077
AYP	304.1656	332.1605	AYPS	391.1976	419.1925	AYPSV	490.2660	518.2609
AYPSVL	603.3501	631.3450	AYPSVLG	660.3715	688.3664	YP	233.1285	261.1234
YPS	320.1605	348.1554	YPSV	419.2289	447.2238	YPSVL	532.3130	560.3079
YPSVLG	589.3344	617.3293	PS	157.0972	185.0921	PSV	256.1656	284.1605
PSVL	369.2496	397.2445	PSVLG	426.2711	454.2660	PSVLGQ	554.3297	582.3246
PSVLGQT	655.3773	683.3723	SV	159.1128	187.1077	SVL	272.1969	300.1918
SVLG	329.2183	357.2132	SVLGQ	457.2769	485.2718	SVLGQT	558.3246	586.3195
SVLGQTI	671.4086	699.4036	VL	185.1648	213.1597	VLG	242.1863	270.1812
VLGQ	370.2449	398.2398	VLGQT	471.2926	499.2875	VLGQTI	584.3766	612.3715
LG	143.1179	171.1128	LGQ	271.1765	299.1714	LGQT	372.2241	400.2191
LGQTI	485.3082	513.3031	GQ	158.0924	186.0873	GQT	259.1401	287.1350
GQTI	372.2241	400.2191	QT	202.1186	230.1135	QTI	315.2027	343.1976
TI	187.1441	215.1390						

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Index

	Accession	Mass	Score	Description
1.	gi|54144332	56979	342	pollen allergen Phl p 4 [Phleum pratense]
2.	gi|189014266	56147	342	pollen allergen Phl p 4.0102 [Phleum pratense]
3.	gi|82492267	58590	295	major pollen allergen Phl p 4 precursor [Phleum pratense]
4.	gi|54144334	56741	295	pollen allergen Phl p 4 [Phleum pratense]
5.	gi|189014268	55889	295	pollen allergen Phl p 4.0202 [Phleum pratense]
6.	gi|189014270	55917	295	pollen allergen Phl p 4.0203 [Phleum pratense]
7.	gi|189014272	55931	295	pollen allergen Phl p 4.0204 [Phleum pratense]
8.	gi|67035869	23333	53	small ribosomal protein subunit 4 [Mastopoma subfiliferum]
9.	gi|147853034	132842	50	hypothetical protein [Vitis vinifera]
10.	gi|217070948	26255	48	unknown [Medicago truncatula]

Results List

1. gi|54144332 **Mass:** 56979 **Score:** 342 **Expect:** 3.8e-029 **Queries matched:** 17

pollen allergen Phl p 4 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
885.4438	884.4365	884.4140	0.0225	442	448	0	---	QAYANYR
1001.5672	1000.5599	1000.5453	0.0146	119	127	1	---	AVWVDGKAR
1059.5465	1058.5392	1058.5297	0.0095	474	481	1	---	YFKGNFQR
1197.6021	1196.5948	1196.5825	0.0123	487	496	1	---	GKVDPTDYFR
1199.7263	1198.7190	1198.7073	0.0117	26	35	1	42	EIPPRLLYAK
1199.7263	1198.7190	1198.7073	0.0117	26	35	1	---	EIPPRLLYAK
1320.5905	1319.5832	1319.5717	0.0116	203	213	0	---	SMGDDHFWAVR
1336.5818	1335.5745	1335.5666	0.0080	203	213	0	---	SMGDDHFWAVR + Oxidation (M)
1340.6173	1339.6100	1339.5792	0.0308	91	102	0	---	SGGHDYEGLSYR
1475.8011	1474.7938	1474.7779	0.0159	36	49	0	103	SSPAYPSVLGQTIR
1475.8011	1474.7938	1474.7779	0.0159	36	49	0	---	SSPAYPSVLGQTIR
1561.8225	1560.8152	1560.8035	0.0118	103	116	0	---	SLQPEEFAVVDLSK
1832.9778	1831.9705	1831.9540	0.0165	36	52	1	69	SSPAYPSVLGQTIRNSR
1832.9778	1831.9705	1831.9540	0.0165	36	52	1	---	SSPAYPSVLGQTIRNSR
1848.9823	1847.9750	1847.9451	0.0300	103	118	1	---	SLQPEEFAVVDLSKMR
1864.9657	1863.9584	1863.9400	0.0185	103	118	1	---	SLQPEEFAVVDLSKMR + Oxidation (M)
1902.9281	1901.9208	1901.8981	0.0227	427	441	1	---	EIYNYMEPYVSKNPR

No match to: 878.4976, 1465.7828, 1598.8328, 1614.8396, 1628.8484, 1628.8484, 1682.9828, 1682.9828, 1700.0026, 1730.8870, 1760.8839, 1847.9846, 2445.3079, 2608.3657

2. gi|189014266 **Mass:** 56147 **Score:** 342 **Expect:** 3.8e-029 **Queries matched:** 17

pollen allergen Phl p 4.0102 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
885.4438	884.4365	884.4140	0.0225	434 -	440	0	---	QAYANYR
1001.5672	1000.5599	1000.5453	0.0146	111 -	119	1	---	AVWVDGKAR
1059.5465	1058.5392	1058.5297	0.0095	466 -	473	1	---	YFKGNFQR
1197.6021	1196.5948	1196.5825	0.0123	479 -	488	1	---	GKVDPTDYFR
1199.7263	1198.7190	1198.7073	0.0117	18 -	27	1	42	EIPPRLLYAK
1199.7263	1198.7190	1198.7073	0.0117	18 -	27	1	---	EIPPRLLYAK
1320.5905	1319.5832	1319.5717	0.0116	195 -	205	0	---	SMGDDHFWAVR
1336.5818	1335.5745	1335.5666	0.0080	195 -	205	0	---	SMGDDHFWAVR + Oxidation (M)
1340.6173	1339.6100	1339.5792	0.0308	83 -	94	0	---	SGGHDYEGLSYR
1475.8011	1474.7938	1474.7779	0.0159	28 -	41	0	103	SSPAYPSVLGQTIR
1475.8011	1474.7938	1474.7779	0.0159	28 -	41	0	---	SSPAYPSVLGQTIR
1561.8225	1560.8152	1560.8035	0.0118	95 -	108	0	---	SLQPEEFAVVDLSK
1832.9778	1831.9705	1831.9540	0.0165	28 -	44	1	69	SSPAYPSVLGQTIRNSR
1832.9778	1831.9705	1831.9540	0.0165	28 -	44	1	---	SSPAYPSVLGQTIRNSR
1848.9823	1847.9750	1847.9451	0.0300	95 -	110	1	---	SLQPEEFAVVDLSKMR
1864.9657	1863.9584	1863.9400	0.0185	95 -	110	1	---	SLQPEEFAVVDLSKMR + Oxidation (M)
1902.9281	1901.9208	1901.8981	0.0227	419 -	433	1	---	EIYNYMEPYVSKNPR

No match to: 878.4976, 1465.7828, 1598.8328, 1614.8396, 1628.8484, 1628.8484, 1682.9828, 1682.9828, 1700.0026, 1730.8870, 1760.8839, 1847.9846, 2445.3079, 2608.3657

3. gi|82492267 **Mass:** 58590 **Score:** 295 **Expect:** 1.9e-024 **Queries matched:** 13

major pollen allergen Phl p 4 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
885.4438	884.4365	884.4140	0.0225	459 -	465	0	---	QAYANYR
1001.5672	1000.5599	1000.5453	0.0146	136 -	144	1	---	AVWVDGKAR
1197.6021	1196.5948	1196.5825	0.0123	504 -	513	1	---	GKVDPTDYFR
1199.7263	1198.7190	1198.7073	0.0117	43 -	52	1	42	EIPPRLLYAK
1199.7263	1198.7190	1198.7073	0.0117	43 -	52	1	---	EIPPRLLYAK
1320.5905	1319.5832	1319.5717	0.0116	220 -	230	0	---	SMGDDHFWAVR
1336.5818	1335.5745	1335.5666	0.0080	220 -	230	0	---	SMGDDHFWAVR + Oxidation (M)
1340.6173	1339.6100	1339.5792	0.0308	108 -	119	0	---	SGGHDYEGLSYR
1475.8011	1474.7938	1474.7779	0.0159	53 -	66	0	103	SSPAYPSVLGQTIR
1475.8011	1474.7938	1474.7779	0.0159	53 -	66	0	---	SSPAYPSVLGQTIR
1832.9778	1831.9705	1831.9540	0.0165	53 -	69	1	69	SSPAYPSVLGQTIRNSR
1832.9778	1831.9705	1831.9540	0.0165	53 -	69	1	---	SSPAYPSVLGQTIRNSR
1847.9846	1846.9773	1846.9611	0.0163	120 -	135	1	---	SLQPETFAVVDLNKMR

No match to: 878.4976, 1059.5465, 1465.7828, 1561.8225, 1598.8328, 1614.8396, 1628.8484, 1628.8484, 1682.9828, 1682.9828, 1700.0026, 1730.8870, 1760.8839, 1848.9823, 1864.9657, 1902.9281, 2445.3079, 2608.3657

4. gi|54144334 **Mass:** 56741 **Score:** 295 **Expect:** 1.9e-024 **Queries matched:** 13

pollen allergen Phl p 4 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
885.4438	884.4365	884.4140	0.0225	442	448	0	---	QAYANYR
1001.5672	1000.5599	1000.5453	0.0146	119	127	1	---	AVWVDGKAR
1197.6021	1196.5948	1196.5825	0.0123	487	496	1	---	GKVDPTDYFR
1199.7263	1198.7190	1198.7073	0.0117	26	35	1	42	EIPPRLLYAK
1199.7263	1198.7190	1198.7073	0.0117	26	35	1	---	EIPPRLLYAK
1320.5905	1319.5832	1319.5717	0.0116	203	213	0	---	SMGDDHFWAVR
1336.5818	1335.5745	1335.5666	0.0080	203	213	0	---	SMGDDHFWAVR + Oxidation (M)
1340.6173	1339.6100	1339.5792	0.0308	91	102	0	---	SGGHDYEGLSYR
1475.8011	1474.7938	1474.7779	0.0159	36	49	0	103	SSPAYPSVLGQTIR
1475.8011	1474.7938	1474.7779	0.0159	36	49	0	---	SSPAYPSVLGQTIR
1832.9778	1831.9705	1831.9540	0.0165	36	52	1	69	SSPAYPSVLGQTIRNSR
1832.9778	1831.9705	1831.9540	0.0165	36	52	1	---	SSPAYPSVLGQTIRNSR
1847.9846	1846.9773	1846.9611	0.0163	103	118	1	---	SLQPETFAVVDLNKMR

No match to: 878.4976, 1059.5465, 1465.7828, 1561.8225, 1598.8328, 1614.8396, 1628.8484, 1628.8484, 1682.9828, 1682.9828, 1700.0026, 1730.8870, 1760.8839, 1848.9823, 1864.9657, 1902.9281, 2445.3079, 2608.3657

5. gi|189014268 **Mass:** 55889 **Score:** 295 **Expect:** 1.9e-024 **Queries matched:** 13

pollen allergen Phl p 4.0202 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
885.4438	884.4365	884.4140	0.0225	434	440	0	---	QAYANYR
1001.5672	1000.5599	1000.5453	0.0146	111	119	1	---	AVWVDGKAR
1197.6021	1196.5948	1196.5825	0.0123	479	488	1	---	GKVDPTDYFR
1199.7263	1198.7190	1198.7073	0.0117	18	27	1	42	EIPPRLLYAK
1199.7263	1198.7190	1198.7073	0.0117	18	27	1	---	EIPPRLLYAK
1320.5905	1319.5832	1319.5717	0.0116	195	205	0	---	SMGDDHFWAVR
1336.5818	1335.5745	1335.5666	0.0080	195	205	0	---	SMGDDHFWAVR + Oxidation (M)
1340.6173	1339.6100	1339.5792	0.0308	83	94	0	---	SGGHDYEGLSYR
1475.8011	1474.7938	1474.7779	0.0159	28	41	0	103	SSPAYPSVLGQTIR
1475.8011	1474.7938	1474.7779	0.0159	28	41	0	---	SSPAYPSVLGQTIR
1832.9778	1831.9705	1831.9540	0.0165	28	44	1	69	SSPAYPSVLGQTIRNSR
1832.9778	1831.9705	1831.9540	0.0165	28	44	1	---	SSPAYPSVLGQTIRNSR
1847.9846	1846.9773	1846.9611	0.0163	95	110	1	---	SLQPETFAVVDLNKMR

No match to: 878.4976, 1059.5465, 1465.7828, 1561.8225, 1598.8328, 1614.8396, 1628.8484, 1628.8484, 1682.9828, 1682.9828, 1700.0026, 1730.8870, 1760.8839, 1848.9823, 1864.9657, 1902.9281, 2445.3079, 2608.3657

6. gi|189014270 **Mass:** 55917 **Score:** 295 **Expect:** 1.9e-024 **Queries matched:** 13

pollen allergen Phl p 4.0203 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
885.4438	884.4365	884.4140	0.0225	434	440	0	---	QAYANYR

1001.5672	1000.5599	1000.5453	0.0146	111 - 119	1	---	AVWVDGKAR
1197.6021	1196.5948	1196.5825	0.0123	479 - 488	1	---	GKVDPTDYFR
1199.7263	1198.7190	1198.7073	0.0117	18 - 27	1	42	EIPPRLLYAK
1199.7263	1198.7190	1198.7073	0.0117	18 - 27	1	---	EIPPRLLYAK
1320.5905	1319.5832	1319.5717	0.0116	195 - 205	0	---	SMGDDHFWAVR
1336.5818	1335.5745	1335.5666	0.0080	195 - 205	0	---	SMGDDHFWAVR + Oxidation (M)
1340.6173	1339.6100	1339.5792	0.0308	83 - 94	0	---	SGGHDYEGLSYR
1475.8011	1474.7938	1474.7779	0.0159	28 - 41	0	103	SSPAYPSVLGQTIR
1475.8011	1474.7938	1474.7779	0.0159	28 - 41	0	---	SSPAYPSVLGQTIR
1832.9778	1831.9705	1831.9540	0.0165	28 - 44	1	69	SSPAYPSVLGQTIRNSR
1832.9778	1831.9705	1831.9540	0.0165	28 - 44	1	---	SSPAYPSVLGQTIRNSR
1847.9846	1846.9773	1846.9611	0.0163	95 - 110	1	---	SLQPETFAVVDLNKMR

No match to: 878.4976, 1059.5465, 1465.7828, 1561.8225, 1598.8328, 1614.8396, 1628.8484, 1628.8484, 1682.9828, 1682.9828, 1700.0026, 1730.8870, 1760.8839, 1848.9823, 1864.9657, 1902.9281, 2445.3079, 2608.3657

7. gi|189014272 **Mass:** 55931 **Score:** 295 **Expect:** 1.9e-024 **Queries matched:** 13

pollen allergen Phl p 4.0204 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
885.4438	884.4365	884.4140	0.0225	434 - 440		0	---	QAYANYR
1001.5672	1000.5599	1000.5453	0.0146	111 - 119		1	---	AVWVDGKAR
1197.6021	1196.5948	1196.5825	0.0123	479 - 488		1	---	GKVDPTDYFR
1199.7263	1198.7190	1198.7073	0.0117	18 - 27		1	42	EIPPRLLYAK
1199.7263	1198.7190	1198.7073	0.0117	18 - 27		1	---	EIPPRLLYAK
1320.5905	1319.5832	1319.5717	0.0116	195 - 205		0	---	SMGDDHFWAVR
1336.5818	1335.5745	1335.5666	0.0080	195 - 205		0	---	SMGDDHFWAVR + Oxidation (M)
1340.6173	1339.6100	1339.5792	0.0308	83 - 94		0	---	SGGHDYEGLSYR
1475.8011	1474.7938	1474.7779	0.0159	28 - 41		0	103	SSPAYPSVLGQTIR
1475.8011	1474.7938	1474.7779	0.0159	28 - 41		0	---	SSPAYPSVLGQTIR
1832.9778	1831.9705	1831.9540	0.0165	28 - 44		1	69	SSPAYPSVLGQTIRNSR
1832.9778	1831.9705	1831.9540	0.0165	28 - 44		1	---	SSPAYPSVLGQTIRNSR
1847.9846	1846.9773	1846.9611	0.0163	95 - 110		1	---	SLQPETFAVVDLNKMR

No match to: 878.4976, 1059.5465, 1465.7828, 1561.8225, 1598.8328, 1614.8396, 1628.8484, 1628.8484, 1682.9828, 1682.9828, 1700.0026, 1730.8870, 1760.8839, 1848.9823, 1864.9657, 1902.9281, 2445.3079, 2608.3657

8. gi|67035869 **Mass:** 23333 **Score:** 53 **Expect:** 3.3 **Queries matched:** 5

small ribosomal protein subunit 4 [Mastopoma subfiliferum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1561.8225	1560.8152	1560.8181	-0.0028	75 - 88		0	---	GSTGEVLLQLLEMR + Oxidation (M)
1700.0026	1698.9953	1698.8828	0.1125	142 - 155		1	---	SETIISKNIEFYQK
1760.8839	1759.8766	1759.9501	-0.0735	73 - 88		1	---	AKGSTGEVLLQLLEMR + Oxidation (M)
1848.9823	1847.9750	1847.9224	0.0526	22 - 38		1	---	TPQLESSSINQSTSNKK

1902.9281	1901.9208	1902.0257	-0.1049	96 - 112	1	---	LGMAPTIPEARQLVNHR

No match to: 878.4976, 885.4438, 1001.5672, 1059.5465, 1197.6021, 1199.7263, 1199.7263, 1320.5905, 1336.5818, 1340.6173, 1465.7828, 1475.8011, 1475.8011, 1598.8328, 1614.8396, 1628.8484, 1628.8484, 1682.9828, 1682.9828, 1730.8870, 1832.9778, 1832.9778, 1847.9846, 1864.9657, 2445.3079, 2608.3657

9. gi|147853034 **Mass:** 132842 **Score:** 50 **Expect:** 5.9 **Queries matched:** 11

hypothetical protein [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1197.6021	1196.5948	1196.6625	-0.0677	565 -	574	0	---	RPAQLQTQQK
1475.8011	1474.7938	1474.7878	0.0060	1058 -	1071	1	11	LAVSATSDVDLKEK
1475.8011	1474.7938	1474.7085	0.0853	869 -	881	1	---	LADKDNLEDMVGR
1561.8225	1560.8152	1560.8663	-0.0511	27 -	40	0	---	SSLNLFFIPPASIR
1598.8328	1597.8255	1597.8796	-0.0541	760 -	773	1	---	THCALVLMLIGRSK
1614.8396	1613.8323	1613.8745	-0.0422	760 -	773	1	---	THCALVLMLIGRSK + Oxidation (M)
1628.8484	1627.8411	1627.8780	-0.0369	1140 -	1153	1	---	IAELEAQIQKEQTK
1628.8484	1627.8411	1627.8780	-0.0369	1140 -	1153	1	---	IAELEAQIQKEQTK
1832.9778	1831.9705	1831.9250	0.0455	496 -	511	1	---	INCNSSDVFTKHILGK
1832.9778	1831.9705	1831.9250	0.0455	496 -	511	1	---	INCNSSDVFTKHILGK
1848.9823	1847.9750	1847.8570	0.1180	1100 -	1115	1	---	AKEEAEDLAQEMAELR + Oxidation (M)

No match to: 878.4976, 885.4438, 1001.5672, 1059.5465, 1199.7263, 1199.7263, 1320.5905, 1336.5818, 1340.6173, 1465.7828, 1682.9828, 1682.9828, 1700.0026, 1730.8870, 1760.8839, 1847.9846, 1864.9657, 1902.9281, 2445.3079, 2608.3657

10. gi|217070948 **Mass:** 26255 **Score:** 48 **Expect:** 9.6 **Queries matched:** 6

unknown [Medicago truncatula]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1199.7263	1198.7190	1198.6743	0.0447	57 -	66	1	---	TVLMDHKLVK + Oxidation (M)
1199.7263	1198.7190	1198.6743	0.0447	57 -	66	1	---	TVLMDHKLVK + Oxidation (M)
1598.8328	1597.8255	1597.8198	0.0057	138 -	151	1	---	EVPIEEAEDLAKQK
1614.8396	1613.8323	1613.8525	-0.0202	64 -	77	1	---	LVKAQIWDTAGQER
1902.9281	1901.9208	1902.0284	-0.1076	47 -	63	1	---	ATIGVEFLTKTVLMDHK
2445.3079	2444.3006	2444.2634	0.0373	110 -	130	1	---	WLDELHNHADKNIVVMLVGNK

No match to: 878.4976, 885.4438, 1001.5672, 1059.5465, 1197.6021, 1320.5905, 1336.5818, 1340.6173, 1465.7828, 1475.8011, 1475.8011, 1561.8225, 1628.8484, 1628.8484, 1682.9828, 1682.9828, 1700.0026, 1730.8870, 1760.8839, 1832.9778, 1832.9778, 1847.9846, 1848.9823, 1864.9657, 2608.3657

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 31

Protein View

Match to: **gi|189014266** Score: **342** Expect: **3.8e-029**
pollen allergen Phl p 4.0102 [Phleum pratense]

Nominal mass (M_r): **56147**; Calculated pI value: **9.05**
NCBI BLAST search of gi|189014266 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **23%**

Matched peptides shown in **Bold Red**

```
     1 YYPTPLAKED FLRCLVKEIP PRLLYAKSSP AYPSVLGQTI RNSRWSSPDN
    51 VKPIYIVTPT NASHIQSAVV CGRRHGVRIR VRSGGHDYEG LSYRSLQPEE
   101 FAVVDLSKMR AVWVDGKART AWVDSGAQLG ELYYAIHKAS TVLAFPAGVC
   151 PTIGVGGNFA GGGFGMLLRK YGIAAENVID VKLVDANGTL HDKKSMGDDH
   201 FWAVRGGGGE SFGIVVAWKV RLLPVPPTVT VFKIPKKASE GAVDIINRWQ
   251 VVAPQLPDDL MIRVIAQGPT ATFEAMYLGT CQTLTPMMGS KFPELGMNAS
   301 HCNEMSWIQS IPFVHLGHRD NIEDDLLNRN NTFKPFAEYK SDYVYEPFPK
   351 RVWEQIFSTW LLKPGAGIMI FDPYGATISA TPEWATPFPH RKGVLFNIQY
   401 VNYWFAPGAG AAPLSWSKEI YNYMEPYVSK NPRQAYANYR DIDLGRNEVV
   451 NDVSTFSSGL VWGQKYFKGN FQRLAITKGK VDPTDYFRNE QSIPPLIQKY
   501
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
18 - 27	1199.7263	1198.7190	1198.7073	0.0117	1	**EIPPRLLYAK** (Ions score 42)
18 - 27	1199.7263	1198.7190	1198.7073	0.0117	1	**EIPPRLLYAK** (No match)
28 - 41	1475.8011	1474.7938	1474.7779	0.0159	0	**SSPAYPSVLGQTIR** (Ions score 103)
28 - 41	1475.8011	1474.7938	1474.7779	0.0159	0	**SSPAYPSVLGQTIR** (No match)
28 - 44	1832.9778	1831.9705	1831.9540	0.0165	1	**SSPAYPSVLGQTIRNSR** (Ions score 69)
28 - 44	1832.9778	1831.9705	1831.9540	0.0165	1	**SSPAYPSVLGQTIRNSR** (No match)
83 - 94	1340.6173	1339.6100	1339.5792	0.0308	0	**SGGHDYEGLSYR** (No match)
95 - 108	1561.8225	1560.8152	1560.8035	0.0118	0	**SLQPEEFAVVDLSK** (No match)
95 - 110	1848.9823	1847.9750	1847.9451	0.0300	1	**SLQPEEFAVVDLSKMR** (No match)
95 - 110	1864.9657	1863.9584	1863.9400	0.0185	1	**SLQPEEFAVVDLSKMR** Oxidation (M) (No match)
111 - 119	1001.5672	1000.5599	1000.5453	0.0146	1	**AVWVDGKAR** (No match)
195 - 205	1320.5905	1319.5832	1319.5717	0.0116	0	**SMGDDHFWAVR** (No match)
195 - 205	1336.5818	1335.5745	1335.5666	0.0080	0	**SMGDDHFWAVR** Oxidation (M) (No match)
419 - 433	1902.9281	1901.9208	1901.8981	0.0227	1	**EIYNYMEPYVSKNPR** (No match)
434 - 440	885.4438	884.4365	884.4140	0.0225	0	**QAYANYR** (No match)
466 - 473	1059.5465	1058.5392	1058.5297	0.0095	1	**YFKGNFQR** (No match)
479 - 488	1197.6021	1196.5948	1196.5825	0.0123	1	**GKVDPTDYFR** (No match)

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	Accession	Mass	Score	Description
1.	gi|54144334	56741	277	pollen allergen Phl p 4 [Phleum pratense]
2.	gi|189014268	55889	277	pollen allergen Phl p 4.0202 [Phleum pratense]
3.	gi|189014270	55917	277	pollen allergen Phl p 4.0203 [Phleum pratense]
4.	gi|189014272	55931	277	pollen allergen Phl p 4.0204 [Phleum pratense]
5.	gi|82492267	58590	276	major pollen allergen Phl p 4 precursor [Phleum pratense]
6.	gi|54144332	56979	275	pollen allergen Phl p 4 [Phleum pratense]
7.	gi|189014266	56147	274	pollen allergen Phl p 4.0102 [Phleum pratense]
8.	gi|55859464	47178	82	pollen allergen Lol p 4 [Lolium perenne]
9.	gi|224085664	135560	49	chromatin remodeling complex subunit [Populus trichocarpa]
10.	gi|146393844	28907	46	putative NB-ARC domain-containing protein [Oryza sativa]

Results List

1. gi|54144334 **Mass:** 56741 **Score:** 277 **Expect:** 1.2e-022 **Queries matched:** 16

pollen allergen Phl p 4 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
885.4280	884.4207	884.4140	0.0067	442	448	0	---	QAYANYR
1001.5590	1000.5517	1000.5453	0.0064	119	127	1	---	AVWVDGKAR
1060.5247	1059.5174	1059.5137	0.0037	474	481	1	---	YFKGNFER
1197.5724	1196.5651	1196.5825	-0.0174	487	496	1	---	GKVDPTDYFR
1199.7061	1198.6988	1198.7073	-0.0085	26	35	1	22	EIPPRLLYAK
1199.7061	1198.6988	1198.7073	-0.0085	26	35	1	---	EIPPRLLYAK
1320.5770	1319.5697	1319.5717	-0.0019	203	213	0	45	SMGDDHFWAVR
1320.5770	1319.5697	1319.5717	-0.0019	203	213	0	---	SMGDDHFWAVR
1336.5812	1335.5739	1335.5666	0.0073	203	213	0	---	SMGDDHFWAVR + Oxidation (M)
1340.6010	1339.5937	1339.5792	0.0145	91	102	0	---	SGGHDYEGLSYR
1475.7852	1474.7779	1474.7779	-0.0000	36	49	0	---	SSPAYPSVLGQTIR
1475.7852	1474.7779	1474.7779	-0.0000	36	49	0	60	SSPAYPSVLGQTIR
1832.9625	1831.9552	1831.9540	0.0012	36	52	1	47	SSPAYPSVLGQTIRNSR
1832.9625	1831.9552	1831.9540	0.0012	36	52	1	---	SSPAYPSVLGQTIRNSR
1847.9761	1846.9688	1846.9611	0.0078	103	118	1	---	SLQPETFAVVDLNKMR
1863.9578	1862.9505	1862.9560	-0.0054	103	118	1	---	SLQPETFAVVDLNKMR + Oxidation (M)

No match to: 768.5280, 1033.5288, 1059.5372, 1561.8088, 1614.8179, 1628.8334, 1682.9696, 1682.9696, 1698.9532, 1699.9886, 2318.2268, 2445.2991, 2608.3569

2. gi|189014268 **Mass:** 55889 **Score:** 277 **Expect:** 1.2e-022 **Queries matched:** 16

pollen allergen Phl p 4.0202 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide

885.4280	884.4207	884.4140	0.0067	434 - 440	0	---	QAYANYR
1001.5590	1000.5517	1000.5453	0.0064	111 - 119	1	---	AVWVDGKAR
1060.5247	1059.5174	1059.5137	0.0037	466 - 473	1	---	YFKGNFER
1197.5724	1196.5651	1196.5825	-0.0174	479 - 488	1	---	GKVDPTDYFR
1199.7061	1198.6988	1198.7073	-0.0085	18 - 27	1	22	EIPPRLLYAK
1199.7061	1198.6988	1198.7073	-0.0085	18 - 27	1	---	EIPPRLLYAK
1320.5770	1319.5697	1319.5717	-0.0019	195 - 205	0	45	SMGDDHFWAVR
1320.5770	1319.5697	1319.5717	-0.0019	195 - 205	0	---	SMGDDHFWAVR
1336.5812	1335.5739	1335.5666	0.0073	195 - 205	0	---	SMGDDHFWAVR + Oxidation (M)
1340.6010	1339.5937	1339.5792	0.0145	83 - 94	0	---	SGGHDYEGLSYR
1475.7852	1474.7779	1474.7779	-0.0000	28 - 41	0	---	SSPAYPSVLGQTIR
1475.7852	1474.7779	1474.7779	-0.0000	28 - 41	0	60	SSPAYPSVLGQTIR
1832.9625	1831.9552	1831.9540	0.0012	28 - 44	1	47	SSPAYPSVLGQTIRNSR
1832.9625	1831.9552	1831.9540	0.0012	28 - 44	1	---	SSPAYPSVLGQTIRNSR
1847.9761	1846.9688	1846.9611	0.0078	95 - 110	1	---	SLQPETFAVVDLNKMR
1863.9578	1862.9505	1862.9560	-0.0054	95 - 110	1	---	SLQPETFAVVDLNKMR + Oxidation (M)

No match to: 768.5280, 1033.5288, 1059.5372, 1561.8088, 1614.8179, 1628.8334, 1682.9696, 1682.9696, 1698.9532, 1699.9886, 2318.2268, 2445.2991, 2608.3569

3. gi|189014270 **Mass:** 55917 **Score:** 277 **Expect:** 1.2e-022 **Queries matched:** 16

pollen allergen Phl p 4.0203 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
885.4280	884.4207	884.4140	0.0067	434 - 440		0	---	QAYANYR
1001.5590	1000.5517	1000.5453	0.0064	111 - 119		1	---	AVWVDGKAR
1060.5247	1059.5174	1059.5137	0.0037	466 - 473		1	---	YFKGNFER
1197.5724	1196.5651	1196.5825	-0.0174	479 - 488		1	---	GKVDPTDYFR
1199.7061	1198.6988	1198.7073	-0.0085	18 - 27		1	22	EIPPRLLYAK
1199.7061	1198.6988	1198.7073	-0.0085	18 - 27		1	---	EIPPRLLYAK
1320.5770	1319.5697	1319.5717	-0.0019	195 - 205		0	45	SMGDDHFWAVR
1320.5770	1319.5697	1319.5717	-0.0019	195 - 205		0	---	SMGDDHFWAVR
1336.5812	1335.5739	1335.5666	0.0073	195 - 205		0	---	SMGDDHFWAVR + Oxidation (M)
1340.6010	1339.5937	1339.5792	0.0145	83 - 94		0	---	SGGHDYEGLSYR
1475.7852	1474.7779	1474.7779	-0.0000	28 - 41		0	---	SSPAYPSVLGQTIR
1475.7852	1474.7779	1474.7779	-0.0000	28 - 41		0	60	SSPAYPSVLGQTIR
1832.9625	1831.9552	1831.9540	0.0012	28 - 44		1	47	SSPAYPSVLGQTIRNSR
1832.9625	1831.9552	1831.9540	0.0012	28 - 44		1	---	SSPAYPSVLGQTIRNSR
1847.9761	1846.9688	1846.9611	0.0078	95 - 110		1	---	SLQPETFAVVDLNKMR
1863.9578	1862.9505	1862.9560	-0.0054	95 - 110		1	---	SLQPETFAVVDLNKMR + Oxidation (M)

No match to: 768.5280, 1033.5288, 1059.5372, 1561.8088, 1614.8179, 1628.8334, 1682.9696, 1682.9696, 1698.9532, 1699.9886, 2318.2268, 2445.2991, 2608.3569

4. gi|189014272 **Mass:** 55931 **Score:** 277 **Expect:** 1.2e-022 **Queries matched:** 16

pollen allergen Phl p 4.0204 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
885.4280	884.4207	884.4140	0.0067	434	440	0	---	QAYANYR
1001.5590	1000.5517	1000.5453	0.0064	111	119	1	---	AVWVDGKAR
1060.5247	1059.5174	1059.5137	0.0037	466	473	1	---	YFKGNFER
1197.5724	1196.5651	1196.5825	-0.0174	479	488	1	---	GKVDPTDYFR
1199.7061	1198.6988	1198.7073	-0.0085	18	27	1	22	EIPPRLLYAK
1199.7061	1198.6988	1198.7073	-0.0085	18	27	1	---	EIPPRLLYAK
1320.5770	1319.5697	1319.5717	-0.0019	195	205	0	45	SMGDDHFWAVR
1320.5770	1319.5697	1319.5717	-0.0019	195	205	0	---	SMGDDHFWAVR
1336.5812	1335.5739	1335.5666	0.0073	195	205	0	---	SMGDDHFWAVR + Oxidation (M)
1340.6010	1339.5937	1339.5792	0.0145	83	94	0	---	SGGHDYEGLSYR
1475.7852	1474.7779	1474.7779	-0.0000	28	41	0	---	SSPAYPSVLGQTIR
1475.7852	1474.7779	1474.7779	-0.0000	28	41	0	60	SSPAYPSVLGQTIR
1832.9625	1831.9552	1831.9540	0.0012	28	44	1	47	SSPAYPSVLGQTIRNSR
1832.9625	1831.9552	1831.9540	0.0012	28	44	1	---	SSPAYPSVLGQTIRNSR
1847.9761	1846.9688	1846.9611	0.0078	95	110	1	---	SLQPETFAVVDLNKMR
1863.9578	1862.9505	1862.9560	-0.0054	95	110	1	---	SLQPETFAVVDLNKMR + Oxidation (M)

No match to: 768.5280, 1033.5288, 1059.5372, 1561.8088, 1614.8179, 1628.8334, 1682.9696, 1682.9696, 1698.9532, 1699.9886, 2318.2268, 2445.2991, 2608.3569

5. gi|82492267 **Mass:** 58590 **Score:** 276 **Expect:** 1.5e-022 **Queries matched:** 16

major pollen allergen Phl p 4 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
885.4280	884.4207	884.4140	0.0067	459	465	0	---	QAYANYR
1001.5590	1000.5517	1000.5453	0.0064	136	144	1	---	AVWVDGKAR
1060.5247	1059.5174	1059.5137	0.0037	491	498	1	---	YFKGNFER
1197.5724	1196.5651	1196.5825	-0.0174	504	513	1	---	GKVDPTDYFR
1199.7061	1198.6988	1198.7073	-0.0085	43	52	1	22	EIPPRLLYAK
1199.7061	1198.6988	1198.7073	-0.0085	43	52	1	---	EIPPRLLYAK
1320.5770	1319.5697	1319.5717	-0.0019	220	230	0	45	SMGDDHFWAVR
1320.5770	1319.5697	1319.5717	-0.0019	220	230	0	---	SMGDDHFWAVR
1336.5812	1335.5739	1335.5666	0.0073	220	230	0	---	SMGDDHFWAVR + Oxidation (M)
1340.6010	1339.5937	1339.5792	0.0145	108	119	0	---	SGGHDYEGLSYR
1475.7852	1474.7779	1474.7779	-0.0000	53	66	0	---	SSPAYPSVLGQTIR
1475.7852	1474.7779	1474.7779	-0.0000	53	66	0	60	SSPAYPSVLGQTIR
1832.9625	1831.9552	1831.9540	0.0012	53	69	1	47	SSPAYPSVLGQTIRNSR
1832.9625	1831.9552	1831.9540	0.0012	53	69	1	---	SSPAYPSVLGQTIRNSR
1847.9761	1846.9688	1846.9611	0.0078	120	135	1	---	SLQPETFAVVDLNKMR
1863.9578	1862.9505	1862.9560	-0.0054	120	135	1	---	SLQPETFAVVDLNKMR + Oxidation (M)

No match to: 768.5280, 1033.5288, 1059.5372, 1561.8088, 1614.8179, 1628.8334, 1682.9696, 1682.9696, 1698.9532, 1699.9886, 2318.2268, 2445.2991, 2608.3569

6. gi|54144332 **Mass:** 56979 **Score:** 275 **Expect:** 1.9e-022 **Queries matched:** 15

pollen allergen Phl p 4 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
885.4280	884.4207	884.4140	0.0067	442	448	0	---	QAYANYR
1001.5590	1000.5517	1000.5453	0.0064	119	127	1	---	AVWVDGKAR
1059.5372	1058.5299	1058.5297	0.0002	474	481	1	---	YFKGNFQR
1197.5724	1196.5651	1196.5825	-0.0174	487	496	1	---	GKVDPTDYFR
1199.7061	1198.6988	1198.7073	-0.0085	26	35	1	22	EIPPRLLYAK
1199.7061	1198.6988	1198.7073	-0.0085	26	35	1	---	EIPPRLLYAK
1320.5770	1319.5697	1319.5717	-0.0019	203	213	0	45	SMGDDHFWAVR
1320.5770	1319.5697	1319.5717	-0.0019	203	213	0	---	SMGDDHFWAVR
1336.5812	1335.5739	1335.5666	0.0073	203	213	0	---	SMGDDHFWAVR + Oxidation (M)
1340.6010	1339.5937	1339.5792	0.0145	91	102	0	---	SGGHDYEGLSYR
1475.7852	1474.7779	1474.7779	-0.0000	36	49	0	---	SSPAYPSVLGQTIR
1475.7852	1474.7779	1474.7779	-0.0000	36	49	0	60	SSPAYPSVLGQTIR
1561.8088	1560.8015	1560.8035	-0.0019	103	116	0	---	SLQPEEFAVVDLSK
1832.9625	1831.9552	1831.9540	0.0012	36	52	1	47	SSPAYPSVLGQTIRNSR
1832.9625	1831.9552	1831.9540	0.0012	36	52	1	---	SSPAYPSVLGQTIRNSR

No match to: 768.5280, 1033.5288, 1060.5247, 1614.8179, 1628.8334, 1682.9696, 1682.9696, 1698.9532, 1699.9886, 1847.9761, 1863.9578, 2318.2268, 2445.2991, 2608.3569

7. gi|189014266 **Mass:** 56147 **Score:** 274 **Expect:** 2.4e-022 **Queries matched:** 15

pollen allergen Phl p 4.0102 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
885.4280	884.4207	884.4140	0.0067	434	440	0	---	QAYANYR
1001.5590	1000.5517	1000.5453	0.0064	111	119	1	---	AVWVDGKAR
1059.5372	1058.5299	1058.5297	0.0002	466	473	1	---	YFKGNFQR
1197.5724	1196.5651	1196.5825	-0.0174	479	488	1	---	GKVDPTDYFR
1199.7061	1198.6988	1198.7073	-0.0085	18	27	1	22	EIPPRLLYAK
1199.7061	1198.6988	1198.7073	-0.0085	18	27	1	---	EIPPRLLYAK
1320.5770	1319.5697	1319.5717	-0.0019	195	205	0	45	SMGDDHFWAVR
1320.5770	1319.5697	1319.5717	-0.0019	195	205	0	---	SMGDDHFWAVR
1336.5812	1335.5739	1335.5666	0.0073	195	205	0	---	SMGDDHFWAVR + Oxidation (M)
1340.6010	1339.5937	1339.5792	0.0145	83	94	0	---	SGGHDYEGLSYR
1475.7852	1474.7779	1474.7779	-0.0000	28	41	0	---	SSPAYPSVLGQTIR
1475.7852	1474.7779	1474.7779	-0.0000	28	41	0	60	SSPAYPSVLGQTIR
1561.8088	1560.8015	1560.8035	-0.0019	95	108	0	---	SLQPEEFAVVDLSK
1832.9625	1831.9552	1831.9540	0.0012	28	44	1	47	SSPAYPSVLGQTIRNSR

1832.9625	1831.9552	1831.9540	0.0012	28 - 44	1	---	SSPAYPSVLGQTIRNSR

No match to: 768.5280, 1033.5288, 1060.5247, 1614.8179, 1628.8334, 1682.9696, 1682.9696, 1698.9532, 1699.9886, 1847.9761, 1863.9578, 2318.2268, 2445.2991, 2608.3569

8. gi|55859464 **Mass:** 47178 **Score:** 82 **Expected:** 0.0042 **Queries matched:** 7

pollen allergen Lol p 4 [Lolium perenne]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
885.4280	884.4207	884.4140	0.0067	367 -	373	0	---	QAYANYR
1060.5247	1059.5174	1059.5137	0.0037	399 -	406	1	---	YFKGNFER
1197.5724	1196.5651	1196.5825	-0.0174	412 -	421	1	---	GKVDPTDYFR
1320.5770	1319.5697	1319.5717	-0.0019	128 -	138	0	45	SMGDDHFWAVR
1320.5770	1319.5697	1319.5717	-0.0019	128 -	138	0	---	SMGDDHFWAVR
1336.5812	1335.5739	1335.5666	0.0073	128 -	138	0	---	SMGDDHFWAVR + Oxidation (M)
1340.6010	1339.5937	1339.5792	0.0145	16 -	27	0	---	SGGHDYEGLSYR

No match to: 768.5280, 1001.5590, 1033.5288, 1059.5372, 1199.7061, 1199.7061, 1475.7852, 1475.7852, 1561.8088, 1614.8179, 1628.8334, 1682.9696, 1682.9696, 1698.9532, 1699.9886, 1832.9625, 1832.9625, 1847.9761, 1863.9578, 2318.2268, 2445.2991, 2608.3569

9. gi|224085664 **Mass:** 135560 **Score:** 49 **Expected:** 8.2 **Queries matched:** 10

chromatin remodeling complex subunit [Populus trichocarpa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1001.5590	1000.5517	1000.5413	0.0104	1014 -	1022	1	---	AAEALRQSR
1060.5247	1059.5174	1059.5811	-0.0637	862 -	871	0	---	LITGGTIEEK
1340.6010	1339.5937	1339.6215	-0.0278	1063 -	1075	1	---	SSDSSSSNKSNLK
1561.8088	1560.8015	1560.7678	0.0337	1001 -	1013	1	---	MRLEEQASQVAQR + Oxidation (M)
1682.9696	1681.9623	1681.8933	0.0690	268 -	283	1	---	AAHSMLEAAKARPTTK
1682.9696	1681.9623	1681.8933	0.0690	268 -	283	1	---	AAHSMLEAAKARPTTK
1698.9532	1697.9459	1697.9028	0.0431	383 -	396	1	---	IPEAIFSKLFDYQK
1847.9761	1846.9688	1847.0161	-0.0472	641 -	655	1	---	CAVVLRDLIMPYLLR + Oxidation (M)
1863.9578	1862.9505	1862.9373	0.0132	49 -	65	1	---	LENVDPSSANQAKLYSK
2445.2991	2444.2918	2444.1918	0.1001	3 -	25	0	---	VDEDSVLLSSLGVTSANPEDIER

No match to: 768.5280, 885.4280, 1033.5288, 1059.5372, 1197.5724, 1199.7061, 1199.7061, 1320.5770, 1320.5770, 1336.5812, 1475.7852, 1475.7852, 1614.8179, 1628.8334, 1699.9886, 1832.9625, 1832.9625, 2318.2268, 2608.3569

10. gi|146393844 **Mass:** 28907 **Score:** 46 **Expected:** 14 **Queries matched:** 7

putative NB-ARC domain-containing protein [Oryza sativa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
885.4280	884.4207	884.4279	-0.0072	248 -	254	0	---	YFEQLVS
1001.5590	1000.5517	1000.5301	0.0216	176 -	184	1	---	DAGNRDLLK
1059.5372	1058.5299	1058.5607	-0.0308	46 -	54	1	---	LEEELNGKK
1199.7061	1198.6988	1198.7033	-0.0045	95 -	106	1	---	SKDALVALGAVR
1199.7061	1198.6988	1198.7033	-0.0045	95 -	106	1	---	SKDALVALGAVR

1320.5770 1319.5697 1319.5791 -0.0093 204 - 213 0 --- CFAYCSIFPR
1320.5770 1319.5697 1319.5791 -0.0093 204 - 213 0 --- CFAYCSIFPR

No match to: 768.5280, 1033.5288, 1060.5247, 1197.5724, 1336.5812, 1340.6010, 1475.7852, 1475.7852, 1561.8088, 1614.8179, 1628.8334, 1682.9696, 1682.9696, 1698.9532, 1699.9886, 1832.9625, 1832.9625, 1847.9761, 1863.9578, 2318.2268, 2445.2991, 2608.3569

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 29

Protein View

Match to: **gi|189014268** Score: **277** Expect: **1.2e-022**
pollen allergen Phl p 4.0202 [Phleum pratense]

Nominal mass (M_r): **55889**; Calculated pI value: **9.19**
NCBI BLAST search of gi|189014268 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **20%**

Matched peptides shown in **Bold Red**

```
  1 YFPPPAAKED FLGCLVKEIP PRLLYAKSSP AYPSVLGQTI RNSRWSSPDN
 51 VKPLYIITPT NVSHIQSAVV CGRRHTVRIR VRSGGHDYEG LSYRSLQPET
101 FAVVDLNKMR AVWVDGKART AWVDSGAQLG ELYYAIYKAS PTLAFPAGVC
151 PTIGVGGNFA GGGFGMLLRK YGIAAENVID VKLVDANGKL HDKKSMGDDH
201 FWAVRGGGGE SFGIVVAWQV KLLPVPPTVT IFKISKTVSE GAVDIINKWQ
251 VVAPQLPADL MIRIIAQGPK ATFEAMYLGT CKTLTPLMSS KFPELGMNPS
301 HCNEMSWIQS IPFVHLGHRD ALEDDLLNRN NSFKPFAEYK SDYVYQPFPK
351 TVWEQILNTW LVKPGAGIMI FDPYGATISA TPESATPFPH RKGVLFNIQY
401 VNYWFAPGAA AAPLSWSKDI YNYMEPYVSK NPRQAYANYR DIDLGRNEVV
451 NDVSTYASGK VWGQKYFKGN FERLAITKGK VDPTDYFRNE QSIPPLIKKY
501
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
18 - 27	1199.7061	1198.6988	1198.7073	-0.0085	1	**EIPPRLLYAK** (Ions score 22)
18 - 27	1199.7061	1198.6988	1198.7073	-0.0085	1	**EIPPRLLYAK** (No match)
28 - 41	1475.7852	1474.7779	1474.7779	-0.0000	0	**SSPAYPSVLGQTIR** (No match)
28 - 41	1475.7852	1474.7779	1474.7779	-0.0000	0	**SSPAYPSVLGQTIR** (Ions score 60)
28 - 44	1832.9625	1831.9552	1831.9540	0.0012	1	**SSPAYPSVLGQTIRNSR** (Ions score 47)
28 - 44	1832.9625	1831.9552	1831.9540	0.0012	1	**SSPAYPSVLGQTIRNSR** (No match)
83 - 94	1340.6010	1339.5937	1339.5792	0.0145	0	**SGGHDYEGLSYR** (No match)
95 - 110	1847.9761	1846.9688	1846.9611	0.0078	1	**SLQPETFAVVDLNKMR** (No match)
95 - 110	1863.9578	1862.9505	1862.9560	-0.0054	1	**SLQPETFAVVDLNKMR** Oxidation (M) (No match)
111 - 119	1001.5590	1000.5517	1000.5453	0.0064	1	**AVWVDGKAR** (No match)
195 - 205	1320.5770	1319.5697	1319.5717	-0.0019	0	**SMGDDHFWAVR** (Ions score 45)
195 - 205	1320.5770	1319.5697	1319.5717	-0.0019	0	**SMGDDHFWAVR** (No match)
195 - 205	1336.5812	1335.5739	1335.5666	0.0073	0	**SMGDDHFWAVR** Oxidation (M) (No match)
434 - 440	885.4280	884.4207	884.4140	0.0067	0	**QAYANYR** (No match)
466 - 473	1060.5247	1059.5174	1059.5137	0.0037	1	**YFKGNFER** (No match)
479 - 488	1197.5724	1196.5651	1196.5825	-0.0174	1	**GKVDPTDYFR** (No match)

Spot 31

Index

	Accession	Mass	Score	Description
1.	gi|82492267	58590	308	major pollen allergen Phl p 4 precursor [Phleum pratense]
2.	gi|54144334	56741	308	pollen allergen Phl p 4 [Phleum pratense]
3.	gi|189014268	55889	308	pollen allergen Phl p 4.0202 [Phleum pratense]
4.	gi|189014270	55917	308	pollen allergen Phl p 4.0203 [Phleum pratense]
5.	gi|189014272	55931	308	pollen allergen Phl p 4.0204 [Phleum pratense]
6.	gi|54144332	56979	288	pollen allergen Phl p 4 [Phleum pratense]
7.	gi|189014266	56147	288	pollen allergen Phl p 4.0102 [Phleum pratense]
8.	gi|15229765	24902	45	HR3 (HOMOLOG OF RPW8 3) [Arabidopsis thaliana]
9.	gi|37359455	24878	45	HR3 [Arabidopsis lyrata]
10.	gi|8778337	22145	44	F15O4.9 [Arabidopsis thaliana]

Results List

1. gi|82492267 **Mass:** 58590 **Score:** 308 **Expect:** 9.6e-026 **Queries matched:** 15

major pollen allergen Phl p 4 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
885.4604	884.4531	884.4140	0.0391	459	465	0	---	QAYANYR
1001.5833	1000.5760	1000.5453	0.0307	136	144	1	---	AVWVDGKAR
1060.5532	1059.5459	1059.5137	0.0322	491	498	1	---	YFKGNFER
1199.7549	1198.7476	1198.7073	0.0403	43	52	1	24	EIPPRLLYAK
1199.7549	1198.7476	1198.7073	0.0403	43	52	1	---	EIPPRLLYAK
1320.6262	1319.6189	1319.5717	0.0473	220	230	0	---	SMGDDHFWAVR
1336.6031	1335.5958	1335.5666	0.0293	220	230	0	---	SMGDDHFWAVR + Oxidation (M)
1340.6310	1339.6237	1339.5792	0.0445	108	119	0	---	SGGHDYEGLSYR
1475.8303	1474.8230	1474.7779	0.0451	53	66	0	100	SSPAYPSVLGQTIR
1475.8303	1474.8230	1474.7779	0.0451	53	66	0	---	SSPAYPSVLGQTIR
1833.0223	1832.0150	1831.9540	0.0610	53	69	1	---	SSPAYPSVLGQTIRNSR
1833.0223	1832.0150	1831.9540	0.0610	53	69	1	81	SSPAYPSVLGQTIRNSR
1848.0256	1847.0183	1846.9611	0.0573	120	135	1	---	SLQPETFAVVDLNKMR
1848.0256	1847.0183	1846.9611	0.0573	120	135	1	14	SLQPETFAVVDLNKMR
1864.0217	1863.0144	1862.9560	0.0585	120	135	1	---	SLQPETFAVVDLNKMR + Oxidation (M)

No match to: 768.5477, 1033.5535, 1561.8638, 1614.8732, 1628.8885, 1683.0228, 1683.0228, 1700.0385, 1865.0155, 1905.9573, 2317.3013, 2445.3728, 2608.4565

2. gi|54144334 **Mass:** 56741 **Score:** 308 **Expect:** 9.6e-026 **Queries matched:** 15

pollen allergen Phl p 4 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
885.4604	884.4531	884.4140	0.0391	442	448	0	---	QAYANYR

1001.5833	1000.5760	1000.5453	0.0307	119 - 127	1	---	AVWVDGKAR
1060.5532	1059.5459	1059.5137	0.0322	474 - 481	1	---	YFKGNFER
1199.7549	1198.7476	1198.7073	0.0403	26 - 35	1	24	EIPPRLLYAK
1199.7549	1198.7476	1198.7073	0.0403	26 - 35	1	---	EIPPRLLYAK
1320.6262	1319.6189	1319.5717	0.0473	203 - 213	0	---	SMGDDHFWAVR
1336.6031	1335.5958	1335.5666	0.0293	203 - 213	0	---	SMGDDHFWAVR + Oxidation (M)
1340.6310	1339.6237	1339.5792	0.0445	91 - 102	0	---	SGGHDYEGLSYR
1475.8303	1474.8230	1474.7779	0.0451	36 - 49	0	100	SSPAYPSVLGQTIR
1475.8303	1474.8230	1474.7779	0.0451	36 - 49	0	---	SSPAYPSVLGQTIR
1833.0223	1832.0150	1831.9540	0.0610	36 - 52	1	---	SSPAYPSVLGQTIRNSR
1833.0223	1832.0150	1831.9540	0.0610	36 - 52	1	81	SSPAYPSVLGQTIRNSR
1848.0256	1847.0183	1846.9611	0.0573	103 - 118	1	---	SLQPETFAVVDLNKMR
1848.0256	1847.0183	1846.9611	0.0573	103 - 118	1	14	SLQPETFAVVDLNKMR
1864.0217	1863.0144	1862.9560	0.0585	103 - 118	1	---	SLQPETFAVVDLNKMR + Oxidation (M)

No match to: 768.5477, 1033.5535, 1561.8638, 1614.8732, 1628.8885, 1683.0228, 1683.0228, 1700.0385, 1865.0155, 1905.9573, 2317.3013, 2445.3728, 2608.4565

3. gi|189014268 **Mass:** 55889 **Score:** 308 **Expect:** 9.6e-026 **Queries matched:** 15

pollen allergen Phl p 4.0202 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
885.4604	884.4531	884.4140	0.0391	434 - 440		0	---	QAYANYR
1001.5833	1000.5760	1000.5453	0.0307	111 - 119		1	---	AVWVDGKAR
1060.5532	1059.5459	1059.5137	0.0322	466 - 473		1	---	YFKGNFER
1199.7549	1198.7476	1198.7073	0.0403	18 - 27		1	24	EIPPRLLYAK
1199.7549	1198.7476	1198.7073	0.0403	18 - 27		1	---	EIPPRLLYAK
1320.6262	1319.6189	1319.5717	0.0473	195 - 205		0	---	SMGDDHFWAVR
1336.6031	1335.5958	1335.5666	0.0293	195 - 205		0	---	SMGDDHFWAVR + Oxidation (M)
1340.6310	1339.6237	1339.5792	0.0445	83 - 94		0	---	SGGHDYEGLSYR
1475.8303	1474.8230	1474.7779	0.0451	28 - 41		0	100	SSPAYPSVLGQTIR
1475.8303	1474.8230	1474.7779	0.0451	28 - 41		0	---	SSPAYPSVLGQTIR
1833.0223	1832.0150	1831.9540	0.0610	28 - 44		1	---	SSPAYPSVLGQTIRNSR
1833.0223	1832.0150	1831.9540	0.0610	28 - 44		1	81	SSPAYPSVLGQTIRNSR
1848.0256	1847.0183	1846.9611	0.0573	95 - 110		1	---	SLQPETFAVVDLNKMR
1848.0256	1847.0183	1846.9611	0.0573	95 - 110		1	14	SLQPETFAVVDLNKMR
1864.0217	1863.0144	1862.9560	0.0585	95 - 110		1	---	SLQPETFAVVDLNKMR + Oxidation (M)

No match to: 768.5477, 1033.5535, 1561.8638, 1614.8732, 1628.8885, 1683.0228, 1683.0228, 1700.0385, 1865.0155, 1905.9573, 2317.3013, 2445.3728, 2608.4565

4. gi|189014270 **Mass:** 55917 **Score:** 308 **Expect:** 9.6e-026 **Queries matched:** 15

pollen allergen Phl p 4.0203 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide

885.4604	884.4531	884.4140	0.0391	434 - 440	0	---	QAYANYR
1001.5833	1000.5760	1000.5453	0.0307	111 - 119	1	---	AVWVDGKAR
1060.5532	1059.5459	1059.5137	0.0322	466 - 473	1	---	YFKGNFER
1199.7549	1198.7476	1198.7073	0.0403	18 - 27	1	24	EIPPRLLYAK
1199.7549	1198.7476	1198.7073	0.0403	18 - 27	1	---	EIPPRLLYAK
1320.6262	1319.6189	1319.5717	0.0473	195 - 205	0	---	SMGDDHFWAVR
1336.6031	1335.5958	1335.5666	0.0293	195 - 205	0	---	SMGDDHFWAVR + Oxidation (M)
1340.6310	1339.6237	1339.5792	0.0445	83 - 94	0	---	SGGHDYEGLSYR
1475.8303	1474.8230	1474.7779	0.0451	28 - 41	0	100	SSPAYPSVLGQTIR
1475.8303	1474.8230	1474.7779	0.0451	28 - 41	0	---	SSPAYPSVLGQTIR
1833.0223	1832.0150	1831.9540	0.0610	28 - 44	1	---	SSPAYPSVLGQTIRNSR
1833.0223	1832.0150	1831.9540	0.0610	28 - 44	1	81	SSPAYPSVLGQTIRNSR
1848.0256	1847.0183	1846.9611	0.0573	95 - 110	1	---	SLQPETFAVVDLNKMR
1848.0256	1847.0183	1846.9611	0.0573	95 - 110	1	14	SLQPETFAVVDLNKMR
1864.0217	1863.0144	1862.9560	0.0585	95 - 110	1	---	SLQPETFAVVDLNKMR + Oxidation (M)

No match to: 768.5477, 1033.5535, 1561.8638, 1614.8732, 1628.8885, 1683.0228, 1683.0228, 1700.0385, 1865.0155, 1905.9573, 2317.3013, 2445.3728, 2608.4565

5. gi|189014272 **Mass:** 55931 **Score:** 308 **Expect:** 9.6e-026 **Queries matched:** 15

pollen allergen Phl p 4.0204 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
885.4604	884.4531	884.4140	0.0391	434 - 440	0	---	QAYANYR
1001.5833	1000.5760	1000.5453	0.0307	111 - 119	1	---	AVWVDGKAR
1060.5532	1059.5459	1059.5137	0.0322	466 - 473	1	---	YFKGNFER
1199.7549	1198.7476	1198.7073	0.0403	18 - 27	1	24	EIPPRLLYAK
1199.7549	1198.7476	1198.7073	0.0403	18 - 27	1	---	EIPPRLLYAK
1320.6262	1319.6189	1319.5717	0.0473	195 - 205	0	---	SMGDDHFWAVR
1336.6031	1335.5958	1335.5666	0.0293	195 - 205	0	---	SMGDDHFWAVR + Oxidation (M)
1340.6310	1339.6237	1339.5792	0.0445	83 - 94	0	---	SGGHDYEGLSYR
1475.8303	1474.8230	1474.7779	0.0451	28 - 41	0	100	SSPAYPSVLGQTIR
1475.8303	1474.8230	1474.7779	0.0451	28 - 41	0	---	SSPAYPSVLGQTIR
1833.0223	1832.0150	1831.9540	0.0610	28 - 44	1	---	SSPAYPSVLGQTIRNSR
1833.0223	1832.0150	1831.9540	0.0610	28 - 44	1	81	SSPAYPSVLGQTIRNSR
1848.0256	1847.0183	1846.9611	0.0573	95 - 110	1	---	SLQPETFAVVDLNKMR
1848.0256	1847.0183	1846.9611	0.0573	95 - 110	1	14	SLQPETFAVVDLNKMR
1864.0217	1863.0144	1862.9560	0.0585	95 - 110	1	---	SLQPETFAVVDLNKMR + Oxidation (M)

No match to: 768.5477, 1033.5535, 1561.8638, 1614.8732, 1628.8885, 1683.0228, 1683.0228, 1700.0385, 1865.0155, 1905.9573, 2317.3013, 2445.3728, 2608.4565

6. gi|54144332 **Mass:** 56979 **Score:** 288 **Expect:** 9.6e-024 **Queries matched:** 13

pollen allergen Phl p 4 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
885.4604	884.4531	884.4140	0.0391	442 -	448	0	---	QAYANYR
1001.5833	1000.5760	1000.5453	0.0307	119 -	127	1	---	AVWVDGKAR
1199.7549	1198.7476	1198.7073	0.0403	26 -	35	1	24	EIPPRLLYAK
1199.7549	1198.7476	1198.7073	0.0403	26 -	35	1	---	EIPPRLLYAK
1320.6262	1319.6189	1319.5717	0.0473	203 -	213	0	---	SMGDDHFWAVR
1336.6031	1335.5958	1335.5666	0.0293	203 -	213	0	---	SMGDDHFWAVR + Oxidation (M)
1340.6310	1339.6237	1339.5792	0.0445	91 -	102	0	---	SGGHDYEGLSYR
1475.8303	1474.8230	1474.7779	0.0451	36 -	49	0	100	SSPAYPSVLGQTIR
1475.8303	1474.8230	1474.7779	0.0451	36 -	49	0	---	SSPAYPSVLGQTIR
1561.8638	1560.8565	1560.8035	0.0531	103 -	116	0	---	SLQPEEFAVVDLSK
1833.0223	1832.0150	1831.9540	0.0610	36 -	52	1	---	SSPAYPSVLGQTIRNSR
1833.0223	1832.0150	1831.9540	0.0610	36 -	52	1	81	SSPAYPSVLGQTIRNSR
1865.0155	1864.0082	1863.9400	0.0683	103 -	118	1	---	SLQPEEFAVVDLSKMR + Oxidation (M)

No match to: 768.5477, 1033.5535, 1060.5532, 1614.8732, 1628.8885, 1683.0228, 1683.0228, 1700.0385, 1848.0256, 1848.0256, 1864.0217, 1905.9573, 2317.3013, 2445.3728, 2608.4565

7. gi|189014266 **Mass:** 56147 **Score:** 288 **Expect:** 9.6e-024 **Queries matched:** 13

pollen allergen Phl p 4.0102 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
885.4604	884.4531	884.4140	0.0391	434 -	440	0	---	QAYANYR
1001.5833	1000.5760	1000.5453	0.0307	111 -	119	1	---	AVWVDGKAR
1199.7549	1198.7476	1198.7073	0.0403	18 -	27	1	24	EIPPRLLYAK
1199.7549	1198.7476	1198.7073	0.0403	18 -	27	1	---	EIPPRLLYAK
1320.6262	1319.6189	1319.5717	0.0473	195 -	205	0	---	SMGDDHFWAVR
1336.6031	1335.5958	1335.5666	0.0293	195 -	205	0	---	SMGDDHFWAVR + Oxidation (M)
1340.6310	1339.6237	1339.5792	0.0445	83 -	94	0	---	SGGHDYEGLSYR
1475.8303	1474.8230	1474.7779	0.0451	28 -	41	0	100	SSPAYPSVLGQTIR
1475.8303	1474.8230	1474.7779	0.0451	28 -	41	0	---	SSPAYPSVLGQTIR
1561.8638	1560.8565	1560.8035	0.0531	95 -	108	0	---	SLQPEEFAVVDLSK
1833.0223	1832.0150	1831.9540	0.0610	28 -	44	1	---	SSPAYPSVLGQTIRNSR
1833.0223	1832.0150	1831.9540	0.0610	28 -	44	1	81	SSPAYPSVLGQTIRNSR
1865.0155	1864.0082	1863.9400	0.0683	95 -	110	1	---	SLQPEEFAVVDLSKMR + Oxidation (M)

No match to: 768.5477, 1033.5535, 1060.5532, 1614.8732, 1628.8885, 1683.0228, 1683.0228, 1700.0385, 1848.0256, 1848.0256, 1864.0217, 1905.9573, 2317.3013, 2445.3728, 2608.4565

8. gi|15229765 **Mass:** 24902 **Score:** 45 **Expect:** 19 **Queries matched:** 4

HR3 (HOMOLOG OF RPW8 3) [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1320.6262	1319.6189	1319.7084	-0.0895	79 -	90	0	---	AVSLVEAYAELR
2317.3013	2316.2940	2316.2874	0.0066	2 -	24	0	---	PVSEIMAGAALGLALQVLHDAIK
2445.3728	2444.3655	2444.3824	-0.0169	2 -	25	1	---	PVSEIMAGAALGLALQVLHDAIKK

2608.4565	2607.4492	2607.4127	0.0365	1 - 25	1	---	MPVSEIMAGAALGLALQVLHDAIKK + 2 Oxidation (M)

No match to: 768.5477, 885.4604, 1001.5833, 1033.5535, 1060.5532, 1199.7549, 1199.7549, 1336.6031, 1340.6310, 1475.8303, 1475.8303, 1561.8638, 1614.8732, 1628.8885, 1683.0228, 1683.0228, 1700.0385, 1833.0223, 1833.0223, 1848.0256, 1848.0256, 1864.0217, 1865.0155, 1905.9573

9. gi|37359455 **Mass:** 24878 **Score:** 45 **Expect:** 19 **Queries matched:** 4

HR3 [Arabidopsis lyrata]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1320.6262	1319.6189	1319.7084	-0.0895	79 -	90	0	---	AVSLVEAYAELR
2317.3013	2316.2940	2316.2874	0.0066	2 -	24	0	---	PVSELMAGAALGLALQVLHDAIK
2445.3728	2444.3655	2444.3824	-0.0169	2 -	25	1	---	PVSELMAGAALGLALQVLHDAIKK
2608.4565	2607.4492	2607.4127	0.0365	1 -	25	1	---	MPVSELMAGAALGLALQVLHDAIKK + 2 Oxidation (M)

No match to: 768.5477, 885.4604, 1001.5833, 1033.5535, 1060.5532, 1199.7549, 1199.7549, 1336.6031, 1340.6310, 1475.8303, 1475.8303, 1561.8638, 1614.8732, 1628.8885, 1683.0228, 1683.0228, 1700.0385, 1833.0223, 1833.0223, 1848.0256, 1848.0256, 1864.0217, 1865.0155, 1905.9573

10. gi|8778337 **Mass:** 22145 **Score:** 44 **Expect:** 26 **Queries matched:** 7

F15O4.9 [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1033.5535	1032.5462	1032.5293	0.0169	86 -	92	1	---	RYWPHFK
1199.7549	1198.7476	1198.7073	0.0403	45 -	54	1	10	VLHDFITKVK
1199.7549	1198.7476	1198.7073	0.0403	45 -	54	1	---	VLHDFITKVK
1833.0223	1832.0150	1831.9364	0.0786	4 -	18	1	---	LSSAQKMLFWYAMLK + Oxidation (M)
1833.0223	1832.0150	1831.9364	0.0786	4 -	18	1	---	LSSAQKMLFWYAMLK + Oxidation (M)
1848.0256	1847.0183	1847.0226	-0.0043	24 -	40	0	---	YLKPSTLCGLPILSGTK
1848.0256	1847.0183	1847.0226	-0.0043	24 -	40	0	---	YLKPSTLCGLPILSGTK

No match to: 768.5477, 885.4604, 1001.5833, 1060.5532, 1320.6262, 1336.6031, 1340.6310, 1475.8303, 1475.8303, 1561.8638, 1614.8732, 1628.8885, 1683.0228, 1683.0228, 1700.0385, 1864.0217, 1865.0155, 1905.9573, 2317.3013, 2445.3728, 2608.4565

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 28

Protein View

Match to: **gi|54144334** Score: **308** Expect: **9.6e-026**
pollen allergen Phl p 4 [Phleum pratense]

Nominal mass (M_r): **56741**; Calculated pI value: **9.16**
NCBI BLAST search of gi|54144334 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **17%**

Matched peptides shown in **Bold Red**

```
   1 SSCQVAFSYF PPPAAKEDFL GCLVKEIPPR LLYAKSSPAY PSVLGQTIRN
  51 SRWSSPDNVK PLYIITPTNV SHIQSAVVCG RRHSVRIRVR SGGHDYEGLS
 101 YRSLQPETFA VVDLNKMRAV WVDGKARTAW VDSGAQLGEL YYAIYKASPT
 151 LAFPAGVCPT IGVGGNFAGG GFGMLLRKYG IAAENVIDVK LVDANGKLHD
 201 KKSMGDDHFW AVRGGGGESF GIVVAWQVKL LPVPPTVTIF KISKTVSEGA
 251 VDIINKWQVV APQLPADLMI RIIAQGPKAT FEAMYLGTCK TLTPLMSSKF
 301 PELGMNPSHC NEMSWIQSIP FVHLGHRDAL EDDLLNRNNS FKPFAEYKSD
 351 YVYQPFPKTV WEQILNTWLV KPGAGIMIFD PYGATISATP ESATPFPHRK
 401 GVLFNIQYVN YWFAPGAAAA PLSWSKDIYN YMEPYVSKNP RQAYANYRDI
 451 DLGRNEVVND VSTYASGKVW GQKYFKGNFE RLAITKGKVD PTDYFRNEQS
 501 IPPLIKKY
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
26 - 35	1199.7549	1198.7476	1198.7073	0.0403	1	EIPPRLLYAK	(Ions score 24)
26 - 35	1199.7549	1198.7476	1198.7073	0.0403	1	EIPPRLLYAK	(No match)
36 - 49	1475.8303	1474.8230	1474.7779	0.0451	0	SSPAYPSVLGQTIR	(Ions score 100)
36 - 49	1475.8303	1474.8230	1474.7779	0.0451	0	SSPAYPSVLGQTIR	(No match)
36 - 52	1833.0223	1832.0150	1831.9540	0.0610	1	SSPAYPSVLGQTIRNSR	(No match)
36 - 52	1833.0223	1832.0150	1831.9540	0.0610	1	SSPAYPSVLGQTIRNSR	(Ions score 81)
91 - 102	1340.6310	1339.6237	1339.5792	0.0445	0	SGGHDYEGLSYR	(No match)
103 - 118	1848.0256	1847.0183	1846.9611	0.0573	1	SLQPETFAVVDLNKMR	(No match)
103 - 118	1848.0256	1847.0183	1846.9611	0.0573	1	SLQPETFAVVDLNKMR	(Ions score 14)
103 - 118	1864.0217	1863.0144	1862.9560	0.0585	1	SLQPETFAVVDLNKMR	Oxidation (M) (No match)
119 - 127	1001.5833	1000.5760	1000.5453	0.0307	1	AVWVDGKAR	(No match)
203 - 213	1320.6262	1319.6189	1319.5717	0.0473	0	SMGDDHFWAVR	(No match)
203 - 213	1336.6031	1335.5958	1335.5666	0.0293	0	SMGDDHFWAVR	Oxidation (M) (No match)
442 - 448	885.4604	884.4531	884.4140	0.0391	0	QAYANYR	(No match)
474 - 481	1060.5532	1059.5459	1059.5137	0.0322	1	YFKGNFER	(No match)

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	Accession	Mass	Score	Description
1.	gi|54144334	56741	399	pollen allergen Phl p 4 [Phleum pratense]
2.	gi|189014268	55889	398	pollen allergen Phl p 4.0202 [Phleum pratense]
3.	gi|189014270	55917	398	pollen allergen Phl p 4.0203 [Phleum pratense]
4.	gi|189014272	55931	398	pollen allergen Phl p 4.0204 [Phleum pratense]
5.	gi|82492267	58590	397	major pollen allergen Phl p 4 precursor [Phleum pratense]
6.	gi|54144332	56979	294	pollen allergen Phl p 4 [Phleum pratense]
7.	gi|189014266	56147	293	pollen allergen Phl p 4.0102 [Phleum pratense]
8.	gi|2244938	67168	53	hypothetical protein [Arabidopsis thaliana]
9.	gi|145348829	28139	49	predicted protein [Ostreococcus lucimarinus CCE9901]
10.	gi|218194159	74490	47	hypothetical protein OsI_14434 [Oryza sativa Indica Group]

Results List

1. gi|54144334 **Mass:** 56741 **Score:** 399 **Expect:** 7.6e-035 **Queries matched:** 18

pollen allergen Phl p 4 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
885.4393	884.4320	884.4140	0.0180	442	448	0	---	QAYANYR
1001.5771	1000.5698	1000.5453	0.0245	119	127	1	---	AVWVDGKAR
1060.5387	1059.5314	1059.5137	0.0177	474	481	1	---	YFKGNFER
1197.6237	1196.6164	1196.5825	0.0339	487	496	1	---	GKVDPTDYFR
1199.7288	1198.7215	1198.7073	0.0142	26	35	1	---	EIPPRLLYAK
1199.7288	1198.7215	1198.7073	0.0142	26	35	1	36	EIPPRLLYAK
1320.5977	1319.5904	1319.5717	0.0188	203	213	0	---	SMGDDHFWAVR
1336.6028	1335.5955	1335.5666	0.0290	203	213	0	---	SMGDDHFWAVR + Oxidation (M)
1340.6198	1339.6125	1339.5792	0.0333	91	102	0	---	SGGHDYEGLSYR
1475.8070	1474.7997	1474.7779	0.0218	36	49	0	103	SSPAYPSVLGQTIR
1475.8070	1474.7997	1474.7779	0.0218	36	49	0	---	SSPAYPSVLGQTIR
1832.9880	1831.9807	1831.9540	0.0267	36	52	1	---	SSPAYPSVLGQTIRNSR
1832.9880	1831.9807	1831.9540	0.0267	36	52	1	66	SSPAYPSVLGQTIRNSR
1847.9949	1846.9876	1846.9611	0.0266	103	118	1	---	SLQPETFAVVDLNKMR
1847.9949	1846.9876	1846.9611	0.0266	103	118	1	62	SLQPETFAVVDLNKMR
1863.9833	1862.9760	1862.9560	0.0201	103	118	1	---	SLQPETFAVVDLNKMR + Oxidation (M)
1888.9153	1887.9080	1887.8825	0.0255	427	441	1	---	DIYNYMEPYVSKNPR
1904.9189	1903.9116	1903.8774	0.0342	427	441	1	---	DIYNYMEPYVSKNPR + Oxidation (M)

No match to: 768.5497, 1561.8572, 1659.8685, 2317.2444, 2445.3513, 2608.4097, 2608.4097, 2808.3555

2. gi|189014268 **Mass:** 55889 **Score:** 398 **Expect:** 9.6e-035 **Queries matched:** 18

pollen allergen Phl p 4.0202 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
885.4393	884.4320	884.4140	0.0180	434	440	0	---	QAYANYR
1001.5771	1000.5698	1000.5453	0.0245	111	119	1	---	AVWVDGKAR
1060.5387	1059.5314	1059.5137	0.0177	466	473	1	---	YFKGNFER
1197.6237	1196.6164	1196.5825	0.0339	479	488	1	---	GKVDPTDYFR
1199.7288	1198.7215	1198.7073	0.0142	18	27	1	---	EIPPRLLYAK
1199.7288	1198.7215	1198.7073	0.0142	18	27	1	36	EIPPRLLYAK
1320.5977	1319.5904	1319.5717	0.0188	195	205	0	---	SMGDDHFWAVR
1336.6028	1335.5955	1335.5666	0.0290	195	205	0	---	SMGDDHFWAVR + Oxidation (M)
1340.6198	1339.6125	1339.5792	0.0333	83	94	0	---	SGGHDYEGLSYR
1475.8070	1474.7997	1474.7779	0.0218	28	41	0	103	SSPAYPSVLGQTIR
1475.8070	1474.7997	1474.7779	0.0218	28	41	0	---	SSPAYPSVLGQTIR
1832.9880	1831.9807	1831.9540	0.0267	28	44	1	---	SSPAYPSVLGQTIRNSR
1832.9880	1831.9807	1831.9540	0.0267	28	44	1	66	SSPAYPSVLGQTIRNSR
1847.9949	1846.9876	1846.9611	0.0266	95	110	1	---	SLQPETFAVVDLNKMR
1847.9949	1846.9876	1846.9611	0.0266	95	110	1	62	SLQPETFAVVDLNKMR
1863.9833	1862.9760	1862.9560	0.0201	95	110	1	---	SLQPETFAVVDLNKMR + Oxidation (M)
1888.9153	1887.9080	1887.8825	0.0255	419	433	1	---	DIYNYMEPYVSKNPR
1904.9189	1903.9116	1903.8774	0.0342	419	433	1	---	DIYNYMEPYVSKNPR + Oxidation (M)

No match to: 768.5497, 1561.8572, 1659.8685, 2317.2444, 2445.3513, 2608.4097, 2608.4097, 2808.3555

3. gi|189014270 **Mass:** 55917 **Score:** 398 **Expect:** 9.6e-035 **Queries matched:** 18

pollen allergen Phl p 4.0203 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
885.4393	884.4320	884.4140	0.0180	434	440	0	---	QAYANYR
1001.5771	1000.5698	1000.5453	0.0245	111	119	1	---	AVWVDGKAR
1060.5387	1059.5314	1059.5137	0.0177	466	473	1	---	YFKGNFER
1197.6237	1196.6164	1196.5825	0.0339	479	488	1	---	GKVDPTDYFR
1199.7288	1198.7215	1198.7073	0.0142	18	27	1	---	EIPPRLLYAK
1199.7288	1198.7215	1198.7073	0.0142	18	27	1	36	EIPPRLLYAK
1320.5977	1319.5904	1319.5717	0.0188	195	205	0	---	SMGDDHFWAVR
1336.6028	1335.5955	1335.5666	0.0290	195	205	0	---	SMGDDHFWAVR + Oxidation (M)
1340.6198	1339.6125	1339.5792	0.0333	83	94	0	---	SGGHDYEGLSYR
1475.8070	1474.7997	1474.7779	0.0218	28	41	0	103	SSPAYPSVLGQTIR
1475.8070	1474.7997	1474.7779	0.0218	28	41	0	---	SSPAYPSVLGQTIR
1832.9880	1831.9807	1831.9540	0.0267	28	44	1	---	SSPAYPSVLGQTIRNSR
1832.9880	1831.9807	1831.9540	0.0267	28	44	1	66	SSPAYPSVLGQTIRNSR
1847.9949	1846.9876	1846.9611	0.0266	95	110	1	---	SLQPETFAVVDLNKMR
1847.9949	1846.9876	1846.9611	0.0266	95	110	1	62	SLQPETFAVVDLNKMR

1863.9833	1862.9760	1862.9560	0.0201	95 - 110	1	---	SLQPETFAVVDLNKMR + Oxidation (M)
1888.9153	1887.9080	1887.8825	0.0255	419 - 433	1	---	DIYNYMEPYVSKNPR
1904.9189	1903.9116	1903.8774	0.0342	419 - 433	1	---	DIYNYMEPYVSKNPR + Oxidation (M)

No match to: 768.5497, 1561.8572, 1659.8685, 2317.2444, 2445.3513, 2608.4097, 2608.4097, 2808.3555

4. gi|189014272 **Mass:** 55931 **Score:** 398 **Expect:** 9.6e-035 **Queries matched:** 18

pollen allergen Phl p 4.0204 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
885.4393	884.4320	884.4140	0.0180	434 -	440	0	---	QAYANYR
1001.5771	1000.5698	1000.5453	0.0245	111 -	119	1	---	AVWVDGKAR
1060.5387	1059.5314	1059.5137	0.0177	466 -	473	1	---	YFKGNFER
1197.6237	1196.6164	1196.5825	0.0339	479 -	488	1	---	GKVDPTDYFR
1199.7288	1198.7215	1198.7073	0.0142	18 -	27	1	---	EIPPRLLYAK
1199.7288	1198.7215	1198.7073	0.0142	18 -	27	1	36	EIPPRLLYAK
1320.5977	1319.5904	1319.5717	0.0188	195 -	205	0	---	SMGDDHFWAVR
1336.6028	1335.5955	1335.5666	0.0290	195 -	205	0	---	SMGDDHFWAVR + Oxidation (M)
1340.6198	1339.6125	1339.5792	0.0333	83 -	94	0	---	SGGHDYEGLSYR
1475.8070	1474.7997	1474.7779	0.0218	28 -	41	0	103	SSPAYPSVLGQTIR
1475.8070	1474.7997	1474.7779	0.0218	28 -	41	0	---	SSPAYPSVLGQTIR
1832.9880	1831.9807	1831.9540	0.0267	28 -	44	1	---	SSPAYPSVLGQTIRNSR
1832.9880	1831.9807	1831.9540	0.0267	28 -	44	1	66	SSPAYPSVLGQTIRNSR
1847.9949	1846.9876	1846.9611	0.0266	95 -	110	1	---	SLQPETFAVVDLNKMR
1847.9949	1846.9876	1846.9611	0.0266	95 -	110	1	62	SLQPETFAVVDLNKMR
1863.9833	1862.9760	1862.9560	0.0201	95 -	110	1	---	SLQPETFAVVDLNKMR + Oxidation (M)
1888.9153	1887.9080	1887.8825	0.0255	419 -	433	1	---	DIYNYMEPYVSKNPR
1904.9189	1903.9116	1903.8774	0.0342	419 -	433	1	---	DIYNYMEPYVSKNPR + Oxidation (M)

No match to: 768.5497, 1561.8572, 1659.8685, 2317.2444, 2445.3513, 2608.4097, 2608.4097, 2808.3555

5. gi|82492267 **Mass:** 58590 **Score:** 397 **Expect:** 1.2e-034 **Queries matched:** 18

major pollen allergen Phl p 4 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
885.4393	884.4320	884.4140	0.0180	459 -	465	0	---	QAYANYR
1001.5771	1000.5698	1000.5453	0.0245	136 -	144	1	---	AVWVDGKAR
1060.5387	1059.5314	1059.5137	0.0177	491 -	498	1	---	YFKGNFER
1197.6237	1196.6164	1196.5825	0.0339	504 -	513	1	---	GKVDPTDYFR
1199.7288	1198.7215	1198.7073	0.0142	43 -	52	1	---	EIPPRLLYAK
1199.7288	1198.7215	1198.7073	0.0142	43 -	52	1	36	EIPPRLLYAK
1320.5977	1319.5904	1319.5717	0.0188	220 -	230	0	---	SMGDDHFWAVR
1336.6028	1335.5955	1335.5666	0.0290	220 -	230	0	---	SMGDDHFWAVR + Oxidation (M)
1340.6198	1339.6125	1339.5792	0.0333	108 -	119	0	---	SGGHDYEGLSYR
1475.8070	1474.7997	1474.7779	0.0218	53 -	66	0	103	SSPAYPSVLGQTIR

1475.8070	1474.7997	1474.7779	0.0218	53 - 66	0	---	SSPAYPSVLGQTIR
1832.9880	1831.9807	1831.9540	0.0267	53 - 69	1	---	SSPAYPSVLGQTIRNSR
1832.9880	1831.9807	1831.9540	0.0267	53 - 69	1	66	SSPAYPSVLGQTIRNSR
1847.9949	1846.9876	1846.9611	0.0266	120 - 135	1	---	SLQPETFAVVDLNKMR
1847.9949	1846.9876	1846.9611	0.0266	120 - 135	1	62	SLQPETFAVVDLNKMR
1863.9833	1862.9760	1862.9560	0.0201	120 - 135	1	---	SLQPETFAVVDLNKMR + Oxidation (M)
1888.9153	1887.9080	1887.8825	0.0255	444 - 458	1	---	DIYNYMEPYVSKNPR
1904.9189	1903.9116	1903.8774	0.0342	444 - 458	1	---	DIYNYMEPYVSKNPR + Oxidation (M)

No match to: 768.5497, 1561.8572, 1659.8685, 2317.2444, 2445.3513, 2608.4097, 2608.4097, 2808.3555

6. gi|54144332 **Mass:** 56979 **Score:** 294 **Expect:** 2.4e-024 **Queries matched:** 13

pollen allergen Phl p 4 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
885.4393	884.4320	884.4140	0.0180	442 - 448		0	---	QAYANYR
1001.5771	1000.5698	1000.5453	0.0245	119 - 127		1	---	AVWVDGKAR
1197.6237	1196.6164	1196.5825	0.0339	487 - 496		1	---	GKVDPTDYFR
1199.7288	1198.7215	1198.7073	0.0142	26 - 35		1	---	EIPPRLLYAK
1199.7288	1198.7215	1198.7073	0.0142	26 - 35		1	36	EIPPRLLYAK
1320.5977	1319.5904	1319.5717	0.0188	203 - 213		0	---	SMGDDHFWAVR
1336.6028	1335.5955	1335.5666	0.0290	203 - 213		0	---	SMGDDHFWAVR + Oxidation (M)
1340.6198	1339.6125	1339.5792	0.0333	91 - 102		0	---	SGGHDYEGLSYR
1475.8070	1474.7997	1474.7779	0.0218	36 - 49		0	103	SSPAYPSVLGQTIR
1475.8070	1474.7997	1474.7779	0.0218	36 - 49		0	---	SSPAYPSVLGQTIR
1561.8572	1560.8499	1560.8035	0.0465	103 - 116		0	---	SLQPEEFAVVDLSK
1832.9880	1831.9807	1831.9540	0.0267	36 - 52		1	---	SSPAYPSVLGQTIRNSR
1832.9880	1831.9807	1831.9540	0.0267	36 - 52		1	66	SSPAYPSVLGQTIRNSR

No match to: 768.5497, 1060.5387, 1659.8685, 1847.9949, 1847.9949, 1863.9833, 1888.9153, 1904.9189, 2317.2444, 2445.3513, 2608.4097, 2608.4097, 2808.3555

7. gi|189014266 **Mass:** 56147 **Score:** 293 **Expect:** 3e-024 **Queries matched:** 13

pollen allergen Phl p 4.0102 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
885.4393	884.4320	884.4140	0.0180	434 - 440		0	---	QAYANYR
1001.5771	1000.5698	1000.5453	0.0245	111 - 119		1	---	AVWVDGKAR
1197.6237	1196.6164	1196.5825	0.0339	479 - 488		1	---	GKVDPTDYFR
1199.7288	1198.7215	1198.7073	0.0142	18 - 27		1	---	EIPPRLLYAK
1199.7288	1198.7215	1198.7073	0.0142	18 - 27		1	36	EIPPRLLYAK
1320.5977	1319.5904	1319.5717	0.0188	195 - 205		0	---	SMGDDHFWAVR
1336.6028	1335.5955	1335.5666	0.0290	195 - 205		0	---	SMGDDHFWAVR + Oxidation (M)
1340.6198	1339.6125	1339.5792	0.0333	83 - 94		0	---	SGGHDYEGLSYR
1475.8070	1474.7997	1474.7779	0.0218	28 - 41		0	103	SSPAYPSVLGQTIR

1475.8070	1474.7997	1474.7779	0.0218	28 - 41	0	---	SSPAYPSVLGQTIR
1561.8572	1560.8499	1560.8035	0.0465	95 - 108	0	---	SLQPEEFAVVDLSK
1832.9880	1831.9807	1831.9540	0.0267	28 - 44	1	---	SSPAYPSVLGQTIRNSR
1832.9880	1831.9807	1831.9540	0.0267	28 - 44	1	66	SSPAYPSVLGQTIRNSR

No match to: 768.5497, 1060.5387, 1659.8685, 1847.9949, 1847.9949, 1863.9833, 1888.9153, 1904.9189, 2317.2444, 2445.3513, 2608.4097, 2608.4097, 2808.3555

8. gi|2244938 **Mass:** 67168 **Score:** 53 **Expect:** 3.2 **Queries matched:** 9

hypothetical protein [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
885.4393	884.4320	884.4351	-0.0031	278 - 285		1	---	EAHKSEGK
1060.5387	1059.5314	1059.5066	0.0249	87 - 94		1	---	AMMLHNRR + 2 Oxidation (M)
1475.8070	1474.7997	1474.7052	0.0946	388 - 399		0	---	NPEEQLQESVFR
1475.8070	1474.7997	1474.7052	0.0946	388 - 399		0	---	NPEEQLQESVFR
1863.9833	1862.9760	1862.9737	0.0023	549 - 565		1	---	DLYEEVSSGGKNVIVVR
1904.9189	1903.9116	1903.8911	0.0205	384 - 399		1	---	DGEKNPEEQLQESVFR
2317.2444	2316.2371	2316.1170	0.1202	59 - 77		1	---	YTKDDLCEAFVAMEVIVWK
2608.4097	2607.4024	2607.3543	0.0481	31 - 55		1	---	GFSESTVAAARIETIPGFSDSIKPK
2608.4097	2607.4024	2607.3543	0.0481	31 - 55		1	---	GFSESTVAAARIETIPGFSDSIKPK

No match to: 768.5497, 1001.5771, 1197.6237, 1199.7288, 1199.7288, 1320.5977, 1336.6028, 1340.6198, 1561.8572, 1659.8685, 1832.9880, 1832.9880, 1847.9949, 1847.9949, 1888.9153, 2445.3513, 2808.3555

9. gi|145348829 **Mass:** 28139 **Score:** 49 **Expect:** 8.6 **Queries matched:** 7

predicted protein [Ostreococcus lucimarinus CCE9901]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1060.5387	1059.5314	1059.5672	-0.0358	61 - 70		1	---	TVVDGTKNAR
1475.8070	1474.7997	1474.7173	0.0824	12 - 23		1	---	RIHELGMFAMDR
1475.8070	1474.7997	1474.7173	0.0824	12 - 23		1	---	RIHELGMFAMDR
1832.9880	1831.9807	1831.8709	0.1099	13 - 27		1	---	IHELGMFAMDRIDPR + 2 Oxidation (M)
1832.9880	1831.9807	1831.8709	0.1099	13 - 27		1	---	IHELGMFAMDRIDPR + 2 Oxidation (M)
1904.9189	1903.9116	1903.9486	-0.0370	122 - 140		1	---	TTDEAAAKAVEADVLGSTR
2445.3513	2444.3440	2444.2984	0.0456	33 - 55		1	---	EMPKILSSVEIVYPSGVDVGAVR

No match to: 768.5497, 885.4393, 1001.5771, 1197.6237, 1199.7288, 1199.7288, 1320.5977, 1336.6028, 1340.6198, 1561.8572, 1659.8685, 1847.9949, 1847.9949, 1863.9833, 1888.9153, 2317.2444, 2608.4097, 2608.4097, 2808.3555

10. gi|218194159 **Mass:** 74490 **Score:** 47 **Expect:** 11 **Queries matched:** 10

hypothetical protein OsI_14434 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
885.4393	884.4320	884.4796	-0.0475	386 - 392		0	---	YPAFLFK
1832.9880	1831.9807	1831.9964	-0.0157	143 - 158		1	---	LKALVVSLETNIEEMK + Oxidation (M)
1832.9880	1831.9807	1831.9964	-0.0157	143 - 158		1	---	LKALVVSLETNIEEMK + Oxidation (M)
1847.9949	1846.9876	1846.9709	0.0167	145 - 160		1	---	ALVVSLETNIEEMKQK + Oxidation (M)

1847.9949	1846.9876	1846.9709	0.0167	145 - 160	1	---	ALVVSLETNIEEMKQK + Oxidation (M)
1888.9153	1887.9080	1887.9724	-0.0643	369 - 385	1	---	ASNITVDMDLVRQVEAK
1904.9189	1903.9116	1903.9673	-0.0556	369 - 385	1	---	ASNITVDMDLVRQVEAK + Oxidation (M)
2445.3513	2444.3440	2444.1787	0.1653	187 - 207	1	---	SMMQSLQEKLNSTEAENHVLR
2608.4097	2607.4024	2607.3558	0.0466	386 - 407	1	---	YPAFLFKQQLTAFVEGLYGMIR + Oxidation (M)
2608.4097	2607.4024	2607.3558	0.0466	386 - 407	1	---	YPAFLFKQQLTAFVEGLYGMIR + Oxidation (M)

No match to: 768.5497, 1001.5771, 1060.5387, 1197.6237, 1199.7288, 1199.7288, 1320.5977, 1336.6028, 1340.6198, 1475.8070, 1475.8070, 1561.8572, 1659.8685, 1863.9833, 2317.2444, 2808.3555

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 26

Protein View

Match to: **gi|54144334** Score: **399** Expect: **7.6e-035**
pollen allergen Phl p 4 [Phleum pratense]

Nominal mass (M_r): **56741**; Calculated pI value: **9.16**
NCBI BLAST search of gi|54144334 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **22%**

Matched peptides shown in **Bold Red**

```
   1 SSCQVAFSYF PPPAAKEDFL GCLVKEIPPR LLYAKSSPAY PSVLGQTIRN
  51 SRWSSPDNVK PLYIITPTNV SHIQSAVVCG RRHSVRIRVR SGGHDYEGLS
 101 YRSLQPETFA VVDLNKMRAV WVDGKARTAW VDSGAQLGEL YYAIYKASPT
 151 LAFPAGVCPT IGVGGNFAGG GFGMLLRKYG IAAENVIDVK LVDANGKLHD
 201 KKSMGDDHFW AVRGGGGESF GIVVAWQVKL LPVPPTVTIF KISKTVSEGA
 251 VDIINKWQVV APQLPADLMI RIIAQGPKAT FEAMYLGTCK TLTPLMSSKF
 301 PELGMNPSHC NEMSWIQSIP FVHLGHRDAL EDDLLNRNNS FKPFAEYKSD
 351 YVYQPFPKTV WEQILNTWLV KPGAGIMIFD PYGATISATP ESATPFPHRK
 401 GVLFNIQYVN YWFAPGAAAA PLSWSKDIYN YMEPYVSKNP RQAYANYRDI
 451 DLGRNEVVND VSTYASGKVW GQKYFKGNFE RLAITKGKVD PTDYFRNEQS
 501 IPPLIKKY
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
26 - 35	1199.7288	1198.7215	1198.7073	0.0142	1	**EIPPRLLYAK** (No match)
26 - 35	1199.7288	1198.7215	1198.7073	0.0142	1	**EIPPRLLYAK** (Ions score 36)
36 - 49	1475.8070	1474.7997	1474.7779	0.0218	0	**SSPAYPSVLGQTIR** (Ions score 103)
36 - 49	1475.8070	1474.7997	1474.7779	0.0218	0	**SSPAYPSVLGQTIR** (No match)
36 - 52	1832.9880	1831.9807	1831.9540	0.0267	1	**SSPAYPSVLGQTIRNSR** (No match)
36 - 52	1832.9880	1831.9807	1831.9540	0.0267	1	**SSPAYPSVLGQTIRNSR** (Ions score 66)
91 - 102	1340.6198	1339.6125	1339.5792	0.0333	0	**SGGHDYEGLSYR** (No match)
103 - 118	1847.9949	1846.9876	1846.9611	0.0266	1	**SLQPETFAVVDLNKMR** (No match)
103 - 118	1847.9949	1846.9876	1846.9611	0.0266	1	**SLQPETFAVVDLNKMR** (Ions score 62)
103 - 118	1863.9833	1862.9760	1862.9560	0.0201	1	**SLQPETFAVVDLNKMR** Oxidation (M) (No match)
119 - 127	1001.5771	1000.5698	1000.5453	0.0245	1	**AVWVDGKAR** (No match)
203 - 213	1320.5977	1319.5904	1319.5717	0.0188	0	**SMGDDHFWAVR** (No match)
203 - 213	1336.6028	1335.5955	1335.5666	0.0290	0	**SMGDDHFWAVR** Oxidation (M) (No match)
427 - 441	1888.9153	1887.9080	1887.8825	0.0255	1	**DIYNYMEPYVSKNPR** (No match)
427 - 441	1904.9189	1903.9116	1903.8774	0.0342	1	**DIYNYMEPYVSKNPR** Oxidation (M) (No match)
442 - 448	885.4393	884.4320	884.4140	0.0180	0	**QAYANYR** (No match)
474 - 481	1060.5387	1059.5314	1059.5137	0.0177	1	**YFKGNFER** (No match)
487 - 496	1197.6237	1196.6164	1196.5825	0.0339	1	**GKVDPTDYFR** (No match)

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	Accession	Mass	Score	Description
1.	gi|4826572	42579	133	polygalacturonase [Phleum pratense]
2.	gi|89257456	23442	45	hypothetical protein 24.t00034 [Brassica oleracea]
3.	gi|157352945	28636	44	unnamed protein product [Vitis vinifera]
4.	gi|222637196	39314	42	hypothetical protein OsJ_24578 [Oryza sativa Japonica Group]
5.	gi|168009401	18535	41	predicted protein [Physcomitrella patens subsp. patens]

Results List

1. gi|4826572 **Mass:** 42579 **Score:** 133 **Expect:** 3e-008 **Queries matched:** 14

polygalacturonase [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
866.4921	865.4848	865.4545	0.0303	288	294	0	---	LTYENVK
1032.5355	1031.5282	1031.5222	0.0060	101	108	0	---	ANWIEIMR
1048.5221	1047.5148	1047.5171	-0.0023	101	108	0	---	ANWIEIMR + Oxidation (M)
1064.6129	1063.6056	1063.6025	0.0031	323	331	1	---	VTVKDVTFR
1323.6919	1322.6846	1322.6805	0.0041	99	108	1	---	YKANWIEIMR
1323.6919	1322.6846	1322.6805	0.0041	99	108	1	13	YKANWIEIMR
1339.6820	1338.6747	1338.6754	-0.0007	99	108	1	---	YKANWIEIMR + Oxidation (M)
1339.6820	1338.6747	1338.6754	-0.0007	99	108	1	(11)	YKANWIEIMR + Oxidation (M)
1388.6094	1387.6021	1387.6053	-0.0031	166	175	0	71	FFHMNIYECK
1388.6094	1387.6021	1387.6053	-0.0031	166	175	0	---	FFHMNIYECK
1404.6180	1403.6107	1403.6002	0.0106	166	175	0	---	FFHMNIYECK + Oxidation (M)
1520.7656	1519.7583	1519.7592	-0.0009	295	307	0	---	MEDVGYPIIIDQK
2368.2092	2367.2019	2367.2031	-0.0012	288	307	1	---	LTYENVKMEDVGYPIIIDQK
2384.2161	2383.2088	2383.1980	0.0108	288	307	1	---	LTYENVKMEDVGYPIIIDQK + Oxidation (M)

No match to: 713.4069, 724.4938, 736.4924, 750.5172, 768.5211, 838.5248, 864.5213, 1199.7067, 1279.7648, 1303.7540, 1334.8795, 1355.6735, 1448.9131, 1475.7852, 1553.8090, 1618.0675, 1682.9750, 1756.8140, 1756.8140, 1832.9614, 2107.0872, 2168.1404, 2296.2239, 2296.2239, 2333.1372, 2564.1990, 2782.4028, 2923.3806, 2985.4529

2. gi|89257456 **Mass:** 23442 **Score:** 45 **Expect:** 20 **Queries matched:** 6

hypothetical protein 24.t00034 [Brassica oleracea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
866.4921	865.4848	865.4545	0.0304	177	184	0	---	SFGLVESK
1048.5221	1047.5148	1047.4767	0.0381	135	143	1	---	RSPSNNMDK
1475.7852	1474.7779	1474.7528	0.0251	124	135	1	---	WESVVQTSVERR
2168.1404	2167.1331	2167.1021	0.0310	155	175	0	---	QVAGAAWVLSDSSGHVLLDSR
2296.2239	2295.2166	2295.1971	0.0196	154	175	1	---	KQVAGAAWVLSDSSGHVLLDSR

2296.2239	2295.2166	2295.1971	0.0196	154 - 175	1	---	KQVAGAAWVLSDSSGHVLLDSR

No match to: 713.4069, 724.4938, 736.4924, 750.5172, 768.5211, 838.5248, 864.5213, 1032.5355, 1064.6129, 1199.7067, 1279.7648, 1303.7540, 1323.6919, 1323.6919, 1334.8795, 1339.6820, 1339.6820, 1355.6735, 1388.6094, 1388.6094, 1404.6180, 1448.9131, 1520.7656, 1553.8090, 1618.0675, 1682.9750, 1756.8140, 1756.8140, 1832.9614, 2107.0872, 2333.1372, 2368.2092, 2384.2161, 2564.1990, 2782.4028, 2923.3806, 2985.4529

3. gi|157352945 **Mass:** 28636 **Score:** 44 **Expect:** 25 **Queries matched:** 5

unnamed protein product [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1475.7852	1474.7779	1474.7204	0.0575	162 -	173	1	---	GSKEIYFQQYGR
1553.8090	1552.8017	1552.7820	0.0197	50 -	62	1	---	STFPDLMNFRVAR
1832.9614	1831.9541	1831.9117	0.0424	165 -	178	1	---	EIYFQQYGRHNIHK
2333.1372	2332.1299	2332.2096	-0.0796	24 -	46	0	---	VLSPDGGLGLLSVCGFGSLLSER
2564.1990	2563.1917	2563.2165	-0.0248	139 -	159	1	---	LFTTPAVLCARYSDEEFFQNR

No match to: 713.4069, 724.4938, 736.4924, 750.5172, 768.5211, 838.5248, 864.5213, 866.4921, 1032.5355, 1048.5221, 1064.6129, 1199.7067, 1279.7648, 1303.7540, 1323.6919, 1323.6919, 1334.8795, 1339.6820, 1339.6820, 1355.6735, 1388.6094, 1388.6094, 1404.6180, 1448.9131, 1520.7656, 1618.0675, 1682.9750, 1756.8140, 1756.8140, 2107.0872, 2168.1404, 2296.2239, 2296.2239, 2368.2092, 2384.2161, 2782.4028, 2923.3806, 2985.4529

4. gi|222637196 **Mass:** 39314 **Score:** 42 **Expect:** 36 **Queries matched:** 7

hypothetical protein OsJ_24578 [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
866.4921	865.4848	865.5133	-0.0285	163 -	169	1	---	VVHRDLK
1303.7540	1302.7467	1302.7142	0.0325	72 -	84	1	---	LSKSSAQGVGELK
1339.6820	1338.6747	1338.6931	-0.0184	46 -	58	1	---	NKLGEGGFGAVYK
1339.6820	1338.6747	1338.6931	-0.0184	46 -	58	1	---	NKLGEGGFGAVYK
1832.9614	1831.9541	1831.9172	0.0370	167 -	182	1	---	DLKASNILLDMNMNPK + Oxidation (M)
2168.1404	2167.1331	2167.1749	-0.0417	144 -	162	1	---	IINGIARGLQYLHEDSQLK
2368.2092	2367.2019	2367.1009	0.1010	332 -	359	1	---	RNGGTGGAGASSGGTSSGTSTAASVQGK

No match to: 713.4069, 724.4938, 736.4924, 750.5172, 768.5211, 838.5248, 864.5213, 1032.5355, 1048.5221, 1064.6129, 1199.7067, 1279.7648, 1323.6919, 1323.6919, 1334.8795, 1355.6735, 1388.6094, 1388.6094, 1404.6180, 1448.9131, 1475.7852, 1520.7656, 1553.8090, 1618.0675, 1682.9750, 1756.8140, 1756.8140, 2107.0872, 2296.2239, 2296.2239, 2333.1372, 2384.2161, 2564.1990, 2782.4028, 2923.3806, 2985.4529

5. gi|168009401 **Mass:** 18535 **Score:** 41 **Expect:** 45 **Queries matched:** 7

predicted protein [Physcomitrella patens subsp. patens]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1323.6919	1322.6846	1322.6553	0.0293	56 -	66	1	---	SRWVGFVADMR
1323.6919	1322.6846	1322.6553	0.0293	56 -	66	1	---	SRWVGFVADMR
1339.6820	1338.6747	1338.6502	0.0245	56 -	66	1	---	SRWVGFVADMR + Oxidation (M)
1339.6820	1338.6747	1338.6502	0.0245	56 -	66	1	---	SRWVGFVADMR + Oxidation (M)
1355.6735	1354.6662	1354.6741	-0.0079	2 -	13	0	---	EQWGPRPATTGR
2384.2161	2383.2088	2383.1815	0.0274	1 -	22	1	---	MEQWGPRPATTGRTGTSGPLQR

2782.4028 2781.3955 2781.3108 0.0847 32 - 55 1 --- NGEGPDPASISCPLRLRPCCEQLR

No match to: 713.4069, 724.4938, 736.4924, 750.5172, 768.5211, 838.5248, 864.5213, 866.4921, 1032.5355, 1048.5221, 1064.6129, 1199.7067, 1279.7648, 1303.7540, 1334.8795, 1388.6094, 1388.6094, 1404.6180, 1448.9131, 1475.7852, 1520.7656, 1553.8090, 1618.0675, 1682.9750, 1756.8140, 1756.8140, 1832.9614, 2107.0872, 2168.1404, 2296.2239, 2296.2239, 2333.1372, 2368.2092, 2564.1990, 2923.3806, 2985.4529

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 43

Protein View

Match to: **gi|4826572** Score: **133** Expect: **3e-008**
polygalacturonase [Phleum pratense]

Nominal mass (M_r): **42579**; Calculated pI value: **7.83**
NCBI BLAST search of gi|4826572 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **12%**

Matched peptides shown in **Bold Red**

```
   1 GKKEEKKEEK KESGDAASGA DGTYDITKLG AKPDGKTDCT KEVEEAWASA
  51 CGGTGKNTIV IPKGDFLTGP LNFTGPCKGD SVTIKLDGNL LSSNDLAKYK
 101 ANWIEIMRIK KLTITGKGTL DGQGKAVWGK NSCAKNYNCK ILPNTLVLDF
 151 CDDALIEGIT LLNAKFFHMN IYECKGVTVK DVTITAPGDS PNTDGIHIGD
 201 SSKVTITDTT IGTGDDCISI GPGSTGLNIT GVTCGPGHGI SVGSLGRYKD
 251 EKDVTDITVK NCVLKKSTNG LRIKSYEDAK SPLTASKLTY ENVKMEDVGY
 301 PIIIDQKYCP NKICTSKGDS ARVTVKDVTF RNITGTSSTP EAVSLLCSDK
 351 QPCNGVTMND VKIEYSGTNN KTMAVCTNAK VTAKGVSEAN TCAA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
99 - 108	1323.6919	1322.6846	1322.6805	0.0041	1	**YKANWIEIMR** (No match)
99 - 108	1323.6919	1322.6846	1322.6805	0.0041	1	**YKANWIEIMR** (Ions score 13)
99 - 108	1339.6820	1338.6747	1338.6754	-0.0007	1	**YKANWIEIMR** Oxidation (M) (No match)
99 - 108	1339.6820	1338.6747	1338.6754	-0.0007	1	**YKANWIEIMR** Oxidation (M) (Ions score 11)
101 - 108	1032.5355	1031.5282	1031.5222	0.0060	0	**ANWIEIMR** (No match)
101 - 108	1048.5221	1047.5148	1047.5171	-0.0023	0	**ANWIEIMR** Oxidation (M) (No match)
166 - 175	1388.6094	1387.6021	1387.6053	-0.0031	0	**FFHMNIYECK** (Ions score 71)
166 - 175	1388.6094	1387.6021	1387.6053	-0.0031	0	**FFHMNIYECK** (No match)
166 - 175	1404.6180	1403.6107	1403.6002	0.0106	0	**FFHMNIYECK** Oxidation (M) (No match)
288 - 294	866.4921	865.4848	865.4545	0.0303	0	**LTYENVK** (No match)
288 - 307	2368.2092	2367.2019	2367.2031	-0.0012	1	**LTYENVKMEDVGYPIIIDQK** (No match)
288 - 307	2384.2161	2383.2088	2383.1980	0.0108	1	**LTYENVKMEDVGYPIIIDQK** Oxidation (M) (No match)
295 - 307	1520.7656	1519.7583	1519.7592	-0.0009	0	**MEDVGYPIIIDQK** (No match)
323 - 331	1064.6129	1063.6056	1063.6025	0.0031	1	**VTVKDVTFR** (No match)

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	Accession	Mass	Score	Description
1.	gi|4826572	42579	121	polygalacturonase [Phleum pratense]
2.	gi|51458190	22454	65	ribosomal protein small subunit 4 [Asplenium theciferum]
3.	gi|157338773	67512	39	unnamed protein product [Vitis vinifera]
4.	gi|145341167	33229	38	predicted protein [Ostreococcus lucimarinus CCE9901]
5.	gi|158979033	55961	36	menthofuran synthase [Mentha arvensis]
6.	gi|205686197	2335	35	RecName: Full=Pollen allergen Beta v 1; AltName: Allergen=Beta v 1
7.	gi|147816687	19465	35	hypothetical protein [Vitis vinifera]
8.	gi|145351165	7997	35	predicted protein [Ostreococcus lucimarinus CCE9901]
9.	gi|30349136	28393	35	STF-1 [Triticum monococcum]
10.	gi|147782427	42646	35	hypothetical protein [Vitis vinifera]

Results List

1. gi|4826572 **Mass:** 42579 **Score:** 121 **Expect:** 4.8e-007 **Queries matched:** 16

polygalacturonase [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1032.5328	1031.5255	1031.5222	0.0033	101	108	0	---	ANWIEIMR
1048.5223	1047.5150	1047.5171	-0.0021	101	108	0	---	ANWIEIMR + Oxidation (M)
1064.6063	1063.5990	1063.6025	-0.0035	323	331	1	---	VTVKDVTFR
1323.6919	1322.6846	1322.6805	0.0041	99	108	1	5	YKANWIEIMR
1323.6919	1322.6846	1322.6805	0.0041	99	108	1	---	YKANWIEIMR
1339.6818	1338.6745	1338.6754	-0.0009	99	108	1	---	YKANWIEIMR + Oxidation (M)
1339.6818	1338.6745	1338.6754	-0.0009	99	108	1	---	YKANWIEIMR + Oxidation (M)
1388.6149	1387.6076	1387.6053	0.0024	166	175	0	---	FFHMNIYECK
1404.6091	1403.6018	1403.6002	0.0017	166	175	0	---	FFHMNIYECK + Oxidation (M)
1404.6091	1403.6018	1403.6002	0.0017	166	175	0	46	FFHMNIYECK + Oxidation (M)
1520.7626	1519.7553	1519.7592	-0.0039	295	307	0	---	MEDVGYPIIIDQK
1536.7584	1535.7511	1535.7541	-0.0030	295	307	0	---	MEDVGYPIIIDQK + Oxidation (M)
1785.8330	1784.8257	1784.8064	0.0193	11	28	1	---	KESGDAASGADGTYDITK
2368.2346	2367.2273	2367.2031	0.0242	288	307	1	---	LTYENVKMEDVGYPIIIDQK
2384.2300	2383.2227	2383.1980	0.0247	288	307	1	---	LTYENVKMEDVGYPIIIDQK + Oxidation (M)
2781.4192	2780.4119	2780.3828	0.0292	176	203	1	---	GVTVKDVTITAPGDSPNTDGIHIGDSSK

No match to: 713.4088, 724.4930, 734.4893, 736.5028, 750.5183, 768.5239, 886.9948, 1303.7548, 1307.7356, 1334.8832, 1355.6758, 1448.9238, 1553.8009, 1618.0693, 1732.1025, 1756.8175, 1756.8175, 1902.2510, 2091.9736, 2168.1392, 2296.2278, 2296.2278, 2333.1631, 2772.5083, 2895.4133, 2923.3718, 2985.4812

2. gi|51458190 **Mass:** 22454 **Score:** 65 **Expect:** 0.21 **Queries matched:** 6

ribosomal protein small subunit 4 [Asplenium theciferum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1303.7548	1302.7475	1302.7156	0.0319	133	143	1	---	NRPTSFNALRK
1536.7584	1535.7511	1535.7289	0.0222	6	20	0	---	DLPGFMGGGETTNLK
2168.1392	2167.1319	2167.1160	0.0159	176	193	0	---	ESINLNINELLVVEYYSR
2296.2278	2295.2205	2295.1607	0.0598	151	171	0	---	TPDHLTFALSEGDRPTGLVNR
2296.2278	2295.2205	2295.2110	0.0096	176	194	1	---	ESINLNINELLVVEYYSRK
2895.4133	2894.4060	2894.4885	-0.0825	145	171	1	---	SLVGDKTPDHLTFALSEGDRPTGLVNR

No match to: 713.4088, 724.4930, 734.4893, 736.5028, 750.5183, 768.5239, 886.9948, 1032.5328, 1048.5223, 1064.6063, 1307.7356, 1323.6919, 1323.6919, 1334.8832, 1339.6818, 1339.6818, 1355.6758, 1388.6149, 1404.6091, 1404.6091, 1448.9238, 1520.7626, 1553.8009, 1618.0693, 1732.1025, 1756.8175, 1756.8175, 1785.8330, 1902.2510, 2091.9736, 2333.1631, 2368.2346, 2384.2300, 2772.5083, 2781.4192, 2923.3718, 2985.4812

3. gi|157338773 **Mass:** 67512 **Score:** 39 **Expect:** 71 **Queries matched:** 8

unnamed protein product [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1307.7356	1306.7283	1306.6954	0.0329	558	568	1	---	MAVNFKDLLEK
1323.6919	1322.6846	1322.6904	-0.0057	558	568	1	---	MAVNFKDLLEK + Oxidation (M)
1323.6919	1322.6846	1322.6904	-0.0057	558	568	1	---	MAVNFKDLLEK + Oxidation (M)
1520.7626	1519.7553	1519.7113	0.0440	69	83	1	---	GLSSKNDSLEGNGDK
2091.9736	2090.9663	2090.9194	0.0469	43	58	1	---	YGDSWYLRHDETEHQR
2368.2346	2367.2273	2367.2191	0.0083	351	369	1	---	NHLCLVFESLHMNLREVLK + Oxidation (M)
2772.5083	2771.5010	2771.3952	0.1058	27	50	1	---	TTLASVESLTMPLVNRYGDSWYLR
2781.4192	2780.4119	2780.3771	0.0348	398	421	1	---	NCGVLHCDIKPDNMLVNEAKNVLK

No match to: 713.4088, 724.4930, 734.4893, 736.5028, 750.5183, 768.5239, 886.9948, 1032.5328, 1048.5223, 1064.6063, 1303.7548, 1334.8832, 1339.6818, 1339.6818, 1355.6758, 1388.6149, 1404.6091, 1404.6091, 1448.9238, 1536.7584, 1553.8009, 1618.0693, 1732.1025, 1756.8175, 1756.8175, 1785.8330, 1902.2510, 2168.1392, 2296.2278, 2296.2278, 2333.1631, 2384.2300, 2895.4133, 2923.3718, 2985.4812

4. gi|145341167 **Mass:** 33229 **Score:** 38 **Expect:** 94 **Queries matched:** 4

predicted protein [Ostreococcus lucimarinus CCE9901]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1339.6818	1338.6745	1338.6640	0.0106	4	16	1	13	EGDPNGASRAPLR
1339.6818	1338.6745	1338.6640	0.0106	4	16	1	---	EGDPNGASRAPLR
2772.5083	2771.5010	2771.4890	0.0120	150	175	1	---	LAACGIYEVVKLENILVGGEEVLAGR
2985.4812	2984.4739	2984.3643	0.1096	191	218	0	---	VDVVPDEVMHVGDSWTADMVGAENAGLR + Oxidation (M)

No match to: 713.4088, 724.4930, 734.4893, 736.5028, 750.5183, 768.5239, 886.9948, 1032.5328, 1048.5223, 1064.6063, 1303.7548, 1307.7356, 1323.6919, 1323.6919, 1334.8832, 1355.6758, 1388.6149, 1404.6091, 1404.6091, 1448.9238, 1520.7626, 1536.7584, 1553.8009, 1618.0693, 1732.1025, 1756.8175, 1756.8175, 1785.8330, 1902.2510, 2091.9736, 2168.1392, 2296.2278, 2296.2278, 2333.1631, 2368.2346, 2384.2300, 2781.4192, 2895.4133, 2923.3718

5. gi|158979033 **Mass:** 55961 **Score:** 36 **Expect:** 1.4e+002 **Queries matched:** 6

menthofuran synthase [Mentha arvensis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide

1048.5223	1047.5150	1047.4720	0.0430	333 - 342	0	---	GGITEDDVDK
1064.6063	1063.5990	1063.5848	0.0142	343 - 351	1	---	MPYLRAVSK
1785.8330	1784.8257	1784.8495	-0.0237	114 - 128	1	---	DVAFAAYGEHWRHAR
2168.1392	2167.1319	2167.0909	0.0410	254 - 272	1	---	KVGDDATTNFVDTLLQFQR
2384.2300	2383.2227	2383.1655	0.0572	255 - 275	1	---	VGDDATTNFVDTLLQFQRESK
2985.4812	2984.4739	2984.5027	-0.0288	287 - 313	0	---	ALILDMFVGGTDTTFAALEWTMAELIR

No match to: 713.4088, 724.4930, 734.4893, 736.5028, 750.5183, 768.5239, 886.9948, 1032.5328, 1303.7548, 1307.7356, 1323.6919, 1323.6919, 1334.8832, 1339.6818, 1339.6818, 1355.6758, 1388.6149, 1404.6091, 1404.6091, 1448.9238, 1520.7626, 1536.7584, 1553.8009, 1618.0693, 1732.1025, 1756.8175, 1756.8175, 1902.2510, 2091.9736, 2296.2278, 2296.2278, 2333.1631, 2368.2346, 2772.5083, 2781.4192, 2895.4133, 2923.3718

6. gi|205686197 **Mass:** 2335 **Score:** 35 **Expect:** 1.7e+002 **Queries matched:** 3

RecName: Full=Pollen allergen Beta v 1; AltName: Allergen=Beta v 1

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1388.6149	1387.6076	1387.5683	0.0394	1 -	11	0	---	VQGMVYCDTCR
1404.6091	1403.6018	1403.5632	0.0387	1 -	11	0	---	VQGMVYCDTCR + Oxidation (M)
1404.6091	1403.6018	1403.5632	0.0387	1 -	11	0	24	VQGMVYCDTCR + Oxidation (M)

No match to: 713.4088, 724.4930, 734.4893, 736.5028, 750.5183, 768.5239, 886.9948, 1032.5328, 1048.5223, 1064.6063, 1303.7548, 1307.7356, 1323.6919, 1323.6919, 1334.8832, 1339.6818, 1339.6818, 1355.6758, 1448.9238, 1520.7626, 1536.7584, 1553.8009, 1618.0693, 1732.1025, 1756.8175, 1756.8175, 1785.8330, 1902.2510, 2091.9736, 2168.1392, 2296.2278, 2296.2278, 2333.1631, 2368.2346, 2384.2300, 2772.5083, 2781.4192, 2895.4133, 2923.3718, 2985.4812

7. gi|147816687 **Mass:** 19465 **Score:** 35 **Expect:** 1.8e+002 **Queries matched:** 5

hypothetical protein [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1388.6149	1387.6076	1387.6441	-0.0365	158 - 169		1	---	DYVDRLGLGSFM + Oxidation (M)
2168.1392	2167.1319	2167.1632	-0.0313	131 - 149		0	---	TMVIEHVSIELMIVDPLTK
2296.2278	2295.2205	2295.2582	-0.0376	130 - 149		1	---	KTMVIEHVSIELMIVDPLTK
2296.2278	2295.2205	2295.2582	-0.0376	130 - 149		1	---	KTMVIEHVSIELMIVDPLTK
2781.4192	2780.4119	2780.4890	-0.0770	131 - 155		1	---	TMVIEHVSIELMIVDPLTKGMPSLK

No match to: 713.4088, 724.4930, 734.4893, 736.5028, 750.5183, 768.5239, 886.9948, 1032.5328, 1048.5223, 1064.6063, 1303.7548, 1307.7356, 1323.6919, 1323.6919, 1334.8832, 1339.6818, 1339.6818, 1355.6758, 1404.6091, 1404.6091, 1448.9238, 1520.7626, 1536.7584, 1553.8009, 1618.0693, 1732.1025, 1756.8175, 1756.8175, 1785.8330, 1902.2510, 2091.9736, 2333.1631, 2368.2346, 2384.2300, 2772.5083, 2895.4133, 2923.3718, 2985.4812

8. gi|145351165 **Mass:** 7997 **Score:** 35 **Expect:** 1.9e+002 **Queries matched:** 3

predicted protein [Ostreococcus lucimarinus CCE9901]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1355.6758	1354.6685	1354.6993	-0.0308	33 -	43	1	---	STEAYRTFRPK
1553.8009	1552.7936	1552.7885	0.0051	8 -	20	1	---	SQTDPLKYGIFER
2091.9736	2090.9663	2091.0061	-0.0397	15 -	32	1	---	YGIFERYASLDAYASTHK

No match to: 713.4088, 724.4930, 734.4893, 736.5028, 750.5183, 768.5239, 886.9948, 1032.5328, 1048.5223,

1064.6063, 1303.7548, 1307.7356, 1323.6919, 1323.6919, 1334.8832, 1339.6818, 1339.6818, 1388.6149, 1404.6091, 1404.6091, 1448.9238, 1520.7626, 1536.7584, 1618.0693, 1732.1025, 1756.8175, 1756.8175, 1785.8330, 1902.2510, 2168.1392, 2296.2278, 2296.2278, 2333.1631, 2368.2346, 2384.2300, 2772.5083, 2781.4192, 2895.4133, 2923.3718, 2985.4812

9. gi|30349136 **Mass:** 28393 **Score:** 35 **Expect:** 2e+002 **Queries matched:** 5

STF-1 [Triticum monococcum]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1756.8175	1755.8102	1755.8614	-0.0511	66	-	81	0	---	SGTTWLNALTFATMAR + Oxidation (M)
1756.8175	1755.8102	1755.8614	-0.0511	66	-	81	0	---	SGTTWLNALTFATMAR + Oxidation (M)
1785.8330	1784.8257	1784.9032	-0.0774	150	-	163	1	---	EPKDMVISQWHFLR
2091.9736	2090.9663	2090.9079	0.0584	125	-	143	0	---	LMNTHMPIDMIMPGGGGCK + 2 Oxidation (M)
2923.3718	2922.3645	2922.4046	-0.0401	117	-	143	1	---	LEALPSPRLMNTHMPIDMIMPGGGGCK

No match to: 713.4088, 724.4930, 734.4893, 736.5028, 750.5183, 768.5239, 886.9948, 1032.5328, 1048.5223, 1064.6063, 1303.7548, 1307.7356, 1323.6919, 1323.6919, 1334.8832, 1339.6818, 1339.6818, 1355.6758, 1388.6149, 1404.6091, 1404.6091, 1448.9238, 1520.7626, 1536.7584, 1553.8009, 1618.0693, 1732.1025, 1902.2510, 2168.1392, 2296.2278, 2296.2278, 2333.1631, 2368.2346, 2384.2300, 2772.5083, 2781.4192, 2895.4133, 2985.4812

10. gi|147782427 **Mass:** 42646 **Score:** 35 **Expect:** 2e+002 **Queries matched:** 7

hypothetical protein [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1048.5223	1047.5150	1047.5600	-0.0450	3	-	11	0	---	NLLLGDEFK
1339.6818	1338.6745	1338.7383	-0.0638	186	-	195	1	---	KGWLLIMHWR
1339.6818	1338.6745	1338.7383	-0.0638	187	-	196	1	---	GWLLIMHWRK
1355.6758	1354.6685	1354.7332	-0.0647	187	-	196	1	---	GWLLIMHWRK + Oxidation (M)
2368.2346	2367.2273	2367.1239	0.1035	29	-	48	0	---	LEGMHDLLDMIWDSDVVVHK + Oxidation (M)
2384.2300	2383.2227	2383.1188	0.1040	29	-	48	0	---	LEGMHDLLDMIWDSDVVVHK + 2 Oxidation (M)
2895.4133	2894.4060	2894.4095	-0.0034	29	-	52	1	---	LEGMHDLLDMIWDSDVVVHKNWVK + Oxidation (M)

No match to: 713.4088, 724.4930, 734.4893, 736.5028, 750.5183, 768.5239, 886.9948, 1032.5328, 1064.6063, 1303.7548, 1307.7356, 1323.6919, 1323.6919, 1334.8832, 1388.6149, 1404.6091, 1404.6091, 1448.9238, 1520.7626, 1536.7584, 1553.8009, 1618.0693, 1732.1025, 1756.8175, 1756.8175, 1785.8330, 1902.2510, 2091.9736, 2168.1392, 2296.2278, 2296.2278, 2333.1631, 2772.5083, 2781.4192, 2923.3718, 2985.4812

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 43

Protein View

Match to: **gi|4826572** Score: **121** Expect: **4.8e-007**
polygalacturonase [Phleum pratense]

Nominal mass (M_r): **42579**; Calculated pI value: **7.83**
NCBI BLAST search of gi|4826572 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **24%**

Matched peptides shown in **Bold Red**

```
     1 GKKEEKKEEK KESGDAASGA DGTYDITKLG AKPDGKTDCT KEVEEAWASA
    51 CGGTGKNTIV IPKGDFLTGP LNFTGPCKGD SVTIKLDGNL LSSNDLAKYK
   101 ANWIEIMRIK KLTITGKGTL DGQGKAVWGK NSCAKNYNCK ILPNTLVLDF
   151 CDDALIEGIT LLNAKFFHMN IYECKGVTVK DVTITAPGDS PNTDGIHIGD
   201 SSKVTITDTT IGTGDDCISI GPGSTGLNIT GVTCGPGHGI SVGSLGRYKD
   251 EKDVTDITVK NCVLKKSTNG LRIKSYEDAK SPLTASKLTY ENVKMEDVGY
   301 PIIIDQKYCP NKICTSKGDS ARVTVKDVTF RNITGTSSTP EAVSLLCSDK
   351 QPCNGVTMND VKIEYSGTNN KTMAVCTNAK VTAKGVSEAN TCAA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
11 - 28	1785.8330	1784.8257	1784.8064	0.0193	1	**KESGDAASGADGTYDITK** (No match)
99 - 108	1323.6919	1322.6846	1322.6805	0.0041	1	**YKANWIEIMR** (Ions score 5)
99 - 108	1323.6919	1322.6846	1322.6805	0.0041	1	**YKANWIEIMR** (No match)
99 - 108	1339.6818	1338.6745	1338.6754	-0.0009	1	**YKANWIEIMR** Oxidation (M) (No match)
99 - 108	1339.6818	1338.6745	1338.6754	-0.0009	1	**YKANWIEIMR** Oxidation (M) (No match)
101 - 108	1032.5328	1031.5255	1031.5222	0.0033	0	**ANWIEIMR** (No match)
101 - 108	1048.5223	1047.5150	1047.5171	-0.0021	0	**ANWIEIMR** Oxidation (M) (No match)
166 - 175	1388.6149	1387.6076	1387.6053	0.0024	0	**FFHMNIYECK** (No match)
166 - 175	1404.6091	1403.6018	1403.6002	0.0017	0	**FFHMNIYECK** Oxidation (M) (No match)
166 - 175	1404.6091	1403.6018	1403.6002	0.0017	0	**FFHMNIYECK** Oxidation (M) (Ions score 46)
176 - 203	2781.4192	2780.4119	2780.3828	0.0292	1	**GVTVKDVTITAPGDSPNTDGIHIGDSSK** (No match)
288 - 307	2368.2346	2367.2273	2367.2031	0.0242	1	**LTYENVKMEDVGYPIIIDQK** (No match)
288 - 307	2384.2300	2383.2227	2383.1980	0.0247	1	**LTYENVKMEDVGYPIIIDQK** Oxidation (M) (No match)
295 - 307	1520.7626	1519.7553	1519.7592	-0.0039	0	**MEDVGYPIIIDQK** (No match)
295 - 307	1536.7584	1535.7511	1535.7541	-0.0030	0	**MEDVGYPIIIDQK** Oxidation (M) (No match)
323 - 331	1064.6063	1063.5990	1063.6025	-0.0035	1	**VTVKDVTFR** (No match)

Spot 35

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	Accession	Mass	Score	Description
1.	gi|4826572	42579	141	polygalacturonase [Phleum pratense]
2.	gi|223539340	9908	46	conserved hypothetical protein [Ricinus communis]
3.	gi|51458190	22454	45	ribosomal protein small subunit 4 [Asplenium theciferum]
4.	gi|21666264	15417	43	ascorbate peroxidase [Triticum aestivum]
5.	gi|115470395	27205	40	Os07g0123300 [Oryza sativa (japonica cultivar-group)]
6.	gi|25992557	41411	40	thylakoid-bound ascorbate peroxidase [Triticum aestivum]
7.	gi|125582491	43582	38	hypothetical protein OsJ_07113 [Oryza sativa Japonica Group]
8.	gi|50725765	44389	38	putative thylakoid-bound ascorbate peroxidase [Oryza sativa Japonica Group]
9.	gi|2160156	123854	38	Strong similarity to S. pombe leucyl-tRNA synthetase (gb|Z73100). [Arabidopsis thaliana]
10.	gi|79339972	124513	38	ATP binding / aminoacyl-tRNA ligase [Arabidopsis thaliana]

Results List

1. gi|4826572 **Mass:** 42579 **Score:** 141 **Expect:** 4.8e-009 **Queries matched:** 16

polygalacturonase [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1032.5315	1031.5242	1031.5222	0.0020	101	108	0	---	ANWIEIMR
1048.5239	1047.5166	1047.5171	-0.0005	101	108	0	---	ANWIEIMR + Oxidation (M)
1064.6011	1063.5938	1063.6025	-0.0087	323	331	1	---	VTVKDVTFR
1120.5594	1119.5521	1119.5495	0.0027	126	135	1	---	AVWGKNSCAK
1323.6957	1322.6884	1322.6805	0.0079	99	108	1	11	YKANWIEIMR
1323.6957	1322.6884	1322.6805	0.0079	99	108	1	---	YKANWIEIMR
1339.6835	1338.6762	1338.6754	0.0008	99	108	1	(1)	YKANWIEIMR + Oxidation (M)
1339.6835	1338.6762	1338.6754	0.0008	99	108	1	---	YKANWIEIMR + Oxidation (M)
1388.6150	1387.6077	1387.6053	0.0025	166	175	0	65	FFHMNIYECK
1388.6150	1387.6077	1387.6053	0.0025	166	175	0	---	FFHMNIYECK
1404.6116	1403.6043	1403.6002	0.0042	166	175	0	---	FFHMNIYECK + Oxidation (M)
1520.7637	1519.7564	1519.7592	-0.0028	295	307	0	---	MEDVGYPIIIDQK
1536.7599	1535.7526	1535.7541	-0.0015	295	307	0	---	MEDVGYPIIIDQK + Oxidation (M)
2368.2236	2367.2163	2367.2031	0.0132	288	307	1	---	LTYENVKMEDVGYPIIIDQK
2384.2134	2383.2061	2383.1980	0.0081	288	307	1	---	LTYENVKMEDVGYPIIIDQK + Oxidation (M)
2781.4268	2780.4195	2780.3828	0.0368	176	203	1	---	GVTVKDVTITAPGDSPNTDGIHIGDSSK

No match to: 713.4100, 734.4906, 736.4909, 750.5137, 768.5228, 887.0035, 1279.7703, 1334.8861, 1350.6915, 1355.6747, 1371.6752, 1448.9235, 1553.8030, 1618.0640, 1637.8765, 1732.1014, 1756.8159, 1756.8159, 1784.8224, 1791.7297, 1902.2487, 2168.1350, 2296.2302, 2296.2302, 2487.3247, 2565.1877, 2772.4985, 2824.3088, 2923.3665, 2926.4819, 2985.4487

2. gi|223539340 **Mass:** 9908 **Score:** 46 **Expect:** 16 **Queries matched:** 5

conserved hypothetical protein [Ricinus communis]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1553.8030	1552.7957	1552.7919	0.0038	3	-	15	1	---	EELKTFMTSLQAR
1756.8159	1755.8086	1755.8825	-0.0739	24	-	39	0	---	QVADPPCALTIDLTSR
1756.8159	1755.8086	1755.8825	-0.0739	24	-	39	0	---	QVADPPCALTIDLTSR
1784.8224	1783.8151	1783.8886	-0.0735	7	-	23	1	---	TFMTSLQARQAASSASK
2487.3247	2486.3174	2486.2435	0.0740	16	-	39	1	---	QAASSASKQVADPPCALTIDLTSR

No match to: 713.4100, 734.4906, 736.4909, 750.5137, 768.5228, 887.0035, 1032.5315, 1048.5239, 1064.6011, 1120.5594, 1279.7703, 1323.6957, 1323.6957, 1334.8861, 1339.6835, 1339.6835, 1350.6915, 1355.6747, 1371.6752, 1388.6150, 1388.6150, 1404.6116, 1448.9235, 1520.7637, 1536.7599, 1618.0640, 1637.8765, 1732.1014, 1791.7297, 1902.2487, 2168.1350, 2296.2302, 2296.2302, 2368.2236, 2384.2134, 2565.1877, 2772.4985, 2781.4268, 2824.3088, 2923.3665, 2926.4819, 2985.4487

3. gi|51458190 **Mass:** 22454 **Score:** 45 **Expect:** 20 **Queries matched:** 5

ribosomal protein small subunit 4 [Asplenium theciferum]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1350.6915	1349.6842	1349.7125	-0.0283	34	-	44	1	---	ISQFCVRLEAK
1536.7599	1535.7526	1535.7289	0.0237	6	-	20	0	---	DLPGFMGGGETTNLK
2168.1350	2167.1277	2167.1160	0.0117	176	-	193	0	---	ESINLNINELLVVEYYSR
2296.2302	2295.2229	2295.2110	0.0120	176	-	194	1	---	ESINLNINELLVVEYYSRK
2296.2302	2295.2229	2295.1607	0.0622	151	-	171	0	---	TPDHLTFALSEGDRPTGLVNR

No match to: 713.4100, 734.4906, 736.4909, 750.5137, 768.5228, 887.0035, 1032.5315, 1048.5239, 1064.6011, 1120.5594, 1279.7703, 1323.6957, 1323.6957, 1334.8861, 1339.6835, 1339.6835, 1355.6747, 1371.6752, 1388.6150, 1388.6150, 1404.6116, 1448.9235, 1520.7637, 1553.8030, 1618.0640, 1637.8765, 1732.1014, 1756.8159, 1756.8159, 1784.8224, 1791.7297, 1902.2487, 2368.2236, 2384.2134, 2487.3247, 2565.1877, 2772.4985, 2781.4268, 2824.3088, 2923.3665, 2926.4819, 2985.4487

4. gi|21666264 **Mass:** 15417 **Score:** 43 **Expect:** 31 **Queries matched:** 5

ascorbate peroxidase [Triticum aestivum]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1323.6957	1322.6884	1322.7306	-0.0422	34	-	46	0	14	EIVALSGAHTLGR
1323.6957	1322.6884	1322.7306	-0.0422	34	-	46	0	---	EIVALSGAHTLGR
1388.6150	1387.6077	1387.6441	-0.0364	23	-	33	1	---	EVFYRMGLDDK + Oxidation (M)
1388.6150	1387.6077	1387.6441	-0.0364	23	-	33	1	---	EVFYRMGLDDK + Oxidation (M)
2824.3088	2823.3015	2823.4218	-0.1202	94	-	118	1	---	DQELLVLPTDAALFDDPSFKVYAEK

No match to: 713.4100, 734.4906, 736.4909, 750.5137, 768.5228, 887.0035, 1032.5315, 1048.5239, 1064.6011, 1120.5594, 1279.7703, 1334.8861, 1339.6835, 1339.6835, 1350.6915, 1355.6747, 1371.6752, 1404.6116, 1448.9235, 1520.7637, 1536.7599, 1553.8030, 1618.0640, 1637.8765, 1732.1014, 1756.8159, 1756.8159, 1784.8224, 1791.7297, 1902.2487, 2168.1350, 2296.2302, 2296.2302, 2368.2236, 2384.2134, 2487.3247, 2565.1877, 2772.4985, 2781.4268, 2923.3665, 2926.4819, 2985.4487

5. gi|115470395 **Mass:** 27205 **Score:** 40 **Expect:** 56 **Queries matched:** 7

Os07g0123300 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide

713.4100	712.4027	712.3690	0.0337	221 - 226	0	---	AHCVVK
1032.5315	1031.5242	1031.5399	-0.0157	173 - 182	0	---	AAGYEPVIGR
1388.6150	1387.6077	1387.6262	-0.0185	138 - 151	0	---	NGSMPNGNSQGGIR
1388.6150	1387.6077	1387.6262	-0.0185	138 - 151	0	---	NGSMPNGNSQGGIR
1404.6116	1403.6043	1403.6211	-0.0168	138 - 151	0	---	NGSMPNGNSQGGIR + Oxidation (M)
1791.7297	1790.7224	1790.7675	-0.0451	114 - 130	0	---	CMHNGLGSGGTNQDVTK + Oxidation (M)
2565.1877	2564.1804	2564.1798	0.0006	1 - 23	0	---	MEGEEEEVESLVGISNALESLER + Oxidation (M)

No match to: 734.4906, 736.4909, 750.5137, 768.5228, 887.0035, 1048.5239, 1064.6011, 1120.5594, 1279.7703, 1323.6957, 1323.6957, 1334.8861, 1339.6835, 1339.6835, 1350.6915, 1355.6747, 1371.6752, 1448.9235, 1520.7637, 1536.7599, 1553.8030, 1618.0640, 1637.8765, 1732.1014, 1756.8159, 1756.8159, 1784.8224, 1902.2487, 2168.1350, 2296.2302, 2296.2302, 2368.2236, 2384.2134, 2487.3247, 2772.4985, 2781.4268, 2824.3088, 2923.3665, 2926.4819, 2985.4487

6. gi|25992557 **Mass:** 41411 **Score:** 40 **Expect:** 66 **Queries matched:** 6

thylakoid-bound ascorbate peroxidase [Triticum aestivum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1323.6957	1322.6884	1322.7306	-0.0422	164 - 176	0	14		EIVALSGAHTLGR
1323.6957	1322.6884	1322.7306	-0.0422	164 - 176	0	---		EIVALSGAHTLGR
1388.6150	1387.6077	1387.6441	-0.0364	153 - 163	1	---		EVFYRMGLDDK + Oxidation (M)
1388.6150	1387.6077	1387.6441	-0.0364	153 - 163	1	---		EVFYRMGLDDK + Oxidation (M)
1784.8224	1783.8151	1783.8601	-0.0450	51 - 66	1	---		NIEEWPQRGGADGSLR
2824.3088	2823.3015	2823.4218	-0.1202	224 - 248	1	---		DQELLVLPTDAALFDDPSFKVYAEK

No match to: 713.4100, 734.4906, 736.4909, 750.5137, 768.5228, 887.0035, 1032.5315, 1048.5239, 1064.6011, 1120.5594, 1279.7703, 1334.8861, 1339.6835, 1339.6835, 1350.6915, 1355.6747, 1371.6752, 1404.6116, 1448.9235, 1520.7637, 1536.7599, 1553.8030, 1618.0640, 1637.8765, 1732.1014, 1756.8159, 1756.8159, 1791.7297, 1902.2487, 2168.1350, 2296.2302, 2296.2302, 2368.2236, 2384.2134, 2487.3247, 2565.1877, 2772.4985, 2781.4268, 2923.3665, 2926.4819, 2985.4487

7. gi|125582491 **Mass:** 43582 **Score:** 38 **Expect:** 87 **Queries matched:** 6

hypothetical protein OsJ_07113 [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1323.6957	1322.6884	1322.7306	-0.0422	161 - 173	0	14		EIVALSGAHTLGR
1323.6957	1322.6884	1322.7306	-0.0422	161 - 173	0	---		EIVALSGAHTLGR
1388.6150	1387.6077	1387.6441	-0.0364	150 - 160	1	---		EVFYRMGLDDK + Oxidation (M)
1388.6150	1387.6077	1387.6441	-0.0364	150 - 160	1	---		EVFYRMGLDDK + Oxidation (M)
1784.8224	1783.8151	1783.8601	-0.0450	48 - 63	1	---		NIEEWPQRGGADGSLR
2824.3088	2823.3015	2823.4218	-0.1202	221 - 245	1	---		DQDLLVLPTDAALFEDPSFKVYAEK

No match to: 713.4100, 734.4906, 736.4909, 750.5137, 768.5228, 887.0035, 1032.5315, 1048.5239, 1064.6011, 1120.5594, 1279.7703, 1334.8861, 1339.6835, 1339.6835, 1350.6915, 1355.6747, 1371.6752, 1404.6116, 1448.9235, 1520.7637, 1536.7599, 1553.8030, 1618.0640, 1637.8765, 1732.1014, 1756.8159, 1756.8159, 1791.7297, 1902.2487, 2168.1350, 2296.2302, 2296.2302, 2368.2236, 2384.2134, 2487.3247, 2565.1877, 2772.4985, 2781.4268, 2923.3665, 2926.4819, 2985.4487

8. gi|50725765 **Mass:** 44389 **Score:** 38 **Expect:** 87 **Queries matched:** 6

putative thylakoid-bound ascorbate peroxidase [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1323.6957	1322.6884	1322.7306	-0.0422	167 -	179	0	14	EIVALSGAHTLGR
1323.6957	1322.6884	1322.7306	-0.0422	167 -	179	0	---	EIVALSGAHTLGR
1388.6150	1387.6077	1387.6441	-0.0364	156 -	166	1	---	EVFYRMGLDDK + Oxidation (M)
1388.6150	1387.6077	1387.6441	-0.0364	156 -	166	1	---	EVFYRMGLDDK + Oxidation (M)
1784.8224	1783.8151	1783.8601	-0.0450	54 -	69	1	---	NIEEWPQRGGADGSLR
2824.3088	2823.3015	2823.4218	-0.1202	227 -	251	1	---	DQDLLVLPTDAALFEDPSFKVYAEK

No match to: 713.4100, 734.4906, 736.4909, 750.5137, 768.5228, 887.0035, 1032.5315, 1048.5239, 1064.6011, 1120.5594, 1279.7703, 1334.8861, 1339.6835, 1339.6835, 1350.6915, 1355.6747, 1371.6752, 1404.6116, 1448.9235, 1520.7637, 1536.7599, 1553.8030, 1618.0640, 1637.8765, 1732.1014, 1756.8159, 1756.8159, 1791.7297, 1902.2487, 2168.1350, 2296.2302, 2296.2302, 2368.2236, 2384.2134, 2487.3247, 2565.1877, 2772.4985, 2781.4268, 2923.3665, 2926.4819, 2985.4487

9. gi|2160156 **Mass:** 123854 **Score:** 38 **Expect:** 92 **Queries matched:** 10

Strong similarity to S. pombe leucyl-tRNA synthetase (gb|Z73100). [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
713.4100	712.4027	712.4119	-0.0092	283 -	289	0	---	LGPLEGK
1339.6835	1338.6762	1338.6931	-0.0169	334 -	345	0	---	AALNLAYQNFSK
1339.6835	1338.6762	1338.6931	-0.0169	334 -	345	0	---	AALNLAYQNFSK
1350.6915	1349.6842	1349.7199	-0.0357	994 -	1004	1	---	AIQKVCMPFLK + Oxidation (M)
1637.8765	1636.8692	1636.8606	0.0086	898 -	911	1	---	SANKYLQDSIVLMR
2296.2302	2295.2229	2295.1608	0.0621	469 -	488	1	---	LTYLKGFTEGTMLIGEFFGR + Oxidation (M)
2296.2302	2295.2229	2295.1608	0.0621	469 -	488	1	0	LTYLKGFTEGTMLIGEFFGR + Oxidation (M)
2772.4985	2771.4912	2771.4785	0.0128	420 -	443	1	---	YGVKTEWLPTEIIPIINIPEFGDK
2824.3088	2823.3015	2823.3518	-0.0503	46 -	69	0	---	FFSTFPFPYMNGYLHIGHAFSLSK + Oxidation (M)
2985.4487	2984.4414	2984.3836	0.0578	624 -	647	0	---	SLIRPQQMNDEVWEYLFCDGPYPK

No match to: 734.4906, 736.4909, 750.5137, 768.5228, 887.0035, 1032.5315, 1048.5239, 1064.6011, 1120.5594, 1279.7703, 1323.6957, 1323.6957, 1334.8861, 1355.6747, 1371.6752, 1388.6150, 1388.6150, 1404.6116, 1448.9235, 1520.7637, 1536.7599, 1553.8030, 1618.0640, 1732.1014, 1756.8159, 1756.8159, 1784.8224, 1791.7297, 1902.2487, 2168.1350, 2368.2236, 2384.2134, 2487.3247, 2565.1877, 2781.4268, 2923.3665, 2926.4819

10. gi|79339972 **Mass:** 124513 **Score:** 38 **Expect:** 96 **Queries matched:** 10

ATP binding / aminoacyl-tRNA ligase [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
713.4100	712.4027	712.4119	-0.0092	283 -	289	0	---	LGPLEGK
1339.6835	1338.6762	1338.6931	-0.0169	334 -	345	0	---	AALNLAYQNFSK
1339.6835	1338.6762	1338.6931	-0.0169	334 -	345	0	---	AALNLAYQNFSK
1350.6915	1349.6842	1349.7199	-0.0357	994 -	1004	1	---	AIQKVCMPFLK + Oxidation (M)
1637.8765	1636.8692	1636.8606	0.0086	898 -	911	1	---	SANKYLQDSIVLMR
2296.2302	2295.2229	2295.1608	0.0621	469 -	488	1	---	LTYLKGFTEGTMLIGEFFGR + Oxidation (M)
2296.2302	2295.2229	2295.1608	0.0621	469 -	488	1	0	LTYLKGFTEGTMLIGEFFGR + Oxidation (M)

2772.4985	2771.4912	2771.4785	0.0128	420 -	443	1	---	YGVKTEWLPTEIIPIINIPEFGDK
2824.3088	2823.3015	2823.3518	-0.0503	46 -	69	0	---	FFSTFPFPYMNGYLHIGHAFSLSK + Oxidation (M)
2985.4487	2984.4414	2984.3836	0.0578	624 -	647	0	---	SLIRPQQMNDEVWEYLFCDGPYPK

No match to: 734.4906, 736.4909, 750.5137, 768.5228, 887.0035, 1032.5315, 1048.5239, 1064.6011, 1120.5594, 1279.7703, 1323.6957, 1323.6957, 1334.8861, 1355.6747, 1371.6752, 1388.6150, 1388.6150, 1404.6116, 1448.9235, 1520.7637, 1536.7599, 1553.8030, 1618.0640, 1732.1014, 1756.8159, 1756.8159, 1784.8224, 1791.7297, 1902.2487, 2168.1350, 2368.2236, 2384.2134, 2487.3247, 2565.1877, 2781.4268, 2923.3665, 2926.4819

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 47

Protein View

Match to: **gi|4826572** Score: **141** Expect: **4.8e-009**
polygalacturonase [Phleum pratense]

Nominal mass (M_r): **42579**; Calculated pI value: **7.83**
NCBI BLAST search of gi|4826572 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **22%**

Matched peptides shown in **Bold Red**

```
   1 GKKEEKKEEK KESGDAASGA DGTYDITKLG AKPDGKTDCT KEVEEAWASA
  51 CGGTGKNTIV IPKGDFLTGP LNFTGPCKGD SVTIKLDGNL LSSNDLAKYK
 101 ANWIEIMRIK KLTITGKGTL DGQGKAVWGK NSCAKNYNCK ILPNTLVLDF
 151 CDDALIEGIT LLNAKFFHMN IYECKGVTVK DVTITAPGDS PNTDGIHIGD
 201 SSKVTITDTT IGTGDDCISI GPGSTGLNIT GVTCGPGHGI SVGSLGRYKD
 251 EKDVTDITVK NCVLKKSTNG LRIKSYEDAK SPLTASKLTY ENVKMEDVGY
 301 PIIIDQKYCP NKICTSKGDS ARVTVKDVTF RNITGTSSTP EAVSLLCSDK
 351 QPCNGVTMND VKIEYSGTNN KTMAVCTNAK VTAKGVSEAN TCAA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
99 - 108	1323.6957	1322.6884	1322.6805	0.0079	1	**YKANWIEIMR** (Ions score 11)
99 - 108	1323.6957	1322.6884	1322.6805	0.0079	1	**YKANWIEIMR** (No match)
99 - 108	1339.6835	1338.6762	1338.6754	0.0008	1	**YKANWIEIMR** Oxidation (M) (Ions score 1)
99 - 108	1339.6835	1338.6762	1338.6754	0.0008	1	**YKANWIEIMR** Oxidation (M) (No match)
101 - 108	1032.5315	1031.5242	1031.5222	0.0020	0	**ANWIEIMR** (No match)
101 - 108	1048.5239	1047.5166	1047.5171	-0.0005	0	**ANWIEIMR** Oxidation (M) (No match)
126 - 135	1120.5594	1119.5521	1119.5495	0.0027	1	**AVWGKNSCAK** (No match)
166 - 175	1388.6150	1387.6077	1387.6053	0.0025	0	**FFHMNIYECK** (Ions score 65)
166 - 175	1388.6150	1387.6077	1387.6053	0.0025	0	**FFHMNIYECK** (No match)
166 - 175	1404.6116	1403.6043	1403.6002	0.0042	0	**FFHMNIYECK** Oxidation (M) (No match)
176 - 203	2781.4268	2780.4195	2780.3828	0.0368	1	**GVTVKDVTITAPGDSPNTDGIHIGDSSK** (No match)
288 - 307	2368.2236	2367.2163	2367.2031	0.0132	1	**LTYENVKMEDVGYPIIIDQK** (No match)
288 - 307	2384.2134	2383.2061	2383.1980	0.0081	1	**LTYENVKMEDVGYPIIIDQK** Oxidation (M) (No match)
295 - 307	1520.7637	1519.7564	1519.7592	-0.0028	0	**MEDVGYPIIIDQK** (No match)
295 - 307	1536.7599	1535.7526	1535.7541	-0.0015	0	**MEDVGYPIIIDQK** Oxidation (M) (No match)
323 - 331	1064.6011	1063.5938	1063.6025	-0.0087	1	**VTVKDVTFR** (No match)

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	Accession	Mass	Score	Description
1.	gi|4826572	42579	77	polygalacturonase [Phleum pratense]
2.	gi|157348939	25389	57	unnamed protein product [Vitis vinifera]
3.	gi|116060270	77618	49	protein T6D22.10 (ISS) [Ostreococcus tauri]
4.	gi|116058504	34634	47	initiation factor 3g (ISS) [Ostreococcus tauri]
5.	gi|52076433	7591	47	hypothetical protein [Oryza sativa Japonica Group]
6.	gi|115442427	37713	47	Os01g0965400 [Oryza sativa (japonica cultivar-group)]
7.	gi|139522556	53750	47	ATP synthase beta subunit [Lysipomia sphagnophila]
8.	gi|3914472	14160	46	RecName: Full=Photosystem II 10 kDa polypeptide, chloroplastic; Short=PII10; Flags: Precursor
9.	gi|218189798	38940	46	hypothetical protein OsI_05332 [Oryza sativa Indica Group]
10.	gi|224061067	43003	45	predicted protein [Populus trichocarpa]

Results List

1. gi|4826572 **Mass:** 42579 **Score:** 77 **Expect:** 0.012 **Queries matched:** 12

polygalacturonase [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1032.5344	1031.5271	1031.5222	0.0049	101	108	0	---	ANWIEIMR
1048.5227	1047.5154	1047.5171	-0.0017	101	108	0	---	ANWIEIMR + Oxidation (M)
1064.6147	1063.6074	1063.6025	0.0049	323	331	1	---	VTVKDVTFR
1094.5579	1093.5506	1093.5186	0.0321	313	322	1	---	ICTSKGDSAR
1323.7002	1322.6929	1322.6805	0.0124	99	108	1	36	YKANWIEIMR
1323.7002	1322.6929	1322.6805	0.0124	99	108	1	---	YKANWIEIMR
1339.6824	1338.6751	1338.6754	-0.0003	99	108	1	(9)	YKANWIEIMR + Oxidation (M)
1339.6824	1338.6751	1338.6754	-0.0003	99	108	1	---	YKANWIEIMR + Oxidation (M)
1388.6215	1387.6142	1387.6053	0.0090	166	175	0	---	FFHMNIYECK
1404.6143	1403.6070	1403.6002	0.0069	166	175	0	---	FFHMNIYECK + Oxidation (M)
2369.2249	2368.2176	2368.0787	0.1389	351	371	1	---	QPCNGVTMNDVKIEYSGTNNK
2781.4167	2780.4094	2780.3828	0.0267	176	203	1	---	GVTVKDVTITAPGDSPNTDGIHIGDSSK

No match to: 713.3977, 724.4932, 734.4839, 750.5103, 768.5106, 782.4767, 797.3663, 848.5228, 864.5171, 982.4987, 1179.6122, 1232.6124, 1277.1881, 1279.7664, 1320.5963, 1350.6975, 1353.6847, 1355.6846, 1448.9091, 1450.6476, 1475.7689, 1637.8795, 1687.9886, 1707.7928, 1756.8297, 1756.8297, 1791.7505, 1838.9305, 1851.9427, 1891.9738, 2091.8955, 2096.9812, 2168.1299, 2199.9675, 2230.2166, 2240.1577, 2286.1460, 2296.2317, 2383.9585, 2383.9585, 2399.0286, 2501.2280, 2564.2007, 2663.3584, 2705.1616, 2705.1616, 2922.3647, 3224.3101, 3333.5669, 3348.6111

2. gi|157348939 **Mass:** 25389 **Score:** 57 **Expect:** 1.1 **Queries matched:** 8

unnamed protein product [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide

1388.6215	1387.6142	1387.5925	0.0217	2 - 14	0	---	VDDGMSPPNVDDK
1404.6143	1403.6070	1403.5874	0.0196	2 - 14	0	---	VDDGMSPPNVDDK + Oxidation (M)
1707.7928	1706.7855	1706.7239	0.0616	1 - 15	1	---	MVDDGMSPPNVDDKR + 2 Oxidation (M)
1851.9427	1850.9354	1850.8733	0.0621	200 - 215	1	---	EWFRANLNCDTGIGAK
1891.9738	1890.9665	1890.8554	0.1111	97 - 114	1	---	AEVEEPSLSSSEGRSGDR
2296.2317	2295.2244	2295.1276	0.0968	18 - 36	1	---	NELVVLQAEIERMHAENER + Oxidation (M)
2501.2280	2500.2207	2500.1438	0.0769	64 - 86	1	---	AENNEEHDQKHSGNNNGGVVVPR
2922.3647	2921.3574	2921.3833	-0.0259	39 - 63	0	---	SMLNQVTNNYNALQVHMVALMQDQK + 2 Oxidation (M)

No match to: 713.3977, 724.4932, 734.4839, 750.5103, 768.5106, 782.4767, 797.3663, 848.5228, 864.5171, 982.4987, 1032.5344, 1048.5227, 1064.6147, 1094.5579, 1179.6122, 1232.6124, 1277.1881, 1279.7664, 1320.5963, 1323.7002, 1323.7002, 1339.6824, 1339.6824, 1350.6975, 1353.6847, 1355.6846, 1448.9091, 1450.6476, 1475.7689, 1637.8795, 1687.9886, 1756.8297, 1756.8297, 1791.7505, 1838.9305, 2091.8955, 2096.9812, 2168.1299, 2199.9675, 2230.2166, 2240.1577, 2286.1460, 2369.2249, 2383.9585, 2383.9585, 2399.0286, 2564.2007, 2663.3584, 2705.1616, 2705.1616, 2781.4167, 3224.3101, 3333.5669, 3348.6111

3. gi|116060270 **Mass:** 77618 **Score:** 49 **Expect:** 8.4 **Queries matched:** 11

protein T6D22.10 (ISS) [Ostreococcus tauri]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
982.4987	981.4914	981.4338	0.0577	472 - 479	0	---	VCESGQFR
1179.6122	1178.6049	1178.6771	-0.0722	252 - 261	1	---	EIDVVALHKR
1232.6124	1231.6051	1231.6893	-0.0841	103 - 112	1	---	MVVMLRKPSR + Oxidation (M)
1323.7002	1322.6929	1322.6466	0.0463	161 - 172	1	---	GYDEAIKANQSK
1323.7002	1322.6929	1322.6466	0.0463	161 - 172	1	---	GYDEAIKANQSK
1448.9091	1447.9018	1447.8146	0.0872	604 - 616	0	---	EDILIVGHQGVLR
1475.7689	1474.7616	1474.7667	-0.0051	592 - 603	0	---	LDPLIQELESYR
2286.1460	2285.1387	2285.1691	-0.0304	114 - 134	1	---	VLSAYEFSIEVAARSFGTNPK
2399.0286	2398.0213	2398.0793	-0.0580	351 - 371	1	---	CGVDVDAVRIHPMSPEGDWSR + Oxidation (M)
2663.3584	2662.3511	2662.2842	0.0669	519 - 539	1	---	VDDLNFLDYELWKFAEELFEK
2781.4167	2780.4094	2780.4357	-0.0263	272 - 297	0	---	TLNIPLNASAHFVHPAHADVATLSER

No match to: 713.3977, 724.4932, 734.4839, 750.5103, 768.5106, 782.4767, 797.3663, 848.5228, 864.5171, 1032.5344, 1048.5227, 1064.6147, 1094.5579, 1277.1881, 1279.7664, 1320.5963, 1339.6824, 1339.6824, 1350.6975, 1353.6847, 1355.6846, 1388.6215, 1404.6143, 1450.6476, 1637.8795, 1687.9886, 1707.7928, 1756.8297, 1756.8297, 1791.7505, 1838.9305, 1851.9427, 1891.9738, 2091.8955, 2096.9812, 2168.1299, 2199.9675, 2230.2166, 2240.1577, 2296.2317, 2369.2249, 2383.9585, 2383.9585, 2501.2280, 2564.2007, 2705.1616, 2705.1616, 2922.3647, 3224.3101, 3333.5669, 3348.6111

4. gi|116058504 **Mass:** 34634 **Score:** 47 **Expect:** 11 **Queries matched:** 8

initiation factor 3g (ISS) [Ostreococcus tauri]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
848.5228	847.5155	847.4915	0.0240	257 - 263	0	---	IYVAINR
1094.5579	1093.5506	1093.4822	0.0684	212 - 223	0	---	AGATGTGASMDR
1756.8297	1755.8224	1755.8903	-0.0679	2 - 16	1	---	AIKPRWDAIDADTER

1756.8297	1755.8224	1755.8903	-0.0679	2 - 16	1	---	AIKPRWDAIDADTER
1838.9305	1837.9232	1837.9573	-0.0341	285 - 300	1	---	AIDKLDGYGYDNLILR
2286.1460	2285.1387	2285.1136	0.0251	116 - 135	0	---	YKPGDESMTAVSLEEIFLEK
2296.2317	2295.2244	2295.0735	0.1509	201 - 223	1	---	KPGGYVPPSMRAGATGTGASMDR + 2 Oxidation (M)
2564.2007	2563.1934	2563.2621	-0.0687	142 - 165	1	---	SELEKASDPLAAMASAQTSLLVCR + Oxidation (M)

No match to: 713.3977, 724.4932, 734.4839, 750.5103, 768.5106, 782.4767, 797.3663, 864.5171, 982.4987, 1032.5344, 1048.5227, 1064.6147, 1179.6122, 1232.6124, 1277.1881, 1279.7664, 1320.5963, 1323.7002, 1323.7002, 1339.6824, 1339.6824, 1350.6975, 1353.6847, 1355.6846, 1388.6215, 1404.6143, 1448.9091, 1450.6476, 1475.7689, 1637.8795, 1687.9886, 1707.7928, 1791.7505, 1851.9427, 1891.9738, 2091.8955, 2096.9812, 2168.1299, 2199.9675, 2230.2166, 2240.1577, 2369.2249, 2383.9585, 2383.9585, 2399.0286, 2501.2280, 2663.3584, 2705.1616, 2705.1616, 2781.4167, 2922.3647, 3224.3101, 3333.5669, 3348.6111

5. gi|52076433 **Mass:** 7591 **Score:** 47 **Expect:** 12 **Queries matched:** 5

hypothetical protein [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1475.7689	1474.7616	1474.7851	-0.0235	51 -	66	1	---	RSGVGVSVSASAAATR
1756.8297	1755.8224	1755.8764	-0.0539	28 -	45	1	---	QAARGWSDGGVSGGKPAR
1756.8297	1755.8224	1755.8764	-0.0539	28 -	45	1	---	QAARGWSDGGVSGGKPAR
1851.9427	1850.9354	1850.8904	0.0450	2 -	20	1	---	TVAATATCEGSRATSGGVR
2096.9812	2095.9739	2096.0544	-0.0805	52 -	72	1	---	SGVGVSVSASAAATRHQPCVR

No match to: 713.3977, 724.4932, 734.4839, 750.5103, 768.5106, 782.4767, 797.3663, 848.5228, 864.5171, 982.4987, 1032.5344, 1048.5227, 1064.6147, 1094.5579, 1179.6122, 1232.6124, 1277.1881, 1279.7664, 1320.5963, 1323.7002, 1323.7002, 1339.6824, 1339.6824, 1350.6975, 1353.6847, 1355.6846, 1388.6215, 1404.6143, 1448.9091, 1450.6476, 1637.8795, 1687.9886, 1707.7928, 1791.7505, 1838.9305, 1891.9738, 2091.8955, 2168.1299, 2199.9675, 2230.2166, 2240.1577, 2286.1460, 2296.2317, 2369.2249, 2383.9585, 2383.9585, 2399.0286, 2501.2280, 2564.2007, 2663.3584, 2705.1616, 2705.1616, 2781.4167, 2922.3647, 3224.3101, 3333.5669, 3348.6111

6. gi|115442427 **Mass:** 37713 **Score:** 47 **Expect:** 12 **Queries matched:** 8

Os01g0965400 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
982.4987	981.4914	981.4953	-0.0039	323 -	331	0	---	VGTFIGCTK
1350.6975	1349.6902	1349.6761	0.0141	198 -	208	1	---	MSEVAEPYIRR
1756.8297	1755.8224	1755.8499	-0.0275	332 -	346	1	---	DQDQIVGNALDQERR
1756.8297	1755.8224	1755.8499	-0.0275	332 -	346	1	---	DQDQIVGNALDQERR
1838.9305	1837.9232	1837.9178	0.0054	2 -	20	0	---	AAAAAAAVACGMSTSFLIR
2096.9812	2095.9739	2096.0762	-0.1023	266 -	283	1	---	NPNARLLEAVSYHEVQTR
2240.1577	2239.1504	2239.1636	-0.0132	219 -	240	0	---	VVIFAAGTGNPFFTTDTAAALR
2564.2007	2563.1934	2563.2336	-0.0402	323 -	345	1	---	VGTFIGCTKDQDQIVGNALDQER

No match to: 713.3977, 724.4932, 734.4839, 750.5103, 768.5106, 782.4767, 797.3663, 848.5228, 864.5171, 1032.5344, 1048.5227, 1064.6147, 1094.5579, 1179.6122, 1232.6124, 1277.1881, 1279.7664, 1320.5963, 1323.7002, 1323.7002, 1339.6824, 1339.6824, 1353.6847, 1355.6846, 1388.6215, 1404.6143, 1448.9091, 1450.6476, 1475.7689, 1637.8795, 1687.9886, 1707.7928, 1791.7505, 1851.9427, 1891.9738, 2091.8955, 2168.1299, 2199.9675, 2230.2166, 2286.1460, 2296.2317, 2369.2249, 2383.9585, 2383.9585, 2399.0286, 2501.2280, 2663.3584, 2705.1616, 2705.1616, 2781.4167,

2922.3647, 3224.3101, 3333.5669, 3348.6111

7. gi|139522556 **Mass:** 53750 **Score:** 47 **Expect:** 13 **Queries matched:** 7

ATP synthase beta subunit [Lysipomia sphagnophila]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1450.6476	1449.6403	1449.6955	-0.0552	487	498	1	---	AMNLEMENNLKK + Oxidation (M)
1851.9427	1850.9354	1850.9230	0.0124	1	17	1	---	MRLNTTPSGSMVSTLEK
2096.9812	2095.9739	2096.0935	-0.1196	88	109	0	---	GMEVIDTGAPLSVPVGGATLGR
2369.2249	2368.2176	2368.2168	0.0008	53	73	0	---	DTLGKPINVTCEVQQLLGNNR
2501.2280	2500.2207	2500.2995	-0.0788	355	378	1	---	GLAAKGIYPAVDPLDSTSTMLQPR
2781.4167	2780.4094	2780.5006	-0.0911	179	205	1	---	TVLIMELINNIAKAHGGVSVFGGVGER
3348.6111	3347.6038	3347.6522	-0.0484	76	109	1	---	AVAMSATDGLMRGMEVIDTGAPLSVPVGGATLGR + 3 Oxidation (M)

No match to: 713.3977, 724.4932, 734.4839, 750.5103, 768.5106, 782.4767, 797.3663, 848.5228, 864.5171, 982.4987, 1032.5344, 1048.5227, 1064.6147, 1094.5579, 1179.6122, 1232.6124, 1277.1881, 1279.7664, 1320.5963, 1323.7002, 1323.7002, 1339.6824, 1339.6824, 1350.6975, 1353.6847, 1355.6846, 1388.6215, 1404.6143, 1448.9091, 1475.7689, 1637.8795, 1687.9886, 1707.7928, 1756.8297, 1756.8297, 1791.7505, 1838.9305, 1891.9738, 2091.8955, 2168.1299, 2199.9675, 2230.2166, 2240.1577, 2286.1460, 2296.2317, 2383.9585, 2383.9585, 2399.0286, 2564.2007, 2663.3584, 2705.1616, 2705.1616, 2922.3647, 3224.3101, 3333.5669

8. gi|3914472 **Mass:** 14160 **Score:** 46 **Expect:** 15 **Queries matched:** 6

RecName: Full=Photosystem II 10 kDa polypeptide, chloroplastic; Short=PII10; Flags: Precursor

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
713.3977	712.3904	712.4231	-0.0327	22	28	0	---	GLPSLAR
1339.6824	1338.6751	1338.6891	-0.0140	29	41	1	---	SSSSFRVQASGVK
1339.6824	1338.6751	1338.6891	-0.0140	29	41	1	---	SSSSFRVQASGVK
1707.7928	1706.7855	1706.8912	-0.1057	2	17	0	---	ASTVMSLKPAPFSVEK + Oxidation (M)
1838.9305	1837.9232	1837.9317	-0.0085	1	17	0	---	MASTVMSLKPAPFSVEK + Oxidation (M)
2296.2317	2295.2244	2295.0913	0.1331	45	66	1	---	TDKPYGINGSMSLRDGVDASGR

No match to: 724.4932, 734.4839, 750.5103, 768.5106, 782.4767, 797.3663, 848.5228, 864.5171, 982.4987, 1032.5344, 1048.5227, 1064.6147, 1094.5579, 1179.6122, 1232.6124, 1277.1881, 1279.7664, 1320.5963, 1323.7002, 1323.7002, 1350.6975, 1353.6847, 1355.6846, 1388.6215, 1404.6143, 1448.9091, 1450.6476, 1475.7689, 1637.8795, 1687.9886, 1756.8297, 1756.8297, 1791.7505, 1851.9427, 1891.9738, 2091.8955, 2096.9812, 2168.1299, 2199.9675, 2230.2166, 2240.1577, 2286.1460, 2369.2249, 2383.9585, 2383.9585, 2399.0286, 2501.2280, 2564.2007, 2663.3584, 2705.1616, 2705.1616, 2781.4167, 2922.3647, 3224.3101, 3333.5669, 3348.6111

9. gi|218189798 **Mass:** 38940 **Score:** 46 **Expect:** 16 **Queries matched:** 8

hypothetical protein OsI_05332 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
982.4987	981.4914	981.4953	-0.0039	335	343	0	---	VGTFIGCTK
1350.6975	1349.6902	1349.6761	0.0141	210	220	1	---	MSEVAEPYIRR
1756.8297	1755.8224	1755.8499	-0.0275	344	358	1	---	DQDQIVGNALDQERR
1756.8297	1755.8224	1755.8499	-0.0275	344	358	1	---	DQDQIVGNALDQERR

1838.9305	1837.9232	1837.9178	0.0054	2 - 20	0	---	AAAAAAAVACGMSTSFLIR
2096.9812	2095.9739	2096.0762	-0.1023	278 - 295	1	---	NPNARLLEAVSYHEVQTR
2240.1577	2239.1504	2239.1636	-0.0132	231 - 252	0	---	VVIFAAGTGNPFFTTDTAAALR
2564.2007	2563.1934	2563.2336	-0.0402	335 - 357	1	---	VGTFIGCTKDQDQIVGNALDQER

No match to: 713.3977, 724.4932, 734.4839, 750.5103, 768.5106, 782.4767, 797.3663, 848.5228, 864.5171, 1032.5344, 1048.5227, 1064.6147, 1094.5579, 1179.6122, 1232.6124, 1277.1881, 1279.7664, 1320.5963, 1323.7002, 1323.7002, 1339.6824, 1339.6824, 1353.6847, 1355.6846, 1388.6215, 1404.6143, 1448.9091, 1450.6476, 1475.7689, 1637.8795, 1687.9886, 1707.7928, 1791.7505, 1851.9427, 1891.9738, 2091.8955, 2168.1299, 2199.9675, 2230.2166, 2286.1460, 2296.2317, 2369.2249, 2383.9585, 2383.9585, 2399.0286, 2501.2280, 2663.3584, 2705.1616, 2705.1616, 2781.4167, 2922.3647, 3224.3101, 3333.5669, 3348.6111

10. gi|224061067 **Mass:** 43003 **Score:** 45 **Expect:** 19 **Queries matched:** 7

predicted protein [Populus trichocarpa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1094.5579	1093.5506	1093.5451	0.0056	25 -	32	1	---	QLCRFSQR
1320.5963	1319.5890	1319.6503	-0.0613	373 -	384	1	---	LVDRMSGSQEAK
1851.9427	1850.9354	1850.8654	0.0700	40 -	56	1	---	HGSVSCSFAPMESAKIK + Oxidation (M)
2091.8955	2090.8882	2091.0312	-0.1430	164 -	182	0	---	EAGYLTVGVVTYPFSFEGR
2096.9812	2095.9739	2095.9666	0.0073	35 -	54	1	---	LSSSKHGSVSCSFAPMESAK
2240.1577	2239.1504	2239.1272	0.0232	343 -	362	0	---	YNGEIHVTIIATGFSQSFQK
2564.2007	2563.1934	2563.2951	-0.1016	136 -	163	0	---	GSDLVFITAGMGGGTGSGAAPVVAQISK + Oxidation (M)

No match to: 713.3977, 724.4932, 734.4839, 750.5103, 768.5106, 782.4767, 797.3663, 848.5228, 864.5171, 982.4987, 1032.5344, 1048.5227, 1064.6147, 1179.6122, 1232.6124, 1277.1881, 1279.7664, 1323.7002, 1323.7002, 1339.6824, 1339.6824, 1350.6975, 1353.6847, 1355.6846, 1388.6215, 1404.6143, 1448.9091, 1450.6476, 1475.7689, 1637.8795, 1687.9886, 1707.7928, 1756.8297, 1756.8297, 1791.7505, 1838.9305, 1891.9738, 2168.1299, 2199.9675, 2230.2166, 2286.1460, 2296.2317, 2369.2249, 2383.9585, 2383.9585, 2399.0286, 2501.2280, 2663.3584, 2705.1616, 2705.1616, 2781.4167, 2922.3647, 3224.3101, 3333.5669, 3348.6111

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 62

Protein View

Match to: **gi|4826572** Score: **77** Expect: **0.012**
polygalacturonase [Phleum pratense]

Nominal mass (M_r): **42579**; Calculated pI value: **7.83**
NCBI BLAST search of gi|4826572 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **22%**

Matched peptides shown in **Bold Red**

```
   1 GKKEEKKEEK KESGDAASGA DGTYDITKLG AKPDGKTDCT KEVEEAWASA
  51 CGGTGKNTIV IPKGDFLTGP LNFTGPCKGD SVTIKLDGNL LSSNDLAKYK
 101 ANWIEIMRIK KLTITGKGTL DGQGKAVWGK NSCAKNYNCK ILPNTLVLDF
 151 CDDALIEGIT LLNAKFFHMN IYECKGVTVK DVTITAPGDS PNTDGIHIGD
 201 SSKVTITDTT IGTGDDCISI GPGSTGLNIT GVTCGPGHGI SVGSLGRYKD
 251 EKDVTDITVK NCVLKKSTNG LRIKSYEDAK SPLTASKLTY ENVKMEDVGY
 301 PIIIDQKYCP NKICTSKGDS ARVTVKDVTF RNITGTSSTP EAVSLLCSDK
 351 QPCNGVTMND VKIEYSGTNN KTMAVCTNAK VTAKGVSEAN TCAA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
99 - 108	1323.7002	1322.6929	1322.6805	0.0124	1	**YKANWIEIMR** (Ions score 36)
99 - 108	1323.7002	1322.6929	1322.6805	0.0124	1	**YKANWIEIMR** (No match)
99 - 108	1339.6824	1338.6751	1338.6754	-0.0003	1	**YKANWIEIMR** Oxidation (M) (Ions score 9)
99 - 108	1339.6824	1338.6751	1338.6754	-0.0003	1	**YKANWIEIMR** Oxidation (M) (No match)
101 - 108	1032.5344	1031.5271	1031.5222	0.0049	0	**ANWIEIMR** (No match)
101 - 108	1048.5227	1047.5154	1047.5171	-0.0017	0	**ANWIEIMR** Oxidation (M) (No match)
166 - 175	1388.6215	1387.6142	1387.6053	0.0090	0	**FFHMNIYECK** (No match)
166 - 175	1404.6143	1403.6070	1403.6002	0.0069	0	**FFHMNIYECK** Oxidation (M) (No match)
176 - 203	2781.4167	2780.4094	2780.3828	0.0267	1	**GVTVKDVTITAPGDSPNTDGIHIGDSSK** (No match)
313 - 322	1094.5579	1093.5506	1093.5186	0.0321	1	**ICTSKGDSAR** (No match)
323 - 331	1064.6147	1063.6074	1063.6025	0.0049	1	**VTVKDVTFR** (No match)
351 - 371	2369.2249	2368.2176	2368.0787	0.1389	1	**QPCNGVTMNDVKIEYSGTNNK** (No match)

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Index

	Accession	Mass	Score	Description
1.	gi|4826572	42579	193	polygalacturonase [Phleum pratense]
2.	gi|115474109	21023	47	Os07g0681400 [Oryza sativa (japonica cultivar-group)]
3.	gi|168013985	21937	43	predicted protein [Physcomitrella patens subsp. patens]
4.	gi|222858686	137957	43	predicted protein [Populus trichocarpa]
5.	gi|87162603	17357	40	hypothetical protein MtrDRAFT_AC148340g14v2 [Medicago truncatula]
6.	gi|198404505	5445	40	DNA-directed RNA polymerase subunit B [Gynostemma pentaphyllum]
7.	gi|45239438	6885	37	COI1 [Nicotiana benthamiana]
8.	gi|66932629	8565	37	isocitrate dehydrogenase [Saltugilia latimeri]
9.	gi|168056286	24881	36	predicted protein [Physcomitrella patens subsp. patens]
10.	gi|168066458	32770	36	predicted protein [Physcomitrella patens subsp. patens]

Results List

1. gi|4826572 **Mass:** 42579 **Score:** 193 **Expect:** 3e-014 **Queries matched:** 20

polygalacturonase [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
775.4343	774.4270	774.4348	-0.0077	266	272	1	---	KSTNGLR
1032.5311	1031.5238	1031.5222	0.0016	101	108	0	---	ANWIEIMR
1048.5239	1047.5166	1047.5171	-0.0005	101	108	0	---	ANWIEIMR + Oxidation (M)
1064.6025	1063.5952	1063.6025	-0.0073	323	331	1	---	VTVKDVTFR
1094.5380	1093.5307	1093.5186	0.0122	313	322	1	---	ICTSKGDSAR
1120.5609	1119.5536	1119.5495	0.0042	126	135	1	---	AVWGKNSCAK
1323.6927	1322.6854	1322.6805	0.0049	99	108	1	24	YKANWIEIMR
1323.6927	1322.6854	1322.6805	0.0049	99	108	1	---	YKANWIEIMR
1339.6825	1338.6752	1338.6754	-0.0002	99	108	1	---	YKANWIEIMR + Oxidation (M)
1339.6825	1338.6752	1338.6754	-0.0002	99	108	1	(15)	YKANWIEIMR + Oxidation (M)
1388.6115	1387.6042	1387.6053	-0.0010	166	175	0	60	FFHMNIYECK
1388.6115	1387.6042	1387.6053	-0.0010	166	175	0	---	FFHMNIYECK
1404.6049	1403.5976	1403.6002	-0.0026	166	175	0	---	FFHMNIYECK + Oxidation (M)
1520.7681	1519.7608	1519.7592	0.0016	295	307	0	---	MEDVGYPIIIDQK
1536.7667	1535.7594	1535.7541	0.0053	295	307	0	---	MEDVGYPIIIDQK + Oxidation (M)
1872.9238	1871.9165	1871.9062	0.0104	166	180	1	---	FFHMNIYECKGVTVK
2368.2368	2367.2295	2367.2031	0.0264	288	307	1	---	LTYENVKMEDVGYPIIIDQK
2384.2234	2383.2161	2383.1980	0.0181	288	307	1	---	LTYENVKMEDVGYPIIIDQK + Oxidation (M)
2771.5273	2770.5200	2770.4826	0.0374	141	165	0	---	ILPNTLVLDFCDDALIEGITLLNAK
2781.4150	2780.4077	2780.3828	0.0250	176	203	1	---	GVTVKDVTITAPGDSPNTDGIHIGDSSK

No match to: 709.3099, 713.4081, 734.4956, 736.5024, 750.5167, 768.5226, 864.5463, 866.5065, 951.6184, 1080.5145,

1277.2272, 1279.7660, 1334.8834, 1355.6804, 1371.6730, 1448.9232, 1553.8102, 1618.0673, 1637.8778, 1732.1171, 1756.8164, 1756.8164, 1784.8204, 1901.2563, 2015.2742, 2168.1387, 2296.2332, 2296.2332, 2318.1804, 2485.3235, 2923.3938, 2926.5046, 2985.4858, 3689.8784

2. gi|115474109 **Mass:** 21023 **Score:** 47 **Expect:** 12 **Queries matched:** 5

Os07g0681400 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1371.6730	1370.6657	1370.6102	0.0555	175	186	1	---	DSDGRVDFGEFK
2168.1387	2167.1314	2167.0684	0.0630	133	152	0	---	VFDVDGDGFISASELQEVLK
2296.2332	2295.2259	2295.1633	0.0626	133	153	1	---	VFDVDGDGFISASELQEVLKK
2296.2332	2295.2259	2295.1566	0.0693	2	22	0	---	EGEQQQQQQQSVAAVRPSLGK
2485.3235	2484.3162	2484.1979	0.1183	50	73	0	---	NGDGEITVDELAQALDALGLEADR

No match to: 709.3099, 713.4081, 734.4956, 736.5024, 750.5167, 768.5226, 775.4343, 864.5463, 866.5065, 951.6184, 1032.5311, 1048.5239, 1064.6025, 1080.5145, 1094.5380, 1120.5609, 1277.2272, 1279.7660, 1323.6927, 1323.6927, 1334.8834, 1339.6825, 1339.6825, 1355.6804, 1388.6115, 1388.6115, 1404.6049, 1448.9232, 1520.7681, 1536.7667, 1553.8102, 1618.0673, 1637.8778, 1732.1171, 1756.8164, 1756.8164, 1784.8204, 1872.9238, 1901.2563, 2015.2742, 2318.1804, 2368.2368, 2384.2234, 2771.5273, 2781.4150, 2923.3938, 2926.5046, 2985.4858, 3689.8784

3. gi|168013985 **Mass:** 21937 **Score:** 43 **Expect:** 31 **Queries matched:** 6

predicted protein [Physcomitrella patens subsp. patens]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1371.6730	1370.6657	1370.6149	0.0508	118	127	1	---	NNELDHRCWK
1536.7667	1535.7594	1535.7732	-0.0138	102	114	1	---	GVQWLDKTFATDR
1553.8102	1552.8029	1552.8321	-0.0292	172	186	1	---	GHVTGVDLQLKSSGR
2368.2368	2367.2295	2367.2177	0.0118	50	70	1	---	FQMGEQSKIVSMTQTIIVEAK
2384.2234	2383.2161	2383.2126	0.0035	50	70	1	---	FQMGEQSKIVSMTQTIIVEAK + Oxidation (M)
2485.3235	2484.3162	2484.2657	0.0506	149	169	1	---	WRLGVIYLYVASMPVCASIDR + Oxidation (M)

No match to: 709.3099, 713.4081, 734.4956, 736.5024, 750.5167, 768.5226, 775.4343, 864.5463, 866.5065, 951.6184, 1032.5311, 1048.5239, 1064.6025, 1080.5145, 1094.5380, 1120.5609, 1277.2272, 1279.7660, 1323.6927, 1323.6927, 1334.8834, 1339.6825, 1339.6825, 1355.6804, 1388.6115, 1388.6115, 1404.6049, 1448.9232, 1520.7681, 1618.0673, 1637.8778, 1732.1171, 1756.8164, 1756.8164, 1784.8204, 1872.9238, 1901.2563, 2015.2742, 2168.1387, 2296.2332, 2296.2332, 2318.1804, 2771.5273, 2781.4150, 2923.3938, 2926.5046, 2985.4858, 3689.8784

4. gi|222858686 **Mass:** 137957 **Score:** 43 **Expect:** 34 **Queries matched:** 12

predicted protein [Populus trichocarpa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
775.4343	774.4270	774.4024	0.0246	14	20	0	---	GLSFHSK
866.5065	865.4992	865.4909	0.0083	2	8	1	---	LTKFETK
1048.5239	1047.5166	1047.5461	-0.0295	1112	1121	0	---	NLATAANFAR
1120.5609	1119.5536	1119.5230	0.0306	171	180	0	---	TVSPADDIMR + Oxidation (M)
1323.6927	1322.6854	1322.6223	0.0631	609	618	1	---	RYDHVMSMIR + Oxidation (M)
1323.6927	1322.6854	1322.6288	0.0566	816	827	0	---	GIFEGGLDNMVR + Oxidation (M)
1339.6825	1338.6752	1338.6172	0.0580	609	618	1	---	RYDHVMSMIR + 2 Oxidation (M)

1339.6825	1338.6752	1338.6172	0.0580	609 - 618	1	---	RYDHVMSMIR + 2 Oxidation (M)
1637.8778	1636.8705	1636.8429	0.0277	1098 - 1111	1	---	LALQNAMTVCFKNK
2771.5273	2770.5200	2770.4588	0.0613	895 - 920	1	---	ASVSARSSVFVAPTPGMPVSQIWIQR
2985.4858	2984.4785	2984.4129	0.0657	610 - 634	1	---	YDHVMSMIRNSQLCGQAMIAYLQQK
3689.8784	3688.8711	3688.8064	0.0647	1079 - 1109	1	---	QQELAAYFTHCNLQAPHLRLALQNAMTVCFK + Oxidation (M)

No match to: 709.3099, 713.4081, 734.4956, 736.5024, 750.5167, 768.5226, 864.5463, 951.6184, 1032.5311, 1064.6025, 1080.5145, 1094.5380, 1277.2272, 1279.7660, 1334.8834, 1355.6804, 1371.6730, 1388.6115, 1388.6115, 1404.6049, 1448.9232, 1520.7681, 1536.7667, 1553.8102, 1618.0673, 1732.1171, 1756.8164, 1756.8164, 1784.8204, 1872.9238, 1901.2563, 2015.2742, 2168.1387, 2296.2332, 2296.2332, 2318.1804, 2368.2368, 2384.2234, 2485.3235, 2781.4150, 2923.3938, 2926.5046

5. gi|87162603 **Mass:** 17357 **Score:** 40 **Expect:** 56 **Queries matched:** 7

hypothetical protein MtrDRAFT_AC148340g14v2 [Medicago truncatula]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
866.5065	865.4992	865.5133	-0.0141	132 - 138	1	---	RLIHAEK
1388.6115	1387.6042	1387.6554	-0.0511	121 - 132	1	---	FNFSMAEGVSKR + Oxidation (M)
1388.6115	1387.6042	1387.6554	-0.0511	121 - 132	1	---	FNFSMAEGVSKR + Oxidation (M)
1756.8164	1755.8091	1755.7919	0.0172	45 - 59	1	---	RACNEGATMDFLEVK + Oxidation (M)
1756.8164	1755.8091	1755.7919	0.0172	45 - 59	1	---	RACNEGATMDFLEVK + Oxidation (M)
1872.9238	1871.9165	1871.8570	0.0595	29 - 45	1	---	VYGMEADGSEVEVTSKR + Oxidation (M)
2318.1804	2317.1731	2317.0630	0.1101	23 - 44	1	---	SLEGSKVYGMEADGSEVEVTSK + Oxidation (M)

No match to: 709.3099, 713.4081, 734.4956, 736.5024, 750.5167, 768.5226, 775.4343, 864.5463, 951.6184, 1032.5311, 1048.5239, 1064.6025, 1080.5145, 1094.5380, 1120.5609, 1277.2272, 1279.7660, 1323.6927, 1323.6927, 1334.8834, 1339.6825, 1339.6825, 1355.6804, 1371.6730, 1404.6049, 1448.9232, 1520.7681, 1536.7667, 1553.8102, 1618.0673, 1637.8778, 1732.1171, 1784.8204, 1901.2563, 2015.2742, 2168.1387, 2296.2332, 2296.2332, 2368.2368, 2384.2234, 2485.3235, 2771.5273, 2781.4150, 2923.3938, 2926.5046, 2985.4858, 3689.8784

6. gi|198404505 **Mass:** 5445 **Score:** 40 **Expect:** 62 **Queries matched:** 3

DNA-directed RNA polymerase subunit B [Gynostemma pentaphyllum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
713.4081	712.4008	712.3690	0.0318	34 - 40	0	---	VAAHMGK
1080.5145	1079.5072	1079.4771	0.0301	41 - 51	0	---	GGDATPFTDVT
3689.8784	3688.8711	3688.9142	-0.0431	1 - 33	1	---	WTVEGITPDIIVNPHAIPSRMTIGQLIECIMGK

No match to: 709.3099, 734.4956, 736.5024, 750.5167, 768.5226, 775.4343, 864.5463, 866.5065, 951.6184, 1032.5311, 1048.5239, 1064.6025, 1094.5380, 1120.5609, 1277.2272, 1279.7660, 1323.6927, 1323.6927, 1334.8834, 1339.6825, 1339.6825, 1355.6804, 1371.6730, 1388.6115, 1388.6115, 1404.6049, 1448.9232, 1520.7681, 1536.7667, 1553.8102, 1618.0673, 1637.8778, 1732.1171, 1756.8164, 1756.8164, 1784.8204, 1872.9238, 1901.2563, 2015.2742, 2168.1387, 2296.2332, 2296.2332, 2318.1804, 2368.2368, 2384.2234, 2485.3235, 2771.5273, 2781.4150, 2923.3938, 2926.5046, 2985.4858

7. gi|45239438 **Mass:** 6885 **Score:** 37 **Expect:** 1.2e+002 **Queries matched:** 2

COI1 [Nicotiana benthamiana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
2296.2332	2295.2259	2295.2487	-0.0227	20 - 40	1	---	RFALYVRPGGLTDVGLSYVGR

2296.2332	2295.2259	2295.2487	-0.0227	20 - 40	1	26		RFALYVRPGGLTDVGLSYVGR

No match to: 709.3099, 713.4081, 734.4956, 736.5024, 750.5167, 768.5226, 775.4343, 864.5463, 866.5065, 951.6184, 1032.5311, 1048.5239, 1064.6025, 1080.5145, 1094.5380, 1120.5609, 1277.2272, 1279.7660, 1323.6927, 1323.6927, 1334.8834, 1339.6825, 1339.6825, 1355.6804, 1371.6730, 1388.6115, 1388.6115, 1404.6049, 1448.9232, 1520.7681, 1536.7667, 1553.8102, 1618.0673, 1637.8778, 1732.1171, 1756.8164, 1756.8164, 1784.8204, 1872.9238, 1901.2563, 2015.2742, 2168.1387, 2318.1804, 2368.2368, 2384.2234, 2485.3235, 2771.5273, 2781.4150, 2923.3938, 2926.5046, 2985.4858, 3689.8784

8. gi|66932629 **Mass:** 8565 **Score:** 37 **Expect:** 1.3e+002 **Queries matched:** 3

isocitrate dehydrogenase [Saltugilia latimeri]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1355.6804	1354.6731	1354.6840	-0.0109	30 -	42	0	---	TIEAEAAHGTVTR
2318.1804	2317.1731	2317.1563	0.0169	50 -	71	1	---	GGETSTNSIASIFAWSRGLAHR
2985.4858	2984.4785	2984.3895	0.0890	1 -	29	0	---	DGDAQSDFLAQGFGSLGLMTSVLVCPDGK

No match to: 709.3099, 713.4081, 734.4956, 736.5024, 750.5167, 768.5226, 775.4343, 864.5463, 866.5065, 951.6184, 1032.5311, 1048.5239, 1064.6025, 1080.5145, 1094.5380, 1120.5609, 1277.2272, 1279.7660, 1323.6927, 1323.6927, 1334.8834, 1339.6825, 1339.6825, 1371.6730, 1388.6115, 1388.6115, 1404.6049, 1448.9232, 1520.7681, 1536.7667, 1553.8102, 1618.0673, 1637.8778, 1732.1171, 1756.8164, 1756.8164, 1784.8204, 1872.9238, 1901.2563, 2015.2742, 2168.1387, 2296.2332, 2296.2332, 2368.2368, 2384.2234, 2485.3235, 2771.5273, 2781.4150, 2923.3938, 2926.5046, 3689.8784

9. gi|168056286 **Mass:** 24881 **Score:** 36 **Expect:** 1.4e+002 **Queries matched:** 4

predicted protein [Physcomitrella patens subsp. patens]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
2318.1804	2317.1731	2317.1834	-0.0103	29 -	49	1	---	QDGSSVVQGCIISIDEKILEK
2368.2368	2367.2295	2367.1593	0.0702	8 -	28	0	---	SDSLPSINVALVEEYIANYDR
2781.4150	2780.4077	2780.4555	-0.0478	126 -	150	1	---	LEEDLVNIGQAQVSTLPVSKVQEER
2926.5046	2925.4973	2925.3897	0.1077	89 -	111	1	---	TTEAIIPELMEWLCFVLRCEMER

No match to: 709.3099, 713.4081, 734.4956, 736.5024, 750.5167, 768.5226, 775.4343, 864.5463, 866.5065, 951.6184, 1032.5311, 1048.5239, 1064.6025, 1080.5145, 1094.5380, 1120.5609, 1277.2272, 1279.7660, 1323.6927, 1323.6927, 1334.8834, 1339.6825, 1339.6825, 1355.6804, 1371.6730, 1388.6115, 1388.6115, 1404.6049, 1448.9232, 1520.7681, 1536.7667, 1553.8102, 1618.0673, 1637.8778, 1732.1171, 1756.8164, 1756.8164, 1784.8204, 1872.9238, 1901.2563, 2015.2742, 2168.1387, 2296.2332, 2296.2332, 2384.2234, 2485.3235, 2771.5273, 2923.3938, 2985.4858, 3689.8784

10. gi|168066458 **Mass:** 32770 **Score:** 36 **Expect:** 1.5e+002 **Queries matched:** 5

predicted protein [Physcomitrella patens subsp. patens]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1553.8102	1552.8029	1552.7568	0.0461	147 -	158	1	---	MQADWRLPVHER + Oxidation (M)
1637.8778	1636.8705	1636.7952	0.0753	247 -	261	1	---	VMNMKVAAGEAPPYK + 2 Oxidation (M)
2318.1804	2317.1731	2317.1775	-0.0044	7 -	29	0	---	GFAEGGLASMIAGFATHPLDLVK + Oxidation (M)
2923.3938	2922.3865	2922.4803	-0.0938	30 -	58	1	---	VRMQLQGEVASPPLAMALAGSHASSGSVR + Oxidation (M)
2985.4858	2984.4785	2984.4959	-0.0174	123 -	152	1	---	VAAALVSGATGAAVGNPADLAMVRMQADWR + Oxidation (M)

No match to: 709.3099, 713.4081, 734.4956, 736.5024, 750.5167, 768.5226, 775.4343, 864.5463, 866.5065, 951.6184, 1032.5311, 1048.5239, 1064.6025, 1080.5145, 1094.5380, 1120.5609, 1277.2272, 1279.7660, 1323.6927, 1323.6927,

1334.8834, 1339.6825, 1339.6825, 1355.6804, 1371.6730, 1388.6115, 1388.6115, 1404.6049, 1448.9232, 1520.7681, 1536.7667, 1618.0673, 1732.1171, 1756.8164, 1756.8164, 1784.8204, 1872.9238, 1901.2563, 2015.2742, 2168.1387, 2296.2332, 2296.2332, 2368.2368, 2384.2234, 2485.3235, 2771.5273, 2781.4150, 2926.5046, 3689.8784

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 54

Protein View

Match to: **gi|4826572** Score: **193** Expect: **3e-014**
polygalacturonase [Phleum pratense]

Nominal mass (M_r): **42579**; Calculated pI value: **7.83**
NCBI BLAST search of gi|4826572 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **32%**

Matched peptides shown in **Bold Red**

```
     1 GKKEEKKEEK KESGDAASGA DGTYDITKLG AKPDGKTDCT KEVEEAWASA
    51 CGGTGKNTIV IPKGDFLTGP LNFTGPCKGD SVTIKLDGNL LSSNDLAKYK
   101 ANWIEIMRIK KLTITGKGTL DGQGKAVWGK NSCAKNYNCK ILPNTLVLDF
   151 CDDALIEGIT LLNAKFFHMN IYECKGVTVK DVTITAPGDS PNTDGIHIGD
   201 SSKVTITDTT IGTGDDCISI GPGSTGLNIT GVTCGPGHGI SVGSLGRYKD
   251 EKDVTDITVK NCVLKKSTNG LRIKSYEDAK SPLTASKLTY ENVKMEDVGY
   301 PIIIDQKYCP NKICTSKGDS ARVTVKDVTF RNITGTSSTP EAVSLLCSDK
   351 QPCNGVTMND VKIEYSGTNN KTMAVCTNAK VTAKGVSEAN TCAA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
99 - 108	1323.6927	1322.6854	1322.6805	0.0049	1	YKANWIEIMR (Ions score 24)
99 - 108	1323.6927	1322.6854	1322.6805	0.0049	1	YKANWIEIMR (No match)
99 - 108	1339.6825	1338.6752	1338.6754	-0.0002	1	YKANWIEIMR Oxidation (M) (No match)
99 - 108	1339.6825	1338.6752	1338.6754	-0.0002	1	YKANWIEIMR Oxidation (M) (Ions score 15)
101 - 108	1032.5311	1031.5238	1031.5222	0.0016	0	ANWIEIMR (No match)
101 - 108	1048.5239	1047.5166	1047.5171	-0.0005	0	ANWIEIMR Oxidation (M) (No match)
126 - 135	1120.5609	1119.5536	1119.5495	0.0042	1	AVWGKNSCAK (No match)
141 - 165	2771.5273	2770.5200	2770.4826	0.0374	0	ILPNTLVLDFCDDALIEGITLLNAK (No match)
166 - 175	1388.6115	1387.6042	1387.6053	-0.0010	0	FFHMNIYECK (Ions score 60)
166 - 175	1388.6115	1387.6042	1387.6053	-0.0010	0	FFHMNIYECK (No match)
166 - 175	1404.6049	1403.5976	1403.6002	-0.0026	0	FFHMNIYECK Oxidation (M) (No match)
166 - 180	1872.9238	1871.9165	1871.9062	0.0104	1	FFHMNIYECKGVTVK (No match)
176 - 203	2781.4150	2780.4077	2780.3828	0.0250	1	GVTVKDVTITAPGDSPNTDGIHIGDSSK (No match)
266 - 272	775.4343	774.4270	774.4348	-0.0077	1	KSTNGLR (No match)
288 - 307	2368.2368	2367.2295	2367.2031	0.0264	1	LTYENVKMEDVGYPIIIDQK (No match)
288 - 307	2384.2234	2383.2161	2383.1980	0.0181	1	LTYENVKMEDVGYPIIIDQK Oxidation (M) (No match)
295 - 307	1520.7681	1519.7608	1519.7592	0.0016	0	MEDVGYPIIIDQK (No match)
295 - 307	1536.7667	1535.7594	1535.7541	0.0053	0	MEDVGYPIIIDQK Oxidation (M) (No match)
313 - 322	1094.5380	1093.5307	1093.5186	0.0122	1	ICTSKGDSAR (No match)
323 - 331	1064.6025	1063.5952	1063.6025	-0.0073	1	VTVKDVTFR (No match)

Spot 38

Index

	Accession	Mass	Score	Description
1.	gi|4826572	42579	125	polygalacturonase [Phleum pratense]
2.	gi|255585751	22507	46	conserved hypothetical protein [Ricinus communis]
3.	gi|121551197	46896	45	thylakoid bound ascorbate peroxidase [Triticum aestivum]
4.	gi|90652448	111128	45	phosphoenolpyrovate carboxylase [Lupinus luteus]
5.	gi|22037346	21037	44	disease resistance-like protein GS3-7 [Glycine max]
6.	gi|21666264	15417	43	ascorbate peroxidase [Triticum aestivum]
7.	gi|225430676	41281	43	PREDICTED: hypothetical protein [Vitis vinifera]
8.	gi|125564123	99127	42	hypothetical protein OsI_31776 [Oryza sativa Indica Group]
9.	gi|25992557	41411	41	thylakoid-bound ascorbate peroxidase [Triticum aestivum]
10.	gi|145348905	35874	41	predicted protein [Ostreococcus lucimarinus CCE9901]

Results List

1. gi|4826572 **Mass:** 42579 **Score:** 125 **Expect:** 1.9e-007 **Queries matched:** 15

polygalacturonase [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1032.5364	1031.5291	1031.5222	0.0069	101	108	0	---	ANWIEIMR
1032.5364	1031.5291	1031.5222	0.0069	101	108	0	11	ANWIEIMR
1048.5121	1047.5048	1047.5171	-0.0123	101	108	0	---	ANWIEIMR + Oxidation (M)
1064.6066	1063.5993	1063.6025	-0.0032	323	331	1	---	VTVKDVTFR
1323.6903	1322.6830	1322.6805	0.0025	99	108	1	---	YKANWIEIMR
1323.6903	1322.6830	1322.6805	0.0025	99	108	1	---	YKANWIEIMR
1339.6696	1338.6623	1338.6754	-0.0131	99	108	1	4	YKANWIEIMR + Oxidation (M)
1339.6696	1338.6623	1338.6754	-0.0131	99	108	1	---	YKANWIEIMR + Oxidation (M)
1388.6100	1387.6027	1387.6053	-0.0025	166	175	0	57	FFHMNIYECK
1388.6100	1387.6027	1387.6053	-0.0025	166	175	0	---	FFHMNIYECK
1404.6035	1403.5962	1403.6002	-0.0040	166	175	0	---	FFHMNIYECK + Oxidation (M)
2369.2246	2368.2173	2368.0787	0.1387	351	371	1	---	QPCNGVTMNDVKIEYSGTNNK
2385.2195	2384.2122	2384.0736	0.1386	351	371	1	---	QPCNGVTMNDVKIEYSGTNNK + Oxidation (M)
2781.4016	2780.3943	2780.3828	0.0116	176	203	1	---	GVTVKDVTITAPGDSPNTDGIHIGDSSK
3339.7781	3338.7708	3338.5428	0.2280	332	362	1	---	NITGTSSTPEAVSLLCSDKQPCNGVTMNDVK + Oxidation (M)

No match to: 713.3959, 724.4827, 734.4888, 736.4824, 744.3909, 750.5089, 768.5094, 782.4706, 838.5156, 848.5186, 864.5176, 881.2809, 1201.6028, 1277.1808, 1279.7418, 1320.5891, 1334.8646, 1355.6810, 1448.8967, 1493.7418, 1562.9358, 1638.8817, 1707.7816, 1732.0823, 1756.8195, 1756.8195, 2015.2649, 2143.0430, 2168.1279, 2230.2129, 2296.2246, 2400.0366, 2564.1987, 2662.4023, 2790.3215, 2824.3210, 2909.4448, 2922.3713, 3331.5798, 3348.6213

2. gi|255585751 **Mass:** 22507 **Score:** 46 **Expect:** 14 **Queries matched:** 7

conserved hypothetical protein [Ricinus communis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
744.3909	743.3836	743.4177	-0.0341	133	138	0	---	NQLLEK
1032.5364	1031.5291	1031.5260	0.0031	164	172	1	---	TFPQGGRNR
1032.5364	1031.5291	1031.5260	0.0031	164	172	1	---	TFPQGGRNR
1493.7418	1492.7345	1492.8071	-0.0726	19	31	1	---	GLIYMDILTNGRK
2143.0430	2142.0357	2141.9461	0.0896	174	191	1	---	QEQDIDIDSEDNTNHKNK
2168.1279	2167.1206	2167.1017	0.0190	34	54	0	---	ALIDMGATNNFITGTMASVLK
2790.3215	2789.3142	2789.4455	-0.1313	34	59	1	---	ALIDMGATNNFITGTMASVLKLEVHK + Oxidation (M)

No match to: 713.3959, 724.4827, 734.4888, 736.4824, 750.5089, 768.5094, 782.4706, 838.5156, 848.5186, 864.5176, 881.2809, 1048.5121, 1064.6066, 1201.6028, 1277.1808, 1279.7418, 1320.5891, 1323.6903, 1323.6903, 1334.8646, 1339.6696, 1339.6696, 1355.6810, 1388.6100, 1388.6100, 1404.6035, 1448.8967, 1562.9358, 1638.8817, 1707.7816, 1732.0823, 1756.8195, 1756.8195, 2015.2649, 2230.2129, 2296.2246, 2369.2246, 2385.2195, 2400.0366, 2564.1987, 2662.4023, 2781.4016, 2824.3210, 2909.4448, 2922.3713, 3331.5798, 3339.7781, 3348.6213

3. gi|121551197 **Mass:** 46896 **Score:** 45 **Expect:** 19 **Queries matched:** 9

thylakoid bound ascorbate peroxidase [Triticum aestivum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
713.3959	712.3886	712.3544	0.0343	210	214	0	---	EVFYR
744.3909	743.3836	743.4289	-0.0453	25	32	0	---	AAVASGLR
864.5176	863.5103	863.4687	0.0416	175	181	1	---	LPMKYGR
1323.6903	1322.6830	1322.7306	-0.0476	221	233	0	---	EIVALSGAHTLGR
1323.6903	1322.6830	1322.7306	-0.0476	221	233	0	7	EIVALSGAHTLGR
1388.6100	1387.6027	1387.6441	-0.0414	210	220	1	---	EVFYRMGLDDK + Oxidation (M)
1388.6100	1387.6027	1387.6441	-0.0414	210	220	1	---	EVFYRMGLDDK + Oxidation (M)
1493.7418	1492.7345	1492.7126	0.0219	65	78	1	---	CMAASEAAQLKSAR
2824.3210	2823.3137	2823.4218	-0.1080	281	305	1	---	DQELLVLPTDAALFDDPSFKVYAEK

No match to: 724.4827, 734.4888, 736.4824, 750.5089, 768.5094, 782.4706, 838.5156, 848.5186, 881.2809, 1032.5364, 1032.5364, 1048.5121, 1064.6066, 1201.6028, 1277.1808, 1279.7418, 1320.5891, 1334.8646, 1339.6696, 1339.6696, 1355.6810, 1404.6035, 1448.8967, 1562.9358, 1638.8817, 1707.7816, 1732.0823, 1756.8195, 1756.8195, 2015.2649, 2143.0430, 2168.1279, 2230.2129, 2296.2246, 2369.2246, 2385.2195, 2400.0366, 2564.1987, 2662.4023, 2781.4016, 2790.3215, 2909.4448, 2922.3713, 3331.5798, 3339.7781, 3348.6213

4. gi|90652448 **Mass:** 111128 **Score:** 45 **Expect:** 20 **Queries matched:** 11

phosphoenolpyrovate carboxylase [Lupinus luteus]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
734.4888	733.4815	733.4374	0.0441	146	151	0	---	LVFDLK
1334.8646	1333.8573	1333.7870	0.0704	554	564	1	---	HPLRVVPLFEK
1638.8817	1637.8744	1637.9100	-0.0356	833	848	1	---	GDPGIAALNDRLLVSK
1756.8195	1755.8122	1755.8171	-0.0049	712	726	0	---	ALMDQMAVIATEEYR + Oxidation (M)
1756.8195	1755.8122	1755.8171	-0.0049	712	726	0	---	ALMDQMAVIATEEYR + Oxidation (M)
2143.0430	2142.0357	2142.1419	-0.1062	77	97	0	---	LEEIGNVITSLDAGDSIVVAK
2168.1279	2167.1206	2167.1789	-0.0583	890	907	1	---	LRHSYITTLNVFQAYTLK
2230.2129	2229.2056	2229.1247	0.0809	181	199	0	---	SLLQSMLGYEIAYLICMPK

2296.2246	2295.2173	2295.1429	0.0744	98 - 117	0	---	SFSHMLNLANLAEEVQISHR
2824.3210	2823.3137	2823.1722	0.1415	309 - 330	0	---	MMAANMYYSQIEDLMFELSMWR + 4 Oxidation (M)
2909.4448	2908.4375	2908.4653	-0.0278	687 - 711	1	---	TLQRYTAATLEHGMNPPISPKPEWR + Oxidation (M)

No match to: 713.3959, 724.4827, 736.4824, 744.3909, 750.5089, 768.5094, 782.4706, 838.5156, 848.5186, 864.5176, 881.2809, 1032.5364, 1032.5364, 1048.5121, 1064.6066, 1201.6028, 1277.1808, 1279.7418, 1320.5891, 1323.6903, 1323.6903, 1339.6696, 1339.6696, 1355.6810, 1388.6100, 1388.6100, 1404.6035, 1448.8967, 1493.7418, 1562.9358, 1707.7816, 1732.0823, 2015.2649, 2369.2246, 2385.2195, 2400.0366, 2564.1987, 2662.4023, 2781.4016, 2790.3215, 2922.3713, 3331.5798, 3339.7781, 3348.6213

5. gi|22037346 **Mass:** 21037 **Score:** 44 **Expect:** 26 **Queries matched:** 6

disease resistance-like protein GS3-7 [Glycine max]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1320.5891	1319.5818	1319.6357	-0.0539	19 -	29	0	---	IDPSYEDVLNR
1339.6696	1338.6623	1338.7005	-0.0382	88 -	98	0	---	NVFLDIAFCLK
1339.6696	1338.6623	1338.7005	-0.0382	88 -	98	0	---	NVFLDIAFCLK
2143.0430	2142.0357	2141.9254	0.1103	102 -	118	0	---	LTEVEHMLCSLYDNCMK
2230.2129	2229.2056	2229.1687	0.0369	134 -	152	1	---	HGIVEMHDLIQVVGREIER
2296.2246	2295.2173	2295.2183	-0.0010	30 -	51	0	---	VVTYASGLPLALEIIGSNMFGK + Oxidation (M)

No match to: 713.3959, 724.4827, 734.4888, 736.4824, 744.3909, 750.5089, 768.5094, 782.4706, 838.5156, 848.5186, 864.5176, 881.2809, 1032.5364, 1032.5364, 1048.5121, 1064.6066, 1201.6028, 1277.1808, 1279.7418, 1323.6903, 1323.6903, 1334.8646, 1355.6810, 1388.6100, 1388.6100, 1404.6035, 1448.8967, 1493.7418, 1562.9358, 1638.8817, 1707.7816, 1732.0823, 1756.8195, 1756.8195, 2015.2649, 2168.1279, 2369.2246, 2385.2195, 2400.0366, 2564.1987, 2662.4023, 2781.4016, 2790.3215, 2824.3210, 2909.4448, 2922.3713, 3331.5798, 3339.7781, 3348.6213

6. gi|21666264 **Mass:** 15417 **Score:** 43 **Expect:** 29 **Queries matched:** 6

ascorbate peroxidase [Triticum aestivum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
713.3959	712.3886	712.3544	0.0343	23 -	27	0	---	EVFYR
1323.6903	1322.6830	1322.7306	-0.0476	34 -	46	0	---	EIVALSGAHTLGR
1323.6903	1322.6830	1322.7306	-0.0476	34 -	46	0	7	EIVALSGAHTLGR
1388.6100	1387.6027	1387.6441	-0.0414	23 -	33	1	---	EVFYRMGLDDK + Oxidation (M)
1388.6100	1387.6027	1387.6441	-0.0414	23 -	33	1	---	EVFYRMGLDDK + Oxidation (M)
2824.3210	2823.3137	2823.4218	-0.1080	94 -	118	1	---	DQELLVLPTDAALFDDPSFKVYAEK

No match to: 724.4827, 734.4888, 736.4824, 744.3909, 750.5089, 768.5094, 782.4706, 838.5156, 848.5186, 864.5176, 881.2809, 1032.5364, 1032.5364, 1048.5121, 1064.6066, 1201.6028, 1277.1808, 1279.7418, 1320.5891, 1334.8646, 1339.6696, 1339.6696, 1355.6810, 1404.6035, 1448.8967, 1493.7418, 1562.9358, 1638.8817, 1707.7816, 1732.0823, 1756.8195, 1756.8195, 2015.2649, 2143.0430, 2168.1279, 2230.2129, 2296.2246, 2369.2246, 2385.2195, 2400.0366, 2564.1987, 2662.4023, 2781.4016, 2790.3215, 2909.4448, 2922.3713, 3331.5798, 3339.7781, 3348.6213

7. gi|225430676 **Mass:** 41281 **Score:** 43 **Expect:** 32 **Queries matched:** 7

PREDICTED: hypothetical protein [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1032.5364	1031.5291	1031.4746	0.0545	192 -	199	0	---	TDFSMFLR + Oxidation (M)

1032.5364	1031.5291	1031.4746	0.0545	192 - 199	0	---	TDFSMFLR + Oxidation (M)
1355.6810	1354.6737	1354.6802	-0.0065	351 - 362	0	---	TEFVNVTVSMTK
1638.8817	1637.8744	1637.8008	0.0736	11 - 26	1	---	GGNGDTSYAKNSLVQK
2385.2195	2384.2122	2384.2375	-0.0253	316 - 337	0	---	AVAEPLLVSHFGDGIIEEVFSR
2922.3713	2921.3640	2921.4745	-0.1104	83 - 107	1	---	MGRQLPEIQVFLNDLPGNDFNTIFK + Oxidation (M)
3339.7781	3338.7708	3338.6526	0.1183	48 - 78	0	---	FPTSLCIADLGCSSGPNTLFAVLEVVTTVDR

No match to: 713.3959, 724.4827, 734.4888, 736.4824, 744.3909, 750.5089, 768.5094, 782.4706, 838.5156, 848.5186, 864.5176, 881.2809, 1048.5121, 1064.6066, 1201.6028, 1277.1808, 1279.7418, 1320.5891, 1323.6903, 1323.6903, 1334.8646, 1339.6696, 1339.6696, 1388.6100, 1388.6100, 1404.6035, 1448.8967, 1493.7418, 1562.9358, 1707.7816, 1732.0823, 1756.8195, 1756.8195, 2015.2649, 2143.0430, 2168.1279, 2230.2129, 2296.2246, 2369.2246, 2400.0366, 2564.1987, 2662.4023, 2781.4016, 2790.3215, 2824.3210, 2909.4448, 3331.5798, 3348.6213

8. gi|125564123 **Mass:** 99127 **Score:** 42 **Expect:** 37 **Queries matched:** 10

hypothetical protein OsI_31776 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
744.3909	743.3836	743.4038	-0.0202	132 - 137		1	---	ADRINR
1048.5121	1047.5048	1047.5752	-0.0704	847 - 856		0	---	ILGGSGWVFI
1064.6066	1063.5993	1063.6654	-0.0661	559 - 566		1	---	LRHLLVWK
1201.6028	1200.5955	1200.6688	-0.0733	208 - 219		0	---	IIAVWGMGGLGK
1732.0823	1731.0750	1730.9719	0.1032	462 - 475		1	---	LIRLWISEGFIEQK
2143.0430	2142.0357	2141.9649	0.0709	85 - 102		0	---	LAHDMEDVVDEFMYVIGK + 2 Oxidation (M)
2369.2246	2368.2173	2368.1078	0.1095	85 - 104		1	---	LAHDMEDVVDEFMYVIGKNK + Oxidation (M)
2385.2195	2384.2122	2384.1027	0.1095	85 - 104		1	---	LAHDMEDVVDEFMYVIGKNK + 2 Oxidation (M)
2824.3210	2823.3137	2823.4741	-0.1604	753 - 776		0	---	QIFIQEGALANLHYLHIDSLMELR
3348.6213	3347.6140	3347.5920	0.0220	574 - 600		1	---	SLNNWESMEPFEGLWDLKELHYLNEVR

No match to: 713.3959, 724.4827, 734.4888, 736.4824, 750.5089, 768.5094, 782.4706, 838.5156, 848.5186, 864.5176, 881.2809, 1032.5364, 1032.5364, 1277.1808, 1279.7418, 1320.5891, 1323.6903, 1323.6903, 1334.8646, 1339.6696, 1339.6696, 1355.6810, 1388.6100, 1388.6100, 1404.6035, 1448.8967, 1493.7418, 1562.9358, 1638.8817, 1707.7816, 1756.8195, 1756.8195, 2015.2649, 2168.1279, 2230.2129, 2296.2246, 2400.0366, 2564.1987, 2662.4023, 2781.4016, 2790.3215, 2909.4448, 2922.3713, 3331.5798, 3339.7781

9. gi|25992557 **Mass:** 41411 **Score:** 41 **Expect:** 45 **Queries matched:** 8

thylakoid-bound ascorbate peroxidase [Triticum aestivum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
713.3959	712.3886	712.3544	0.0343	153 - 157		0	---	EVFYR
864.5176	863.5103	863.4687	0.0416	118 - 124		1	---	LPMKYGR
1323.6903	1322.6830	1322.7306	-0.0476	164 - 176		0	---	EIVALSGAHTLGR
1323.6903	1322.6830	1322.7306	-0.0476	164 - 176		0	7	EIVALSGAHTLGR
1388.6100	1387.6027	1387.6441	-0.0414	153 - 163		1	---	EVFYRMGLDDK + Oxidation (M)
1388.6100	1387.6027	1387.6441	-0.0414	153 - 163		1	---	EVFYRMGLDDK + Oxidation (M)
1493.7418	1492.7345	1492.7126	0.0219	8 - 21		1	---	CMAASEAAQLKSAR
2824.3210	2823.3137	2823.4218	-0.1080	224 - 248		1	---	DQELLVLPTDAALFDDPSFKVYAEK

No match to: 724.4827, 734.4888, 736.4824, 744.3909, 750.5089, 768.5094, 782.4706, 838.5156, 848.5186, 881.2809,

1032.5364, 1032.5364, 1048.5121, 1064.6066, 1201.6028, 1277.1808, 1279.7418, 1320.5891, 1334.8646, 1339.6696, 1339.6696, 1355.6810, 1404.6035, 1448.8967, 1562.9358, 1638.8817, 1707.7816, 1732.0823, 1756.8195, 1756.8195, 2015.2649, 2143.0430, 2168.1279, 2230.2129, 2296.2246, 2369.2246, 2385.2195, 2400.0366, 2564.1987, 2662.4023, 2781.4016, 2790.3215, 2909.4448, 2922.3713, 3331.5798, 3339.7781, 3348.6213

10. gi|145348905 **Mass:** 35874 **Score:** 41 **Expect:** 46 **Queries matched:** 8

predicted protein [Ostreococcus lucimarinus CCE9901]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1032.5364	1031.5291	1031.5148	0.0143	136	143	1	---	DEWRVATR
1032.5364	1031.5291	1031.5148	0.0143	136	143	1	---	DEWRVATR
1404.6035	1403.5962	1403.6317	-0.0354	3	15	0	---	AIVADGDDASEWR
1707.7816	1706.7743	1706.7682	0.0062	1	15	1	---	MRAIVADGDDASEWR + Oxidation (M)
1756.8195	1755.8122	1755.8613	-0.0491	172	185	1	---	ENTEFAIVMFDLRR + Oxidation (M)
1756.8195	1755.8122	1755.8613	-0.0491	172	185	1	---	ENTEFAIVMFDLRR + Oxidation (M)
2369.2246	2368.2173	2368.1910	0.0264	228	248	1	---	EYAANVEETQRLLDSATFALK
2400.0366	2399.0293	2399.1573	-0.1280	112	132	1	---	SLTGDQMGTLATYQQMLQNKR + Oxidation (M)

No match to: 713.3959, 724.4827, 734.4888, 736.4824, 744.3909, 750.5089, 768.5094, 782.4706, 838.5156, 848.5186, 864.5176, 881.2809, 1048.5121, 1064.6066, 1201.6028, 1277.1808, 1279.7418, 1320.5891, 1323.6903, 1323.6903, 1334.8646, 1339.6696, 1339.6696, 1355.6810, 1388.6100, 1388.6100, 1448.8967, 1493.7418, 1562.9358, 1638.8817, 1732.0823, 2015.2649, 2143.0430, 2168.1279, 2230.2129, 2296.2246, 2385.2195, 2564.1987, 2662.4023, 2781.4016, 2790.3215, 2824.3210, 2909.4448, 2922.3713, 3331.5798, 3339.7781, 3348.6213

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 55

Protein View

Match to: **gi|4826572** Score: **125** Expect: **1.9e-007**
polygalacturonase [Phleum pratense]

Nominal mass (M_r): **42579**; Calculated pI value: **7.83**
NCBI BLAST search of gi|4826572 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **24%**

Matched peptides shown in **Bold Red**

```
   1 GKKEEKKEEK KESGDAASGA DGTYDITKLG AKPDGKTDCT KEVEEAWASA
  51 CGGTGKNTIV IPKGDFLTGP LNFTGPCKGD SVTIKLDGNL LSSNDLAKYK
 101 ANWIEIMRIK KLTITGKGTL DGQGKAVWGK NSCAKNYNCK ILPNTLVLDF
 151 CDDALIEGIT LLNAKFFHMN IYECKGVTVK DVTITAPGDS PNTDGIHIGD
 201 SSKVTITDTT IGTGDDCISI GPGSTGLNIT GVTCGPGHGI SVGSLGRYKD
 251 EKDVTDITVK NCVLKKSTNG LRIKSYEDAK SPLTASKLTY ENVKMEDVGY
 301 PIIIDQKYCP NKICTSKGDS ARVTVKDVTF RNITGTSSTP EAVSLLCSDK
 351 QPCNGVTMND VKIEYSGTNN KTMAVCTNAK VTAKGVSEAN TCAA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
99 - 108	1323.6903	1322.6830	1322.6805	0.0025	1	YKANWIEIMR (No match)
99 - 108	1323.6903	1322.6830	1322.6805	0.0025	1	YKANWIEIMR (No match)
99 - 108	1339.6696	1338.6623	1338.6754	-0.0131	1	YKANWIEIMR Oxidation (M) (Ions score 4)
99 - 108	1339.6696	1338.6623	1338.6754	-0.0131	1	YKANWIEIMR Oxidation (M) (No match)
101 - 108	1032.5364	1031.5291	1031.5222	0.0069	0	ANWIEIMR (No match)
101 - 108	1032.5364	1031.5291	1031.5222	0.0069	0	ANWIEIMR (Ions score 11)
101 - 108	1048.5121	1047.5048	1047.5171	-0.0123	0	ANWIEIMR Oxidation (M) (No match)
166 - 175	1388.6100	1387.6027	1387.6053	-0.0025	0	FFHMNIYECK (Ions score 57)
166 - 175	1388.6100	1387.6027	1387.6053	-0.0025	0	FFHMNIYECK (No match)
166 - 175	1404.6035	1403.5962	1403.6002	-0.0040	0	FFHMNIYECK Oxidation (M) (No match)
176 - 203	2781.4016	2780.3943	2780.3828	0.0116	1	GVTVKDVTITAPGDSPNTDGIHIGDSSK (No match)
323 - 331	1064.6066	1063.5993	1063.6025	-0.0032	1	VTVKDVTFR (No match)
332 - 362	3339.7781	3338.7708	3338.5428	0.2280	1	NITGTSSTPEAVSLLCSDKQPCNGVTMNDVK Oxidation (M) (No match)
351 - 371	2369.2246	2368.2173	2368.0787	0.1387	1	QPCNGVTMNDVKIEYSGTNNK (No match)
351 - 371	2385.2195	2384.2122	2384.0736	0.1386	1	QPCNGVTMNDVKIEYSGTNNK Oxidation (M) (No match)

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	Accession	Mass	Score	Description
1.	gi|4826572	42579	152	polygalacturonase [Phleum pratense]
2.	gi|34394307	8524	49	hypothetical protein [Oryza sativa Japonica Group]
3.	gi|147855451	91852	45	hypothetical protein [Vitis vinifera]
4.	gi|27819107	57538	39	ADP-glucose pyrophosphorylase small subunit [Solanum tuberosum]
5.	gi|51458190	22454	39	ribosomal protein small subunit 4 [Asplenium theciferum]
6.	gi|159468568	22282	38	predicted protein [Chlamydomonas reinhardtii]
7.	gi|145334527	60668	38	unknown protein [Arabidopsis thaliana]
8.	gi|147816687	19465	37	hypothetical protein [Vitis vinifera]
9.	gi|147823327	30971	37	hypothetical protein [Vitis vinifera]
10.	gi|78191069	37233	37	carotene cleavage dioxygenase [Nicotiana langsdorffii x Nicotiana sanderae]

Results List

1. gi|4826572 **Mass:** 42579 **Score:** 152 **Expect:** 3.8e-010 **Queries matched:** 17

polygalacturonase [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1032.5322	1031.5249	1031.5222	0.0027	101	108	0	---	ANWIEIMR
1048.5238	1047.5165	1047.5171	-0.0006	101	108	0	---	ANWIEIMR + Oxidation (M)
1064.6013	1063.5940	1063.6025	-0.0085	323	331	1	---	VTVKDVTFR
1094.5376	1093.5303	1093.5186	0.0118	313	322	1	---	ICTSKGDSAR
1323.6885	1322.6812	1322.6805	0.0007	99	108	1	---	YKANWIEIMR
1323.6885	1322.6812	1322.6805	0.0007	99	108	1	---	YKANWIEIMR
1339.6805	1338.6732	1338.6754	-0.0022	99	108	1	---	YKANWIEIMR + Oxidation (M)
1339.6805	1338.6732	1338.6754	-0.0022	99	108	1	---	YKANWIEIMR + Oxidation (M)
1388.6141	1387.6068	1387.6053	0.0016	166	175	0	---	FFHMNIYECK
1388.6141	1387.6068	1387.6053	0.0016	166	175	0	62	FFHMNIYECK
1404.6049	1403.5976	1403.6002	-0.0026	166	175	0	---	FFHMNIYECK + Oxidation (M)
1520.7607	1519.7534	1519.7592	-0.0058	295	307	0	---	MEDVGYPIIIDQK
1536.7573	1535.7500	1535.7541	-0.0041	295	307	0	---	MEDVGYPIIIDQK + Oxidation (M)
2368.2332	2367.2259	2367.2031	0.0228	288	307	1	---	LTYENVKMEDVGYPIIIDQK
2384.2183	2383.2110	2383.1980	0.0130	288	307	1	---	LTYENVKMEDVGYPIIIDQK + Oxidation (M)
2771.5024	2770.4951	2770.4826	0.0125	141	165	0	---	ILPNTLVLDFCDDALIEGITLLNAK
2781.4065	2780.3992	2780.3828	0.0165	176	203	1	---	GVTVKDVTITAPGDSPNTDGIHIGDSSK

No match to: 709.3157, 713.4075, 734.4991, 750.5170, 768.5210, 864.9976, 886.9797, 1334.8853, 1355.6716, 1448.9133, 1553.8007, 1618.0607, 1637.8737, 1756.8154, 1756.8154, 1784.8260, 1892.9554, 2168.1316, 2296.2305, 2296.2305, 2923.3794, 2986.4895

2. gi|34394307 **Mass:** 8524 **Score:** 49 **Expect:** 8.5 **Queries matched:** 5

hypothetical protein [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
768.5210	767.5137	767.4766	0.0372	48	53	0	---	RPVQLR
1323.6885	1322.6812	1322.6214	0.0598	37	47	1	---	REGYENEASLR
1323.6885	1322.6812	1322.6214	0.0598	37	47	1	---	REGYENEASLR
1637.8737	1636.8664	1636.8532	0.0132	2	17	1	---	AASTRAAVLGSTETFR
1784.8260	1783.8187	1783.8886	-0.0699	1	17	1	---	MAASTRAAVLGSTETFR + Oxidation (M)

No match to: 709.3157, 713.4075, 734.4991, 750.5170, 864.9976, 886.9797, 1032.5322, 1048.5238, 1064.6013, 1094.5376, 1334.8853, 1339.6805, 1339.6805, 1355.6716, 1388.6141, 1388.6141, 1404.6049, 1448.9133, 1520.7607, 1536.7573, 1553.8007, 1618.0607, 1756.8154, 1756.8154, 1892.9554, 2168.1316, 2296.2305, 2296.2305, 2368.2332, 2384.2183, 2771.5024, 2781.4065, 2923.3794, 2986.4895

3. gi|147855451 **Mass:** 91852 **Score:** 45 **Expect:** 21 **Queries matched:** 12

hypothetical protein [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
709.3157	708.3084	708.3224	-0.0140	38	43	1	---	KDGSMR + Oxidation (M)
1048.5238	1047.5165	1047.5569	-0.0404	648	656	1	---	VSPMKSIMR
1064.6013	1063.5940	1063.5518	0.0422	648	656	1	---	VSPMKSIMR + Oxidation (M)
1323.6885	1322.6812	1322.7207	-0.0395	743	753	1	---	HAVVKVQWSNR
1323.6885	1322.6812	1322.7207	-0.0395	743	753	1	---	HAVVKVQWSNR
1388.6141	1387.6068	1387.6554	-0.0486	39	49	1	---	DGSMRLYIDYR
1388.6141	1387.6068	1387.6554	-0.0486	39	49	1	---	DGSMRLYIDYR
1404.6049	1403.5976	1403.6503	-0.0527	39	49	1	---	DGSMRLYIDYR + Oxidation (M)
1448.9133	1447.9060	1447.8775	0.0285	348	360	1	---	FVGPLAAIRVHIR
2168.1316	2167.1243	2167.1928	-0.0685	206	224	1	---	FIEGFSKIALPLTSFQELK
2384.2183	2383.2110	2383.1571	0.0539	284	301	1	---	IWRHFLFGETCEIFTYHK
2986.4895	2985.4822	2985.4397	0.0425	92	117	1	---	VRSEDILVMPFSLTNAPAAFMDLMNR + 3 Oxidation (M)

No match to: 713.4075, 734.4991, 750.5170, 768.5210, 864.9976, 886.9797, 1032.5322, 1094.5376, 1334.8853, 1339.6805, 1339.6805, 1355.6716, 1520.7607, 1536.7573, 1553.8007, 1618.0607, 1637.8737, 1756.8154, 1756.8154, 1784.8260, 1892.9554, 2296.2305, 2296.2305, 2368.2332, 2771.5024, 2781.4065, 2923.3794

4. gi|27819107 **Mass:** 57538 **Score:** 39 **Expect:** 74 **Queries matched:** 6

ADP-glucose pyrophosphorylase small subunit [Solanum tuberosum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1032.5322	1031.5249	1031.5400	-0.0150	378	386	0	---	SAPIYTQPR
1520.7607	1519.7534	1519.6797	0.0737	10	22	1	---	SSPSSNNCINERR
1553.8007	1552.7934	1552.7555	0.0380	248	261	1	---	ATAFGLMKIDEEGR + Oxidation (M)
1637.8737	1636.8664	1636.8568	0.0096	293	307	0	---	EMPLVASMGIYVISK
1892.9554	1891.9481	1891.9387	0.0094	28	45	1	---	AVSSRNLSFSSSHLTGDK
2384.2183	2383.2110	2383.1960	0.0150	367	386	1	---	KPVPDFSFYDRSAPIYTQPR

No match to: 709.3157, 713.4075, 734.4991, 750.5170, 768.5210, 864.9976, 886.9797, 1048.5238, 1064.6013, 1094.5376, 1323.6885, 1323.6885, 1334.8853, 1339.6805, 1339.6805, 1355.6716, 1388.6141, 1388.6141, 1404.6049, 1448.9133, 1536.7573, 1618.0607, 1756.8154, 1756.8154, 1784.8260, 2168.1316, 2296.2305, 2296.2305, 2368.2332,

2771.5024, 2781.4065, 2923.3794, 2986.4895

5. gi|51458190 **Mass:** 22454 **Score:** 39 **Expect:** 80 **Queries matched:** 4

ribosomal protein small subunit 4 [Asplenium theciferum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1536.7573	1535.7500	1535.7289	0.0211	6	20	0	---	DLPGFMGGGETTNLK
2168.1316	2167.1243	2167.1160	0.0083	176	193	0	---	ESINLNINELLVVEYYSR
2296.2305	2295.2232	2295.2110	0.0123	176	194	1	---	ESINLNINELLVVEYYSRK
2296.2305	2295.2232	2295.1607	0.0625	151	171	0	---	TPDHLTFALSEGDRPTGLVNR

No match to: 709.3157, 713.4075, 734.4991, 750.5170, 768.5210, 864.9976, 886.9797, 1032.5322, 1048.5238, 1064.6013, 1094.5376, 1323.6885, 1323.6885, 1334.8853, 1339.6805, 1339.6805, 1355.6716, 1388.6141, 1388.6141, 1404.6049, 1448.9133, 1520.7607, 1553.8007, 1618.0607, 1637.8737, 1756.8154, 1756.8154, 1784.8260, 1892.9554, 2368.2332, 2384.2183, 2771.5024, 2781.4065, 2923.3794, 2986.4895

6. gi|159468568 **Mass:** 22282 **Score:** 38 **Expect:** 1.1e+002 **Queries matched:** 4

predicted protein [Chlamydomonas reinhardtii]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1032.5322	1031.5249	1031.4784	0.0465	135	143	0	---	SHISFNDGR
1784.8260	1783.8187	1783.8853	-0.0665	135	150	1	---	SHISFNDGRTPSIPEK
1892.9554	1891.9481	1891.9639	-0.0157	2	20	0	---	GEGALGVPPLPVTASNEER
2384.2183	2383.2110	2383.1478	0.0633	104	125	0	---	TSQLVPDVSQFPGYIACASSTR

No match to: 709.3157, 713.4075, 734.4991, 750.5170, 768.5210, 864.9976, 886.9797, 1048.5238, 1064.6013, 1094.5376, 1323.6885, 1323.6885, 1334.8853, 1339.6805, 1339.6805, 1355.6716, 1388.6141, 1388.6141, 1404.6049, 1448.9133, 1520.7607, 1536.7573, 1553.8007, 1618.0607, 1637.8737, 1756.8154, 1756.8154, 2168.1316, 2296.2305, 2296.2305, 2368.2332, 2771.5024, 2781.4065, 2923.3794, 2986.4895

7. gi|145334527 **Mass:** 60668 **Score:** 38 **Expect:** 1.1e+002 **Queries matched:** 5

unknown protein [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1323.6885	1322.6812	1322.6830	-0.0017	119	130	1	14	KGEHEVIASEPK
1323.6885	1322.6812	1322.6830	-0.0017	119	130	1	---	KGEHEVIASEPK
1892.9554	1891.9481	1891.9475	0.0007	365	380	1	---	IDVLVMNTGHHWNRGK + Oxidation (M)
2368.2332	2367.2259	2367.1906	0.0354	360	378	1	---	QYLQKIDVLVMNTGHHWNR + Oxidation (M)
2781.4065	2780.3992	2780.2753	0.1239	263	287	1	---	TLAFVGDSLGRQQFQSMMCMISGGK + 2 Oxidation (M)

No match to: 709.3157, 713.4075, 734.4991, 750.5170, 768.5210, 864.9976, 886.9797, 1032.5322, 1048.5238, 1064.6013, 1094.5376, 1334.8853, 1339.6805, 1339.6805, 1355.6716, 1388.6141, 1388.6141, 1404.6049, 1448.9133, 1520.7607, 1536.7573, 1553.8007, 1618.0607, 1637.8737, 1756.8154, 1756.8154, 1784.8260, 2168.1316, 2296.2305, 2296.2305, 2384.2183, 2771.5024, 2923.3794, 2986.4895

8. gi|147816687 **Mass:** 19465 **Score:** 37 **Expect:** 1.1e+002 **Queries matched:** 6

hypothetical protein [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1388.6141	1387.6068	1387.6441	-0.0373	158	169	1	---	DYVDRLGLGSFM + Oxidation (M)

1388.6141	1387.6068	1387.6441	-0.0373	158 - 169	1	---	DYVDRLGLGSFM + Oxidation (M)
2168.1316	2167.1243	2167.1632	-0.0389	131 - 149	0	---	TMVIEHVSIELMIVDPLTK
2296.2305	2295.2232	2295.2582	-0.0349	130 - 149	1	---	KTMVIEHVSIELMIVDPLTK
2296.2305	2295.2232	2295.2582	-0.0349	130 - 149	1	---	KTMVIEHVSIELMIVDPLTK
2781.4065	2780.3992	2780.4890	-0.0897	131 - 155	1	---	TMVIEHVSIELMIVDPLTKGMPSLK

No match to: 709.3157, 713.4075, 734.4991, 750.5170, 768.5210, 864.9976, 886.9797, 1032.5322, 1048.5238, 1064.6013, 1094.5376, 1323.6885, 1323.6885, 1334.8853, 1339.6805, 1339.6805, 1355.6716, 1404.6049, 1448.9133, 1520.7607, 1536.7573, 1553.8007, 1618.0607, 1637.8737, 1756.8154, 1756.8154, 1784.8260, 1892.9554, 2368.2332, 2384.2183, 2771.5024, 2923.3794, 2986.4895

9. gi|147823327 **Mass:** 30971 **Score:** 37 **Expect:** 1.2e+002 **Queries matched:** 6

hypothetical protein [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
709.3157	708.3084	708.3298	-0.0214	1 -	6	0	---	MACSLK
1094.5376	1093.5303	1093.4961	0.0342	240 -	249	0	---	GEVMEDSALK + Oxidation (M)
1756.8154	1755.8081	1755.8436	-0.0354	117 -	131	1	---	LVVVDFYSPRCGGCK
1756.8154	1755.8081	1755.8436	-0.0354	117 -	131	1	---	LVVVDFYSPRCGGCK
1784.8260	1783.8187	1783.8419	-0.0232	7 -	22	0	---	TGLCISGMMEASFRPK
2771.5024	2770.4951	2770.3723	0.1229	152 -	173	1	---	VDYEELKTMCHALHIHVLPFFR + Oxidation (M)

No match to: 713.4075, 734.4991, 750.5170, 768.5210, 864.9976, 886.9797, 1032.5322, 1048.5238, 1064.6013, 1323.6885, 1323.6885, 1334.8853, 1339.6805, 1339.6805, 1355.6716, 1388.6141, 1388.6141, 1404.6049, 1448.9133, 1520.7607, 1536.7573, 1553.8007, 1618.0607, 1637.8737, 1892.9554, 2168.1316, 2296.2305, 2296.2305, 2368.2332, 2384.2183, 2781.4065, 2923.3794, 2986.4895

10. gi|78191069 **Mass:** 37233 **Score:** 37 **Expect:** 1.2e+002 **Queries matched:** 5

carotene cleavage dioxygenase [Nicotiana langsdorffii x Nicotiana sanderae]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1064.6013	1063.5940	1063.6178	-0.0238	97 -	105	1	---	FGILPRYAK
1094.5376	1093.5303	1093.5516	-0.0212	191 -	199	1	---	INENYTGRK
1892.9554	1891.9481	1891.8774	0.0708	158 -	172	1	---	DGFTNELYEMRFNIK + Oxidation (M)
2368.2332	2367.2259	2367.1534	0.0725	308 -	327	0	---	VPYGFHAFFVTEEQIQEQAK
2384.2183	2383.2110	2383.2668	-0.0557	284 -	306	1	---	SSVNVIDAKTMSAEPVAVVELPK

No match to: 709.3157, 713.4075, 734.4991, 750.5170, 768.5210, 864.9976, 886.9797, 1032.5322, 1048.5238, 1323.6885, 1323.6885, 1334.8853, 1339.6805, 1339.6805, 1355.6716, 1388.6141, 1388.6141, 1404.6049, 1448.9133, 1520.7607, 1536.7573, 1553.8007, 1618.0607, 1637.8737, 1756.8154, 1756.8154, 1784.8260, 2168.1316, 2296.2305, 2296.2305, 2771.5024, 2781.4065, 2923.3794, 2986.4895

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 39

Protein View

Match to: **gi|4826572** Score: **152** Expect: **3.8e-010**
polygalacturonase [Phleum pratense]

Nominal mass (M_r): **42579**; Calculated pI value: **7.83**
NCBI BLAST search of gi|4826572 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **28%**

Matched peptides shown in **Bold Red**

```
     1 GKKEEKKEEK KESGDAASGA DGTYDITKLG AKPDGKTDCT KEVEEAWASA
    51 CGGTGKNTIV IPKGDFLTGP LNFTGPCKGD SVTIKLDGNL LSSNDLAKYK
   101 ANWIEIMRIK KLTITGKGTL DGQGKAVWGK NSCAKNYNCK ILPNTLVLDF
   151 CDDALIEGIT LLNAKFFHMN IYECKGVTVK DVTITAPGDS PNTDGIHIGD
   201 SSKVTITDTT IGTGDDCISI GPGSTGLNIT GVTCGPGHGI SVGSLGRYKD
   251 EKDVTDITVK NCVLKKSTNG LRIKSYEDAK SPLTASKLTY ENVKMEDVGY
   301 PIIIDQKYCP NKICTSKGDS ARVTVKDVTF RNITGTSSTP EAVSLLCSDK
   351 QPCNGVTMND VKIEYSGTNN KTMAVCTNAK VTAKGVSEAN TCAA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
99 - 108	1323.6885	1322.6812	1322.6805	0.0007	1	YKANWIEIMR (No match)
99 - 108	1323.6885	1322.6812	1322.6805	0.0007	1	YKANWIEIMR (No match)
99 - 108	1339.6805	1338.6732	1338.6754	-0.0022	1	YKANWIEIMR Oxidation (M) (No match)
99 - 108	1339.6805	1338.6732	1338.6754	-0.0022	1	YKANWIEIMR Oxidation (M) (No match)
101 - 108	1032.5322	1031.5249	1031.5222	0.0027	0	ANWIEIMR (No match)
101 - 108	1048.5238	1047.5165	1047.5171	-0.0006	0	ANWIEIMR Oxidation (M) (No match)
141 - 165	2771.5024	2770.4951	2770.4826	0.0125	0	ILPNTLVLDFCDDALIEGITLLNAK (No match)
166 - 175	1388.6141	1387.6068	1387.6053	0.0016	0	FFHMNIYECK (No match)
166 - 175	1388.6141	1387.6068	1387.6053	0.0016	0	FFHMNIYECK (Ions score 62)
166 - 175	1404.6049	1403.5976	1403.6002	-0.0026	0	FFHMNIYECK Oxidation (M) (No match)
176 - 203	2781.4065	2780.3992	2780.3828	0.0165	1	GVTVKDVTITAPGDSPNTDGIHIGDSSK (No match)
288 - 307	2368.2332	2367.2259	2367.2031	0.0228	1	LTYENVKMEDVGYPIIIDQK (No match)
288 - 307	2384.2183	2383.2110	2383.1980	0.0130	1	LTYENVKMEDVGYPIIIDQK Oxidation (M) (No match)
295 - 307	1520.7607	1519.7534	1519.7592	-0.0058	0	MEDVGYPIIIDQK (No match)
295 - 307	1536.7573	1535.7500	1535.7541	-0.0041	0	MEDVGYPIIIDQK Oxidation (M) (No match)
313 - 322	1094.5376	1093.5303	1093.5186	0.0118	1	ICTSKGDSAR (No match)
323 - 331	1064.6013	1063.5940	1063.6025	-0.0085	1	VTVKDVTFR (No match)

Spot 40

Index

	Accession	Mass	Score	Description
1.	gi|4826572	42579	110	polygalacturonase [Phleum pratense]
2.	gi|157348939	25389	53	unnamed protein product [Vitis vinifera]
3.	gi|157357859	8456	49	unnamed protein product [Vitis vinifera]
4.	gi|145356423	81220	48	predicted protein [Ostreococcus lucimarinus CCE9901]
5.	gi|51997092	61056	47	maturase K [Xanthoceras sorbifolium]
6.	gi|224121292	7051	47	predicted protein [Populus trichocarpa]
7.	gi|38607373	70992	46	ethylene receptor [Zea mays]
8.	gi|145348905	35874	45	predicted protein [Ostreococcus lucimarinus CCE9901]
9.	gi|34394307	8524	45	hypothetical protein [Oryza sativa Japonica Group]
10.	gi|25986843	125895	44	phytochrome [Physcomitrella patens]

Results List

1. gi|4826572 **Mass:** 42579 **Score:** 110 **Expect:** 6.1e-006 **Queries matched:** 14

polygalacturonase [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1032.5325	1031.5252	1031.5222	0.0030	101	108	0	---	ANWIEIMR
1032.5325	1031.5252	1031.5222	0.0030	101	108	0	19	ANWIEIMR
1048.5188	1047.5115	1047.5171	-0.0056	101	108	0	---	ANWIEIMR + Oxidation (M)
1064.6068	1063.5995	1063.6025	-0.0030	323	331	1	---	VTVKDVTFR
1323.6929	1322.6856	1322.6805	0.0051	99	108	1	37	YKANWIEIMR
1323.6929	1322.6856	1322.6805	0.0051	99	108	1	---	YKANWIEIMR
1339.6735	1338.6662	1338.6754	-0.0092	99	108	1	---	YKANWIEIMR + Oxidation (M)
1339.6735	1338.6662	1338.6754	-0.0092	99	108	1	---	YKANWIEIMR + Oxidation (M)
1388.6089	1387.6016	1387.6053	-0.0036	166	175	0	---	FFHMNIYECK
1404.6034	1403.5961	1403.6002	-0.0040	166	175	0	---	FFHMNIYECK + Oxidation (M)
2369.2090	2368.2017	2368.0787	0.1231	351	371	1	---	QPCNGVTMNDVKIEYSGTNNK
2384.2100	2383.2027	2383.1980	0.0047	288	307	1	---	LTYENVKMEDVGYPIIIDQK + Oxidation (M)
2384.9683	2383.9610	2384.0736	-0.1126	351	371	1	---	QPCNGVTMNDVKIEYSGTNNK + Oxidation (M)
2781.3953	2780.3880	2780.3828	0.0053	176	203	1	---	GVTVKDVTITAPGDSPNTDGIHIGDSSK

No match to: 713.4025, 724.4829, 734.4869, 768.5142, 1183.5134, 1277.2260, 1279.7540, 1307.7150, 1336.6490, 1353.6753, 1355.6724, 1448.8948, 1476.7743, 1637.8738, 1638.8727, 1707.7844, 1756.8197, 1756.8197, 1784.8275, 1891.9630, 2015.2642, 2168.1365, 2230.2188, 2239.1426, 2296.2271, 2296.2271, 2564.1951, 2663.3835, 2825.3242, 2909.4363, 2922.3782, 3332.5593, 3349.5994

2. gi|157348939 **Mass:** 25389 **Score:** 53 **Expect:** 2.9 **Queries matched:** 8

unnamed protein product [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1388.6089	1387.6016	1387.5925	0.0091	2 -	14	0	---	VDDGMSPPNVDDK
1404.6034	1403.5961	1403.5874	0.0087	2 -	14	0	---	VDDGMSPPNVDDK + Oxidation (M)
1476.7743	1475.7670	1475.6739	0.0931	97 -	110	0	---	AEVEEPSLSSSEGR
1707.7844	1706.7771	1706.7239	0.0532	1 -	15	1	---	MVDDGMSPPNVDDKR + 2 Oxidation (M)
1891.9630	1890.9557	1890.8554	0.1003	97 -	114	1	---	AEVEEPSLSSSEGRSGDR
2296.2271	2295.2198	2295.1276	0.0922	18 -	36	1	---	NELVVLQAEIERMHAENER + Oxidation (M)
2296.2271	2295.2198	2295.1276	0.0922	18 -	36	1	---	NELVVLQAEIERMHAENER + Oxidation (M)
2922.3782	2921.3709	2921.3833	-0.0124	39 -	63	0	---	SMLNQVTNNYNALQVHMVALMQDQK + 2 Oxidation (M)

No match to: 713.4025, 724.4829, 734.4869, 768.5142, 1032.5325, 1032.5325, 1048.5188, 1064.6068, 1183.5134, 1277.2260, 1279.7540, 1307.7150, 1323.6929, 1323.6929, 1336.6490, 1339.6735, 1339.6735, 1353.6753, 1355.6724, 1448.8948, 1637.8738, 1638.8727, 1756.8197, 1756.8197, 1784.8275, 2015.2642, 2168.1365, 2230.2188, 2239.1426, 2369.2090, 2384.2100, 2384.9683, 2564.1951, 2663.3835, 2781.3953, 2825.3242, 2909.4363, 3332.5593, 3349.5994

3. gi|157357859 **Mass:** 8456 **Score:** 49 **Expect:** 8 **Queries matched:** 5

unnamed protein product [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1307.7150	1306.7077	1306.7496	-0.0419	2 -	13	0	---	IIFALSQSTISK
1476.7743	1475.7670	1475.6827	0.0843	14 -	26	0	---	LDSHASFLGMDQR
2369.2090	2368.2017	2368.0820	0.1197	54 -	74	0	---	FLSASEAMEFGFIDGILETEY
2384.9683	2383.9610	2384.0769	-0.1159	54 -	74	0	---	FLSASEAMEFGFIDGILETEY + Oxidation (M)
2781.3953	2780.3880	2780.4166	-0.0286	2 -	26	1	---	IIFALSQSTISKLDSHASFLGMDQR + Oxidation (M)

No match to: 713.4025, 724.4829, 734.4869, 768.5142, 1032.5325, 1032.5325, 1048.5188, 1064.6068, 1183.5134, 1277.2260, 1279.7540, 1323.6929, 1323.6929, 1336.6490, 1339.6735, 1339.6735, 1353.6753, 1355.6724, 1388.6089, 1404.6034, 1448.8948, 1637.8738, 1638.8727, 1707.7844, 1756.8197, 1756.8197, 1784.8275, 1891.9630, 2015.2642, 2168.1365, 2230.2188, 2239.1426, 2296.2271, 2296.2271, 2384.2100, 2564.1951, 2663.3835, 2825.3242, 2909.4363, 2922.3782, 3332.5593, 3349.5994

4. gi|145356423 **Mass:** 81220 **Score:** 48 **Expect:** 11 **Queries matched:** 10

predicted protein [Ostreococcus lucimarinus CCE9901]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1032.5325	1031.5252	1031.5247	0.0005	448 -	457	0	---	STALDGVVDR
1032.5325	1031.5252	1031.5247	0.0005	448 -	457	0	---	STALDGVVDR
1323.6929	1322.6856	1322.6830	0.0027	446 -	457	1	---	YKSTALDGVVDR
1323.6929	1322.6856	1322.6830	0.0027	446 -	457	1	---	YKSTALDGVVDR
1353.6753	1352.6680	1352.7564	-0.0884	603 -	614	0	---	KPNTPPRPTFAK
1355.6724	1354.6651	1354.6728	-0.0077	720 -	733	0	---	TNDSPALAAPPSSK
1891.9630	1890.9557	1890.8240	0.1317	314 -	329	1	---	ENEMCYKHVTPPGDSK
2369.2090	2368.2017	2368.2420	-0.0403	253 -	273	1	---	AMLELAELVRDDNADLLAIQR
2909.4363	2908.4290	2908.5745	-0.1455	621 -	648	0	---	RPTVATMPNPPPLPPNPPPLPSGKPPAR + Oxidation (M)
2922.3782	2921.3709	2921.3862	-0.0153	409 -	438	1	---	AITSAASGGASSTNAGATSTNYDVEGLHRR

No match to: 713.4025, 724.4829, 734.4869, 768.5142, 1048.5188, 1064.6068, 1183.5134, 1277.2260, 1279.7540,

1307.7150, 1336.6490, 1339.6735, 1339.6735, 1388.6089, 1404.6034, 1448.8948, 1476.7743, 1637.8738, 1638.8727, 1707.7844, 1756.8197, 1756.8197, 1784.8275, 2015.2642, 2168.1365, 2230.2188, 2239.1426, 2296.2271, 2296.2271, 2384.2100, 2384.9683, 2564.1951, 2663.3835, 2781.3953, 2825.3242, 3332.5593, 3349.5994

5. gi|51997092 **Mass:** 61056 **Score:** 47 **Expect:** 12 **Queries matched:** 7

maturase K [Xanthoceras sorbifolium]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1048.5188	1047.5115	1047.5560	-0.0445	235	244	0	---	STSSGVLLER
1756.8197	1755.8124	1755.8171	-0.0047	346	360	0	---	SQMLENAFLIDNAMK + 2 Oxidation (M)
1756.8197	1755.8124	1755.9227	-0.1103	229	244	1	---	QSSHLRSTSSGVLLER
2384.2100	2383.2027	2383.1379	0.0649	380	400	0	---	FCNPLGHPISKPIWADSSDSR
2564.1951	2563.1878	2563.2667	-0.0789	89	110	0	---	NFYSEMISEGFAVIVEIPFSLR + Oxidation (M)
2781.3953	2780.3880	2780.3678	0.0203	207	227	0	---	FFFFLYNSHVYEYESIFLFLR
2909.4363	2908.4290	2908.4627	-0.0337	207	228	1	---	FFFFLYNSHVYEYESIFLFLRK

No match to: 713.4025, 724.4829, 734.4869, 768.5142, 1032.5325, 1032.5325, 1064.6068, 1183.5134, 1277.2260, 1279.7540, 1307.7150, 1323.6929, 1323.6929, 1336.6490, 1339.6735, 1339.6735, 1353.6753, 1355.6724, 1388.6089, 1404.6034, 1448.8948, 1476.7743, 1637.8738, 1638.8727, 1707.7844, 1784.8275, 1891.9630, 2015.2642, 2168.1365, 2230.2188, 2239.1426, 2296.2271, 2296.2271, 2369.2090, 2384.9683, 2663.3835, 2825.3242, 2922.3782, 3332.5593, 3349.5994

6. gi|224121292 **Mass:** 7051 **Score:** 47 **Expect:** 12 **Queries matched:** 6

predicted protein [Populus trichocarpa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1032.5325	1031.5252	1031.5399	-0.0147	4	12	0	---	VYVGNLDPR
1032.5325	1031.5252	1031.5399	-0.0147	4	12	0	---	VYVGNLDPR
1183.5134	1182.5061	1182.5153	-0.0091	50	60	0	---	DAQDAIHELDG
1339.6735	1338.6662	1338.6164	0.0499	49	60	1	---	RDAQDAIHELDG
1339.6735	1338.6662	1338.6164	0.0499	49	60	1	---	RDAQDAIHELDG
2239.1426	2238.1353	2238.1221	0.0132	30	48	1	---	SVWVARRPPGYAFIDFDDK

No match to: 713.4025, 724.4829, 734.4869, 768.5142, 1048.5188, 1064.6068, 1277.2260, 1279.7540, 1307.7150, 1323.6929, 1323.6929, 1336.6490, 1353.6753, 1355.6724, 1388.6089, 1404.6034, 1448.8948, 1476.7743, 1637.8738, 1638.8727, 1707.7844, 1756.8197, 1756.8197, 1784.8275, 1891.9630, 2015.2642, 2168.1365, 2230.2188, 2296.2271, 2296.2271, 2369.2090, 2384.2100, 2384.9683, 2564.1951, 2663.3835, 2781.3953, 2825.3242, 2909.4363, 2922.3782, 3332.5593, 3349.5994

7. gi|38607373 **Mass:** 70992 **Score:** 46 **Expect:** 16 **Queries matched:** 9

ethylene receptor [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
768.5142	767.5069	767.4765	0.0304	235	241	0	---	VRPLAGR
1064.6068	1063.5995	1063.5769	0.0226	82	91	0	---	TVAMVMTIAK
1307.7150	1306.7077	1306.6928	0.0149	145	154	1	---	HVRMLTHEIR + Oxidation (M)
1448.8948	1447.8875	1447.8108	0.0767	425	437	0	---	EVMGFIKPIASIK + Oxidation (M)

1476.7743	1475.7670	1475.6649	0.1021	345 - 356	0	---	NDFLAVMNHEMR
1637.8738	1636.8665	1636.8317	0.0349	272 - 286	0	---	SFAIMVLMLPSDSAR
1756.8197	1755.8124	1755.9301	-0.1177	321 - 335	1	---	DLLMEQNVALDLARR
1756.8197	1755.8124	1755.9301	-0.1177	321 - 335	1	---	DLLMEQNVALDLARR
2909.4363	2908.4290	2908.3674	0.0616	517 - 543	1	---	DTGCGVSPQDLPHVFTKFAHPQSGGNR

No match to: 713.4025, 724.4829, 734.4869, 1032.5325, 1032.5325, 1048.5188, 1183.5134, 1277.2260, 1279.7540, 1323.6929, 1323.6929, 1336.6490, 1339.6735, 1339.6735, 1353.6753, 1355.6724, 1388.6089, 1404.6034, 1638.8727, 1707.7844, 1784.8275, 1891.9630, 2015.2642, 2168.1365, 2230.2188, 2239.1426, 2296.2271, 2296.2271, 2369.2090, 2384.2100, 2384.9683, 2564.1951, 2663.3835, 2781.3953, 2825.3242, 2922.3782, 3332.5593, 3349.5994

8. gi|145348905 **Mass:** 35874 **Score:** 45 **Expect:** 20 **Queries matched:** 8

predicted protein [Ostreococcus lucimarinus CCE9901]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1032.5325	1031.5252	1031.5148	0.0104	136 - 143		1	---	DEWRVATR
1032.5325	1031.5252	1031.5148	0.0104	136 - 143		1	---	DEWRVATR
1404.6034	1403.5961	1403.6317	-0.0355	3 - 15		0	---	AIVADGDDASEWR
1707.7844	1706.7771	1706.7682	0.0090	1 - 15		1	---	MRAIVADGDDASEWR + Oxidation (M)
1756.8197	1755.8124	1755.8613	-0.0489	172 - 185		1	---	ENTEFAIVMFDLRR + Oxidation (M)
1756.8197	1755.8124	1755.8613	-0.0489	172 - 185		1	---	ENTEFAIVMFDLRR + Oxidation (M)
2369.2090	2368.2017	2368.1910	0.0108	228 - 248		1	---	EYAANVEETQRLLDSATFALK
2384.2100	2383.2027	2383.1624	0.0403	112 - 132		1	---	SLTGDQMGTLATYQQMLQNKR

No match to: 713.4025, 724.4829, 734.4869, 768.5142, 1048.5188, 1064.6068, 1183.5134, 1277.2260, 1279.7540, 1307.7150, 1323.6929, 1323.6929, 1336.6490, 1339.6735, 1339.6735, 1353.6753, 1355.6724, 1388.6089, 1448.8948, 1476.7743, 1637.8738, 1638.8727, 1784.8275, 1891.9630, 2015.2642, 2168.1365, 2230.2188, 2239.1426, 2296.2271, 2296.2271, 2384.9683, 2564.1951, 2663.3835, 2781.3953, 2825.3242, 2909.4363, 2922.3782, 3332.5593, 3349.5994

9. gi|34394307 **Mass:** 8524 **Score:** 45 **Expect:** 21 **Queries matched:** 5

hypothetical protein [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
768.5142	767.5069	767.4766	0.0304	48 - 53		0	---	RPVQLR
1323.6929	1322.6856	1322.6214	0.0642	37 - 47		1	---	REGYENEASLR
1323.6929	1322.6856	1322.6214	0.0642	37 - 47		1	---	REGYENEASLR
1637.8738	1636.8665	1636.8532	0.0133	2 - 17		1	---	AASTRAAVLGSTETFR
1784.8275	1783.8202	1783.8886	-0.0684	1 - 17		1	---	MAASTRAAVLGSTETFR + Oxidation (M)

No match to: 713.4025, 724.4829, 734.4869, 1032.5325, 1032.5325, 1048.5188, 1064.6068, 1183.5134, 1277.2260, 1279.7540, 1307.7150, 1336.6490, 1339.6735, 1339.6735, 1353.6753, 1355.6724, 1388.6089, 1404.6034, 1448.8948, 1476.7743, 1638.8727, 1707.7844, 1756.8197, 1756.8197, 1891.9630, 2015.2642, 2168.1365, 2230.2188, 2239.1426, 2296.2271, 2296.2271, 2369.2090, 2384.2100, 2384.9683, 2564.1951, 2663.3835, 2781.3953, 2825.3242, 2909.4363, 2922.3782, 3332.5593, 3349.5994

10. gi|25986843 **Mass:** 125895 **Score:** 44 **Expect:** 25 **Queries matched:** 10

phytochrome [Physcomitrella patens]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
713.4025	712.3952	712.3980	-0.0028	16	-	21	1	---	SKHSVR
1183.5134	1182.5061	1182.4901	0.0160	533	-	542	1	---	HDPDEKDDGR
1448.8948	1447.8875	1447.8034	0.0841	841	-	853	1	---	QGKYVDALLTVNK
1637.8738	1636.8665	1636.8619	0.0046	1040	-	1053	1	---	RLGGGIHVMHLEFR + Oxidation (M)
1638.8727	1637.8654	1637.8195	0.0460	1092	-	1105	1	---	LMNGNVQYIRETGK + Oxidation (M)
1784.8275	1783.8202	1783.7869	0.0333	817	-	832	0	---	FMIALNSAMDGQDTDR
2369.2090	2368.2017	2368.1732	0.0285	561	-	580	0	---	SLPWEDIEMDAIHSLQLISR + Oxidation (M)
2564.1951	2563.1878	2563.0988	0.0890	810	-	832	1	---	GQDAMTKFMIALNSAMDGQDTDR + 3 Oxidation (M)
3332.5593	3331.5520	3331.6362	-0.0842	130	-	160	1	---	TLFTPSSAAALEKCAGAVDVTMLNPISVHCR + Oxidation (M)
3349.5994	3348.5921	3348.7135	-0.1214	854	-	883	1	---	RTDAEGSITGVFCFLHTTSVELLQALTVQR

No match to: 724.4829, 734.4869, 768.5142, 1032.5325, 1032.5325, 1048.5188, 1064.6068, 1277.2260, 1279.7540, 1307.7150, 1323.6929, 1323.6929, 1336.6490, 1339.6735, 1339.6735, 1353.6753, 1355.6724, 1388.6089, 1404.6034, 1476.7743, 1707.7844, 1756.8197, 1756.8197, 1891.9630, 2015.2642, 2168.1365, 2230.2188, 2239.1426, 2296.2271, 2296.2271, 2384.2100, 2384.9683, 2663.3835, 2781.3953, 2825.3242, 2909.4363, 2922.3782

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 47

Protein View

Match to: **gi|4826572** Score: **110** Expect: **6.1e-006**
polygalacturonase [Phleum pratense]

Nominal mass (M_r): **42579**; Calculated pI value: **7.83**
NCBI BLAST search of gi|4826572 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **24%**

Matched peptides shown in **Bold Red**

```
   1 GKKEEKKEEK KESGDAASGA DGTYDITKLG AKPDGKTDCT KEVEEAWASA
  51 CGGTGKNTIV IPKGDFLTGP LNFTGPCKGD SVTIKLDGNL LSSNDLAKYK
 101 ANWIEIMRIK KLTITGKGTL DGQGKAVWGK NSCAKNYNCK ILPNTLVLDF
 151 CDDALIEGIT LLNAKFFHMN IYECKGVTVK DVTITAPGDS PNTDGIHIGD
 201 SSKVTITDTT IGTGDDCISI GPGSTGLNIT GVTCGPGHGI SVGSLGRYKD
 251 EKDVTDITVK NCVLKKSTNG LRIKSYEDAK SPLTASKLTY ENVKMEDVGY
 301 PIIIDQKYCP NKICTSKGDS ARVTVKDVTF RNITGTSSTP EAVSLLCSDK
 351 QPCNGVTMND VKIEYSGTNN KTMAVCTNAK VTAKGVSEAN TCAA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
99 - 108	1323.6929	1322.6856	1322.6805	0.0051	1	YKANWIEIMR (Ions score 37)
99 - 108	1323.6929	1322.6856	1322.6805	0.0051	1	YKANWIEIMR (No match)
99 - 108	1339.6735	1338.6662	1338.6754	-0.0092	1	YKANWIEIMR Oxidation (M) (No match)
99 - 108	1339.6735	1338.6662	1338.6754	-0.0092	1	YKANWIEIMR Oxidation (M) (No match)
101 - 108	1032.5325	1031.5252	1031.5222	0.0030	0	ANWIEIMR (No match)
101 - 108	1032.5325	1031.5252	1031.5222	0.0030	0	ANWIEIMR (Ions score 19)
101 - 108	1048.5188	1047.5115	1047.5171	-0.0056	0	ANWIEIMR Oxidation (M) (No match)
166 - 175	1388.6089	1387.6016	1387.6053	-0.0036	0	FFHMNIYECK (No match)
166 - 175	1404.6034	1403.5961	1403.6002	-0.0040	0	FFHMNIYECK Oxidation (M) (No match)
176 - 203	2781.3953	2780.3880	2780.3828	0.0053	1	GVTVKDVTITAPGDSPNTDGIHIGDSSK (No match)
288 - 307	2384.2100	2383.2027	2383.1980	0.0047	1	LTYENVKMEDVGYPIIIDQK Oxidation (M) (No match)
323 - 331	1064.6068	1063.5995	1063.6025	-0.0030	1	VTVKDVTFR (No match)
351 - 371	2369.2090	2368.2017	2368.0787	0.1231	1	QPCNGVTMNDVKIEYSGTNNK (No match)
351 - 371	2384.9683	2383.9610	2384.0736	-0.1126	1	QPCNGVTMNDVKIEYSGTNNK Oxidation (M) (No match)

Spot 41

Index

	Accession	Mass	Score	Description
1.	gi|4826572	42579	133	polygalacturonase [Phleum pratense]
2.	gi|34398265	12619	52	protein phosphatase 2A catalytic subunit [Nicotiana benthamiana]
3.	gi|87162769	15504	48	F-box protein interaction domain; Galactose oxidase, central, putative [Medicago truncatula]
4.	gi|223537353	7032	42	conserved hypothetical protein [Ricinus communis]
5.	gi|222845743	36753	41	predicted protein [Populus trichocarpa]

Results List

1. gi|4826572 **Mass:** 42579 **Score:** 133 **Expect:** 3e-008 **Queries matched:** 11

polygalacturonase [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1032.5333	1031.5260	1031.5222	0.0038	101	108	0	---	ANWIEIMR
1048.5243	1047.5170	1047.5171	-0.0001	101	108	0	---	ANWIEIMR + Oxidation (M)
1064.6107	1063.6034	1063.6025	0.0009	323	331	1	---	VTVKDVTFR
1323.6898	1322.6825	1322.6805	0.0020	99	108	1	23	YKANWIEIMR
1323.6898	1322.6825	1322.6805	0.0020	99	108	1	---	YKANWIEIMR
1339.6766	1338.6693	1338.6754	-0.0061	99	108	1	(15)	YKANWIEIMR + Oxidation (M)
1339.6766	1338.6693	1338.6754	-0.0061	99	108	1	---	YKANWIEIMR + Oxidation (M)
1388.6134	1387.6061	1387.6053	0.0009	166	175	0	76	FFHMNIYECK
1388.6134	1387.6061	1387.6053	0.0009	166	175	0	---	FFHMNIYECK
1404.6298	1403.6225	1403.6002	0.0223	166	175	0	---	FFHMNIYECK + Oxidation (M)
2781.4236	2780.4163	2780.3828	0.0336	176	203	1	---	GVTVKDVTITAPGDSPNTDGIHIGDSSK

No match to: 713.4097, 724.4962, 734.4909, 750.5182, 768.5233, 838.5305, 886.9864, 1133.7191, 1279.7672, 1334.8867, 1355.6732, 1404.1549, 1448.9174, 1521.7570, 1562.9480, 1618.0675, 1732.0962, 1756.8085, 1756.8085, 1758.0470, 2168.1223, 2230.2190, 2240.1411, 2296.2288, 2296.2288, 2369.2170, 2385.2153, 2564.1965, 2823.3337, 2922.3694, 2986.4873

2. gi|34398265 **Mass:** 12619 **Score:** 52 **Expect:** 3.8 **Queries matched:** 4

protein phosphatase 2A catalytic subunit [Nicotiana benthamiana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
2230.2190	2229.2117	2229.2157	-0.0039	87	105	1	---	GYYSVETVTLLVALQVRYR
2369.2170	2368.2097	2368.2208	-0.0111	27	46	1	---	TLCDQARAILVEEWNVQPVK
2823.3337	2822.3264	2822.3578	-0.0314	2	26	0	---	PSHGDLDQQIAQLMECKPLSEAEVK
2986.4873	2985.4800	2985.3881	0.0919	1	26	0	---	MPSHGDLDQQIAQLMECKPLSEAEVK + 2 Oxidation (M)

No match to: 713.4097, 724.4962, 734.4909, 750.5182, 768.5233, 838.5305, 886.9864, 1032.5333, 1048.5243, 1064.6107, 1133.7191, 1279.7672, 1323.6898, 1323.6898, 1334.8867, 1339.6766, 1339.6766, 1355.6732, 1388.6134, 1388.6134, 1404.1549, 1404.6298, 1448.9174, 1521.7570, 1562.9480, 1618.0675, 1732.0962, 1756.8085, 1756.8085, 1758.0470, 2168.1223, 2240.1411, 2296.2288, 2296.2288, 2385.2153, 2564.1965, 2781.4236, 2922.3694

3. gi|87162769 **Mass:** 15504 **Score:** 48 **Expect:** 11 **Queries matched:** 4

F-box protein interaction domain; Galactose oxidase, central, putative [Medicago truncatula]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
2168.1223	2167.1150	2167.0354	0.0796	118	137	0	---	SQMAVYIESLLSLPDGTEQA + Oxidation (M)
2230.2190	2229.2117	2229.1945	0.0172	26	44	0	---	GIYDLLVFHGLISVWNVER
2781.4236	2780.4163	2780.3036	0.1127	114	137	1	---	YFMRSQMAVYIESLLSLPDGTEQA + 2 Oxidation (M)
2823.3337	2822.3264	2822.3652	-0.0388	1	25	1	---	MDVIIAFDLKEATMAEIALPNDCSR

No match to: 713.4097, 724.4962, 734.4909, 750.5182, 768.5233, 838.5305, 886.9864, 1032.5333, 1048.5243, 1064.6107, 1133.7191, 1279.7672, 1323.6898, 1323.6898, 1334.8867, 1339.6766, 1339.6766, 1355.6732, 1388.6134, 1388.6134, 1404.1549, 1404.6298, 1448.9174, 1521.7570, 1562.9480, 1618.0675, 1732.0962, 1756.8085, 1756.8085, 1758.0470, 2240.1411, 2296.2288, 2296.2288, 2369.2170, 2385.2153, 2564.1965, 2922.3694, 2986.4873

4. gi|223537353 **Mass:** 7032 **Score:** 42 **Expect:** 40 **Queries matched:** 4

conserved hypothetical protein [Ricinus communis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
2296.2288	2295.2215	2295.1641	0.0574	29	49	0	---	MNQILTQTPTVTHDSAAAQIR
2296.2288	2295.2215	2295.1641	0.0574	29	49	0	---	MNQILTQTPTVTHDSAAAQIR
2823.3337	2822.3264	2822.3855	-0.0591	2	26	1	---	STQTNLIDVKQISEDSMTNTLEDLK
2986.4873	2985.4800	2985.4158	0.0642	1	26	1	---	MSTQTNLIDVKQISEDSMTNTLEDLK + 2 Oxidation (M)

No match to: 713.4097, 724.4962, 734.4909, 750.5182, 768.5233, 838.5305, 886.9864, 1032.5333, 1048.5243, 1064.6107, 1133.7191, 1279.7672, 1323.6898, 1323.6898, 1334.8867, 1339.6766, 1339.6766, 1355.6732, 1388.6134, 1388.6134, 1404.1549, 1404.6298, 1448.9174, 1521.7570, 1562.9480, 1618.0675, 1732.0962, 1756.8085, 1756.8085, 1758.0470, 2168.1223, 2230.2190, 2240.1411, 2369.2170, 2385.2153, 2564.1965, 2781.4236, 2922.3694

5. gi|222845743 **Mass:** 36753 **Score:** 41 **Expect:** 54 **Queries matched:** 9

predicted protein [Populus trichocarpa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1323.6898	1322.6825	1322.6726	0.0099	225	235	0	---	LCVLGQDFLMK
1323.6898	1322.6825	1322.6726	0.0099	225	235	0	---	LCVLGQDFLMK
1339.6766	1338.6693	1338.6675	0.0018	225	235	0	---	LCVLGQDFLMK + Oxidation (M)
1339.6766	1338.6693	1338.6675	0.0018	225	235	0	---	LCVLGQDFLMK + Oxidation (M)
1355.6732	1354.6659	1354.7067	-0.0408	163	174	0	---	GSPLWMAPEVIR
1756.8085	1755.8012	1755.8725	-0.0713	7	22	1	---	CIGRGSYGTVNLAFNK
1756.8085	1755.8012	1755.8725	-0.0713	7	22	1	---	CIGRGSYGTVNLAFNK
2230.2190	2229.2117	2229.1429	0.0689	11	31	1	---	GSYGTVNLAFNKQTDAVFAVK
2385.2153	2384.2080	2384.2045	0.0035	96	116	1	---	LADVDEQAVRSFTYCIVSALK

No match to: 713.4097, 724.4962, 734.4909, 750.5182, 768.5233, 838.5305, 886.9864, 1032.5333, 1048.5243, 1064.6107, 1133.7191, 1279.7672, 1334.8867, 1388.6134, 1388.6134, 1404.1549, 1404.6298, 1448.9174, 1521.7570, 1562.9480, 1618.0675, 1732.0962, 1758.0470, 2168.1223, 2240.1411, 2296.2288, 2296.2288, 2369.2170, 2564.1965, 2781.4236, 2823.3337, 2922.3694, 2986.4873

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 42

Protein View

Match to: **gi|4826572** Score: **133** Expect: **3e-008**
polygalacturonase [Phleum pratense]

Nominal mass (M_r): **42579**; Calculated pI value: **7.83**
NCBI BLAST search of gi|4826572 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **14%**

Matched peptides shown in **Bold Red**

```
     1 GKKEEKKEEK KESGDAASGA DGTYDITKLG AKPDGKTDCT KEVEEAWASA
    51 CGGTGKNTIV IPKGDFLTGP LNFTGPCKGD SVTIKLDGNL LSSNDLAKYK
   101 ANWIEIMRIK KLTITGKGTL DGQGKAVWGK NSCAKNYNCK ILPNTLVLDF
   151 CDDALIEGIT LLNAKFFHMN IYECKGVTVK DVTITAPGDS PNTDGIHIGD
   201 SSKVTITDTT IGTGDDCISI GPGSTGLNIT GVTCGPGHGI SVGSLGRYKD
   251 EKDVTDITVK NCVLKKSTNG LRIKSYEDAK SPLTASKLTY ENVKMEDVGY
   301 PIIIDQKYCP NKICTSKGDS ARVTVKDVTF RNITGTSSTP EAVSLLCSDK
   351 QPCNGVTMND VKIEYSGTNN KTMAVCTNAK VTAKGVSEAN TCAA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
99 - 108	1323.6898	1322.6825	1322.6805	0.0020	1	**YKANWIEIMR** (Ions score 23)
99 - 108	1323.6898	1322.6825	1322.6805	0.0020	1	**YKANWIEIMR** (No match)
99 - 108	1339.6766	1338.6693	1338.6754	-0.0061	1	**YKANWIEIMR** Oxidation (M) (Ions score 15)
99 - 108	1339.6766	1338.6693	1338.6754	-0.0061	1	**YKANWIEIMR** Oxidation (M) (No match)
101 - 108	1032.5333	1031.5260	1031.5222	0.0038	0	**ANWIEIMR** (No match)
101 - 108	1048.5243	1047.5170	1047.5171	-0.0001	0	**ANWIEIMR** Oxidation (M) (No match)
166 - 175	1388.6134	1387.6061	1387.6053	0.0009	0	**FFHMNIYECK** (Ions score 76)
166 - 175	1388.6134	1387.6061	1387.6053	0.0009	0	**FFHMNIYECK** (No match)
166 - 175	1404.6298	1403.6225	1403.6002	0.0223	0	**FFHMNIYECK** Oxidation (M) (No match)
176 - 203	2781.4236	2780.4163	2780.3828	0.0336	1	**GVTVKDVTITAPGDSPNTDGIHIGDSSK** (No match)
323 - 331	1064.6107	1063.6034	1063.6025	0.0009	1	**VTVKDVTFR** (No match)

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	Accession	Mass	Score	Description
1.	gi|125581161	27071	122	hypothetical protein OsJ_05753 [Oryza sativa Japonica Group]
2.	gi|2832691	39669	121	polygalacturonase-like protein [Arabidopsis thaliana]
3.	gi|218190250	40600	121	hypothetical protein OsI_06235 [Oryza sativa Indica Group]
4.	gi|224102769	44771	120	predicted protein [Populus trichocarpa]
5.	gi|15236790	45764	120	glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein [Arabidop
6.	gi|226502274	44631	120	hypothetical protein LOC100273946 [Zea mays]
7.	gi|49388133	44519	120	putative exopolygalacturonase precursor [Oryza sativa Japonica Group]
8.	gi|115444829	47052	120	Os02g0196700 [Oryza sativa (japonica cultivar-group)]
9.	gi|15225803	76008	118	glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein [Arabidop
10.	gi|255576408	42131	78	Polygalacturonase precursor, putative [Ricinus communis]

Results List

1. gi|125581161 **Mass:** 27071 **Score:** 122 **Expect:** 3.8e-007 **Queries matched:** 2

hypothetical protein OsJ_05753 [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1353.6807	1352.6734	1352.6618	0.0116	92 -	105	0	---	CGPGHGISVGSLGR
1353.6807	1352.6734	1352.6618	0.0116	92 -	105	0	107	CGPGHGISVGSLGR

No match to: 713.4023, 768.5151

2. gi|2832691 **Mass:** 39669 **Score:** 121 **Expect:** 4.8e-007 **Queries matched:** 2

polygalacturonase-like protein [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1353.6807	1352.6734	1352.6618	0.0116	193 -	206	0	---	CGPGHGISVGSLGR
1353.6807	1352.6734	1352.6618	0.0116	193 -	206	0	107	CGPGHGISVGSLGR

No match to: 713.4023, 768.5151

3. gi|218190250 **Mass:** 40600 **Score:** 121 **Expect:** 4.8e-007 **Queries matched:** 2

hypothetical protein OsI_06235 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1353.6807	1352.6734	1352.6618	0.0116	226 -	239	0	---	CGPGHGISVGSLGR
1353.6807	1352.6734	1352.6618	0.0116	226 -	239	0	107	CGPGHGISVGSLGR

No match to: 713.4023, 768.5151

4. gi|224102769 **Mass:** 44771 **Score:** 120 **Expect:** 6.1e-007 **Queries matched:** 2

predicted protein [Populus trichocarpa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1353.6807	1352.6734	1352.6618	0.0116	252 -	265	0	---	CGPGHGISVGSLGR

1353.6807 1352.6734 1352.6618 0.0116 252 - 265 0 107 CGPGHGISVGSLGR
No match to: 713.4023, 768.5151

5. gi|15236790 **Mass:** 45764 **Score:** 120 **Expect:** 6.1e-007 **Queries matched:** 2
glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein [Arabidopsis t

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1353.6807	1352.6734	1352.6618	0.0116	245	258	0	---	CGPGHGISVGSLGR
1353.6807	1352.6734	1352.6618	0.0116	245	258	0	107	CGPGHGISVGSLGR

No match to: 713.4023, 768.5151

6. gi|226502274 **Mass:** 44631 **Score:** 120 **Expect:** 6.1e-007 **Queries matched:** 2
hypothetical protein LOC100273946 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1353.6807	1352.6734	1352.6618	0.0116	260	273	0	---	CGPGHGISVGSLGR
1353.6807	1352.6734	1352.6618	0.0116	260	273	0	107	CGPGHGISVGSLGR

No match to: 713.4023, 768.5151

7. gi|49388133 **Mass:** 44519 **Score:** 120 **Expect:** 6.1e-007 **Queries matched:** 2
putative exopolygalacturonase precursor [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1353.6807	1352.6734	1352.6618	0.0116	264	277	0	---	CGPGHGISVGSLGR
1353.6807	1352.6734	1352.6618	0.0116	264	277	0	107	CGPGHGISVGSLGR

No match to: 713.4023, 768.5151

8. gi|115444829 **Mass:** 47052 **Score:** 120 **Expect:** 6.1e-007 **Queries matched:** 2
Os02g0196700 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1353.6807	1352.6734	1352.6618	0.0116	291	304	0	---	CGPGHGISVGSLGR
1353.6807	1352.6734	1352.6618	0.0116	291	304	0	107	CGPGHGISVGSLGR

No match to: 713.4023, 768.5151

9. gi|15225803 **Mass:** 76008 **Score:** 118 **Expect:** 9.6e-007 **Queries matched:** 2
glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein [Arabidopsis t

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1353.6807	1352.6734	1352.6618	0.0116	243	256	0	---	CGPGHGISVGSLGR
1353.6807	1352.6734	1352.6618	0.0116	243	256	0	107	CGPGHGISVGSLGR

No match to: 713.4023, 768.5151

10. gi|255576408 **Mass:** 42131 **Score:** 78 **Expect:** 0.01 **Queries matched:** 2
Polygalacturonase precursor, putative [Ricinus communis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1353.6807	1352.6734	1352.6618	0.0116	233	246	0	---	CGPGHGVSIGSLGR

1353.6807 1352.6734 1352.6618 0.0116 233 - 246 0 65 CGPGHGVSIGSLGR

No match to: 713.4023, 768.5151

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 4

Protein View

Match to: **gi|125581161** Score: **122** Expect: **3.8e-007**
hypothetical protein OsJ_05753 [Oryza sativa Japonica Group]

Nominal mass (M_r): **27071**; Calculated pI value: **8.02**
NCBI BLAST search of gi|125581161 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Oryza sativa Japonica Group

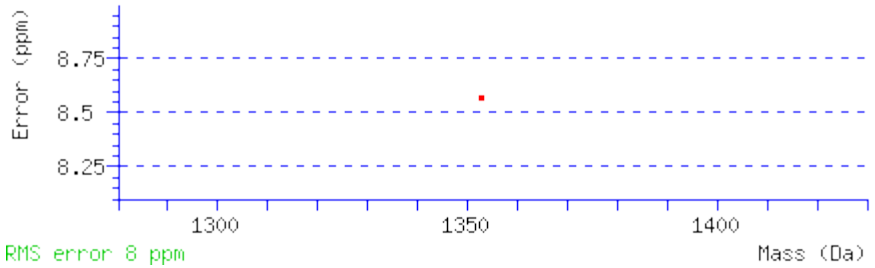
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **5%**

Matched peptides shown in **Bold Red**

```
     1 MQSLVIDYST NVTVRGITLK NSKFFHLNIY ESKNVVIDKV TITSPGDSPN
    51 TDGIHVGDST NITISSTTIA AGDDCISIGP GTKMVRVNGV RCGPGHGISV
   101 GSLGRYKDEK DVEDIIVTNC TIKGTTNGLR IKSYEDSKSQ LRATKFLYDG
   151 ITMDNVSYPI IIDQKYCPNN ICSASGTSKV AVTDIVFKNI VGTSATPEAV
   201 TLNCANNLPC QGIQLHNVDL KYAGQGNTTL SVCKNVAGKS SNVAKELACV
   251
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
92 - 105	1353.6807	1352.6734	1352.6618	0.0116	0	CGPGHGISVGSLGR	(No match)
92 - 105	1353.6807	1352.6734	1352.6618	0.0116	0	CGPGHGISVGSLGR	(Ions score 107)



Peptide View

MS/MS Fragmentation of **CGPGHGISVGSLGR**
Found in **gi|125581161**, hypothetical protein OsJ_05753 [Oryza sativa Japonica Group]

Match to Query 4: 1352.673424 from(1353.680700,1+)
MaldiWellID: 81768, SpectrumID: 213572,

Click mouse within plot area to zoom in by factor of two about that point
Or, to Da
MONOISOTOPIC mass of neutral peptide Mr(calc): 1352.6618
Fixed modifications: Carbamidomethyl (C)
Ions Score: 107 **Expect:** 1.5e-008
Matches (Bold Red): 54/204 fragment ions using 51 most intense peaks

#	Immon.	a	a^0	b	b^0	Seq.	v	y	y*	y^0	#
1	**133.0430**	**133.0430**		161.0379		C					14
2	30.0338	**190.0645**		**218.0594**		G		1193.6385	1176.6120	1175.6279	13
3	**70.0651**	287.1172		**315.1121**		P	1094.5701	**1136.6170**	1119.5905	1118.6065	12
4	30.0338	344.1387		**372.1336**		G		1039.5643	1022.5377	1021.5537	11
5	**110.0713**	**481.1976**		**509.1925**		H	900.4897	**982.5428**	965.5163	964.5323	10
6	30.0338	538.2191		**566.2140**		G		**845.4839**	828.4574	827.4734	9

7	86.0964	651.3031		679.2980		I	730.3842	788.4625	771.4359	770.4519	8
8	60.0444	738.3352	720.3246	766.3301	748.3195	S	643.3522	675.3784	658.3519	657.3678	7
9	72.0808	837.4036	819.3930	865.3985	847.3879	V	544.2838	588.3464	571.3198	570.3358	6
10	30.0338	894.4250	876.4145	922.4199	904.4094	G		489.2780	472.2514	471.2674	5
11	60.0444	981.4571	963.4465	1009.4520	991.4414	S	400.2303	432.2565	415.2300	414.2459	4
12	86.0964	1094.5411	1076.5306	1122.5360	1104.5255	L	287.1462	345.2245	328.1979		3
13	30.0338	1151.5626	1133.5520	1179.5575	1161.5469	G		232.1404	215.1139		2
14	129.1135					R	74.0236	175.1189	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
GP	127.0866	155.0815	GPG	184.1080	212.1030	GPGH	321.1670	349.1619
GPGHG	378.1884	406.1833	GPGHGI	491.2725	519.2674	GPGHGIS	578.3045	606.2994
GPGHGISV	677.3729	705.3678	PG	127.0866	155.0815	PGH	264.1455	292.1404
PGHG	321.1670	349.1619	PGHGI	434.2510	462.2459	PGHGIS	521.2830	549.2780
PGHGISV	620.3515	648.3464	PGHGISVG	677.3729	705.3678	GH	167.0927	195.0876
GHG	224.1142	252.1091	GHGI	337.1983	365.1932	GHGIS	424.2303	452.2252
GHGISV	523.2987	551.2936	GHGISVG	580.3202	608.3151	GHGISVGS	667.3522	695.3471
HG	167.0927	195.0876	HGI	280.1768	308.1717	HGIS	367.2088	395.2037
HGISV	466.2772	494.2721	HGISVG	523.2987	551.2936	HGISVGS	610.3307	638.3256
GI	143.1179	171.1128	GIS	230.1499	258.1448	GISV	329.2183	357.2132
GISVG	386.2398	414.2347	GISVGS	473.2718	501.2667	GISVGSL	586.3559	614.3508
GISVGSLG	643.3773	671.3722	IS	173.1285	201.1234	ISV	272.1969	300.1918
ISVG	329.2183	357.2132	ISVGS	416.2504	444.2453	ISVGSL	529.3344	557.3293
ISVGSLG	586.3559	614.3508	SV	159.1128	187.1077	SVG	216.1343	244.1292
SVGS	303.1663	331.1612	SVGSL	416.2504	444.2453	SVGSLG	473.2718	501.2667
VG	129.1022	157.0971	VGS	216.1343	244.1292	VGSL	329.2183	357.2132
VGSLG	386.2398	414.2347	GS	117.0659	145.0608	GSL	230.1499	258.1448
GSLG	287.1714	315.1663	SL	173.1285	201.1234	SLG	230.1499	258.1448
LG	143.1179	171.1128						

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	Accession	Mass	Score	Description
1.	gi|218190250	40600	97	hypothetical protein OsI_06235 [Oryza sativa Indica Group]
2.	gi|49388133	44519	96	putative exopolygalacturonase precursor [Oryza sativa Japonica Group]
3.	gi|115444829	47052	95	Os02g0196700 [Oryza sativa (japonica cultivar-group)]
4.	gi|222849203	44771	95	predicted protein [Populus trichocarpa]
5.	gi|125581161	27071	86	hypothetical protein OsJ_05753 [Oryza sativa Japonica Group]
6.	gi|2832691	39669	85	polygalacturonase-like protein [Arabidopsis thaliana]
7.	gi|15236790	45764	85	glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein [Arabidop
8.	gi|194706004	44631	85	unknown [Zea mays]
9.	gi|15225803	76008	83	glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein [Arabidop
10.	gi|223536326	42374	54	Polygalacturonase precursor, putative [Ricinus communis]

Results List

1. gi|218190250 **Mass:** 40600 **Score:** 97 **Expect:** 0.00013 **Queries matched:** 3

hypothetical protein OsI_06235 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1353.6693	1352.6620	1352.6618	0.0002	226	239	0	---	CGPGHGISVGSLGR
1353.6693	1352.6620	1352.6618	0.0002	226	239	0	76	CGPGHGISVGSLGR
1903.9689	1902.9616	1903.0414	-0.0798	133	149	0	---	ILPNSLVIDYSTNVTVR

No match to: 713.4065, 768.5187, 1183.4996, 1320.5951, 1320.5951, 1336.6504, 1336.6504, 1352.6478

2. gi|49388133 **Mass:** 44519 **Score:** 96 **Expect:** 0.00016 **Queries matched:** 3

putative exopolygalacturonase precursor [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1353.6693	1352.6620	1352.6618	0.0002	264	277	0	---	CGPGHGISVGSLGR
1353.6693	1352.6620	1352.6618	0.0002	264	277	0	76	CGPGHGISVGSLGR
1903.9689	1902.9616	1903.0414	-0.0798	171	187	0	---	ILPNSLVIDYSTNVTVR

No match to: 713.4065, 768.5187, 1183.4996, 1320.5951, 1320.5951, 1336.6504, 1336.6504, 1352.6478

3. gi|115444829 **Mass:** 47052 **Score:** 95 **Expect:** 0.00018 **Queries matched:** 3

Os02g0196700 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1353.6693	1352.6620	1352.6618	0.0002	291	304	0	---	CGPGHGISVGSLGR
1353.6693	1352.6620	1352.6618	0.0002	291	304	0	76	CGPGHGISVGSLGR
1903.9689	1902.9616	1903.0414	-0.0798	198	214	0	---	ILPNSLVIDYSTNVTVR

No match to: 713.4065, 768.5187, 1183.4996, 1320.5951, 1320.5951, 1336.6504, 1336.6504, 1352.6478

4. gi|222849203 **Mass:** 44771 **Score:** 95 **Expect:** 0.00018 **Queries matched:** 3

predicted protein [Populus trichocarpa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1352.6478	1351.6405	1351.6772	-0.0366	56 -	67	1	---	TDDSKAFIAAWK
1353.6693	1352.6620	1352.6618	0.0002	252 -	265	0	---	CGPGHGISVGSLGR
1353.6693	1352.6620	1352.6618	0.0002	252 -	265	0	76	CGPGHGISVGSLGR

No match to: 713.4065, 768.5187, 1183.4996, 1320.5951, 1320.5951, 1336.6504, 1336.6504, 1903.9689

5. gi|125581161 **Mass:** 27071 **Score:** 86 **Expect:** 0.0014 **Queries matched:** 2

hypothetical protein OsJ_05753 [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1353.6693	1352.6620	1352.6618	0.0002	92 -	105	0	---	CGPGHGISVGSLGR
1353.6693	1352.6620	1352.6618	0.0002	92 -	105	0	76	CGPGHGISVGSLGR

No match to: 713.4065, 768.5187, 1183.4996, 1320.5951, 1320.5951, 1336.6504, 1336.6504, 1352.6478, 1903.9689

6. gi|2832691 **Mass:** 39669 **Score:** 85 **Expect:** 0.0019 **Queries matched:** 2

polygalacturonase-like protein [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1353.6693	1352.6620	1352.6618	0.0002	193 -	206	0	---	CGPGHGISVGSLGR
1353.6693	1352.6620	1352.6618	0.0002	193 -	206	0	76	CGPGHGISVGSLGR

No match to: 713.4065, 768.5187, 1183.4996, 1320.5951, 1320.5951, 1336.6504, 1336.6504, 1352.6478, 1903.9689

7. gi|15236790 **Mass:** 45764 **Score:** 85 **Expect:** 0.0021 **Queries matched:** 2

glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein [Arabidopsis t

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1353.6693	1352.6620	1352.6618	0.0002	245 -	258	0	---	CGPGHGISVGSLGR
1353.6693	1352.6620	1352.6618	0.0002	245 -	258	0	76	CGPGHGISVGSLGR

No match to: 713.4065, 768.5187, 1183.4996, 1320.5951, 1320.5951, 1336.6504, 1336.6504, 1352.6478, 1903.9689

8. gi|194706004 **Mass:** 44631 **Score:** 85 **Expect:** 0.0021 **Queries matched:** 2

unknown [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1353.6693	1352.6620	1352.6618	0.0002	260 -	273	0	---	CGPGHGISVGSLGR
1353.6693	1352.6620	1352.6618	0.0002	260 -	273	0	76	CGPGHGISVGSLGR

No match to: 713.4065, 768.5187, 1183.4996, 1320.5951, 1320.5951, 1336.6504, 1336.6504, 1352.6478, 1903.9689

9. gi|15225803 **Mass:** 76008 **Score:** 83 **Expect:** 0.003 **Queries matched:** 2

glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein [Arabidopsis t

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1353.6693	1352.6620	1352.6618	0.0002	243 -	256	0	---	CGPGHGISVGSLGR
1353.6693	1352.6620	1352.6618	0.0002	243 -	256	0	76	CGPGHGISVGSLGR

No match to: 713.4065, 768.5187, 1183.4996, 1320.5951, 1320.5951, 1336.6504, 1336.6504, 1352.6478, 1903.9689

10. gi|223536326 **Mass:** 42374 **Score:** 54 **Expect:** 2.4 **Queries matched:** 4

Polygalacturonase precursor, putative [Ricinus communis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1320.5951	1319.5878	1319.6027	-0.0149	211	223	0	---	TGDDCISIGPGTK
1320.5951	1319.5878	1319.6027	-0.0149	211	223	0	---	TGDDCISIGPGTK
1353.6693	1352.6620	1352.6870	-0.0250	232	245	0	---	CGPGHGISIGSLAK
1353.6693	1352.6620	1352.6870	-0.0250	232	245	0	34	CGPGHGISIGSLAK

No match to: 713.4065, 768.5187, 1183.4996, 1336.6504, 1336.6504, 1352.6478, 1903.9689

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 11

Protein View

Match to: **gi|218190250** Score: **97** Expect: **0.00013**
hypothetical protein OsI_06235 [Oryza sativa Indica Group]

Nominal mass (M_r): **40600**; Calculated pI value: **7.92**
NCBI BLAST search of gi|218190250 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Oryza sativa Indica Group

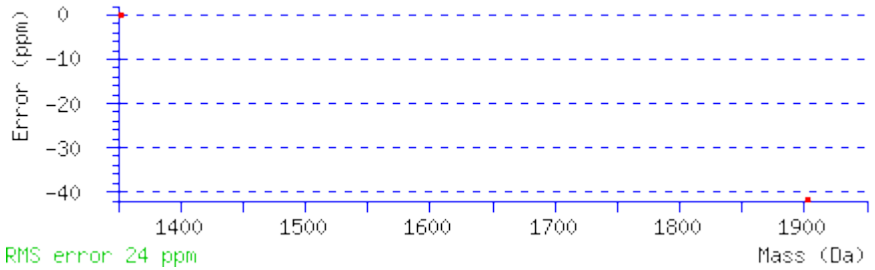
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **8%**

Matched peptides shown in **Bold Red**

```
   1 MVSSTRRTTS SLSATTAAAI AAAAAALMVS VAFATAQYTP ATSAAPGAAA
  51 AGAAAPYTPG AAGAAPSGPC TSSIILRLDG NLLGTGDLNA YKTNWIEVEH
 101 VDNFAINGHG IIDGQGPLVW THNQCNKNYN CKILPNSLVI DYSTNVTVRG
 151 ITLKNSKFFH LNIYESKNVV IDKVTITSPG DSPNTDGIHV GDSTNITISS
 201 TTIAAGDDCI SIGPGTKMVR VNGVRCGPGH GISVGSLGRY KDEKDVEDII
 251 VTNCTIKGTT NGLRIKSYED SKSQLRATKF LYDGITMDNV SYPIIIDQKY
 301 CPNNICSASG TSKVAVTDIV FKNIVGTSAT PEAVTLNCAN NLPCQGIQLH
 351 NVDLKYAGQG NTTLSVCKNV AGKSSNVAKE LACV
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
133 - 149	1903.9689	1902.9616	1903.0414	-0.0798	0	ILPNSLVIDYSTNVTVR	(No match)
226 - 239	1353.6693	1352.6620	1352.6618	0.0002	0	CGPGHGISVGSLGR	(No match)
226 - 239	1353.6693	1352.6620	1352.6618	0.0002	0	CGPGHGISVGSLGR	(Ions score 76)



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	Accession	Mass	Score	Description
1.	gi|222849203	44771	118	predicted protein [Populus trichocarpa]
2.	gi|125581161	27071	107	hypothetical protein OsJ_05753 [Oryza sativa Japonica Group]
3.	gi|218190250	40600	105	hypothetical protein OsI_06235 [Oryza sativa Indica Group]
4.	gi|49388133	44519	105	putative exopolygalacturonase precursor [Oryza sativa Japonica Group]
5.	gi|2832691	39669	105	polygalacturonase-like protein [Arabidopsis thaliana]

Results List

1. gi|222849203 **Mass:** 44771 **Score:** 118 **Expect:** 9.6e-007 **Queries matched:** 5

predicted protein [Populus trichocarpa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1263.6541	1262.6468	1262.6481	-0.0013	184	193	0	---	FFHIALVECK
1352.6384	1351.6311	1351.6772	-0.0460	56	67	1	---	TDDSKAFIAAWK
1353.6709	1352.6636	1352.6618	0.0018	252	265	0	---	CGPGHGISVGSLGR
1353.6709	1352.6636	1352.6618	0.0018	252	265	0	95	CGPGHGISVGSLGR
1622.8765	1621.8692	1621.8470	0.0222	250	265	1	---	IRCGPGHGISVGSLGR

No match to: 713.4082, 750.5129, 768.5212, 838.5275, 886.9892, 933.5367, 1007.4479, 1018.5826, 1183.4999, 1183.4999, 1296.6486, 1315.7222, 1334.8821, 1336.6460, 1336.6460, 1372.6550, 1392.6688, 1448.9081, 1475.7958, 1490.8571, 1687.9056, 1691.8914, 1725.9369, 1774.8618, 1774.8618, 1903.9720, 1903.9720, 2057.1409, 2136.1353, 2139.0874, 2548.3306, 2649.3877, 2690.3884, 2772.5166, 2918.6045

2. gi|125581161 **Mass:** 27071 **Score:** 107 **Expect:** 1.2e-005 **Queries matched:** 3

hypothetical protein OsJ_05753 [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1353.6709	1352.6636	1352.6618	0.0018	92	105	0	---	CGPGHGISVGSLGR
1353.6709	1352.6636	1352.6618	0.0018	92	105	0	95	CGPGHGISVGSLGR
1725.9369	1724.9296	1724.8767	0.0529	1	15	0	---	MQSLVIDYSTNVTVR

No match to: 713.4082, 750.5129, 768.5212, 838.5275, 886.9892, 933.5367, 1007.4479, 1018.5826, 1183.4999, 1183.4999, 1263.6541, 1296.6486, 1315.7222, 1334.8821, 1336.6460, 1336.6460, 1352.6384, 1372.6550, 1392.6688, 1448.9081, 1475.7958, 1490.8571, 1622.8765, 1687.9056, 1691.8914, 1774.8618, 1774.8618, 1903.9720, 1903.9720, 2057.1409, 2136.1353, 2139.0874, 2548.3306, 2649.3877, 2690.3884, 2772.5166, 2918.6045

3. gi|218190250 **Mass:** 40600 **Score:** 105 **Expect:** 1.9e-005 **Queries matched:** 4

hypothetical protein OsI_06235 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1353.6709	1352.6636	1352.6618	0.0018	226	239	0	---	CGPGHGISVGSLGR
1353.6709	1352.6636	1352.6618	0.0018	226	239	0	95	CGPGHGISVGSLGR
1903.9720	1902.9647	1903.0414	-0.0767	133	149	0	---	ILPNSLVIDYSTNVTVR

1903.9720	1902.9647	1903.0414	-0.0767	133 - 149	0	---	ILPNSLVIDYSTNVTVR

No match to: 713.4082, 750.5129, 768.5212, 838.5275, 886.9892, 933.5367, 1007.4479, 1018.5826, 1183.4999, 1183.4999, 1263.6541, 1296.6486, 1315.7222, 1334.8821, 1336.6460, 1336.6460, 1352.6384, 1372.6550, 1392.6688, 1448.9081, 1475.7958, 1490.8571, 1622.8765, 1687.9056, 1691.8914, 1725.9369, 1774.8618, 1774.8618, 2057.1409, 2136.1353, 2139.0874, 2548.3306, 2649.3877, 2690.3884, 2772.5166, 2918.6045

4. gi|49388133 **Mass:** 44519 **Score:** 105 **Expect:** 1.9e-005 **Queries matched:** 4

putative exopolygalacturonase precursor [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1353.6709	1352.6636	1352.6618	0.0018	264 -	277	0	---	CGPGHGISVGSLGR
1353.6709	1352.6636	1352.6618	0.0018	264 -	277	0	95	CGPGHGISVGSLGR
1903.9720	1902.9647	1903.0414	-0.0767	171 -	187	0	---	ILPNSLVIDYSTNVTVR
1903.9720	1902.9647	1903.0414	-0.0767	171 -	187	0	---	ILPNSLVIDYSTNVTVR

No match to: 713.4082, 750.5129, 768.5212, 838.5275, 886.9892, 933.5367, 1007.4479, 1018.5826, 1183.4999, 1183.4999, 1263.6541, 1296.6486, 1315.7222, 1334.8821, 1336.6460, 1336.6460, 1352.6384, 1372.6550, 1392.6688, 1448.9081, 1475.7958, 1490.8571, 1622.8765, 1687.9056, 1691.8914, 1725.9369, 1774.8618, 1774.8618, 2057.1409, 2136.1353, 2139.0874, 2548.3306, 2649.3877, 2690.3884, 2772.5166, 2918.6045

5. gi|2832691 **Mass:** 39669 **Score:** 105 **Expect:** 1.9e-005 **Queries matched:** 3

polygalacturonase-like protein [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1353.6709	1352.6636	1352.6618	0.0018	193 -	206	0	---	CGPGHGISVGSLGR
1353.6709	1352.6636	1352.6618	0.0018	193 -	206	0	95	CGPGHGISVGSLGR
1475.7958	1474.7885	1474.8329	-0.0444	100 -	112	1	---	LLPTSLKFVGMNR

No match to: 713.4082, 750.5129, 768.5212, 838.5275, 886.9892, 933.5367, 1007.4479, 1018.5826, 1183.4999, 1183.4999, 1263.6541, 1296.6486, 1315.7222, 1334.8821, 1336.6460, 1336.6460, 1352.6384, 1372.6550, 1392.6688, 1448.9081, 1490.8571, 1622.8765, 1687.9056, 1691.8914, 1725.9369, 1774.8618, 1774.8618, 1903.9720, 1903.9720, 2057.1409, 2136.1353, 2139.0874, 2548.3306, 2649.3877, 2690.3884, 2772.5166, 2918.6045

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 40

Protein View

Match to: **gi|222849203** Score: **118** Expect: **9.6e-007**
predicted protein [Populus trichocarpa]

Nominal mass (M_r): **44771**; Calculated pI value: **8.88**
NCBI BLAST search of gi|222849203 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Populus trichocarpa

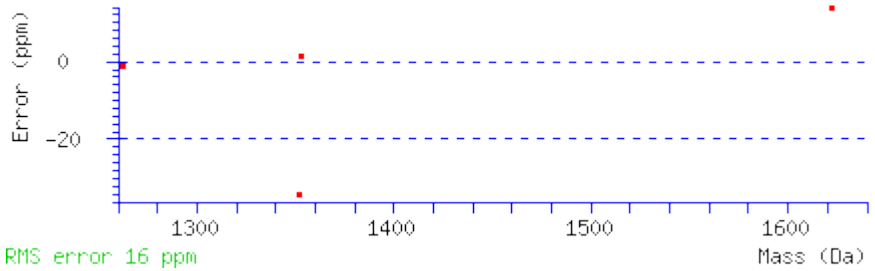
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **9%**

Matched peptides shown in **Bold Red**

```
   1 MLLLLLSFFC FNAVVFTGAD GQGLEAEARR PISHHKGNSS LLFDVKRFGA
  51 RADGRTDDSK AFIAAWKEAC RATGKVELLI PKGTYLIGPV KFAGPCKNVS
 101 SLTGYLKATA KLSRYGSGTG WVEFGWLERL TLTGGGTFDG QGAKAWPYNN
 151 CTNDSKCKLL PTNVKFVAMN QTVVQGITSL NSKFFHIALV ECKNFKGTKI
 201 KISAPADSPN TDGIHVERSS SVYISQSLIG TGDDCISIGQ GNSQVTITRI
 251 RCGPGHGISV GSLGRYEDEG DVSGLVVRDC AISGTMNGIR IKTWANSPGS
 301 SAATNMTFEN IVMNNVTNPI IIDQSYCPFS SCISTEPSKV KLSDIYFKQI
 351 RGTSSSAVAV ALECSKGIPC QNIYLENVHL ELSSGEKQAT SSCKNVRARY
 401 IGEQIPPPCA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
56 - 67	1352.6384	1351.6311	1351.6772	-0.0460	1	TDDSKAFIAAWK	(No match)
184 - 193	1263.6541	1262.6468	1262.6481	-0.0013	0	FFHIALVECK	(No match)
250 - 265	1622.8765	1621.8692	1621.8470	0.0222	1	IRCGPGHGISVGSLGR	(No match)
252 - 265	1353.6709	1352.6636	1352.6618	0.0018	0	CGPGHGISVGSLGR	(No match)
252 - 265	1353.6709	1352.6636	1352.6618	0.0018	0	CGPGHGISVGSLGR	(Ions score 95)



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	Accession	Mass	Score	Description
1.	gi|222849203	44771	100	predicted protein [Populus trichocarpa]
2.	gi|125581161	27071	91	hypothetical protein OsJ_05753 [Oryza sativa Japonica Group]
3.	gi|2832691	39669	90	polygalacturonase-like protein [Arabidopsis thaliana]
4.	gi|218190250	40600	90	hypothetical protein OsI_06235 [Oryza sativa Indica Group]
5.	gi|15236790	45764	89	glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein [Arabidop
6.	gi|194706004	44631	89	unknown [Zea mays]
7.	gi|49388133	44519	89	putative exopolygalacturonase precursor [Oryza sativa Japonica Group]
8.	gi|115444829	47052	89	Os02g0196700 [Oryza sativa (japonica cultivar-group)]
9.	gi|15225803	76008	88	glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein [Arabidop
10.	gi|223531447	42131	57	Polygalacturonase precursor, putative [Ricinus communis]

Results List

1. gi|222849203 **Mass:** 44771 **Score:** 100 **Expect:** 6e-005 **Queries matched:** 3

predicted protein [Populus trichocarpa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1352.6469	1351.6396	1351.6772	-0.0375	56 -	67	1	---	TDDSKAFIAAWK
1353.6776	1352.6703	1352.6618	0.0085	252 -	265	0	---	CGPGHGISVGSLGR
1353.6776	1352.6703	1352.6618	0.0085	252 -	265	0	81	CGPGHGISVGSLGR

No match to: 713.4019, 768.5134, 864.5009, 1183.5145, 1183.5145, 1336.6555, 1336.6555

2. gi|125581161 **Mass:** 27071 **Score:** 91 **Expect:** 0.00047 **Queries matched:** 2

hypothetical protein OsJ_05753 [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1353.6776	1352.6703	1352.6618	0.0085	92 -	105	0	---	CGPGHGISVGSLGR
1353.6776	1352.6703	1352.6618	0.0085	92 -	105	0	81	CGPGHGISVGSLGR

No match to: 713.4019, 768.5134, 864.5009, 1183.5145, 1183.5145, 1336.6555, 1336.6555, 1352.6469

3. gi|2832691 **Mass:** 39669 **Score:** 90 **Expect:** 0.00065 **Queries matched:** 2

polygalacturonase-like protein [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1353.6776	1352.6703	1352.6618	0.0085	193 -	206	0	---	CGPGHGISVGSLGR
1353.6776	1352.6703	1352.6618	0.0085	193 -	206	0	81	CGPGHGISVGSLGR

No match to: 713.4019, 768.5134, 864.5009, 1183.5145, 1183.5145, 1336.6555, 1336.6555, 1352.6469

4. gi|218190250 **Mass:** 40600 **Score:** 90 **Expect:** 0.00068 **Queries matched:** 2

hypothetical protein OsI_06235 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide

1353.6776 1352.6703 1352.6618 0.0085 226 - 239 0 --- CGPGHGISVGSLGR
1353.6776 1352.6703 1352.6618 0.0085 226 - 239 0 81 CGPGHGISVGSLGR
No match to: 713.4019, 768.5134, 864.5009, 1183.5145, 1183.5145, 1336.6555, 1336.6555, 1352.6469

5. gi|15236790 **Mass:** 45764 **Score:** 89 **Expect:** 0.00073 **Queries matched:** 2
glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein [Arabidopsis t

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1353.6776	1352.6703	1352.6618	0.0085	245	258	0	---	CGPGHGISVGSLGR
1353.6776	1352.6703	1352.6618	0.0085	245	258	0	81	CGPGHGISVGSLGR

No match to: 713.4019, 768.5134, 864.5009, 1183.5145, 1183.5145, 1336.6555, 1336.6555, 1352.6469

6. gi|194706004 **Mass:** 44631 **Score:** 89 **Expect:** 0.00073 **Queries matched:** 2
unknown [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1353.6776	1352.6703	1352.6618	0.0085	260	273	0	---	CGPGHGISVGSLGR
1353.6776	1352.6703	1352.6618	0.0085	260	273	0	81	CGPGHGISVGSLGR

No match to: 713.4019, 768.5134, 864.5009, 1183.5145, 1183.5145, 1336.6555, 1336.6555, 1352.6469

7. gi|49388133 **Mass:** 44519 **Score:** 89 **Expect:** 0.00073 **Queries matched:** 2
putative exopolygalacturonase precursor [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1353.6776	1352.6703	1352.6618	0.0085	264	277	0	---	CGPGHGISVGSLGR
1353.6776	1352.6703	1352.6618	0.0085	264	277	0	81	CGPGHGISVGSLGR

No match to: 713.4019, 768.5134, 864.5009, 1183.5145, 1183.5145, 1336.6555, 1336.6555, 1352.6469

8. gi|115444829 **Mass:** 47052 **Score:** 89 **Expect:** 0.00078 **Queries matched:** 2
Os02g0196700 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1353.6776	1352.6703	1352.6618	0.0085	291	304	0	---	CGPGHGISVGSLGR
1353.6776	1352.6703	1352.6618	0.0085	291	304	0	81	CGPGHGISVGSLGR

No match to: 713.4019, 768.5134, 864.5009, 1183.5145, 1183.5145, 1336.6555, 1336.6555, 1352.6469

9. gi|15225803 **Mass:** 76008 **Score:** 88 **Expect:** 0.001 **Queries matched:** 2
glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein [Arabidopsis t

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1353.6776	1352.6703	1352.6618	0.0085	243	256	0	---	CGPGHGISVGSLGR
1353.6776	1352.6703	1352.6618	0.0085	243	256	0	81	CGPGHGISVGSLGR

No match to: 713.4019, 768.5134, 864.5009, 1183.5145, 1183.5145, 1336.6555, 1336.6555, 1352.6469

10. gi|223531447 **Mass:** 42131 **Score:** 57 **Expect:** 1.4 **Queries matched:** 2
Polygalacturonase precursor, putative [Ricinus communis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide

1353.6776 1352.6703 1352.6618 0.0085 233 - 246 0 --- CGPGHGVSIGSLGR
1353.6776 1352.6703 1352.6618 0.0085 233 - 246 0 48 CGPGHGVSIGSLGR
No match to: 713.4019, 768.5134, 864.5009, 1183.5145, 1183.5145, 1336.6555, 1336.6555, 1352.6469

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 10

Protein View

Match to: **gi|222849203** Score: **100** Expect: **6e-005**
predicted protein [Populus trichocarpa]

Nominal mass (M_r): **44771**; Calculated pI value: **8.88**
NCBI BLAST search of gi|222849203 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Populus trichocarpa

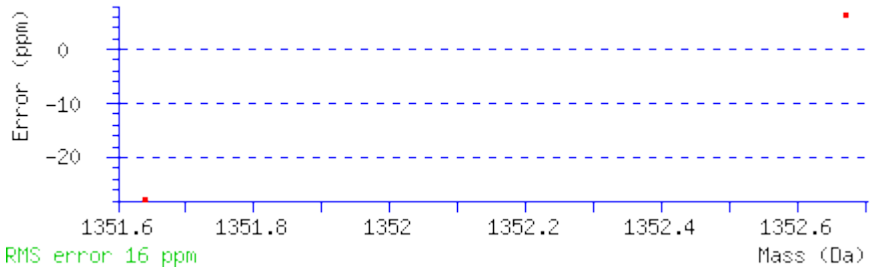
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **6%**

Matched peptides shown in **Bold Red**

```
     1 MLLLLLSFFC FNAVVFTGAD GQGLEAEARR PISHHKGNSS LLFDVKRFGA
    51 RADGRTDDSK AFIAAWKEAC RATGKVELLI PKGTYLIGPV KFAGPCKNVS
   101 SLTGYLKATA KLSRYGSGTG WVEFGWLERL TLTGGGTFDG QGAKAWPYNN
   151 CTNDSKCKLL PTNVKFVAMN QTVVQGITSL NSKFFHIALV ECKNFKGTKI
   201 KISAPADSPN TDGIHVERSS SVYISQSLIG TGDDCISIGQ GNSQVTITRI
   251 RCGPGHGISV GSLGRYEDEG DVSGLVVRDC AISGTMNGIR IKTWANSPGS
   301 SAATNMTFEN IVMNNVTNPI IIDQSYCPFS SCISTEPSKV KLSDIYFKQI
   351 RGTSSSAVAV ALECSKGIPC QNIYLENVHL ELSSGEKQAT SSCKNVRARY
   401 IGEQIPPPCA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
56 - 67	1352.6469	1351.6396	1351.6772	-0.0375	1	TDDSKAFIAAWK	(No match)
252 - 265	1353.6776	1352.6703	1352.6618	0.0085	0	CGPGHGISVGSLGR	(No match)
252 - 265	1353.6776	1352.6703	1352.6618	0.0085	0	CGPGHGISVGSLGR	(Ions score 81)



Peptide View

MS/MS Fragmentation of **CGPGHGISVGSLGR**
Found in **gi|222849203**, predicted protein [Populus trichocarpa]

Match to Query 10: 1352.670324 from(1353.677600,1+)
MaldiWellID: 70975, SpectrumID: 162892,

Click mouse within plot area to zoom in by factor of two about that point
Or, to Da
MONOISOTOPIC mass of neutral peptide Mr(calc): 1352.6618

Fixed modifications: Carbamidomethyl (C)
Ions Score: 81 **Expect:** 6.9e-006
Matches (Bold Red): 29/204 fragment ions using 42 most intense peaks

#	Immon.	a	a^0	b	b^0	Seq.	v	y	y*	y^0	#
1	133.0430	133.0430		161.0379		C					14
2	30.0338	190.0645		**218.0594**		G		1193.6385	1176.6120	1175.6279	13
3	**70.0651**	287.1172		315.1121		P	1094.5701	**1136.6170**	1119.5905	1118.6065	12
4	30.0338	344.1387		372.1336		G		1039.5643	1022.5377	1021.5537	11
5	**110.0713**	**481.1976**		509.1925		H	900.4897	**982.5428**	965.5163	964.5323	10
6	30.0338	538.2191		**566.2140**		G		**845.4839**	828.4574	827.4734	9
7	**86.0964**	651.3031		**679.2980**		I	730.3842	**788.4625**	771.4359	770.4519	8
8	60.0444	738.3352	720.3246	766.3301	748.3195	S	643.3522	**675.3784**	658.3519	657.3678	7
9	72.0808	837.4036	819.3930	865.3985	847.3879	V	544.2838	**588.3464**	571.3198	570.3358	6
10	30.0338	894.4250	876.4145	922.4199	904.4094	G		**489.2780**	472.2514	471.2674	5
11	60.0444	981.4571	963.4465	1009.4520	991.4414	S	400.2303	**432.2565**	415.2300	414.2459	4
12	**86.0964**	1094.5411	1076.5306	1122.5360	1104.5255	L	287.1462	**345.2245**	328.1979		3
13	30.0338	1151.5626	1133.5520	1179.5575	1161.5469	G		**232.1404**	215.1139		2
14	129.1135					R	74.0236	**175.1189**	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
GP	127.0866	155.0815	GPG	**184.1080**	212.1030	GPGH	321.1670	349.1619
GPGHG	378.1884	406.1833	GPGHGI	491.2725	519.2674	GPGHGIS	578.3045	606.2994
GPGHGISV	677.3729	705.3678	PG	127.0866	155.0815	PGH	264.1455	292.1404
PGHG	321.1670	349.1619	PGHGI	434.2510	462.2459	PGHGIS	521.2830	**549.2780**
PGHGISV	620.3515	648.3464	PGHGISVG	677.3729	705.3678	GH	167.0927	**195.0876**
GHG	224.1142	252.1091	GHGI	337.1983	365.1932	GHGIS	424.2303	452.2252
GHGISV	523.2987	551.2936	GHGISVG	580.3202	608.3151	GHGISVGS	667.3522	695.3471
HG	167.0927	**195.0876**	HGI	**280.1768**	308.1717	HGIS	367.2088	395.2037
HGISV	466.2772	494.2721	HGISVG	523.2987	551.2936	HGISVGS	610.3307	638.3256
GI	143.1179	171.1128	GIS	230.1499	**258.1448**	GISV	329.2183	357.2132
GISVG	386.2398	414.2347	GISVGS	473.2718	501.2667	GISVGSL	586.3559	614.3508

GISVGSLG	643.3773	671.3722	**IS**	173.1285	201.1234	**ISV**	272.1969	300.1918
ISVG	329.2183	357.2132	**ISVGS**	416.2504	444.2453	**ISVGSL**	529.3344	557.3293
ISVGSLG	586.3559	614.3508	**SV**	159.1128	187.1077	**SVG**	216.1343	**244.1292**
SVGS	303.1663	331.1612	**SVGSL**	416.2504	444.2453	**SVGSLG**	473.2718	501.2667
VG	129.1022	157.0971	**VGS**	216.1343	**244.1292**	**VGSL**	329.2183	357.2132
VGSLG	386.2398	414.2347	**GS**	117.0659	145.0608	**GSL**	230.1499	**258.1448**
GSLG	287.1714	315.1663	**SL**	173.1285	201.1234	**SLG**	230.1499	**258.1448**
LG	143.1179	171.1128						

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	Accession	Mass	Score	Description
1.	gi|115444197	47393	312	Os02g0146600 [Oryza sativa (japonica cultivar-group)]
2.	gi|63139086	47277	312	eukaryotic initiation factor 4A [Pennisetum glaucum]
3.	gi|1170511	47098	304	RecName: Full=Eukaryotic initiation factor 4A-10; Short=eIF-4A-10; AltName: Full=ATP-dependent
4.	gi|1170506	47084	291	RecName: Full=Eukaryotic initiation factor 4A-2; Short=eIF-4A-2; AltName: Full=ATP-dependent RN
5.	gi|2500516	47152	291	RecName: Full=Eukaryotic initiation factor 4A-7; Short=eIF-4A-7; AltName: Full=ATP-dependent RN

Results List

1. gi|115444197 **Mass:** 47393 **Score:** 312 **Expect:** 3.8e-026 **Queries matched:** 28

Os02g0146600 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
820.4363	819.4290	819.4312	-0.0022	71	77	0	---	GIVPFCK
891.4872	890.4799	890.4796	0.0003	235	241	0	---	FMNKPVR
907.4692	906.4619	906.4745	-0.0126	235	241	0	---	FMNKPVR + Oxidation (M)
936.5051	935.4978	935.5011	-0.0032	170	176	1	---	VFDMLRR
952.4918	951.4845	951.4960	-0.0114	170	176	1	---	VFDMLRR + Oxidation (M)
976.5659	975.5586	975.5501	0.0085	378	386	0	---	GVAINFVTR
1019.5842	1018.5769	1018.5746	0.0024	234	241	1	---	KFMNKPVR
1035.5731	1034.5658	1034.5695	-0.0036	234	241	1	---	KFMNKPVR + Oxidation (M)
1079.5631	1078.5558	1078.5593	-0.0035	320	327	1	---	DIIMREFR
1093.6099	1092.6026	1092.6040	-0.0013	177	185	0	---	QSLRPDHIK
1095.5568	1094.5495	1094.5542	-0.0047	320	327	1	---	DIIMREFR + Oxidation (M)
1104.6506	1103.6433	1103.6451	-0.0017	377	386	1	---	KGVAINFVTR
1114.6785	1113.6712	1113.6757	-0.0045	333	342	0	39	VLITTDLLAR
1114.6785	1113.6712	1113.6757	-0.0045	333	342	0	---	VLITTDLLAR
1249.7041	1248.6968	1248.7051	-0.0082	176	185	1	---	RQSLRPDHIK
1344.7401	1343.7328	1343.7231	0.0098	120	130	1	---	ELAQQIEKVMR
1401.7245	1400.7172	1400.7259	-0.0087	78	91	0	---	GLDVIQQAQSGTGK
1555.7092	1554.7019	1554.7058	-0.0039	186	198	0	---	MFVLDEADEMLSR
1571.7073	1570.7000	1570.7007	-0.0007	186	198	0	---	MFVLDEADEMLSR + Oxidation (M)
1587.6957	1586.6884	1586.6956	-0.0072	186	198	0	---	MFVLDEADEMLSR + 2 Oxidation (M)
1588.8955	1587.8882	1587.8944	-0.0061	328	342	1	---	SGSSRVLITTDLLAR
1670.8010	1669.7937	1669.7954	-0.0017	140	154	1	---	VHACVGGTSVREDQR
1827.9327	1826.9254	1826.9314	-0.0060	55	70	0	---	GIYAYGFEKPSAIQQR
1827.9327	1826.9254	1826.9314	-0.0060	55	70	0	80	GIYAYGFEKPSAIQQR
1919.9247	1918.9174	1918.8804	0.0370	186	201	1	---	MFVLDEADEMLSRGFK + 2 Oxidation (M)

2059.0723	2058.0650	2058.0679	-0.0029	131 - 150	1	---	ALGDYLGVKVHACVGGTSVR
2203.1575	2202.1502	2202.1466	0.0036	71 - 91	1	---	GIVPFCKGLDVIQQAQSGTGK
2911.4919	2910.4846	2910.4875	-0.0029	343 - 367	0	---	GIDVQQVSLVINYDLPTQPENYLHR

No match to: 713.4099, 724.4971, 750.5083, 768.5241, 838.5307, 886.9838, 1008.6342, 1053.6849, 1056.6514, 1160.6410, 1181.7622, 1279.7522, 1291.6815, 1296.7004, 1307.6652, 1334.8792, 1350.5918, 1447.8126, 1447.8126, 1463.7689, 1505.7671, 1590.9094, 1633.8584, 1786.8511, 1994.8928, 1994.8928, 2010.8839, 2010.8839, 2014.8856, 2231.2202, 2240.1350, 2382.3335, 2565.1946, 2587.3076, 2825.3232

2. gi|63139086 **Mass:** 47277 **Score:** 312 **Expect:** 3.8e-026 **Queries matched:** 28

eukaryotic initiation factor 4A [Pennisetum glaucum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
820.4363	819.4290	819.4312	-0.0022	71 -	77	0	---	GIVPFCK
891.4872	890.4799	890.4796	0.0003	235 -	241	0	---	FMNKPVR
907.4692	906.4619	906.4745	-0.0126	235 -	241	0	---	FMNKPVR + Oxidation (M)
936.5051	935.4978	935.5011	-0.0032	170 -	176	1	---	VFDMLRR
952.4918	951.4845	951.4960	-0.0114	170 -	176	1	---	VFDMLRR + Oxidation (M)
976.5659	975.5586	975.5501	0.0085	378 -	386	0	---	GVAINFVTR
1019.5842	1018.5769	1018.5746	0.0024	234 -	241	1	---	KFMNKPVR
1035.5731	1034.5658	1034.5695	-0.0036	234 -	241	1	---	KFMNKPVR + Oxidation (M)
1079.5631	1078.5558	1078.5593	-0.0035	320 -	327	1	---	DIIMREFR
1093.6099	1092.6026	1092.6040	-0.0013	177 -	185	0	---	QSLRPDHIK
1095.5568	1094.5495	1094.5542	-0.0047	320 -	327	1	---	DIIMREFR + Oxidation (M)
1104.6506	1103.6433	1103.6451	-0.0017	377 -	386	1	---	KGVAINFVTR
1114.6785	1113.6712	1113.6757	-0.0045	333 -	342	0	39	VLITTDLLAR
1114.6785	1113.6712	1113.6757	-0.0045	333 -	342	0	---	VLITTDLLAR
1249.7041	1248.6968	1248.7051	-0.0082	176 -	185	1	---	RQSLRPDHIK
1344.7401	1343.7328	1343.7231	0.0098	120 -	130	1	---	ELAQQIEKVMR
1401.7245	1400.7172	1400.7259	-0.0087	78 -	91	0	---	GLDVIQQAQSGTGK
1555.7092	1554.7019	1554.7058	-0.0039	186 -	198	0	---	MFVLDEADEMLSR
1571.7073	1570.7000	1570.7007	-0.0007	186 -	198	0	---	MFVLDEADEMLSR + Oxidation (M)
1587.6957	1586.6884	1586.6956	-0.0072	186 -	198	0	---	MFVLDEADEMLSR + 2 Oxidation (M)
1588.8955	1587.8882	1587.8944	-0.0061	328 -	342	1	---	SGSSRVLITTDLLAR
1670.8010	1669.7937	1669.7954	-0.0017	140 -	154	1	---	VHACVGGTSVREDQR
1827.9327	1826.9254	1826.9314	-0.0060	55 -	70	0	---	GIYAYGFEKPSAIQQR
1827.9327	1826.9254	1826.9314	-0.0060	55 -	70	0	80	GIYAYGFEKPSAIQQR
1919.9247	1918.9174	1918.8804	0.0370	186 -	201	1	---	MFVLDEADEMLSRGFK + 2 Oxidation (M)
2059.0723	2058.0650	2058.0679	-0.0029	131 -	150	1	---	ALGDYLGVKVHACVGGTSVR
2203.1575	2202.1502	2202.1466	0.0036	71 -	91	1	---	GIVPFCKGLDVIQQAQSGTGK
2911.4919	2910.4846	2910.4875	-0.0029	343 -	367	0	---	GIDVQQVSLVINYDLPTQPENYLHR

No match to: 713.4099, 724.4971, 750.5083, 768.5241, 838.5307, 886.9838, 1008.6342, 1053.6849, 1056.6514, 1160.6410, 1181.7622, 1279.7522, 1291.6815, 1296.7004, 1307.6652, 1334.8792, 1350.5918, 1447.8126, 1447.8126, 1463.7689, 1505.7671, 1590.9094, 1633.8584, 1786.8511, 1994.8928, 1994.8928, 2010.8839, 2010.8839, 2014.8856,

2231.2202, 2240.1350, 2382.3335, 2565.1946, 2587.3076, 2825.3232

3. gi|1170511 **Mass:** 47098 **Score:** 304 **Expect:** 2.4e-025 **Queries matched:** 27

RecName: Full=Eukaryotic initiation factor 4A-10; Short=eIF-4A-10; AltName: Full=ATP-dependent RNA

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
820.4363	819.4290	819.4312	-0.0022	70	76	0	---	GIVPFCK
891.4872	890.4799	890.4796	0.0003	234	240	0	---	FMNKPVR
907.4692	906.4619	906.4745	-0.0126	234	240	0	---	FMNKPVR + Oxidation (M)
936.5051	935.4978	935.5011	-0.0032	169	175	1	---	VFDMLRR
952.4918	951.4845	951.4960	-0.0114	169	175	1	---	VFDMLRR + Oxidation (M)
1019.5842	1018.5769	1018.5746	0.0024	233	240	1	---	KFMNKPVR
1035.5731	1034.5658	1034.5695	-0.0036	233	240	1	---	KFMNKPVR + Oxidation (M)
1079.5631	1078.5558	1078.5593	-0.0035	319	326	1	---	DIIMREFR
1093.6099	1092.6026	1092.6040	-0.0013	176	184	0	---	QSLRPDHIK
1095.5568	1094.5495	1094.5542	-0.0047	319	326	1	---	DIIMREFR + Oxidation (M)
1114.6785	1113.6712	1113.6757	-0.0045	332	341	0	39	VLITTDLLAR
1114.6785	1113.6712	1113.6757	-0.0045	332	341	0	---	VLITTDLLAR
1249.7041	1248.6968	1248.7051	-0.0082	175	184	1	---	RQSLRPDHIK
1344.7401	1343.7328	1343.7231	0.0098	119	129	1	---	ELAQQIEKVMR
1401.7245	1400.7172	1400.7259	-0.0087	77	90	0	---	GLDVIQQAQSGTGK
1463.7689	1462.7616	1462.7415	0.0201	377	389	1	---	GVAINFVTKDDER
1555.7092	1554.7019	1554.7058	-0.0039	185	197	0	---	MFVLDEADEMLSR
1571.7073	1570.7000	1570.7007	-0.0007	185	197	0	---	MFVLDEADEMLSR + Oxidation (M)
1587.6957	1586.6884	1586.6956	-0.0072	185	197	0	---	MFVLDEADEMLSR + 2 Oxidation (M)
1588.8955	1587.8882	1587.8944	-0.0061	327	341	1	---	SGSSRVLITTDLLAR
1670.8010	1669.7937	1669.7954	-0.0017	139	153	1	---	VHACVGGTSVREDQR
1827.9327	1826.9254	1826.9314	-0.0060	54	69	0	---	GIYAYGFEKPSAIQQR
1827.9327	1826.9254	1826.9314	-0.0060	54	69	0	80	GIYAYGFEKPSAIQQR
1919.9247	1918.9174	1918.8804	0.0370	185	200	1	---	MFVLDEADEMLSRGFK + 2 Oxidation (M)
2059.0723	2058.0650	2058.0679	-0.0029	130	149	1	---	ALGDYLGVKVHACVGGTSVR
2203.1575	2202.1502	2202.1466	0.0036	70	90	1	---	GIVPFCKGLDVIQQAQSGTGK
2911.4919	2910.4846	2910.4875	-0.0029	342	366	0	---	GIDVQQVSLVINYDLPTQPENYLHR

No match to: 713.4099, 724.4971, 750.5083, 768.5241, 838.5307, 886.9838, 976.5659, 1008.6342, 1053.6849, 1056.6514, 1104.6506, 1160.6410, 1181.7622, 1279.7522, 1291.6815, 1296.7004, 1307.6652, 1334.8792, 1350.5918, 1447.8126, 1447.8126, 1505.7671, 1590.9094, 1633.8584, 1786.8511, 1994.8928, 1994.8928, 2010.8839, 2010.8839, 2014.8856, 2231.2202, 2240.1350, 2382.3335, 2565.1946, 2587.3076, 2825.3232

4. gi|1170506 **Mass:** 47084 **Score:** 291 **Expect:** 4.8e-024 **Queries matched:** 26

RecName: Full=Eukaryotic initiation factor 4A-2; Short=eIF-4A-2; AltName: Full=ATP-dependent RNA he

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
820.4363	819.4290	819.4312	-0.0022	70	76	0	---	GIVPFCK
891.4872	890.4799	890.4796	0.0003	234	240	0	---	FMNKPVR

907.4692	906.4619	906.4745	-0.0126	234 - 240	0	---	FMNKPVR + Oxidation (M)
936.5051	935.4978	935.5011	-0.0032	169 - 175	1	---	VFDMLRR
952.4918	951.4845	951.4960	-0.0114	169 - 175	1	---	VFDMLRR + Oxidation (M)
1019.5842	1018.5769	1018.5746	0.0024	233 - 240	1	---	KFMNKPVR
1035.5731	1034.5658	1034.5695	-0.0036	233 - 240	1	---	KFMNKPVR + Oxidation (M)
1079.5631	1078.5558	1078.5593	-0.0035	319 - 326	1	---	DIIMREFR
1093.6099	1092.6026	1092.6040	-0.0013	176 - 184	0	---	QSLRPDHIK
1095.5568	1094.5495	1094.5542	-0.0047	319 - 326	1	---	DIIMREFR + Oxidation (M)
1114.6785	1113.6712	1113.6757	-0.0045	332 - 341	0	39	VLITTDLLAR
1114.6785	1113.6712	1113.6757	-0.0045	332 - 341	0	---	VLITTDLLAR
1249.7041	1248.6968	1248.7051	-0.0082	175 - 184	1	---	RQSLRPDHIK
1344.7401	1343.7328	1343.7231	0.0098	119 - 129	1	---	ELAQQIEKVMR
1401.7245	1400.7172	1400.7259	-0.0087	77 - 90	0	---	GLDVIQQAQSGTGK
1555.7092	1554.7019	1554.7058	-0.0039	185 - 197	0	---	MFVLDEADEMLSR
1571.7073	1570.7000	1570.7007	-0.0007	185 - 197	0	---	MFVLDEADEMLSR + Oxidation (M)
1587.6957	1586.6884	1586.6956	-0.0072	185 - 197	0	---	MFVLDEADEMLSR + 2 Oxidation (M)
1588.8955	1587.8882	1587.8944	-0.0061	327 - 341	1	---	SGSSRVLITTDLLAR
1670.8010	1669.7937	1669.7954	-0.0017	139 - 153	1	---	VHACVGGTSVREDQR
1827.9327	1826.9254	1826.9314	-0.0060	54 - 69	0	---	GIYAYGFEKPSAIQQR
1827.9327	1826.9254	1826.9314	-0.0060	54 - 69	0	80	GIYAYGFEKPSAIQQR
1919.9247	1918.9174	1918.8804	0.0370	185 - 200	1	---	MFVLDEADEMLSRGFK + 2 Oxidation (M)
2059.0723	2058.0650	2058.0679	-0.0029	130 - 149	1	---	ALGDYLGVKVHACVGGTSVR
2203.1575	2202.1502	2202.1466	0.0036	70 - 90	1	---	GIVPFCKGLDVIQQAQSGTGK
2911.4919	2910.4846	2910.4875	-0.0029	342 - 366	0	---	GIDVQQVSLVINYDLPTQPENYLHR

No match to: 713.4099, 724.4971, 750.5083, 768.5241, 838.5307, 886.9838, 976.5659, 1008.6342, 1053.6849, 1056.6514, 1104.6506, 1160.6410, 1181.7622, 1279.7522, 1291.6815, 1296.7004, 1307.6652, 1334.8792, 1350.5918, 1447.8126, 1447.8126, 1463.7689, 1505.7671, 1590.9094, 1633.8584, 1786.8511, 1994.8928, 1994.8928, 2010.8839, 2010.8839, 2014.8856, 2231.2202, 2240.1350, 2382.3335, 2565.1946, 2587.3076, 2825.3232

5. gi|2500516 **Mass:** 47152 **Score:** 291 **Expect:** 4.8e-024 **Queries matched:** 26

RecName: Full=Eukaryotic initiation factor 4A-7; Short=eIF-4A-7; AltName: Full=ATP-dependent RNA he

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
820.4363	819.4290	819.4312	-0.0022	70 - 76	0	---	GIVPFCK
891.4872	890.4799	890.4796	0.0003	234 - 240	0	---	FMNKPVR
907.4692	906.4619	906.4745	-0.0126	234 - 240	0	---	FMNKPVR + Oxidation (M)
936.5051	935.4978	935.5011	-0.0032	169 - 175	1	---	VFDMLRR
952.4918	951.4845	951.4960	-0.0114	169 - 175	1	---	VFDMLRR + Oxidation (M)
1019.5842	1018.5769	1018.5746	0.0024	233 - 240	1	---	KFMNKPVR
1035.5731	1034.5658	1034.5695	-0.0036	233 - 240	1	---	KFMNKPVR + Oxidation (M)
1079.5631	1078.5558	1078.5593	-0.0035	319 - 326	1	---	DIIMREFR
1093.6099	1092.6026	1092.6040	-0.0013	176 - 184	0	---	QSLRPDHIK

1095.5568	1094.5495	1094.5542	-0.0047	319 - 326	1	---	DIIMREFR + Oxidation (M)
1114.6785	1113.6712	1113.6757	-0.0045	332 - 341	0	39	VLITTDLLAR
1114.6785	1113.6712	1113.6757	-0.0045	332 - 341	0	---	VLITTDLLAR
1249.7041	1248.6968	1248.7051	-0.0082	175 - 184	1	---	RQSLRPDHIK
1344.7401	1343.7328	1343.7231	0.0098	119 - 129	1	---	ELAQQIEKVMR
1401.7245	1400.7172	1400.7259	-0.0087	77 - 90	0	---	GLDVIQQAQSGTGK
1555.7092	1554.7019	1554.7058	-0.0039	185 - 197	0	---	MFVLDEADEMLSR
1571.7073	1570.7000	1570.7007	-0.0007	185 - 197	0	---	MFVLDEADEMLSR + Oxidation (M)
1587.6957	1586.6884	1586.6956	-0.0072	185 - 197	0	---	MFVLDEADEMLSR + 2 Oxidation (M)
1588.8955	1587.8882	1587.8944	-0.0061	327 - 341	1	---	SGSSRVLITTDLLAR
1670.8010	1669.7937	1669.7954	-0.0017	139 - 153	1	---	VHACVGGTSVREDQR
1827.9327	1826.9254	1826.9314	-0.0060	54 - 69	0	---	GIYAYGFEKPSAIQQR
1827.9327	1826.9254	1826.9314	-0.0060	54 - 69	0	80	GIYAYGFEKPSAIQQR
1919.9247	1918.9174	1918.8804	0.0370	185 - 200	1	---	MFVLDEADEMLSRGFK + 2 Oxidation (M)
2059.0723	2058.0650	2058.0679	-0.0029	130 - 149	1	---	ALGDYLGVKVHACVGGTSVR
2203.1575	2202.1502	2202.1466	0.0036	70 - 90	1	---	GIVPFCKGLDVIQQAQSGTGK
2911.4919	2910.4846	2910.4875	-0.0029	342 - 366	0	---	GIDVQQVSLVINYDLPTQPENYLHR

No match to: 713.4099, 724.4971, 750.5083, 768.5241, 838.5307, 886.9838, 976.5659, 1008.6342, 1053.6849, 1056.6514, 1104.6506, 1160.6410, 1181.7622, 1279.7522, 1291.6815, 1296.7004, 1307.6652, 1334.8792, 1350.5918, 1447.8126, 1447.8126, 1463.7689, 1505.7671, 1590.9094, 1633.8584, 1786.8511, 1994.8928, 1994.8928, 2010.8839, 2010.8839, 2014.8856, 2231.2202, 2240.1350, 2382.3335, 2565.1946, 2587.3076, 2825.3232

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 63

Protein View

Match to: **gi|63139086** Score: **312** Expect: **3.8e-026**
eukaryotic initiation factor 4A [Pennisetum glaucum]

Nominal mass (M_r): **47277**; Calculated pI value: **5.36**
NCBI BLAST search of gi|63139086 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Pennisetum glaucum

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **41%**

Matched peptides shown in **Bold Red**

```
   1 MAGMAPEGSQ FDAKHYDSKM QELLSTGETE EFFTSYDEVF ESFDDMGLQE
  51 NLLRGIYAYG FEKPSAIQQR GIVPFCKGLD VIQQAQSGTG KTATFCSGIL
 101 QQLDYGLVEC QALVLAPTRE LAQQIEKVMR ALGDYLGVKV HACVGGTSVR
 151 EDQRILASGV HVVVGTPGRV FDMLRRQSLR PDHIKMFVLD EADEMLSRGF
 201 KDQIYDIFQL LPAKIQVGVF SATMPPEALE ITRKFMNKPV RILVKRDELT
 251 LEGIKQFYVN VEKEDWKLDT LCDLYETLAI TQSVIFVNTR RKVDWLTDKM
 301 RSRDHTVSAT HGDMDQNTRD IIMREFRSGS SRVLITTDLL ARGIDVQQVS
 351 LVINYDLPTQ PENYLHRIGR SGRFGRKGVA INFVTRDDDR MQFDIQRFYS
 401 VVIEELPTNV ADLL
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
55 - 70	1827.9327	1826.9254	1826.9314	-0.0060	0	**GIYAYGFEKPSAIQQR** (No match)
55 - 70	1827.9327	1826.9254	1826.9314	-0.0060	0	**GIYAYGFEKPSAIQQR** (Ions score 80)
71 - 77	820.4363	819.4290	819.4312	-0.0022	0	**GIVPFCK** (No match)
71 - 91	2203.1575	2202.1502	2202.1466	0.0036	1	**GIVPFCKGLDVIQQAQSGTGK** (No match)
78 - 91	1401.7245	1400.7172	1400.7259	-0.0087	0	**GLDVIQQAQSGTGK** (No match)
120 - 130	1344.7401	1343.7328	1343.7231	0.0098	1	**ELAQQIEKVMR** (No match)
131 - 150	2059.0723	2058.0650	2058.0679	-0.0029	1	**ALGDYLGVKVHACVGGTSVR** (No match)
140 - 154	1670.8010	1669.7937	1669.7954	-0.0017	1	**VHACVGGTSVREDQR** (No match)
170 - 176	936.5051	935.4978	935.5011	-0.0032	1	**VFDMLRR** (No match)
170 - 176	952.4918	951.4845	951.4960	-0.0114	1	**VFDMLRR** Oxidation (M) (No match)
176 - 185	1249.7041	1248.6968	1248.7051	-0.0082	1	**RQSLRPDHIK** (No match)
177 - 185	1093.6099	1092.6026	1092.6040	-0.0013	0	**QSLRPDHIK** (No match)
186 - 198	1555.7092	1554.7019	1554.7058	-0.0039	0	**MFVLDEADEMLSR** (No match)
186 - 198	1571.7073	1570.7000	1570.7007	-0.0007	0	**MFVLDEADEMLSR** Oxidation (M) (No match)
186 - 198	1587.6957	1586.6884	1586.6956	-0.0072	0	**MFVLDEADEMLSR** 2 Oxidation (M) (No match)
186 - 201	1919.9247	1918.9174	1918.8804	0.0370	1	**MFVLDEADEMLSRGFK** 2 Oxidation (M) (No match)
234 - 241	1019.5842	1018.5769	1018.5746	0.0024	1	**KFMNKPVR** (No match)
234 - 241	1035.5731	1034.5658	1034.5695	-0.0036	1	**KFMNKPVR** Oxidation (M) (No match)
235 - 241	891.4872	890.4799	890.4796	0.0003	0	**FMNKPVR** (No match)
235 - 241	907.4692	906.4619	906.4745	-0.0126	0	**FMNKPVR** Oxidation (M) (No match)
320 - 327	1079.5631	1078.5558	1078.5593	-0.0035	1	**DIIMREFR** (No match)
320 - 327	1095.5568	1094.5495	1094.5542	-0.0047	1	**DIIMREFR** Oxidation (M) (No match)
328 - 342	1588.8955	1587.8882	1587.8944	-0.0061	1	**SGSSRVLITTDLLAR** (No match)
333 - 342	1114.6785	1113.6712	1113.6757	-0.0045	0	**VLITTDLLAR** (Ions score 39)
333 - 342	1114.6785	1113.6712	1113.6757	-0.0045	0	**VLITTDLLAR** (No match)
343 - 367	2911.4919	2910.4846	2910.4875	-0.0029	0	**GIDVQQVSLVINYDLPTQPENYLHR** (No match)
377 - 386	1104.6506	1103.6433	1103.6451	-0.0017	1	**KGVAINFVTR** (No match)
378 - 386	976.5659	975.5586	975.5501	0.0085	0	**GVAINFVTR** (No match)

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	Accession	Mass	Score	Description
1.	gi|226503683	50808	170	citrate synthase 4 [Zea mays]
2.	gi|8928010	52908	163	RecName: Full=Citrate synthase, mitochondrial; Flags: Precursor
3.	gi|212720950	52651	158	hypothetical protein LOC100194338 [Zea mays]
4.	gi|219884127	52625	155	unknown [Zea mays]
5.	gi|226504136	34249	139	hypothetical protein LOC100279573 [Zea mays]
6.	gi|115444791	52424	129	Os02g0194100 [Oryza sativa (japonica cultivar-group)]
7.	gi|11066954	52423	129	citrate synthase [Oryza sativa]
8.	gi|222622360	54020	129	hypothetical protein OsJ_05734 [Oryza sativa Japonica Group]
9.	gi|218190238	54047	128	hypothetical protein OsI_06215 [Oryza sativa Indica Group]
10.	gi|115485775	52557	128	Os11g0538900 [Oryza sativa (japonica cultivar-group)]

Results List

1. gi|226503683 **Mass:** 50808 **Score:** 170 **Expect:** 6.1e-012 **Queries matched:** 16

citrate synthase 4 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1031.5079	1030.5006	1030.5117	-0.0111	86	94	0	---	GLSIPECQK
1093.6748	1092.6675	1092.6655	0.0021	431	440	0	---	ALGLPLERPK
1093.6748	1092.6675	1092.6655	0.0021	431	440	0	22	ALGLPLERPK
1204.6384	1203.6311	1203.6287	0.0024	409	418	0	39	YYTVLFGVSR
1204.6384	1203.6311	1203.6287	0.0024	409	418	0	---	YYTVLFGVSR
1301.6345	1300.6272	1300.6234	0.0039	347	356	1	---	YSCQREFALK
1334.7007	1333.6934	1333.6812	0.0122	84	94	1	---	FRGLSIPECQK
1362.6899	1361.6826	1361.6761	0.0065	419	430	0	---	SMGIGSQLIWDR
1362.6899	1361.6826	1361.6761	0.0065	419	430	0	26	SMGIGSQLIWDR
1378.6758	1377.6685	1377.6710	-0.0025	419	430	0	---	SMGIGSQLIWDR + Oxidation (M)
1522.8257	1521.8184	1521.8191	-0.0007	357	369	0	---	HLPEDPLFQLVSK
1926.9193	1925.9120	1925.8981	0.0139	185	199	0	---	FWEPTYEDCLNLIAR
2135.0195	2134.0122	2134.0074	0.0048	65	83	0	---	GMTGMLWETSLLDPEEGIR
2142.0452	2141.0379	2141.0251	0.0128	183	199	1	---	SKFWEPTYEDCLNLIAR
2151.0095	2150.0022	2150.0023	-0.0001	65	83	0	---	GMTGMLWETSLLDPEEGIR + Oxidation (M)
2564.1797	2563.1724	2563.2892	-0.1168	409	430	1	---	YYTVLFGVSRSMGIGSQLIWDR + Oxidation (M)

No match to: 713.3937, 724.4756, 734.4897, 750.5082, 768.5119, 782.4727, 848.5277, 864.5253, 1153.6534, 1153.6534, 1195.6522, 1320.5950, 1351.7496, 1351.7496, 1394.6868, 1425.8044, 1448.9039, 1530.8682, 1533.6824, 1601.7721, 1617.7598, 1661.7800, 1677.7855, 1702.9071, 1707.7908, 1718.8966, 1842.9575, 1858.9449, 2230.2185, 2241.1545, 2400.0166, 2483.3445, 2542.2927, 2663.3464, 2769.4600, 2825.3096, 2922.3599, 2932.4197, 2947.4126, 2964.4336, 3332.5544

2. gi|8928010 **Mass:** 52908 **Score:** 163 **Expect:** 3e-011 **Queries matched:** 15

RecName: Full=Citrate synthase, mitochondrial; Flags: Precursor

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
782.4727	781.4654	781.4446	0.0208	59	65	1	---	LKAEHGK
1031.5079	1030.5006	1030.5117	-0.0111	103	111	0	---	GLSIPECQK
1093.6748	1092.6675	1092.6655	0.0021	448	457	0	---	ALGLPLERPK
1093.6748	1092.6675	1092.6655	0.0021	448	457	0	22	ALGLPLERPK
1153.6534	1152.6461	1152.6403	0.0058	348	358	0	33	VVPGYGHGVLR
1153.6534	1152.6461	1152.6403	0.0058	348	358	0	---	VVPGYGHGVLR
1204.6384	1203.6311	1203.6287	0.0024	426	435	0	39	YYTVLFGVSR
1204.6384	1203.6311	1203.6287	0.0024	426	435	0	---	YYTVLFGVSR
1334.7007	1333.6934	1333.6812	0.0122	101	111	1	---	FRGLSIPECQK
1533.6824	1532.6751	1532.6752	-0.0000	458	469	0	---	SVTMEWLENHCK
1661.7800	1660.7727	1660.7701	0.0026	458	470	1	---	SVTMEWLENHCKK
1677.7855	1676.7782	1676.7650	0.0132	458	470	1	---	SVTMEWLENHCKK + Oxidation (M)
1702.9071	1701.8998	1701.8905	0.0093	66	81	0	---	VQLGNITVDMVLGGMR
1718.8966	1717.8893	1717.8854	0.0039	66	81	0	---	VQLGNITVDMVLGGMR + Oxidation (M)
2241.1545	2240.1472	2240.1405	0.0068	61	81	1	---	AEHGKVQLGNITVDMVLGGMR + Oxidation (M)

No match to: 713.3937, 724.4756, 734.4897, 750.5082, 768.5119, 848.5277, 864.5253, 1195.6522, 1301.6345, 1320.5950, 1351.7496, 1351.7496, 1362.6899, 1362.6899, 1378.6758, 1394.6868, 1425.8044, 1448.9039, 1522.8257, 1530.8682, 1601.7721, 1617.7598, 1707.7908, 1842.9575, 1858.9449, 1926.9193, 2135.0195, 2142.0452, 2151.0095, 2230.2185, 2400.0166, 2483.3445, 2542.2927, 2564.1797, 2663.3464, 2769.4600, 2825.3096, 2922.3599, 2932.4197, 2947.4126, 2964.4336, 3332.5544

3. gi|212720950 **Mass:** 52651 **Score:** 158 **Expect:** 9.6e-011 **Queries matched:** 15

hypothetical protein LOC100194338 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1031.5079	1030.5006	1030.5117	-0.0111	102	110	0	---	GLSIPECQK
1093.6748	1092.6675	1092.6655	0.0021	447	456	0	---	ALGLPLERPK
1093.6748	1092.6675	1092.6655	0.0021	447	456	0	22	ALGLPLERPK
1204.6384	1203.6311	1203.6287	0.0024	425	434	0	39	YYTVLFGVSR
1204.6384	1203.6311	1203.6287	0.0024	425	434	0	---	YYTVLFGVSR
1301.6345	1300.6272	1300.6234	0.0039	363	372	1	---	YSCQREFALK
1334.7007	1333.6934	1333.6812	0.0122	100	110	1	---	FRGLSIPECQK
1362.6899	1361.6826	1361.6761	0.0065	435	446	0	---	SMGIGSQLIWDR
1362.6899	1361.6826	1361.6761	0.0065	435	446	0	26	SMGIGSQLIWDR
1378.6758	1377.6685	1377.6710	-0.0025	435	446	0	---	SMGIGSQLIWDR + Oxidation (M)
1522.8257	1521.8184	1521.8191	-0.0007	373	385	0	---	HLPEDPLFQLVSK
1702.9071	1701.8998	1701.8905	0.0093	65	80	0	---	VQLGNITVDMVLGGMR
1718.8966	1717.8893	1717.8854	0.0039	65	80	0	---	VQLGNITVDMVLGGMR + Oxidation (M)

2241.1545	2240.1472	2240.1405	0.0068	60 - 80	1	---	SEHGKVQLGNITVDMVLGGMR
2564.1797	2563.1724	2563.2892	-0.1168	425 - 446	1	---	YYTVLFGVSRSMGIGSQLIWDR + Oxidation (M)

No match to: 713.3937, 724.4756, 734.4897, 750.5082, 768.5119, 782.4727, 848.5277, 864.5253, 1153.6534, 1153.6534, 1195.6522, 1320.5950, 1351.7496, 1351.7496, 1394.6868, 1425.8044, 1448.9039, 1530.8682, 1533.6824, 1601.7721, 1617.7598, 1661.7800, 1677.7855, 1707.7908, 1842.9575, 1858.9449, 1926.9193, 2135.0195, 2142.0452, 2151.0095, 2230.2185, 2400.0166, 2483.3445, 2542.2927, 2663.3464, 2769.4600, 2825.3096, 2922.3599, 2932.4197, 2947.4126, 2964.4336, 3332.5544

4. gi|219884127 **Mass:** 52625 **Score:** 155 **Expect:** 1.9e-010 **Queries matched:** 15

unknown [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1031.5079	1030.5006	1030.5117	-0.0111	102 - 110		0	---	GLSIPECQK
1093.6748	1092.6675	1092.6655	0.0021	447 - 456		0	---	ALGLPLERPK
1093.6748	1092.6675	1092.6655	0.0021	447 - 456		0	22	ALGLPLERPK
1204.6384	1203.6311	1203.6287	0.0024	425 - 434		0	39	YYTVLFGVSR
1204.6384	1203.6311	1203.6287	0.0024	425 - 434		0	---	YYTVLFGVSR
1301.6345	1300.6272	1300.6234	0.0039	363 - 372		1	---	YSCQREFALK
1334.7007	1333.6934	1333.6812	0.0122	100 - 110		1	---	FRGLSIPECQK
1362.6899	1361.6826	1361.6761	0.0065	435 - 446		0	---	SMGIGSQLIWDR
1362.6899	1361.6826	1361.6761	0.0065	435 - 446		0	26	SMGIGSQLIWDR
1378.6758	1377.6685	1377.6710	-0.0025	435 - 446		0	---	SMGIGSQLIWDR + Oxidation (M)
1926.9193	1925.9120	1925.8981	0.0139	201 - 215		0	---	FWEPTYEDCLNLIAR
2135.0195	2134.0122	2134.0074	0.0048	81 - 99		0	---	GMTGMLWETSLLDPEEGIR
2142.0452	2141.0379	2141.0251	0.0128	199 - 215		1	---	SKFWEPTYEDCLNLIAR
2151.0095	2150.0022	2150.0023	-0.0001	81 - 99		0	---	GMTGMLWETSLLDPEEGIR + Oxidation (M)
2564.1797	2563.1724	2563.2892	-0.1168	425 - 446		1	---	YYTVLFGVSRSMGIGSQLIWDR + Oxidation (M)

No match to: 713.3937, 724.4756, 734.4897, 750.5082, 768.5119, 782.4727, 848.5277, 864.5253, 1153.6534, 1153.6534, 1195.6522, 1320.5950, 1351.7496, 1351.7496, 1394.6868, 1425.8044, 1448.9039, 1522.8257, 1530.8682, 1533.6824, 1601.7721, 1617.7598, 1661.7800, 1677.7855, 1702.9071, 1707.7908, 1718.8966, 1842.9575, 1858.9449, 2230.2185, 2241.1545, 2400.0166, 2483.3445, 2542.2927, 2663.3464, 2769.4600, 2825.3096, 2922.3599, 2932.4197, 2947.4126, 2964.4336, 3332.5544

5. gi|226504136 **Mass:** 34249 **Score:** 139 **Expect:** 7.6e-009 **Queries matched:** 11

hypothetical protein LOC100279573 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1093.6748	1092.6675	1092.6655	0.0021	295 - 304		0	---	ALGLPLERPK
1093.6748	1092.6675	1092.6655	0.0021	295 - 304		0	22	ALGLPLERPK
1204.6384	1203.6311	1203.6287	0.0024	273 - 282		0	39	YYTVLFGVSR
1204.6384	1203.6311	1203.6287	0.0024	273 - 282		0	---	YYTVLFGVSR
1301.6345	1300.6272	1300.6234	0.0039	211 - 220		1	---	YSCQREFALK
1362.6899	1361.6826	1361.6761	0.0065	283 - 294		0	---	SMGIGSQLIWDR
1362.6899	1361.6826	1361.6761	0.0065	283 - 294		0	26	SMGIGSQLIWDR

1378.6758	1377.6685	1377.6710	-0.0025	283 - 294	0	---	SMGIGSQLIWDR + Oxidation (M)
1926.9193	1925.9120	1925.8981	0.0139	49 - 63	0	---	FWEPTYEDCLNLIAR
2142.0452	2141.0379	2141.0251	0.0128	47 - 63	1	---	SKFWEPTYEDCLNLIAR
2564.1797	2563.1724	2563.2892	-0.1168	273 - 294	1	---	YYTVLFGVSRSMGIGSQLIWDR + Oxidation (M)

No match to: 713.3937, 724.4756, 734.4897, 750.5082, 768.5119, 782.4727, 848.5277, 864.5253, 1031.5079, 1153.6534, 1153.6534, 1195.6522, 1320.5950, 1334.7007, 1351.7496, 1351.7496, 1394.6868, 1425.8044, 1448.9039, 1522.8257, 1530.8682, 1533.6824, 1601.7721, 1617.7598, 1661.7800, 1677.7855, 1702.9071, 1707.7908, 1718.8966, 1842.9575, 1858.9449, 2135.0195, 2151.0095, 2230.2185, 2241.1545, 2400.0166, 2483.3445, 2542.2927, 2663.3464, 2769.4600, 2825.3096, 2922.3599, 2932.4197, 2947.4126, 2964.4336, 3332.5544

6. gi|115444791 **Mass:** 52424 **Score:** 129 **Expect:** 7.6e-008 **Queries matched:** 14

Os02g0194100 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1031.5079	1030.5006	1030.5117	-0.0111	102 - 110	0	---	GLSIPECQK
1093.6748	1092.6675	1092.6655	0.0021	447 - 456	0	---	ALGLPLERPK
1093.6748	1092.6675	1092.6655	0.0021	447 - 456	0	22	ALGLPLERPK
1204.6384	1203.6311	1203.6287	0.0024	425 - 434	0	39	YYTVLFGVSR
1204.6384	1203.6311	1203.6287	0.0024	425 - 434	0	---	YYTVLFGVSR
1334.7007	1333.6934	1333.6812	0.0122	100 - 110	1	---	FRGLSIPECQK
1533.6824	1532.6751	1532.6752	-0.0000	457 - 468	0	---	SVTMEWLENHCK
1661.7800	1660.7727	1660.7701	0.0026	457 - 469	1	---	SVTMEWLENHCKK
1677.7855	1676.7782	1676.7650	0.0132	457 - 469	1	---	SVTMEWLENHCKK + Oxidation (M)
1702.9071	1701.8998	1701.8905	0.0093	65 - 80	0	---	VQLGNITVDMVLGGMR
1718.8966	1717.8893	1717.8854	0.0039	65 - 80	0	---	VQLGNITVDMVLGGMR + Oxidation (M)
1926.9193	1925.9120	1925.8981	0.0139	201 - 215	0	---	FWEPTYEDCLNLIAR
2142.0452	2141.0379	2141.0251	0.0128	199 - 215	1	---	SKFWEPTYEDCLNLIAR
2241.1545	2240.1472	2240.1405	0.0068	60 - 80	1	---	SEHGKVQLGNITVDMVLGGMR

No match to: 713.3937, 724.4756, 734.4897, 750.5082, 768.5119, 782.4727, 848.5277, 864.5253, 1153.6534, 1153.6534, 1195.6522, 1301.6345, 1320.5950, 1351.7496, 1351.7496, 1362.6899, 1362.6899, 1378.6758, 1394.6868, 1425.8044, 1448.9039, 1522.8257, 1530.8682, 1601.7721, 1617.7598, 1707.7908, 1842.9575, 1858.9449, 2135.0195, 2151.0095, 2230.2185, 2400.0166, 2483.3445, 2542.2927, 2564.1797, 2663.3464, 2769.4600, 2825.3096, 2922.3599, 2932.4197, 2947.4126, 2964.4336, 3332.5544

7. gi|11066954 **Mass:** 52423 **Score:** 129 **Expect:** 7.6e-008 **Queries matched:** 14

citrate synthase [Oryza sativa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1031.5079	1030.5006	1030.5117	-0.0111	102 - 110	0	---	GLSIPECQK
1093.6748	1092.6675	1092.6655	0.0021	447 - 456	0	---	ALGLPLERPK
1093.6748	1092.6675	1092.6655	0.0021	447 - 456	0	22	ALGLPLERPK
1204.6384	1203.6311	1203.6287	0.0024	425 - 434	0	39	YYTVLFGVSR
1204.6384	1203.6311	1203.6287	0.0024	425 - 434	0	---	YYTVLFGVSR
1334.7007	1333.6934	1333.6812	0.0122	100 - 110	1	---	FRGLSIPECQK

1533.6824	1532.6751	1532.6752	-0.0000	457 - 468	0	---	SVTMEWLENHCK
1661.7800	1660.7727	1660.7701	0.0026	457 - 469	1	---	SVTMEWLENHCKK
1677.7855	1676.7782	1676.7650	0.0132	457 - 469	1	---	SVTMEWLENHCKK + Oxidation (M)
1702.9071	1701.8998	1701.8905	0.0093	65 - 80	0	---	VQLGNITVDMVLGGMR
1718.8966	1717.8893	1717.8854	0.0039	65 - 80	0	---	VQLGNITVDMVLGGMR + Oxidation (M)
1926.9193	1925.9120	1925.8981	0.0139	201 - 215	0	---	FWEPTYEDCLNLIAR
2142.0452	2141.0379	2141.0251	0.0128	199 - 215	1	---	SKFWEPTYEDCLNLIAR
2241.1545	2240.1472	2240.1405	0.0068	60 - 80	1	---	SEHGKVQLGNITVDMVLGGMR

No match to: 713.3937, 724.4756, 734.4897, 750.5082, 768.5119, 782.4727, 848.5277, 864.5253, 1153.6534, 1153.6534, 1195.6522, 1301.6345, 1320.5950, 1351.7496, 1351.7496, 1362.6899, 1362.6899, 1378.6758, 1394.6868, 1425.8044, 1448.9039, 1522.8257, 1530.8682, 1601.7721, 1617.7598, 1707.7908, 1842.9575, 1858.9449, 2135.0195, 2151.0095, 2230.2185, 2400.0166, 2483.3445, 2542.2927, 2564.1797, 2663.3464, 2769.4600, 2825.3096, 2922.3599, 2932.4197, 2947.4126, 2964.4336, 3332.5544

8. gi|222622360 **Mass:** 54020 **Score:** 129 **Expect:** 7.6e-008 **Queries matched:** 14

hypothetical protein OsJ_05734 [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1031.5079	1030.5006	1030.5117	-0.0111	102 - 110	0	---	GLSIPECQK
1093.6748	1092.6675	1092.6655	0.0021	462 - 471	0	---	ALGLPLERPK
1093.6748	1092.6675	1092.6655	0.0021	462 - 471	0	22	ALGLPLERPK
1204.6384	1203.6311	1203.6287	0.0024	440 - 449	0	39	YYTVLFGVSR
1204.6384	1203.6311	1203.6287	0.0024	440 - 449	0	---	YYTVLFGVSR
1334.7007	1333.6934	1333.6812	0.0122	100 - 110	1	---	FRGLSIPECQK
1533.6824	1532.6751	1532.6752	-0.0000	472 - 483	0	---	SVTMEWLENHCK
1661.7800	1660.7727	1660.7701	0.0026	472 - 484	1	---	SVTMEWLENHCKK
1677.7855	1676.7782	1676.7650	0.0132	472 - 484	1	---	SVTMEWLENHCKK + Oxidation (M)
1702.9071	1701.8998	1701.8905	0.0093	65 - 80	0	---	VQLGNITVDMVLGGMR
1718.8966	1717.8893	1717.8854	0.0039	65 - 80	0	---	VQLGNITVDMVLGGMR + Oxidation (M)
1926.9193	1925.9120	1925.8981	0.0139	201 - 215	0	---	FWEPTYEDCLNLIAR
2142.0452	2141.0379	2141.0251	0.0128	199 - 215	1	---	SKFWEPTYEDCLNLIAR
2241.1545	2240.1472	2240.1405	0.0068	60 - 80	1	---	SEHGKVQLGNITVDMVLGGMR

No match to: 713.3937, 724.4756, 734.4897, 750.5082, 768.5119, 782.4727, 848.5277, 864.5253, 1153.6534, 1153.6534, 1195.6522, 1301.6345, 1320.5950, 1351.7496, 1351.7496, 1362.6899, 1362.6899, 1378.6758, 1394.6868, 1425.8044, 1448.9039, 1522.8257, 1530.8682, 1601.7721, 1617.7598, 1707.7908, 1842.9575, 1858.9449, 2135.0195, 2151.0095, 2230.2185, 2400.0166, 2483.3445, 2542.2927, 2564.1797, 2663.3464, 2769.4600, 2825.3096, 2922.3599, 2932.4197, 2947.4126, 2964.4336, 3332.5544

9. gi|218190238 **Mass:** 54047 **Score:** 128 **Expect:** 9.6e-008 **Queries matched:** 14

hypothetical protein OsI_06215 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1031.5079	1030.5006	1030.5117	-0.0111	102 - 110	0	---	GLSIPECQK
1093.6748	1092.6675	1092.6655	0.0021	462 - 471	0	---	ALGLPLERPK

1093.6748	1092.6675	1092.6655	0.0021	462 - 471	0	22	ALGLPLERPK
1204.6384	1203.6311	1203.6287	0.0024	440 - 449	0	39	YYTVLFGVSR
1204.6384	1203.6311	1203.6287	0.0024	440 - 449	0	---	YYTVLFGVSR
1334.7007	1333.6934	1333.6812	0.0122	100 - 110	1	---	FRGLSIPECQK
1533.6824	1532.6751	1532.6752	-0.0000	472 - 483	0	---	SVTMEWLENHCK
1661.7800	1660.7727	1660.7701	0.0026	472 - 484	1	---	SVTMEWLENHCKK
1677.7855	1676.7782	1676.7650	0.0132	472 - 484	1	---	SVTMEWLENHCKK + Oxidation (M)
1702.9071	1701.8998	1701.8905	0.0093	65 - 80	0	---	VQLGNITVDMVLGGMR
1718.8966	1717.8893	1717.8854	0.0039	65 - 80	0	---	VQLGNITVDMVLGGMR + Oxidation (M)
1926.9193	1925.9120	1925.8981	0.0139	201 - 215	0	---	FWEPTYEDCLNLIAR
2142.0452	2141.0379	2141.0251	0.0128	199 - 215	1	---	SKFWEPTYEDCLNLIAR
2241.1545	2240.1472	2240.1405	0.0068	60 - 80	1	---	SEHGKVQLGNITVDMVLGGMR

No match to: 713.3937, 724.4756, 734.4897, 750.5082, 768.5119, 782.4727, 848.5277, 864.5253, 1153.6534, 1153.6534, 1195.6522, 1301.6345, 1320.5950, 1351.7496, 1351.7496, 1362.6899, 1362.6899, 1378.6758, 1394.6868, 1425.8044, 1448.9039, 1522.8257, 1530.8682, 1601.7721, 1617.7598, 1707.7908, 1842.9575, 1858.9449, 2135.0195, 2151.0095, 2230.2185, 2400.0166, 2483.3445, 2542.2927, 2564.1797, 2663.3464, 2769.4600, 2825.3096, 2922.3599, 2932.4197, 2947.4126, 2964.4336, 3332.5544

10. gi|115485775 **Mass:** 52557 **Score:** 128 **Expect:** 9.6e-008 **Queries matched:** 14

Os11g0538900 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1031.5079	1030.5006	1030.5117	-0.0111	102 - 110	0	---	GLSIPECQK
1093.6748	1092.6675	1092.6655	0.0021	447 - 456	0	---	ALGLPLERPK
1093.6748	1092.6675	1092.6655	0.0021	447 - 456	0	22	ALGLPLERPK
1204.6384	1203.6311	1203.6287	0.0024	425 - 434	0	39	YYTVLFGVSR
1204.6384	1203.6311	1203.6287	0.0024	425 - 434	0	---	YYTVLFGVSR
1334.7007	1333.6934	1333.6812	0.0122	100 - 110	1	---	FRGLSIPECQK
1533.6824	1532.6751	1532.6752	-0.0000	457 - 468	0	---	SVTMEWLENHCK
1661.7800	1660.7727	1660.7701	0.0026	457 - 469	1	---	SVTMEWLENHCKK
1677.7855	1676.7782	1676.7650	0.0132	457 - 469	1	---	SVTMEWLENHCKK + Oxidation (M)
1702.9071	1701.8998	1701.8905	0.0093	65 - 80	0	---	VQLGNITVDMVLGGMR
1718.8966	1717.8893	1717.8854	0.0039	65 - 80	0	---	VQLGNITVDMVLGGMR + Oxidation (M)
1926.9193	1925.9120	1925.8981	0.0139	201 - 215	0	---	FWEPTYEDCLNLIAR
2142.0452	2141.0379	2141.0251	0.0128	199 - 215	1	---	SKFWEPTYEDCLNLIAR
2241.1545	2240.1472	2240.1405	0.0068	60 - 80	1	---	SEHGKVQLGNITVDMVLGGMR

No match to: 713.3937, 724.4756, 734.4897, 750.5082, 768.5119, 782.4727, 848.5277, 864.5253, 1153.6534, 1153.6534, 1195.6522, 1301.6345, 1320.5950, 1351.7496, 1351.7496, 1362.6899, 1362.6899, 1378.6758, 1394.6868, 1425.8044, 1448.9039, 1522.8257, 1530.8682, 1601.7721, 1617.7598, 1707.7908, 1842.9575, 1858.9449, 2135.0195, 2151.0095, 2230.2185, 2400.0166, 2483.3445, 2542.2927, 2564.1797, 2663.3464, 2769.4600, 2825.3096, 2922.3599, 2932.4197, 2947.4126, 2964.4336, 3332.5544

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Spot of Queries : 57

Protein View

Match to: **gi|226503683** Score: **170** Expect: **6.1e-012**
citrate synthase 4 [Zea mays]

Nominal mass (M_r): **50808**; Calculated pI value: **6.25**
NCBI BLAST search of gi|226503683 against nr
Unformatted sequence string for pasting into other applications
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|195624496 from Zea mays

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **22%**

Matched peptides shown in **Bold Red**

```
     1 MAQEATTLGG VRWLQMQSAS DLDLKSQLQE LIPEQQDRLK KLKSEHGKTQ
    51 LGNITVDMVL GGMRGMTGML WETSLLDPEE GIRFRGLSIP ECQKVLPTAV
   101 KGGEPLPEGL LWLLLTGKVP TKEQVDALSK ELLARSTVPA HVYKTIDALP
   151 VDAHPMTQFT TGVMALQVES EFQKAYDNGL PKSKFWEPTY EDCLNLIARL
   201 PPVSSYVYRR IFKSGKSIEA DNSLDYAANF SHMLGFDDQK MLELMRLYVT
   251 IHTDHEGGNV SAHTGHLVGS ALSDPYLSFA AALNGLAGPL HGLANQEVLL
   301 WIKSVIEETG SGVTTDQLKD YVWKTLKSGK VVPGFGHGVL RKTDPRYSCQ
   351 REFALKHLPE DPLFQLVSKL YEVVPPILTE LGKVKNPWPN VDAHSGVLLN
   401 HFGLSEARYY TVLFGVSRSM GIGSQLIWDR ALGLPLERPK SVTMEWLENY
   451 CKNKAA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
65 - 83	2135.0195	2134.0122	2134.0074	0.0048	0	**GMTGMLWETSLLDPEEGIR** (No match)
65 - 83	2151.0095	2150.0022	2150.0023	-0.0001	0	**GMTGMLWETSLLDPEEGIR** Oxidation (M) (No match)
84 - 94	1334.7007	1333.6934	1333.6812	0.0122	1	**FRGLSIPECQK** (No match)
86 - 94	1031.5079	1030.5006	1030.5117	-0.0111	0	**GLSIPECQK** (No match)
183 - 199	2142.0452	2141.0379	2141.0251	0.0128	1	**SKFWEPTYEDCLNLIAR** (No match)
185 - 199	1926.9193	1925.9120	1925.8981	0.0139	0	**FWEPTYEDCLNLIAR** (No match)
347 - 356	1301.6345	1300.6272	1300.6234	0.0039	1	**YSCQREFALK** (No match)
357 - 369	1522.8257	1521.8184	1521.8191	-0.0007	0	**HLPEDPLFQLVSK** (No match)
409 - 418	1204.6384	1203.6311	1203.6287	0.0024	0	**YYTVLFGVSR** (Ions score 39)
409 - 418	1204.6384	1203.6311	1203.6287	0.0024	0	**YYTVLFGVSR** (No match)
409 - 430	2564.1797	2563.1724	2563.2892	-0.1168	1	**YYTVLFGVSRSMGIGSQLIWDR** Oxidation (M) (No match)
419 - 430	1362.6899	1361.6826	1361.6761	0.0065	0	**SMGIGSQLIWDR** (No match)
419 - 430	1362.6899	1361.6826	1361.6761	0.0065	0	**SMGIGSQLIWDR** (Ions score 26)
419 - 430	1378.6758	1377.6685	1377.6710	-0.0025	0	**SMGIGSQLIWDR** Oxidation (M) (No match)
431 - 440	1093.6748	1092.6675	1092.6655	0.0021	0	**ALGLPLERPK** (No match)
431 - 440	1093.6748	1092.6675	1092.6655	0.0021	0	**ALGLPLERPK** (Ions score 22)

Spot 48

Index

	Accession	Mass	Score	Description
1.	gi|8928010	52908	175	RecName: Full=Citrate synthase, mitochondrial; Flags: Precursor
2.	gi|195624496	50808	166	citrate synthase 4 [Zea mays]
3.	gi|219884127	52625	160	unknown [Zea mays]
4.	gi|212720950	52651	152	hypothetical protein LOC100194338 [Zea mays]
5.	gi|145339693	51920	120	CSY5 (CITRATE SYNTHASE 5); citrate (SI)-synthase [Arabidopsis thaliana]

Results List

1. gi|8928010 **Mass:** 52908 **Score:** 175 **Expect:** 1.9e-012 **Queries matched:** 14

RecName: Full=Citrate synthase, mitochondrial; Flags: Precursor

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1013.5235	1012.5162	1012.5341	-0.0179	153	161	0	---	AAVPEHVYK
1031.5078	1030.5005	1030.5117	-0.0112	103	111	0	---	GLSIPECQK
1093.6729	1092.6656	1092.6655	0.0002	448	457	0	36	ALGLPLERPK
1093.6729	1092.6656	1092.6655	0.0002	448	457	0	---	ALGLPLERPK
1153.6489	1152.6416	1152.6403	0.0013	348	358	0	63	VVPGYGHGVLR
1153.6489	1152.6416	1152.6403	0.0013	348	358	0	---	VVPGYGHGVLR
1204.6379	1203.6306	1203.6287	0.0019	426	435	0	---	YYTVLFGVSR
1334.6921	1333.6848	1333.6812	0.0036	101	111	1	---	FRGLSIPECQK
1533.6871	1532.6798	1532.6752	0.0047	458	469	0	---	SVTMEWLENHCK
1661.7782	1660.7709	1660.7701	0.0008	458	470	1	---	SVTMEWLENHCKK
1677.7734	1676.7661	1676.7650	0.0011	458	470	1	---	SVTMEWLENHCKK + Oxidation (M)
1702.8898	1701.8825	1701.8905	-0.0080	66	81	0	---	VQLGNITVDMVLGGMR
1736.9178	1735.9105	1735.9117	-0.0012	348	363	1	---	VVPGYGHGVLRNTDPR
2963.4517	2962.4444	2962.4896	-0.0452	17	42	1	---	AVQQSNLSNTVRWFQVQTSASDLDLR

No match to: 713.3995, 768.5176, 878.5075, 886.9893, 998.5539, 1101.6794, 1195.6475, 1296.5969, 1301.6317, 1301.6317, 1351.7454, 1351.7454, 1362.6860, 1378.6750, 1424.7258, 1425.7950, 1425.7950, 1464.7181, 1478.7305, 1495.8218, 1523.7642, 1543.9001, 1550.6807, 1566.8691, 1583.8872, 1601.7601, 1617.7554, 1651.8574, 1680.8894, 1739.9720, 1768.0265, 1787.9923, 1842.9432, 1857.9951, 1884.9058, 1892.9548, 1926.9182, 2021.0525, 2054.9929, 2142.0391, 2144.2593, 2426.2349, 2443.2598, 2765.4739, 2931.4146, 2947.4595, 3189.6504, 3206.6516

2. gi|195624496 **Mass:** 50808 **Score:** 166 **Expect:** 1.5e-011 **Queries matched:** 16

citrate synthase 4 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1031.5078	1030.5005	1030.5117	-0.0112	86	94	0	---	GLSIPECQK
1093.6729	1092.6656	1092.6655	0.0002	431	440	0	36	ALGLPLERPK
1093.6729	1092.6656	1092.6655	0.0002	431	440	0	---	ALGLPLERPK

1204.6379	1203.6306	1203.6287	0.0019	409 - 418	0	---	YYTVLFGVSR
1301.6317	1300.6244	1300.6234	0.0011	347 - 356	1	---	YSCQREFALK
1301.6317	1300.6244	1300.6234	0.0011	347 - 356	1	30	YSCQREFALK
1334.6921	1333.6848	1333.6812	0.0036	84 - 94	1	---	FRGLSIPECQK
1362.6860	1361.6787	1361.6761	0.0026	419 - 430	0	---	SMGIGSQLIWDR
1378.6750	1377.6677	1377.6710	-0.0033	419 - 430	0	---	SMGIGSQLIWDR + Oxidation (M)
1550.6807	1549.6734	1549.7446	-0.0712	13 - 25	0	---	WLQMQSASDLDLK + Oxidation (M)
1583.8872	1582.8799	1582.8831	-0.0031	131 - 144	1	---	ELLARSTVPAHVYK
1736.9178	1735.9105	1735.8596	0.0509	49 - 64	0	---	TQLGNITVDMVLGGMR + 2 Oxidation (M)
1739.9720	1738.9647	1738.9651	-0.0003	86 - 101	1	---	GLSIPECQKVLPTAVK
1926.9182	1925.9109	1925.8981	0.0128	185 - 199	0	---	FWEPTYEDCLNLIAR
2142.0391	2141.0318	2141.0251	0.0067	183 - 199	1	---	SKFWEPTYEDCLNLIAR
2765.4739	2764.4666	2764.3523	0.1143	1 - 25	1	---	MAQEATTLGGVRWLQMQSASDLDLK + Oxidation (M)

No match to: 713.3995, 768.5176, 878.5075, 886.9893, 998.5539, 1013.5235, 1101.6794, 1153.6489, 1153.6489, 1195.6475, 1296.5969, 1351.7454, 1351.7454, 1424.7258, 1425.7950, 1425.7950, 1464.7181, 1478.7305, 1495.8218, 1523.7642, 1533.6871, 1543.9001, 1566.8691, 1601.7601, 1617.7554, 1651.8574, 1661.7782, 1677.7734, 1680.8894, 1702.8898, 1768.0265, 1787.9923, 1842.9432, 1857.9951, 1884.9058, 1892.9548, 2021.0525, 2054.9929, 2144.2593, 2426.2349, 2443.2598, 2931.4146, 2947.4595, 2963.4517, 3189.6504, 3206.6516

3. gi|219884127 **Mass:** 52625 **Score:** 160 **Expect:** 6e-011 **Queries matched:** 16

unknown [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1031.5078	1030.5005	1030.5117	-0.0112	102 - 110	0	---	GLSIPECQK
1093.6729	1092.6656	1092.6655	0.0002	447 - 456	0	36	ALGLPLERPK
1093.6729	1092.6656	1092.6655	0.0002	447 - 456	0	---	ALGLPLERPK
1204.6379	1203.6306	1203.6287	0.0019	425 - 434	0	---	YYTVLFGVSR
1301.6317	1300.6244	1300.6234	0.0011	363 - 372	1	---	YSCQREFALK
1301.6317	1300.6244	1300.6234	0.0011	363 - 372	1	30	YSCQREFALK
1334.6921	1333.6848	1333.6812	0.0036	100 - 110	1	---	FRGLSIPECQK
1362.6860	1361.6787	1361.6761	0.0026	435 - 446	0	---	SMGIGSQLIWDR
1378.6750	1377.6677	1377.6710	-0.0033	435 - 446	0	---	SMGIGSQLIWDR + Oxidation (M)
1550.6807	1549.6734	1549.7446	-0.0712	29 - 41	0	---	WLQMQSASDLDLK + Oxidation (M)
1583.8872	1582.8799	1582.8831	-0.0031	147 - 160	1	---	ELLARSTVPAHVYK
1736.9178	1735.9105	1735.8596	0.0509	65 - 80	0	---	TQLGNITVDMVLGGMR + 2 Oxidation (M)
1739.9720	1738.9647	1738.9651	-0.0003	102 - 117	1	---	GLSIPECQKVLPTAVK
1926.9182	1925.9109	1925.8981	0.0128	201 - 215	0	---	FWEPTYEDCLNLIAR
2142.0391	2141.0318	2141.0251	0.0067	199 - 215	1	---	SKFWEPTYEDCLNLIAR
2765.4739	2764.4666	2764.3523	0.1143	17 - 41	1	---	MAQEATTLGGVRWLQMQSASDLDLK + Oxidation (M)

No match to: 713.3995, 768.5176, 878.5075, 886.9893, 998.5539, 1013.5235, 1101.6794, 1153.6489, 1153.6489, 1195.6475, 1296.5969, 1351.7454, 1351.7454, 1424.7258, 1425.7950, 1425.7950, 1464.7181, 1478.7305, 1495.8218, 1523.7642, 1533.6871, 1543.9001, 1566.8691, 1601.7601, 1617.7554, 1651.8574, 1661.7782, 1677.7734, 1680.8894, 1702.8898, 1768.0265, 1787.9923, 1842.9432, 1857.9951, 1884.9058, 1892.9548, 2021.0525, 2054.9929, 2144.2593,

2426.2349, 2443.2598, 2931.4146, 2947.4595, 2963.4517, 3189.6504, 3206.6516

4. gi|212720950 **Mass:** 52651 **Score:** 152 **Expect:** 3.8e-010 **Queries matched:** 15

hypothetical protein LOC100194338 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1031.5078	1030.5005	1030.5117	-0.0112	102	110	0	---	GLSIPECQK
1093.6729	1092.6656	1092.6655	0.0002	447	456	0	36	ALGLPLERPK
1093.6729	1092.6656	1092.6655	0.0002	447	456	0	---	ALGLPLERPK
1204.6379	1203.6306	1203.6287	0.0019	425	434	0	---	YYTVLFGVSR
1301.6317	1300.6244	1300.6234	0.0011	363	372	1	---	YSCQREFALK
1301.6317	1300.6244	1300.6234	0.0011	363	372	1	30	YSCQREFALK
1334.6921	1333.6848	1333.6812	0.0036	100	110	1	---	FRGLSIPECQK
1362.6860	1361.6787	1361.6761	0.0026	435	446	0	---	SMGIGSQLIWDR
1378.6750	1377.6677	1377.6710	-0.0033	435	446	0	---	SMGIGSQLIWDR + Oxidation (M)
1550.6807	1549.6734	1549.7446	-0.0712	29	41	0	---	WLQMQSASDLDLK + Oxidation (M)
1583.8872	1582.8799	1582.8831	-0.0031	147	160	1	---	ELLARSTVPAHVYK
1702.8898	1701.8825	1701.8905	-0.0080	65	80	0	---	VQLGNITVDMVLGGMR
1739.9720	1738.9647	1738.9651	-0.0003	102	117	1	---	GLSIPECQKVLPTAVK
2426.2349	2425.2276	2425.2012	0.0264	320	340	1	---	SVIQETGSDVTTDQLKEYVWK
2765.4739	2764.4666	2764.3523	0.1143	17	41	1	---	MAQEATTLGGVRWLQMQSASDLDLK + Oxidation (M)

No match to: 713.3995, 768.5176, 878.5075, 886.9893, 998.5539, 1013.5235, 1101.6794, 1153.6489, 1153.6489, 1195.6475, 1296.5969, 1351.7454, 1351.7454, 1424.7258, 1425.7950, 1425.7950, 1464.7181, 1478.7305, 1495.8218, 1523.7642, 1533.6871, 1543.9001, 1566.8691, 1601.7601, 1617.7554, 1651.8574, 1661.7782, 1677.7734, 1680.8894, 1736.9178, 1768.0265, 1787.9923, 1842.9432, 1857.9951, 1884.9058, 1892.9548, 1926.9182, 2021.0525, 2054.9929, 2142.0391, 2144.2593, 2443.2598, 2931.4146, 2947.4595, 2963.4517, 3189.6504, 3206.6516

5. gi|145339693 **Mass:** 51920 **Score:** 120 **Expect:** 6e-007 **Queries matched:** 8

CSY5 (CITRATE SYNTHASE 5); citrate (SI)-synthase [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1093.6729	1092.6656	1092.6655	0.0002	440	449	0	36	ALGLPLERPK
1093.6729	1092.6656	1092.6655	0.0002	440	449	0	---	ALGLPLERPK
1153.6489	1152.6416	1152.6403	0.0013	340	350	0	63	VVPGYGHGVLR
1153.6489	1152.6416	1152.6403	0.0013	340	350	0	---	VVPGYGHGVLR
1204.6379	1203.6306	1203.6287	0.0019	418	427	0	---	YYTVLFGVSR
1601.7601	1600.7528	1600.7515	0.0013	39	51	0	---	SQMQEIIPEQQDR
1617.7554	1616.7481	1616.7464	0.0017	39	51	0	---	SQMQEIIPEQQDR + Oxidation (M)
1842.9432	1841.9359	1841.9305	0.0054	39	53	1	---	SQMQEIIPEQQDRLK

No match to: 713.3995, 768.5176, 878.5075, 886.9893, 998.5539, 1013.5235, 1031.5078, 1101.6794, 1195.6475, 1296.5969, 1301.6317, 1301.6317, 1334.6921, 1351.7454, 1351.7454, 1362.6860, 1378.6750, 1424.7258, 1425.7950, 1425.7950, 1464.7181, 1478.7305, 1495.8218, 1523.7642, 1533.6871, 1543.9001, 1550.6807, 1566.8691, 1583.8872, 1651.8574, 1661.7782, 1677.7734, 1680.8894, 1702.8898, 1736.9178, 1739.9720, 1768.0265, 1787.9923, 1857.9951, 1884.9058, 1892.9548, 1926.9182, 2021.0525, 2054.9929, 2142.0391, 2144.2593, 2426.2349, 2443.2598, 2765.4739, 2931.4146, 2947.4595, 2963.4517, 3189.6504, 3206.6516

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 62

Protein View

Match to: **gi|8928010** Score: **175** Expect: **1.9e-012**
RecName: Full=Citrate synthase, mitochondrial; Flags: Precursor

Nominal mass (M_r): **52908**; Calculated pI value: **6.95**
NCBI BLAST search of gi|8928010 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Daucus carota
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|3493367 from Daucus carota

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **23%**

Matched peptides shown in **Bold Red**

```
     1 MVFFRSVSLL NKLRSRAVQQ SNLSNTVRWF QVQTSASDLD LRSQLKELIP
    51 EQQERIKKLK AEHGKVQLGN ITVDMVLGGM RGMTGLLWET SLLDPEEGIR
   101 FRGLSIPECQ KLLPGAKPGG EPLPEGLLWL LLTGKVPTKE QVDALSAELR
   151 SRAAVPEHVY KTIDALPVTA HPMTQFATGV MALQVQSEFQ KAYEKGIHKT
   201 KYWEPTYEDS ITLIAQLPVV AAYIYRRMYK NGQSISTDDS LDYGANFAHM
   251 LGYDSPSMQE LMRLYVTIHT DHEGGNVSAH TGHLVASALS DPYLSFAAAL
   301 NGLAGPLHGL ANQEVLLWIK SVVSECGENV TKEQLKDYIW KTLNSGKVVP
   351 GYGHGVLRNT DPRYICQREF ALKHLPDDPL FQLVSNLFEV VPPILTELGK
   401 VKNPWPNVDA HSGVLLNHYG LTEARYYTVL FGVSRAIGIC SQLVWDRALG
   451 LPLERPKSVT MEWLENHCKK SS
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
17 - 42	2963.4517	2962.4444	2962.4896	-0.0452	1	**AVQQSNLSNTVRWFQVQTSASDLDLR** (No match)
66 - 81	1702.8898	1701.8825	1701.8905	-0.0080	0	**VQLGNITVDMVLGGMR** (No match)
101 - 111	1334.6921	1333.6848	1333.6812	0.0036	1	**FRGLSIPECQK** (No match)
103 - 111	1031.5078	1030.5005	1030.5117	-0.0112	0	**GLSIPECQK** (No match)
153 - 161	1013.5235	1012.5162	1012.5341	-0.0179	0	**AAVPEHVYK** (No match)
348 - 358	1153.6489	1152.6416	1152.6403	0.0013	0	**VVPGYGHGVLR** (Ions score 63)
348 - 358	1153.6489	1152.6416	1152.6403	0.0013	0	**VVPGYGHGVLR** (No match)
348 - 363	1736.9178	1735.9105	1735.9117	-0.0012	1	**VVPGYGHGVLRNTDPR** (No match)
426 - 435	1204.6379	1203.6306	1203.6287	0.0019	0	**YYTVLFGVSR** (No match)
448 - 457	1093.6729	1092.6656	1092.6655	0.0002	0	**ALGLPLERPK** (Ions score 36)
448 - 457	1093.6729	1092.6656	1092.6655	0.0002	0	**ALGLPLERPK** (No match)
458 - 469	1533.6871	1532.6798	1532.6752	0.0047	0	**SVTMEWLENHCK** (No match)
458 - 470	1661.7782	1660.7709	1660.7701	0.0008	1	**SVTMEWLENHCKK** (No match)
458 - 470	1677.7734	1676.7661	1676.7650	0.0011	1	**SVTMEWLENHCKK** Oxidation (M) (No match)

Spot 49

Index

	Accession	Mass	Score	Description
1.	gi|4666287	46716	137	cytosolic monodehydroascorbate reductase [Oryza sativa Japonica Group]
2.	gi|115480733	46758	137	Os09g0567300 [Oryza sativa (japonica cultivar-group)]
3.	gi|125564749	47977	137	hypothetical protein OsI_32437 [Oryza sativa Indica Group]
4.	gi|4760483	43043	87	monodehydroascorbate reductase [Oryza sativa Japonica Group]
5.	gi|115477781	46770	86	Os08g0557600 [Oryza sativa (japonica cultivar-group)]
6.	gi|125562536	46770	86	hypothetical protein OsI_30244 [Oryza sativa Indica Group]
7.	gi|222641005	49149	86	hypothetical protein OsJ_28260 [Oryza sativa Japonica Group]
8.	gi|223947705	46556	85	unknown [Zea mays]
9.	gi|1381678	22638	58	small GTP-binding protein [Glycine max]
10.	gi|450635	24225	58	GTP binding protein [Glycine max]

Results List

1. gi|4666287 **Mass:** 46716 **Score:** 137 **Expect:** 1.2e-008 **Queries matched:** 6

cytosolic monodehydroascorbate reductase [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1118.5892	1117.5819	1117.5740	0.0079	312	320	1	---	RVEHVDHAR
1136.5881	1135.5808	1135.5774	0.0034	54	63	0	56	GYLFPQNAAR
1136.5881	1135.5808	1135.5774	0.0034	54	63	0	---	GYLFPQNAAR
1437.7871	1436.7798	1436.7775	0.0023	9	23	0	---	YVILGGGVAAGYAAR
2388.1072	2387.0999	2387.0956	0.0043	332	351	1	51	GKESGESVVEYDYLPYFYSR
2388.1072	2387.0999	2387.0956	0.0043	332	351	1	---	GKESGESVVEYDYLPYFYSR

No match to: 768.5316, 791.4123, 899.7359, 900.2654, 917.2763, 917.2763, 971.2979, 1056.6587, 1446.7491, 1914.0334, 1937.9391, 1994.0394, 2138.2776, 2185.9756, 2188.9719, 2188.9719, 2241.1719, 2307.2332, 2307.2332, 2564.3232

2. gi|115480733 **Mass:** 46758 **Score:** 137 **Expect:** 1.2e-008 **Queries matched:** 6

Os09g0567300 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1118.5892	1117.5819	1117.5740	0.0079	312	320	1	---	RVEHVDHAR
1136.5881	1135.5808	1135.5774	0.0034	54	63	0	56	GYLFPQNAAR
1136.5881	1135.5808	1135.5774	0.0034	54	63	0	---	GYLFPQNAAR
1437.7871	1436.7798	1436.7775	0.0023	9	23	0	---	YVILGGGVAAGYAAR
2388.1072	2387.0999	2387.0956	0.0043	332	351	1	51	GKESGESVVEYDYLPYFYSR
2388.1072	2387.0999	2387.0956	0.0043	332	351	1	---	GKESGESVVEYDYLPYFYSR

No match to: 768.5316, 791.4123, 899.7359, 900.2654, 917.2763, 917.2763, 971.2979, 1056.6587, 1446.7491, 1914.0334, 1937.9391, 1994.0394, 2138.2776, 2185.9756, 2188.9719, 2188.9719, 2241.1719, 2307.2332, 2307.2332, 2564.3232

3. gi|125564749 **Mass:** 47977 **Score:** 137 **Expect:** 1.2e-008 **Queries matched:** 6

hypothetical protein OsI_32437 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1118.5892	1117.5819	1117.5740	0.0079	324	332	1	---	RVEHVDHAR
1136.5881	1135.5808	1135.5774	0.0034	66	75	0	56	GYLFPQNAAR
1136.5881	1135.5808	1135.5774	0.0034	66	75	0	---	GYLFPQNAAR
1437.7871	1436.7798	1436.7775	0.0023	9	23	0	---	YVILGGGVAAGYAAR
2388.1072	2387.0999	2387.0956	0.0043	344	363	1	51	GKESGESVVEYDYLPYFYSR
2388.1072	2387.0999	2387.0956	0.0043	344	363	1	---	GKESGESVVEYDYLPYFYSR

No match to: 768.5316, 791.4123, 899.7359, 900.2654, 917.2763, 917.2763, 971.2979, 1056.6587, 1446.7491, 1914.0334, 1937.9391, 1994.0394, 2138.2776, 2185.9756, 2188.9719, 2188.9719, 2241.1719, 2307.2332, 2307.2332, 2564.3232

4. gi|4760483 **Mass:** 43043 **Score:** 87 **Expect:** 0.0011 **Queries matched:** 5

monodehydroascorbate reductase [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1118.5892	1117.5819	1117.5740	0.0079	312	320	1	---	RVEHVDHAR
1136.5881	1135.5808	1135.5774	0.0034	54	63	0	56	GYLFPQNAAR
1136.5881	1135.5808	1135.5774	0.0034	54	63	0	---	GYLFPQNAAR
1446.7491	1445.7418	1445.7514	-0.0095	41	53	0	---	ESVAPYERPALSK
2564.3232	2563.3159	2563.3182	-0.0023	41	63	1	---	ESVAPYERPALSKGYLFPQNAAR

No match to: 768.5316, 791.4123, 899.7359, 900.2654, 917.2763, 917.2763, 971.2979, 1056.6587, 1437.7871, 1914.0334, 1937.9391, 1994.0394, 2138.2776, 2185.9756, 2188.9719, 2188.9719, 2241.1719, 2307.2332, 2307.2332, 2388.1072, 2388.1072

5. gi|115477781 **Mass:** 46770 **Score:** 86 **Expect:** 0.0015 **Queries matched:** 5

Os08g0557600 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1118.5892	1117.5819	1117.5740	0.0079	312	320	1	---	RVEHVDHAR
1136.5881	1135.5808	1135.5774	0.0034	54	63	0	56	GYLFPQNAAR
1136.5881	1135.5808	1135.5774	0.0034	54	63	0	---	GYLFPQNAAR
1446.7491	1445.7418	1445.7514	-0.0095	41	53	0	---	ESVAPYERPALSK
2564.3232	2563.3159	2563.3182	-0.0023	41	63	1	---	ESVAPYERPALSKGYLFPQNAAR

No match to: 768.5316, 791.4123, 899.7359, 900.2654, 917.2763, 917.2763, 971.2979, 1056.6587, 1437.7871, 1914.0334, 1937.9391, 1994.0394, 2138.2776, 2185.9756, 2188.9719, 2188.9719, 2241.1719, 2307.2332, 2307.2332, 2388.1072, 2388.1072

6. gi|125562536 **Mass:** 46770 **Score:** 86 **Expect:** 0.0015 **Queries matched:** 5

hypothetical protein OsI_30244 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1118.5892	1117.5819	1117.5740	0.0079	312	320	1	---	RVEHVDHAR
1136.5881	1135.5808	1135.5774	0.0034	54	63	0	56	GYLFPQNAAR

1136.5881	1135.5808	1135.5774	0.0034	54 - 63	0	---	GYLFPQNAAR
1446.7491	1445.7418	1445.7514	-0.0095	41 - 53	0	---	ESVAPYERPALSK
2564.3232	2563.3159	2563.3182	-0.0023	41 - 63	1	---	ESVAPYERPALSKGYLFPQNAAR

No match to: 768.5316, 791.4123, 899.7359, 900.2654, 917.2763, 917.2763, 971.2979, 1056.6587, 1437.7871, 1914.0334, 1937.9391, 1994.0394, 2138.2776, 2185.9756, 2188.9719, 2188.9719, 2241.1719, 2307.2332, 2307.2332, 2388.1072, 2388.1072

7. gi|222641005 **Mass:** 49149 **Score:** 86 **Expect:** 0.0017 **Queries matched:** 5

hypothetical protein OsJ_28260 [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1118.5892	1117.5819	1117.5740	0.0079	312 -	320	1	---	RVEHVDHAR
1136.5881	1135.5808	1135.5774	0.0034	54 -	63	0	56	GYLFPQNAAR
1136.5881	1135.5808	1135.5774	0.0034	54 -	63	0	---	GYLFPQNAAR
1446.7491	1445.7418	1445.7514	-0.0095	41 -	53	0	---	ESVAPYERPALSK
2564.3232	2563.3159	2563.3182	-0.0023	41 -	63	1	---	ESVAPYERPALSKGYLFPQNAAR

No match to: 768.5316, 791.4123, 899.7359, 900.2654, 917.2763, 917.2763, 971.2979, 1056.6587, 1437.7871, 1914.0334, 1937.9391, 1994.0394, 2138.2776, 2185.9756, 2188.9719, 2188.9719, 2241.1719, 2307.2332, 2307.2332, 2388.1072, 2388.1072

8. gi|223947705 **Mass:** 46556 **Score:** 85 **Expect:** 0.0021 **Queries matched:** 5

unknown [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1118.5892	1117.5819	1117.5740	0.0079	310 -	318	1	---	RVEHVDHAR
1136.5881	1135.5808	1135.5774	0.0034	52 -	61	0	56	GYLFPQNAAR
1136.5881	1135.5808	1135.5774	0.0034	52 -	61	0	---	GYLFPQNAAR
1437.7871	1436.7798	1436.7775	0.0023	7 -	21	0	---	YVILGGGVAAGYAAR
1446.7491	1445.7418	1445.7877	-0.0459	266 -	279	1	---	LFIGQAADEKGGLK

No match to: 768.5316, 791.4123, 899.7359, 900.2654, 917.2763, 917.2763, 971.2979, 1056.6587, 1914.0334, 1937.9391, 1994.0394, 2138.2776, 2185.9756, 2188.9719, 2188.9719, 2241.1719, 2307.2332, 2307.2332, 2388.1072, 2388.1072, 2564.3232

9. gi|1381678 **Mass:** 22638 **Score:** 58 **Expect:** 0.88 **Queries matched:** 6

small GTP-binding protein [Glycine max]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1118.5892	1117.5819	1117.5979	-0.0159	49 -	58	1	---	TVEQDGKTIK
1937.9391	1936.9318	1936.9278	0.0040	101 -	116	1	---	QWLSEIDRYASDNVNK
2185.9756	2184.9683	2185.0102	-0.0419	28 -	46	0	---	FSDDSYIESYISTIGVDFK
2241.1719	2240.1646	2240.1728	-0.0082	2 -	21	1	---	NPEYDYLFKLLLIGDSGVGK
2388.1072	2387.0999	2387.2082	-0.1083	1 -	21	1	---	MNPEYDYLFKLLLIGDSGVGK + Oxidation (M)
2388.1072	2387.0999	2387.2082	-0.1083	1 -	21	1	---	MNPEYDYLFKLLLIGDSGVGK + Oxidation (M)

No match to: 768.5316, 791.4123, 899.7359, 900.2654, 917.2763, 917.2763, 971.2979, 1056.6587, 1136.5881, 1136.5881, 1437.7871, 1446.7491, 1914.0334, 1994.0394, 2138.2776, 2188.9719, 2188.9719, 2307.2332, 2307.2332, 2564.3232

10. gi|450635 **Mass:** 24225 **Score:** 58 **Expect:** 1 **Queries matched:** 6

GTP binding protein [Glycine max]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1118.5892	1117.5819	1117.5979	-0.0159	49	58	1	---	TVEQDGKTIK
1937.9391	1936.9318	1936.9278	0.0040	102	117	1	---	QWLSEIDRYASDNVNK
2185.9756	2184.9683	2185.0102	-0.0419	28	46	0	---	FSDDSYIESYISTIGVDFK
2241.1719	2240.1646	2240.1728	-0.0082	2	21	1	---	NPEYDYLFKLLLIGDSGVGK
2388.1072	2387.0999	2387.2082	-0.1083	1	21	1	---	MNPEYDYLFKLLLIGDSGVGK + Oxidation (M)
2388.1072	2387.0999	2387.2082	-0.1083	1	21	1	---	MNPEYDYLFKLLLIGDSGVGK + Oxidation (M)

No match to: 768.5316, 791.4123, 899.7359, 900.2654, 917.2763, 917.2763, 971.2979, 1056.6587, 1136.5881, 1136.5881, 1437.7871, 1446.7491, 1914.0334, 1994.0394, 2138.2776, 2188.9719, 2188.9719, 2307.2332, 2307.2332, 2564.3232

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 269

Protein View

Match to: **gi|115480733** Score: **137** Expect: **1.2e-008**
Os09g0567300 [Oryza sativa (japonica cultivar-group)]

Nominal mass (M_r): **46758**; Calculated pI value: **5.53**
NCBI BLAST search of gi|115480733 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Oryza sativa Japonica Group
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|52077207 from Oryza sativa Japonica Group
gi|113632193 from Oryza sativa Japonica Group

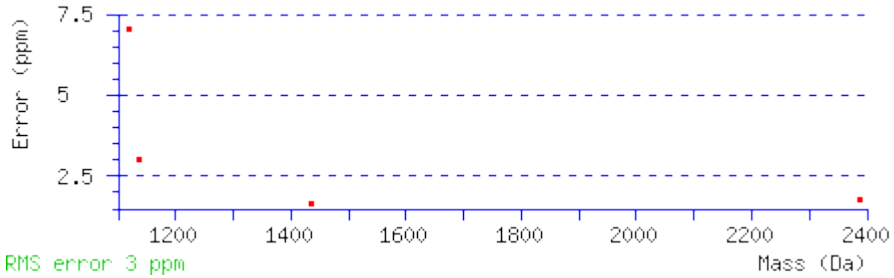
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **12%**

Matched peptides shown in **Bold Red**

```
    1 MASEKHFKYV ILGGGVAAGY AAREFAKQGV KPGELAIISK EAVAPYERPA
   51 LSKGYLFPQN AARLPGFHVC VGSGGERLLP EWYSEKGIEL ILSTEIVKAD
  101 LASKTLTSAV GATFTYEILI IATGSSVIKL SDFGTQGADS NNILYLREVD
  151 DADKLVAAIQ AKKGGKAVIV GGGYIGLELS AALKINDFDV TMVFPEPWCM
  201 PRLFTADIAA FYESYYTNKG VKIVKGTVAV GFDADANGDV TAVNLKNGSV
  251 LEADIVVVGV GGRPLTTLFK GQVAEEKGGI KTDAFFETSV PGVYAVGDVA
  301 TFPMKMYNEL RRVEHVDHAR KSAEQAVKAI KGKESGESVV EYDYLPYFYS
  351 RSFDLGWQFY GDNVGDTILF GDSDPTSAKP KFGSYWIKDG KVLGAFLEGG
  401 SPDENKAIAK VAKTQPPVAN IEELKKEGLQ FASKI
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
9 - 23	1437.7871	1436.7798	1436.7775	0.0023	0	YVILGGGVAAGYAAR	(No match)
54 - 63	1136.5881	1135.5808	1135.5774	0.0034	0	GYLFPQNAAR	(Ions score 56)
54 - 63	1136.5881	1135.5808	1135.5774	0.0034	0	GYLFPQNAAR	(No match)
312 - 320	1118.5892	1117.5819	1117.5740	0.0079	1	RVEHVDHAR	(No match)
332 - 351	2388.1072	2387.0999	2387.0956	0.0043	1	GKESGESVVEYDYLPYFYSR	(Ions score 51)
332 - 351	2388.1072	2387.0999	2387.0956	0.0043	1	GKESGESVVEYDYLPYFYSR	(No match)



Spot 50

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	Accession	Mass	Score	Description
1.	gi|15218574	47083	172	eukaryotic translation initiation factor 4A, putative / eIF-4A, putative [Arabidopsis thaliana
2.	gi|3776021	50232	172	RNA helicase [Arabidopsis thaliana]
3.	gi|15221761	47075	172	EIF4A-2; ATP-dependent helicase/ translation initiation factor [Arabidopsis thaliana]
4.	gi|2500519	40475	161	RecName: Full=Eukaryotic initiation factor 4A-13; Short=eIF-4A-13; AltName: Full=ATP-dependent
5.	gi|152003979	38578	161	eukaryotic initiation factor 4A [Lolium perenne]
6.	gi|217073428	42113	161	unknown [Medicago truncatula]
7.	gi|224153793	44519	160	predicted protein [Populus trichocarpa]
8.	gi|168472719	39817	160	eukaryotic initiation factor 4A [Lolium temulentum]
9.	gi|147834872	46872	160	hypothetical protein [Vitis vinifera]
10.	gi|303844	47187	160	eukaryotic initiation factor 4A [Oryza sativa Japonica Group]

Results List

1. gi|15218574 **Mass:** 47083 **Score:** 172 **Expect:** 3.8e-012 **Queries matched:** 5

eukaryotic translation initiation factor 4A, putative / eIF-4A, putative [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1114.6930	1113.6857	1113.6757	0.0100	333	342	0	---	VLITTDLLAR
1114.6930	1113.6857	1113.6757	0.0100	333	342	0	43	VLITTDLLAR
1633.8827	1632.8754	1632.7637	0.1117	140	154	1	---	AQACVGGTSVREDQR
1827.9497	1826.9424	1826.9314	0.0110	55	70	0	---	GIYAYGFEKPSAIQQR
1827.9497	1826.9424	1826.9314	0.0110	55	70	0	97	GIYAYGFEKPSAIQQR

No match to: 768.5197, 978.5125, 978.5125, 1056.6594, 1056.6594, 1447.7855

2. gi|3776021 **Mass:** 50232 **Score:** 172 **Expect:** 3.8e-012 **Queries matched:** 5

RNA helicase [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1114.6930	1113.6857	1113.6757	0.0100	360	369	0	---	VLITTDLLAR
1114.6930	1113.6857	1113.6757	0.0100	360	369	0	43	VLITTDLLAR
1633.8827	1632.8754	1632.7637	0.1117	167	181	1	---	AQACVGGTSVREDQR
1827.9497	1826.9424	1826.9314	0.0110	82	97	0	---	GIYAYGFEKPSAIQQR
1827.9497	1826.9424	1826.9314	0.0110	82	97	0	97	GIYAYGFEKPSAIQQR

No match to: 768.5197, 978.5125, 978.5125, 1056.6594, 1056.6594, 1447.7855

3. gi|15221761 **Mass:** 47075 **Score:** 172 **Expect:** 3.8e-012 **Queries matched:** 5

EIF4A-2; ATP-dependent helicase/ translation initiation factor [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1114.6930	1113.6857	1113.6757	0.0100	331	340	0	---	VLITTDLLAR
1114.6930	1113.6857	1113.6757	0.0100	331	340	0	43	VLITTDLLAR

1447.7855	1446.7782	1446.7466	0.0316	376 - 388	0	---	GVAINFVTLDDQR
1827.9497	1826.9424	1826.9314	0.0110	53 - 68	0	---	GIYAYGFEKPSAIQQR
1827.9497	1826.9424	1826.9314	0.0110	53 - 68	0	97	GIYAYGFEKPSAIQQR

No match to: 768.5197, 978.5125, 978.5125, 1056.6594, 1056.6594, 1633.8827

4. gi|2500519 **Mass:** 40475 **Score:** 161 **Expect:** 4.8e-011 **Queries matched:** 4

RecName: Full=Eukaryotic initiation factor 4A-13; Short=eIF-4A-13; AltName: Full=ATP-dependent RNA

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1114.6930	1113.6857	1113.6757	0.0100	332 - 341		0	---	VLITTDLLAR
1114.6930	1113.6857	1113.6757	0.0100	332 - 341		0	43	VLITTDLLAR
1827.9497	1826.9424	1826.9314	0.0110	54 - 69		0	---	GIYAYGFEKPSAIQQR
1827.9497	1826.9424	1826.9314	0.0110	54 - 69		0	97	GIYAYGFEKPSAIQQR

No match to: 768.5197, 978.5125, 978.5125, 1056.6594, 1056.6594, 1447.7855, 1633.8827

5. gi|152003979 **Mass:** 38578 **Score:** 161 **Expect:** 4.8e-011 **Queries matched:** 4

eukaryotic initiation factor 4A [Lolium perenne]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1114.6930	1113.6857	1113.6757	0.0100	320 - 329		0	---	VLITTDLLAR
1114.6930	1113.6857	1113.6757	0.0100	320 - 329		0	43	VLITTDLLAR
1827.9497	1826.9424	1826.9314	0.0110	42 - 57		0	---	GIYAYGFEKPSAIQQR
1827.9497	1826.9424	1826.9314	0.0110	42 - 57		0	97	GIYAYGFEKPSAIQQR

No match to: 768.5197, 978.5125, 978.5125, 1056.6594, 1056.6594, 1447.7855, 1633.8827

6. gi|217073428 **Mass:** 42113 **Score:** 161 **Expect:** 4.8e-011 **Queries matched:** 4

unknown [Medicago truncatula]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1114.6930	1113.6857	1113.6757	0.0100	312 - 321		0	---	VLITTDLLAR
1114.6930	1113.6857	1113.6757	0.0100	312 - 321		0	43	VLITTDLLAR
1827.9497	1826.9424	1826.9314	0.0110	54 - 69		0	---	GIYAYGFEKPSAIQQR
1827.9497	1826.9424	1826.9314	0.0110	54 - 69		0	97	GIYAYGFEKPSAIQQR

No match to: 768.5197, 978.5125, 978.5125, 1056.6594, 1056.6594, 1447.7855, 1633.8827

7. gi|224153793 **Mass:** 44519 **Score:** 160 **Expect:** 6.1e-011 **Queries matched:** 4

predicted protein [Populus trichocarpa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1114.6930	1113.6857	1113.6757	0.0100	309 - 318		0	---	VLITTDLLAR
1114.6930	1113.6857	1113.6757	0.0100	309 - 318		0	43	VLITTDLLAR
1827.9497	1826.9424	1826.9314	0.0110	31 - 46		0	---	GIYAYGFEKPSAIQQR
1827.9497	1826.9424	1826.9314	0.0110	31 - 46		0	97	GIYAYGFEKPSAIQQR

No match to: 768.5197, 978.5125, 978.5125, 1056.6594, 1056.6594, 1447.7855, 1633.8827

8. gi|168472719 **Mass:** 39817 **Score:** 160 **Expect:** 6.1e-011 **Queries matched:** 4

eukaryotic initiation factor 4A [Lolium temulentum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1114.6930	1113.6857	1113.6757	0.0100	328	337	0	---	VLITTDLLAR
1114.6930	1113.6857	1113.6757	0.0100	328	337	0	43	VLITTDLLAR
1827.9497	1826.9424	1826.9314	0.0110	50	65	0	---	GIYAYGFEKPSAIQQR
1827.9497	1826.9424	1826.9314	0.0110	50	65	0	97	GIYAYGFEKPSAIQQR

No match to: 768.5197, 978.5125, 978.5125, 1056.6594, 1056.6594, 1447.7855, 1633.8827

9. gi|147834872 **Mass:** 46872 **Score:** 160 **Expect:** 6.1e-011 **Queries matched:** 4

hypothetical protein [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1114.6930	1113.6857	1113.6757	0.0100	332	341	0	---	VLITTDLLAR
1114.6930	1113.6857	1113.6757	0.0100	332	341	0	43	VLITTDLLAR
1827.9497	1826.9424	1826.9314	0.0110	54	69	0	---	GIYAYGFEKPSAIQQR
1827.9497	1826.9424	1826.9314	0.0110	54	69	0	97	GIYAYGFEKPSAIQQR

No match to: 768.5197, 978.5125, 978.5125, 1056.6594, 1056.6594, 1447.7855, 1633.8827

10. gi|303844 **Mass:** 47187 **Score:** 160 **Expect:** 6.1e-011 **Queries matched:** 4

eukaryotic initiation factor 4A [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1114.6930	1113.6857	1113.6757	0.0100	332	341	0	---	VLITTDLLAR
1114.6930	1113.6857	1113.6757	0.0100	332	341	0	43	VLITTDLLAR
1827.9497	1826.9424	1826.9314	0.0110	55	70	0	---	GIYAYGFEKPSAIQQR
1827.9497	1826.9424	1826.9314	0.0110	55	70	0	97	GIYAYGFEKPSAIQQR

No match to: 768.5197, 978.5125, 978.5125, 1056.6594, 1056.6594, 1447.7855, 1633.8827

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 11

Protein View

Match to: **gi|3776021** Score: **172** Expect: **3.8e-012**
RNA helicase [Arabidopsis thaliana]

Nominal mass (M_r): **50232**; Calculated pI value: **5.18**
NCBI BLAST search of gi|3776021 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Arabidopsis thaliana

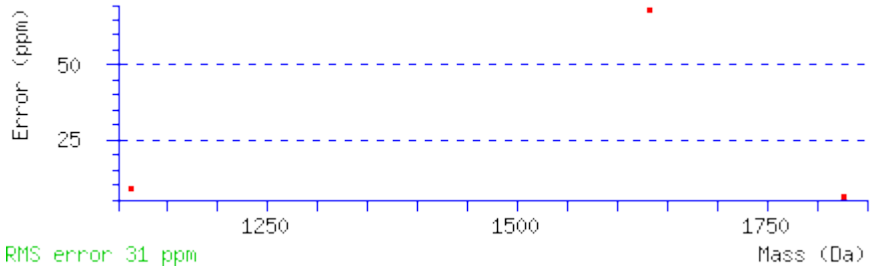
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **9%**

Matched peptides shown in **Bold Red**

```
   1 KSFEFGLCLY LFNLSLSIAL QFDNSKVMAG MASDGTQYDP RQFDTKMNAI
  51 LGEEGEETFY TNYDEVCDTF DAMELQPDLL RGIYAYGFEK PSAIQQRGII
 101 PFCKGLDVIQ QAQSGTGKTA TFCSGVLQQL DISLVQCQAL VLAPTRELAQ
 151 QIEKVMRALG DYLGVKAQAC VGGTSVREDQ RVLQSGVHVV VGTPGRVFDL
 201 LRRQSLRADA IKMFVLDEAD EMLSRGFKDQ IYDIFQLLPS KVQVGVFSAT
 251 MPPEALEITR KFMNKPVRIL VKRDELTLEG IKQFYVNVDK EEWKLETLCD
 301 LYETLAITQS VIFVNTRRKV DWLTDKMRSR DHTVSATHGD MDQNTRDIIM
 351 REFRSGSSRV LITTDLLARG IDVQQVSLVI NFDLPTQPEN YLHRIGRSGR
 401 FGRKGVAINF MTSEDERMMA DIQRFYNVVV EELPSNVADL L
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
82 - 97	1827.9497	1826.9424	1826.9314	0.0110	0	GIYAYGFEKPSAIQQR	(No match)
82 - 97	1827.9497	1826.9424	1826.9314	0.0110	0	GIYAYGFEKPSAIQQR	(Ions score 97)
167 - 181	1633.8827	1632.8754	1632.7637	0.1117	1	AQACVGGTSVREDQR	(No match)
360 - 369	1114.6930	1113.6857	1113.6757	0.0100	0	VLITTDLLAR	(No match)
360 - 369	1114.6930	1113.6857	1113.6757	0.0100	0	VLITTDLLAR	(Ions score 43)



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	Accession	Mass	Score	Description
1.	gi|4666287	46716	191	cytosolic monodehydroascorbate reductase [Oryza sativa Japonica Group]
2.	gi|115480733	46758	191	Os09g0567300 [Oryza sativa (japonica cultivar-group)]
3.	gi|125564749	47977	190	hypothetical protein OsI_32437 [Oryza sativa Indica Group]
4.	gi|4760483	43043	161	monodehydroascorbate reductase [Oryza sativa Japonica Group]
5.	gi|115477781	46770	158	Os08g0557600 [Oryza sativa (japonica cultivar-group)]
6.	gi|125562536	46770	158	hypothetical protein OsI_30244 [Oryza sativa Indica Group]
7.	gi|222641005	49149	157	hypothetical protein OsJ_28260 [Oryza sativa Japonica Group]
8.	gi|223947705	46556	112	unknown [Zea mays]
9.	gi|1170511	47098	84	RecName: Full=Eukaryotic initiation factor 4A-10; Short=eIF-4A-10; AltName: Full=ATP-dependent
10.	gi|115444197	47393	78	Os02g0146600 [Oryza sativa (japonica cultivar-group)]

Results List

1. gi|4666287 **Mass:** 46716 **Score:** 191 **Expect:** 4.8e-014 **Queries matched:** 12

cytosolic monodehydroascorbate reductase [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1118.5748	1117.5675	1117.5740	-0.0065	312	320	1	---	RVEHVDHAR
1136.5850	1135.5777	1135.5774	0.0003	54	63	0	73	GYLFPQNAAR
1136.5850	1135.5777	1135.5774	0.0003	54	63	0	---	GYLFPQNAAR
1200.5917	1199.5844	1199.5974	-0.0130	382	391	1	---	FGSYWIKDGK
1339.7435	1338.7362	1338.7870	-0.0508	28	40	0	---	QGVKPGELAIISK
1437.7883	1436.7810	1436.7775	0.0035	9	23	0	9	YVILGGGVAAGYAAR
1437.7883	1436.7810	1436.7775	0.0035	9	23	0	---	YVILGGGVAAGYAAR
1814.9916	1813.9843	1814.0301	-0.0458	24	40	1	---	EFAKQGVKPGELAIISK
1850.0085	1849.0012	1848.9998	0.0015	6	23	1	---	HFKYVILGGGVAAGYAAR
1913.0332	1912.0259	1912.0205	0.0054	9	27	1	---	YVILGGGVAAGYAAREFAK
2388.1045	2387.0972	2387.0956	0.0016	332	351	1	52	GKESGESVVEYDYLPYFYSR
2388.1045	2387.0972	2387.0956	0.0016	332	351	1	---	GKESGESVVEYDYLPYFYSR

No match to: 713.3984, 768.5125, 791.4080, 881.2817, 952.4984, 1093.6040, 1095.5554, 1104.6547, 1114.6825, 1141.6068, 1158.5604, 1246.6730, 1291.6801, 1322.7177, 1445.6809, 1446.7516, 1446.7516, 1453.7612, 1463.7686, 1468.7084, 1555.7222, 1571.7096, 1581.8556, 1587.6948, 1602.8114, 1633.8654, 1792.8739, 1827.9438, 1880.8871, 1903.9646, 1937.9436, 1959.9911, 1994.0363, 2059.0808, 2138.2734, 2188.9739, 2188.9739, 2204.1472, 2270.2034, 2307.2266, 2363.2002, 2418.2659, 2563.3076, 2564.3208, 2596.4089, 2662.3779, 2700.3225, 2750.4797, 2767.4966, 2782.4683, 2911.4861, 3242.7427, 3348.6348

2. gi|115480733 **Mass:** 46758 **Score:** 191 **Expect:** 4.8e-014 **Queries matched:** 12

Os09g0567300 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1118.5748	1117.5675	1117.5740	-0.0065	312	320	1	---	RVEHVDHAR
1136.5850	1135.5777	1135.5774	0.0003	54	63	0	73	GYLFPQNAAR
1136.5850	1135.5777	1135.5774	0.0003	54	63	0	---	GYLFPQNAAR
1200.5917	1199.5844	1199.5974	-0.0130	382	391	1	---	FGSYWIKDGK
1339.7435	1338.7362	1338.7870	-0.0508	28	40	0	---	QGVKPGELAIISK
1437.7883	1436.7810	1436.7775	0.0035	9	23	0	9	YVILGGGVAAGYAAR
1437.7883	1436.7810	1436.7775	0.0035	9	23	0	---	YVILGGGVAAGYAAR
1814.9916	1813.9843	1814.0301	-0.0458	24	40	1	---	EFAKQGVKPGELAIISK
1850.0085	1849.0012	1848.9998	0.0015	6	23	1	---	HFKYVILGGGVAAGYAAR
1913.0332	1912.0259	1912.0205	0.0054	9	27	1	---	YVILGGGVAAGYAAREFAK
2388.1045	2387.0972	2387.0956	0.0016	332	351	1	52	GKESGESVVEYDYLPYFYSR
2388.1045	2387.0972	2387.0956	0.0016	332	351	1	---	GKESGESVVEYDYLPYFYSR

No match to: 713.3984, 768.5125, 791.4080, 881.2817, 952.4984, 1093.6040, 1095.5554, 1104.6547, 1114.6825, 1141.6068, 1158.5604, 1246.6730, 1291.6801, 1322.7177, 1445.6809, 1446.7516, 1446.7516, 1453.7612, 1463.7686, 1468.7084, 1555.7222, 1571.7096, 1581.8556, 1587.6948, 1602.8114, 1633.8654, 1792.8739, 1827.9438, 1880.8871, 1903.9646, 1937.9436, 1959.9911, 1994.0363, 2059.0808, 2138.2734, 2188.9739, 2188.9739, 2204.1472, 2270.2034, 2307.2266, 2363.2002, 2418.2659, 2563.3076, 2564.3208, 2596.4089, 2662.3779, 2700.3225, 2750.4797, 2767.4966, 2782.4683, 2911.4861, 3242.7427, 3348.6348

3. gi|125564749 **Mass:** 47977 **Score:** 190 **Expect:** 6.1e-014 **Queries matched:** 12

hypothetical protein OsI_32437 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1118.5748	1117.5675	1117.5740	-0.0065	324	332	1	---	RVEHVDHAR
1136.5850	1135.5777	1135.5774	0.0003	66	75	0	73	GYLFPQNAAR
1136.5850	1135.5777	1135.5774	0.0003	66	75	0	---	GYLFPQNAAR
1200.5917	1199.5844	1199.5974	-0.0130	394	403	1	---	FGSYWIKDGK
1339.7435	1338.7362	1338.7870	-0.0508	28	40	0	---	QGVKPGELAIISK
1437.7883	1436.7810	1436.7775	0.0035	9	23	0	9	YVILGGGVAAGYAAR
1437.7883	1436.7810	1436.7775	0.0035	9	23	0	---	YVILGGGVAAGYAAR
1814.9916	1813.9843	1814.0301	-0.0458	24	40	1	---	EFAKQGVKPGELAIISK
1850.0085	1849.0012	1848.9998	0.0015	6	23	1	---	HFKYVILGGGVAAGYAAR
1913.0332	1912.0259	1912.0205	0.0054	9	27	1	---	YVILGGGVAAGYAAREFAK
2388.1045	2387.0972	2387.0956	0.0016	344	363	1	52	GKESGESVVEYDYLPYFYSR
2388.1045	2387.0972	2387.0956	0.0016	344	363	1	---	GKESGESVVEYDYLPYFYSR

No match to: 713.3984, 768.5125, 791.4080, 881.2817, 952.4984, 1093.6040, 1095.5554, 1104.6547, 1114.6825, 1141.6068, 1158.5604, 1246.6730, 1291.6801, 1322.7177, 1445.6809, 1446.7516, 1446.7516, 1453.7612, 1463.7686, 1468.7084, 1555.7222, 1571.7096, 1581.8556, 1587.6948, 1602.8114, 1633.8654, 1792.8739, 1827.9438, 1880.8871, 1903.9646, 1937.9436, 1959.9911, 1994.0363, 2059.0808, 2138.2734, 2188.9739, 2188.9739, 2204.1472, 2270.2034, 2307.2266, 2363.2002, 2418.2659, 2563.3076, 2564.3208, 2596.4089, 2662.3779, 2700.3225, 2750.4797, 2767.4966, 2782.4683, 2911.4861, 3242.7427, 3348.6348

4. gi|4760483 **Mass:** 43043 **Score:** 161 **Expect:** 4.8e-011 **Queries matched:** 12

monodehydroascorbate reductase [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1118.5748	1117.5675	1117.5740	-0.0065	312	320	1	---	RVEHVDHAR
1136.5850	1135.5777	1135.5774	0.0003	54	63	0	73	GYLFPQNAAR
1136.5850	1135.5777	1135.5774	0.0003	54	63	0	---	GYLFPQNAAR
1200.5917	1199.5844	1199.5974	-0.0130	382	391	1	---	FGSYWIKDGK
1339.7435	1338.7362	1338.7870	-0.0508	28	40	0	---	QGVKPGELAIISK
1446.7516	1445.7443	1445.7514	-0.0070	41	53	0	15	ESVAPYERPALSK
1446.7516	1445.7443	1445.7514	-0.0070	41	53	0	---	ESVAPYERPALSK
1633.8654	1632.8581	1632.8028	0.0553	148	162	1	---	DIEDADKLVAAMQAK + Oxidation (M)
1814.9916	1813.9843	1814.0301	-0.0458	24	40	1	---	EFAKQGVKPGELAIISK
2563.3076	2562.3003	2562.2351	0.0652	282	305	0	---	TDAFFETSVPGVYAIADVAAFPMK + Oxidation (M)
2564.3208	2563.3135	2563.3182	-0.0047	41	63	1	---	ESVAPYERPALSKGYLFPQNAAR
2767.4966	2766.4893	2766.5278	-0.0385	28	53	1	---	QGVKPGELAIISKESVAPYERPALSK

No match to: 713.3984, 768.5125, 791.4080, 881.2817, 952.4984, 1093.6040, 1095.5554, 1104.6547, 1114.6825, 1141.6068, 1158.5604, 1246.6730, 1291.6801, 1322.7177, 1437.7883, 1437.7883, 1445.6809, 1453.7612, 1463.7686, 1468.7084, 1555.7222, 1571.7096, 1581.8556, 1587.6948, 1602.8114, 1792.8739, 1827.9438, 1850.0085, 1880.8871, 1903.9646, 1913.0332, 1937.9436, 1959.9911, 1994.0363, 2059.0808, 2138.2734, 2188.9739, 2188.9739, 2204.1472, 2270.2034, 2307.2266, 2363.2002, 2388.1045, 2388.1045, 2418.2659, 2596.4089, 2662.3779, 2700.3225, 2750.4797, 2782.4683, 2911.4861, 3242.7427, 3348.6348

5. gi|115477781 **Mass:** 46770 **Score:** 158 **Expect:** 9.6e-011 **Queries matched:** 12

Os08g0557600 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1118.5748	1117.5675	1117.5740	-0.0065	312	320	1	---	RVEHVDHAR
1136.5850	1135.5777	1135.5774	0.0003	54	63	0	73	GYLFPQNAAR
1136.5850	1135.5777	1135.5774	0.0003	54	63	0	---	GYLFPQNAAR
1200.5917	1199.5844	1199.5974	-0.0130	382	391	1	---	FGSYWIKDGK
1339.7435	1338.7362	1338.7870	-0.0508	28	40	0	---	QGVKPGELAIISK
1446.7516	1445.7443	1445.7514	-0.0070	41	53	0	15	ESVAPYERPALSK
1446.7516	1445.7443	1445.7514	-0.0070	41	53	0	---	ESVAPYERPALSK
1633.8654	1632.8581	1632.8028	0.0553	148	162	1	---	DIEDADKLVAAMQAK + Oxidation (M)
1814.9916	1813.9843	1814.0301	-0.0458	24	40	1	---	EFAKQGVKPGELAIISK
2563.3076	2562.3003	2562.2351	0.0652	282	305	0	---	TDAFFETSVPGVYAIADVAAFPMK + Oxidation (M)
2564.3208	2563.3135	2563.3182	-0.0047	41	63	1	---	ESVAPYERPALSKGYLFPQNAAR
2767.4966	2766.4893	2766.5278	-0.0385	28	53	1	---	QGVKPGELAIISKESVAPYERPALSK

No match to: 713.3984, 768.5125, 791.4080, 881.2817, 952.4984, 1093.6040, 1095.5554, 1104.6547, 1114.6825, 1141.6068, 1158.5604, 1246.6730, 1291.6801, 1322.7177, 1437.7883, 1437.7883, 1445.6809, 1453.7612, 1463.7686, 1468.7084, 1555.7222, 1571.7096, 1581.8556, 1587.6948, 1602.8114, 1792.8739, 1827.9438, 1850.0085, 1880.8871, 1903.9646, 1913.0332, 1937.9436, 1959.9911, 1994.0363, 2059.0808, 2138.2734, 2188.9739, 2188.9739, 2204.1472, 2270.2034, 2307.2266, 2363.2002, 2388.1045, 2388.1045, 2418.2659, 2596.4089, 2662.3779, 2700.3225, 2750.4797,

2782.4683, 2911.4861, 3242.7427, 3348.6348

6. gi|125562536 **Mass:** 46770 **Score:** 158 **Expect:** 9.6e-011 **Queries matched:** 12

hypothetical protein OsI_30244 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1118.5748	1117.5675	1117.5740	-0.0065	312	320	1	---	RVEHVDHAR
1136.5850	1135.5777	1135.5774	0.0003	54	63	0	73	GYLFPQNAAR
1136.5850	1135.5777	1135.5774	0.0003	54	63	0	---	GYLFPQNAAR
1200.5917	1199.5844	1199.5974	-0.0130	382	391	1	---	FGSYWIKDGK
1339.7435	1338.7362	1338.7870	-0.0508	28	40	0	---	QGVKPGELAIISK
1446.7516	1445.7443	1445.7514	-0.0070	41	53	0	15	ESVAPYERPALSK
1446.7516	1445.7443	1445.7514	-0.0070	41	53	0	---	ESVAPYERPALSK
1633.8654	1632.8581	1632.8028	0.0553	148	162	1	---	DIEDADKLVAAMQAK + Oxidation (M)
1814.9916	1813.9843	1814.0301	-0.0458	24	40	1	---	EFAKQGVKPGELAIISK
2563.3076	2562.3003	2562.2351	0.0652	282	305	0	---	TDAFFETSVPGVYAIADVAAFPMK + Oxidation (M)
2564.3208	2563.3135	2563.3182	-0.0047	41	63	1	---	ESVAPYERPALSKGYLFPQNAAR
2767.4966	2766.4893	2766.5278	-0.0385	28	53	1	---	QGVKPGELAIISKESVAPYERPALSK

No match to: 713.3984, 768.5125, 791.4080, 881.2817, 952.4984, 1093.6040, 1095.5554, 1104.6547, 1114.6825, 1141.6068, 1158.5604, 1246.6730, 1291.6801, 1322.7177, 1437.7883, 1437.7883, 1445.6809, 1453.7612, 1463.7686, 1468.7084, 1555.7222, 1571.7096, 1581.8556, 1587.6948, 1602.8114, 1792.8739, 1827.9438, 1850.0085, 1880.8871, 1903.9646, 1913.0332, 1937.9436, 1959.9911, 1994.0363, 2059.0808, 2138.2734, 2188.9739, 2188.9739, 2204.1472, 2270.2034, 2307.2266, 2363.2002, 2388.1045, 2388.1045, 2418.2659, 2596.4089, 2662.3779, 2700.3225, 2750.4797, 2782.4683, 2911.4861, 3242.7427, 3348.6348

7. gi|222641005 **Mass:** 49149 **Score:** 157 **Expect:** 1.2e-010 **Queries matched:** 12

hypothetical protein OsJ_28260 [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1118.5748	1117.5675	1117.5740	-0.0065	312	320	1	---	RVEHVDHAR
1136.5850	1135.5777	1135.5774	0.0003	54	63	0	73	GYLFPQNAAR
1136.5850	1135.5777	1135.5774	0.0003	54	63	0	---	GYLFPQNAAR
1141.6068	1140.5995	1140.6363	-0.0368	384	393	1	---	LVLDQGRQGR
1339.7435	1338.7362	1338.7870	-0.0508	28	40	0	---	QGVKPGELAIISK
1446.7516	1445.7443	1445.7514	-0.0070	41	53	0	15	ESVAPYERPALSK
1446.7516	1445.7443	1445.7514	-0.0070	41	53	0	---	ESVAPYERPALSK
1633.8654	1632.8581	1632.8028	0.0553	148	162	1	---	DIEDADKLVAAMQAK + Oxidation (M)
1814.9916	1813.9843	1814.0301	-0.0458	24	40	1	---	EFAKQGVKPGELAIISK
2563.3076	2562.3003	2562.2351	0.0652	282	305	0	---	TDAFFETSVPGVYAIADVAAFPMK + Oxidation (M)
2564.3208	2563.3135	2563.3182	-0.0047	41	63	1	---	ESVAPYERPALSKGYLFPQNAAR
2767.4966	2766.4893	2766.5278	-0.0385	28	53	1	---	QGVKPGELAIISKESVAPYERPALSK

No match to: 713.3984, 768.5125, 791.4080, 881.2817, 952.4984, 1093.6040, 1095.5554, 1104.6547, 1114.6825, 1158.5604, 1200.5917, 1246.6730, 1291.6801, 1322.7177, 1437.7883, 1437.7883, 1445.6809, 1453.7612, 1463.7686,

1468.7084, 1555.7222, 1571.7096, 1581.8556, 1587.6948, 1602.8114, 1792.8739, 1827.9438, 1850.0085, 1880.8871, 1903.9646, 1913.0332, 1937.9436, 1959.9911, 1994.0363, 2059.0808, 2138.2734, 2188.9739, 2188.9739, 2204.1472, 2270.2034, 2307.2266, 2363.2002, 2388.1045, 2388.1045, 2418.2659, 2596.4089, 2662.3779, 2700.3225, 2750.4797, 2782.4683, 2911.4861, 3242.7427, 3348.6348

8. gi|223947705 **Mass:** 46556 **Score:** 112 **Expect:** 3.8e-006 **Queries matched:** 9

unknown [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1118.5748	1117.5675	1117.5740	-0.0065	310	318	1	---	RVEHVDHAR
1136.5850	1135.5777	1135.5774	0.0003	52	61	0	73	GYLFPQNAAR
1136.5850	1135.5777	1135.5774	0.0003	52	61	0	---	GYLFPQNAAR
1437.7883	1436.7810	1436.7775	0.0035	7	21	0	9	YVILGGGVAAGYAAR
1437.7883	1436.7810	1436.7775	0.0035	7	21	0	---	YVILGGGVAAGYAAR
1446.7516	1445.7443	1445.7877	-0.0434	266	279	1	---	LFIGQAADEKGGLK
1446.7516	1445.7443	1445.7877	-0.0434	266	279	1	---	LFIGQAADEKGGLK
1850.0085	1849.0012	1848.9998	0.0015	4	21	1	---	HFKYVILGGGVAAGYAAR
1913.0332	1912.0259	1912.0205	0.0054	7	25	1	---	YVILGGGVAAGYAAREFAK

No match to: 713.3984, 768.5125, 791.4080, 881.2817, 952.4984, 1093.6040, 1095.5554, 1104.6547, 1114.6825, 1141.6068, 1158.5604, 1200.5917, 1246.6730, 1291.6801, 1322.7177, 1339.7435, 1445.6809, 1453.7612, 1463.7686, 1468.7084, 1555.7222, 1571.7096, 1581.8556, 1587.6948, 1602.8114, 1633.8654, 1792.8739, 1814.9916, 1827.9438, 1880.8871, 1903.9646, 1937.9436, 1959.9911, 1994.0363, 2059.0808, 2138.2734, 2188.9739, 2188.9739, 2204.1472, 2270.2034, 2307.2266, 2363.2002, 2388.1045, 2388.1045, 2418.2659, 2563.3076, 2564.3208, 2596.4089, 2662.3779, 2700.3225, 2750.4797, 2767.4966, 2782.4683, 2911.4861, 3242.7427, 3348.6348

9. gi|1170511 **Mass:** 47098 **Score:** 84 **Expect:** 0.0023 **Queries matched:** 14

RecName: Full=Eukaryotic initiation factor 4A-10; Short=eIF-4A-10; AltName: Full=ATP-dependent RNA

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
952.4984	951.4911	951.4960	-0.0048	169	175	1	---	VFDMLRR + Oxidation (M)
1093.6040	1092.5967	1092.6040	-0.0072	176	184	0	---	QSLRPDHIK
1095.5554	1094.5481	1094.5542	-0.0061	319	326	1	---	DIIMREFR + Oxidation (M)
1114.6825	1113.6752	1113.6757	-0.0005	332	341	0	---	VLITTDLLAR
1463.7686	1462.7613	1462.7415	0.0198	377	389	1	---	GVAINFVTKDDER
1555.7222	1554.7149	1554.7058	0.0091	185	197	0	---	MFVLDEADEMLSR
1571.7096	1570.7023	1570.7007	0.0016	185	197	0	---	MFVLDEADEMLSR + Oxidation (M)
1587.6948	1586.6875	1586.6956	-0.0081	185	197	0	---	MFVLDEADEMLSR + 2 Oxidation (M)
1827.9438	1826.9365	1826.9314	0.0051	54	69	0	---	GIYAYGFEKPSAIQQR
1903.9646	1902.9573	1902.8855	0.0718	185	200	1	---	MFVLDEADEMLSRGFK + Oxidation (M)
2059.0808	2058.0735	2058.0679	0.0056	130	149	1	---	ALGDYLGVKVHACVGGTSVR
2662.3779	2661.3706	2661.2890	0.0816	176	197	1	---	QSLRPDHIKMFVLDEADEMLSR + 2 Oxidation (M)
2750.4797	2749.4724	2749.4247	0.0477	390	413	1	---	MLSDIQKFYNVVIEELPANVADLL + Oxidation (M)
2911.4861	2910.4788	2910.4875	-0.0087	342	366	0	---	GIDVQQVSLVINYDLPTQPENYLHR

No match to: 713.3984, 768.5125, 791.4080, 881.2817, 1104.6547, 1118.5748, 1136.5850, 1136.5850, 1141.6068,

1158.5604, 1200.5917, 1246.6730, 1291.6801, 1322.7177, 1339.7435, 1437.7883, 1437.7883, 1445.6809, 1446.7516, 1446.7516, 1453.7612, 1468.7084, 1581.8556, 1602.8114, 1633.8654, 1792.8739, 1814.9916, 1850.0085, 1880.8871, 1913.0332, 1937.9436, 1959.9911, 1994.0363, 2138.2734, 2188.9739, 2188.9739, 2204.1472, 2270.2034, 2307.2266, 2363.2002, 2388.1045, 2388.1045, 2418.2659, 2563.3076, 2564.3208, 2596.4089, 2700.3225, 2767.4966, 2782.4683, 3242.7427, 3348.6348

10. gi|115444197 **Mass:** 47393 **Score:** 78 **Expect:** 0.011 **Queries matched:** 14

Os02g0146600 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
952.4984	951.4911	951.4960	-0.0048	170	176	1	---	VFDMLRR + Oxidation (M)
1093.6040	1092.5967	1092.6040	-0.0072	177	185	0	---	QSLRPDHIK
1095.5554	1094.5481	1094.5542	-0.0061	320	327	1	---	DIIMREFR + Oxidation (M)
1104.6547	1103.6474	1103.6451	0.0024	377	386	1	---	KGVAINFVTR
1114.6825	1113.6752	1113.6757	-0.0005	333	342	0	---	VLITTDLLAR
1453.7612	1452.7539	1452.6667	0.0872	387	397	1	---	DDERMLFDIQR + Oxidation (M)
1555.7222	1554.7149	1554.7058	0.0091	186	198	0	---	MFVLDEADEMLSR
1571.7096	1570.7023	1570.7007	0.0016	186	198	0	---	MFVLDEADEMLSR + Oxidation (M)
1587.6948	1586.6875	1586.6956	-0.0081	186	198	0	---	MFVLDEADEMLSR + 2 Oxidation (M)
1827.9438	1826.9365	1826.9314	0.0051	55	70	0	---	GIYAYGFEKPSAIQQR
1903.9646	1902.9573	1902.8855	0.0718	186	201	1	---	MFVLDEADEMLSRGFK + Oxidation (M)
2059.0808	2058.0735	2058.0679	0.0056	131	150	1	---	ALGDYLGVKVHACVGGTSVR
2662.3779	2661.3706	2661.2890	0.0816	177	198	1	---	QSLRPDHIKMFVLDEADEMLSR + 2 Oxidation (M)
2911.4861	2910.4788	2910.4875	-0.0087	343	367	0	---	GIDVQQVSLVINYDLPTQPENYLHR

No match to: 713.3984, 768.5125, 791.4080, 881.2817, 1118.5748, 1136.5850, 1136.5850, 1141.6068, 1158.5604, 1200.5917, 1246.6730, 1291.6801, 1322.7177, 1339.7435, 1437.7883, 1437.7883, 1445.6809, 1446.7516, 1446.7516, 1463.7686, 1468.7084, 1581.8556, 1602.8114, 1633.8654, 1792.8739, 1814.9916, 1850.0085, 1880.8871, 1913.0332, 1937.9436, 1959.9911, 1994.0363, 2138.2734, 2188.9739, 2188.9739, 2204.1472, 2270.2034, 2307.2266, 2363.2002, 2388.1045, 2388.1045, 2418.2659, 2563.3076, 2564.3208, 2596.4089, 2700.3225, 2750.4797, 2767.4966, 2782.4683, 3242.7427, 3348.6348

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 65

Protein View

Match to: **gi|4666287** Score: **191** Expect: **4.8e-014**
cytosolic monodehydroascorbate reductase [Oryza sativa Japonica Group]

Nominal mass (M_r): **46716**; Calculated pI value: **5.53**
NCBI BLAST search of gi|4666287 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Oryza sativa Japonica Group

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **19%**

Matched peptides shown in **Bold Red**

```
   1 MASEKHFKYV ILGGGVAAGY AAREFAKQGV KPGELAIISK EAVAPYERPA
  51 LSKGYLFPQN AARLPGFHVC VGSGGERLLP EWYSEKGIEL ILSTEIVKAD
 101 LASKTLTSAV GATFTYEILI IATGSSVIKL SDFGTQGADS NNILYLREVD
 151 DADKLVAAIQ AKKGGKAVIV GGGYIGLELS AALKINDFDV TMVFPEPWCM
 201 PRLFTADIAA FYESYYTNKG VKIVKGTVAV GFDADANGDV TAVNLKNGSV
 251 LEADIVGVGV GGRPLTTLFK GQVAEEKGGI KTDAFFETSV PGVYAVGDVA
 301 TFPMKMYNEL RRVEHVDHAR KSAEQAVKAI KGKESGESVV EYDYLPYFYS
 351 RSFDLGWQFY GDNVGDTILF GDSDPTSAKP KFGSYWIKDG KVLGAFLEGG
 401 SPDENKAIAK VAKTQPPVAN IEELKKEGLQ FASKI
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
6 - 23	1850.0085	1849.0012	1848.9998	0.0015	1	HFKYVILGGGVAAGYAAR	(No match)
9 - 23	1437.7883	1436.7810	1436.7775	0.0035	0	YVILGGGVAAGYAAR	(Ions score 9)
9 - 23	1437.7883	1436.7810	1436.7775	0.0035	0	YVILGGGVAAGYAAR	(No match)
9 - 27	1913.0332	1912.0259	1912.0205	0.0054	1	YVILGGGVAAGYAAREFAK	(No match)
24 - 40	1814.9916	1813.9843	1814.0301	-0.0458	1	EFAKQGVKPGELAIISK	(No match)
28 - 40	1339.7435	1338.7362	1338.7870	-0.0508	0	QGVKPGELAIISK	(No match)
54 - 63	1136.5850	1135.5777	1135.5774	0.0003	0	GYLFPQNAAR	(Ions score 73)
54 - 63	1136.5850	1135.5777	1135.5774	0.0003	0	GYLFPQNAAR	(No match)
312 - 320	1118.5748	1117.5675	1117.5740	-0.0065	1	RVEHVDHAR	(No match)
332 - 351	2388.1045	2387.0972	2387.0956	0.0016	1	GKESGESVVEYDYLPYFYSR	(Ions score 52)
332 - 351	2388.1045	2387.0972	2387.0956	0.0016	1	GKESGESVVEYDYLPYFYSR	(No match)
382 - 391	1200.5917	1199.5844	1199.5974	-0.0130	1	FGSYWIKDGK	(No match)

Spot 52

Index

	Accession	Mass	Score	Description
1.	gi|219363507	46411	279	hypothetical protein LOC100217128 [Zea mays]
2.	gi|15218869	46059	274	isocitrate dehydrogenase, putative / NADP+ isocitrate dehydrogenase, putative [Arabidopsis tha
3.	gi|20260384	46045	274	similar to NADP-specific isocitrate dehydrogenase [Arabidopsis thaliana]
4.	gi|115438939	46356	264	Os01g0654500 [Oryza sativa (japonica cultivar-group)]
5.	gi|226499486	46565	263	hypothetical protein LOC100272371 [Zea mays]
6.	gi|115465563	46457	263	Os05g0573200 [Oryza sativa (japonica cultivar-group)]
7.	gi|213493066	46779	252	NADP-dependent isocitrate dehydrogenase [Passiflora edulis]
8.	gi|19171469	46039	249	isocitrate dehydrogenase [Arabidopsis thaliana]
9.	gi|125553404	48242	248	hypothetical protein OsI_21072 [Oryza sativa Indica Group]
10.	gi|226500532	46536	243	hypothetical protein LOC100274592 [Zea mays]

Results List

1. gi|219363507 **Mass:** 46411 **Score:** 279 **Expect:** 7.6e-023 **Queries matched:** 12

hypothetical protein LOC100217128 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
993.4539	992.4466	992.4464	0.0002	135	142	0	---	HAFGDQYR
993.4539	992.4466	992.4464	0.0002	135	142	0	24	HAFGDQYR
1355.6965	1354.6892	1354.6840	0.0052	302	314	0	---	TIEAEAAHGTVTR
1496.8447	1495.8374	1495.8333	0.0041	122	134	0	---	LVPGWTKPICIGR
1496.8447	1495.8374	1495.8333	0.0041	122	134	0	61	LVPGWTKPICIGR
1773.9766	1772.9693	1772.9606	0.0087	103	117	1	---	NIINGTVFREPIICK
1773.9766	1772.9693	1772.9606	0.0087	103	117	1	30	NIINGTVFREPIICK
1795.9370	1794.9297	1794.9125	0.0173	302	317	1	---	TIEAEAAHGTVTRHFR
1797.8894	1796.8821	1796.8693	0.0129	322	338	0	88	GGETSTNSIASIFAWTR
1797.8894	1796.8821	1796.8693	0.0129	322	338	0	---	GGETSTNSIASIFAWTR
2290.1631	2289.1558	2289.1501	0.0057	318	338	1	---	VHQKGGETSTNSIASIFAWTR
2597.2859	2596.2786	2596.2301	0.0485	8	29	1	---	VSNPIVEMDGDEMTRVFWQSIK + Oxidation (M)

No match to: 713.3889, 768.4931, 825.1118, 845.0977, 854.0434, 864.5004, 930.9944, 1098.0043, 1325.7952, 1513.8556, 1609.7865, 1935.1006, 2018.9972, 2031.0509, 2036.0195, 2036.0195, 2234.1211, 2241.0771, 2301.2473, 2499.3525, 2823.3140, 2923.3491

2. gi|15218869 **Mass:** 46059 **Score:** 274 **Expect:** 2.4e-022 **Queries matched:** 12

isocitrate dehydrogenase, putative / NADP+ isocitrate dehydrogenase, putative [Arabidopsis thaliana

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
993.4539	992.4466	992.4464	0.0002	135	142	0	---	HAFGDQYR
993.4539	992.4466	992.4464	0.0002	135	142	0	24	HAFGDQYR

1355.6965	1354.6892	1354.6840	0.0052	302 - 314	0	---	TIEAEAAHGTVTR
1496.8447	1495.8374	1495.8333	0.0041	122 - 134	0	---	LVPGWTKPICIGR
1496.8447	1495.8374	1495.8333	0.0041	122 - 134	0	61	LVPGWTKPICIGR
1773.9766	1772.9693	1772.9606	0.0087	103 - 117	1	---	NILNGTVFREPIICK
1773.9766	1772.9693	1772.9606	0.0087	103 - 117	1	30	NILNGTVFREPIICK
1795.9370	1794.9297	1794.9125	0.0173	302 - 317	1	---	TIEAEAAHGTVTRHFR
1797.8894	1796.8821	1796.8693	0.0129	322 - 338	0	88	GGETSTNSIASIFAWTR
1797.8894	1796.8821	1796.8693	0.0129	322 - 338	0	---	GGETSTNSIASIFAWTR
1935.1006	1934.0933	1934.0923	0.0010	118 - 134	1	---	NVPKLVPGWTKPICIGR
2290.1631	2289.1558	2289.1501	0.0057	318 - 338	1	---	VHQKGGETSTNSIASIFAWTR

No match to: 713.3889, 768.4931, 825.1118, 845.0977, 854.0434, 864.5004, 930.9944, 1098.0043, 1325.7952, 1513.8556, 1609.7865, 2018.9972, 2031.0509, 2036.0195, 2036.0195, 2234.1211, 2241.0771, 2301.2473, 2499.3525, 2597.2859, 2823.3140, 2923.3491

3. gi|20260384 **Mass:** 46045 **Score:** 274 **Expect:** 2.4e-022 **Queries matched:** 12

similar to NADP-specific isocitrate dehydrogenase [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
993.4539	992.4466	992.4464	0.0002	135 - 142	0	---	HAFGDQYR
993.4539	992.4466	992.4464	0.0002	135 - 142	0	24	HAFGDQYR
1355.6965	1354.6892	1354.6840	0.0052	302 - 314	0	---	TIEAEAAHGTVTR
1496.8447	1495.8374	1495.8333	0.0041	122 - 134	0	---	LVPGWTKPICIGR
1496.8447	1495.8374	1495.8333	0.0041	122 - 134	0	61	LVPGWTKPICIGR
1773.9766	1772.9693	1772.9606	0.0087	103 - 117	1	---	NILNGTVFREPIICK
1773.9766	1772.9693	1772.9606	0.0087	103 - 117	1	30	NILNGTVFREPIICK
1795.9370	1794.9297	1794.9125	0.0173	302 - 317	1	---	TIEAEAAHGTVTRHFR
1797.8894	1796.8821	1796.8693	0.0129	322 - 338	0	88	GGETSTNSIASIFAWTR
1797.8894	1796.8821	1796.8693	0.0129	322 - 338	0	---	GGETSTNSIASIFAWTR
1935.1006	1934.0933	1934.0923	0.0010	118 - 134	1	---	NVPKLVPGWTKPICIGR
2290.1631	2289.1558	2289.1501	0.0057	318 - 338	1	---	VHQKGGETSTNSIASIFAWTR

No match to: 713.3889, 768.4931, 825.1118, 845.0977, 854.0434, 864.5004, 930.9944, 1098.0043, 1325.7952, 1513.8556, 1609.7865, 2018.9972, 2031.0509, 2036.0195, 2036.0195, 2234.1211, 2241.0771, 2301.2473, 2499.3525, 2597.2859, 2823.3140, 2923.3491

4. gi|115438939 **Mass:** 46356 **Score:** 264 **Expect:** 2.4e-021 **Queries matched:** 11

Os01g0654500 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
993.4539	992.4466	992.4464	0.0002	135 - 142	0	---	HAFGDQYR
993.4539	992.4466	992.4464	0.0002	135 - 142	0	24	HAFGDQYR
1355.6965	1354.6892	1354.6840	0.0052	302 - 314	0	---	TIEAEAAHGTVTR
1496.8447	1495.8374	1495.8333	0.0041	122 - 134	0	---	LVPGWTKPICIGR
1496.8447	1495.8374	1495.8333	0.0041	122 - 134	0	61	LVPGWTKPICIGR

1773.9766	1772.9693	1772.9606	0.0087	103 - 117	1	---	NIINGTVFREPIICK
1773.9766	1772.9693	1772.9606	0.0087	103 - 117	1	30	NIINGTVFREPIICK
1795.9370	1794.9297	1794.9125	0.0173	302 - 317	1	---	TIEAEAAHGTVTRHFR
1797.8894	1796.8821	1796.8693	0.0129	322 - 338	0	88	GGETSTNSIASIFAWTR
1797.8894	1796.8821	1796.8693	0.0129	322 - 338	0	---	GGETSTNSIASIFAWTR
2290.1631	2289.1558	2289.1501	0.0057	318 - 338	1	---	VHQKGGETSTNSIASIFAWTR

No match to: 713.3889, 768.4931, 825.1118, 845.0977, 854.0434, 864.5004, 930.9944, 1098.0043, 1325.7952, 1513.8556, 1609.7865, 1935.1006, 2018.9972, 2031.0509, 2036.0195, 2036.0195, 2234.1211, 2241.0771, 2301.2473, 2499.3525, 2597.2859, 2823.3140, 2923.3491

5. gi|226499486 **Mass:** 46565 **Score:** 263 **Expect:** 3e-021 **Queries matched:** 11

hypothetical protein LOC100272371 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
864.5004	863.4931	863.4752	0.0179	352 - 358		0	---	LLDFTQK
993.4539	992.4466	992.4464	0.0002	135 - 142		0	---	HAFGDQYR
993.4539	992.4466	992.4464	0.0002	135 - 142		0	24	HAFGDQYR
1355.6965	1354.6892	1354.6840	0.0052	302 - 314		0	---	TIEAEAAHGTVTR
1496.8447	1495.8374	1495.8333	0.0041	122 - 134		0	---	LVPGWTKPICIGR
1496.8447	1495.8374	1495.8333	0.0041	122 - 134		0	61	LVPGWTKPICIGR
1773.9766	1772.9693	1772.9606	0.0087	103 - 117		1	---	NILNGTVFREPIICK
1773.9766	1772.9693	1772.9606	0.0087	103 - 117		1	30	NILNGTVFREPIICK
1797.8894	1796.8821	1796.8693	0.0129	322 - 338		0	88	GGETSTNSIASIFAWTR
1797.8894	1796.8821	1796.8693	0.0129	322 - 338		0	---	GGETSTNSIASIFAWTR
2290.1631	2289.1558	2289.1501	0.0057	318 - 338		1	---	VHQKGGETSTNSIASIFAWTR

No match to: 713.3889, 768.4931, 825.1118, 845.0977, 854.0434, 930.9944, 1098.0043, 1325.7952, 1513.8556, 1609.7865, 1795.9370, 1935.1006, 2018.9972, 2031.0509, 2036.0195, 2036.0195, 2234.1211, 2241.0771, 2301.2473, 2499.3525, 2597.2859, 2823.3140, 2923.3491

6. gi|115465563 **Mass:** 46457 **Score:** 263 **Expect:** 3e-021 **Queries matched:** 11

Os05g0573200 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
864.5004	863.4931	863.4752	0.0179	352 - 358		0	---	LLDFTQK
993.4539	992.4466	992.4464	0.0002	135 - 142		0	---	HAFGDQYR
993.4539	992.4466	992.4464	0.0002	135 - 142		0	24	HAFGDQYR
1355.6965	1354.6892	1354.6840	0.0052	302 - 314		0	---	TIEAEAAHGTVTR
1496.8447	1495.8374	1495.8333	0.0041	122 - 134		0	---	LVPGWTKPICIGR
1496.8447	1495.8374	1495.8333	0.0041	122 - 134		0	61	LVPGWTKPICIGR
1773.9766	1772.9693	1772.9606	0.0087	103 - 117		1	---	NILNGTVFREPIICK
1773.9766	1772.9693	1772.9606	0.0087	103 - 117		1	30	NILNGTVFREPIICK
1797.8894	1796.8821	1796.8693	0.0129	322 - 338		0	88	GGETSTNSIASIFAWTR
1797.8894	1796.8821	1796.8693	0.0129	322 - 338		0	---	GGETSTNSIASIFAWTR

2290.1631	2289.1558	2289.1501	0.0057	318 - 338	1	---	VHQKGGETSTNSIASIFAWTR

No match to: 713.3889, 768.4931, 825.1118, 845.0977, 854.0434, 930.9944, 1098.0043, 1325.7952, 1513.8556, 1609.7865, 1795.9370, 1935.1006, 2018.9972, 2031.0509, 2036.0195, 2036.0195, 2234.1211, 2241.0771, 2301.2473, 2499.3525, 2597.2859, 2823.3140, 2923.3491

7. gi|213493066 **Mass:** 46779 **Score:** 252 **Expect:** 3.8e-020 **Queries matched:** 10

NADP-dependent isocitrate dehydrogenase [Passiflora edulis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
993.4539	992.4466	992.4464	0.0002	135 - 142		0	---	HAFGDQYR
993.4539	992.4466	992.4464	0.0002	135 - 142		0	24	HAFGDQYR
1355.6965	1354.6892	1354.6840	0.0052	304 - 316		0	---	TIEAEAAHGTVTR
1496.8447	1495.8374	1495.8333	0.0041	122 - 134		0	---	LVPGWTKPICIGR
1496.8447	1495.8374	1495.8333	0.0041	122 - 134		0	61	LVPGWTKPICIGR
1773.9766	1772.9693	1772.9606	0.0087	103 - 117		1	---	NILNGTVFREPILCK
1773.9766	1772.9693	1772.9606	0.0087	103 - 117		1	30	NILNGTVFREPILCK
1797.8894	1796.8821	1796.8693	0.0129	324 - 340		0	88	GGETSTNSIASIFAWTR
1797.8894	1796.8821	1796.8693	0.0129	324 - 340		0	---	GGETSTNSIASIFAWTR
2290.1631	2289.1558	2289.1501	0.0057	320 - 340		1	---	VHQKGGETSTNSIASIFAWTR

No match to: 713.3889, 768.4931, 825.1118, 845.0977, 854.0434, 864.5004, 930.9944, 1098.0043, 1325.7952, 1513.8556, 1609.7865, 1795.9370, 1935.1006, 2018.9972, 2031.0509, 2036.0195, 2036.0195, 2234.1211, 2241.0771, 2301.2473, 2499.3525, 2597.2859, 2823.3140, 2923.3491

8. gi|19171469 **Mass:** 46039 **Score:** 249 **Expect:** 7.6e-020 **Queries matched:** 10

isocitrate dehydrogenase [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
993.4539	992.4466	992.4464	0.0002	135 - 142		0	---	HAFGDQYR
993.4539	992.4466	992.4464	0.0002	135 - 142		0	24	HAFGDQYR
1496.8447	1495.8374	1495.8333	0.0041	122 - 134		0	---	LVPGWTKPICIGR
1496.8447	1495.8374	1495.8333	0.0041	122 - 134		0	61	LVPGWTKPICIGR
1773.9766	1772.9693	1772.9606	0.0087	103 - 117		1	---	NILNGTVFREPIICK
1773.9766	1772.9693	1772.9606	0.0087	103 - 117		1	30	NILNGTVFREPIICK
1797.8894	1796.8821	1796.8693	0.0129	322 - 338		0	88	GGETSTNSIASIFAWTR
1797.8894	1796.8821	1796.8693	0.0129	322 - 338		0	---	GGETSTNSIASIFAWTR
1935.1006	1934.0933	1934.0923	0.0010	118 - 134		1	---	NVPKLVPGWTKPICIGR
2290.1631	2289.1558	2289.1501	0.0057	318 - 338		1	---	VHQKGGETSTNSIASIFAWTR

No match to: 713.3889, 768.4931, 825.1118, 845.0977, 854.0434, 864.5004, 930.9944, 1098.0043, 1325.7952, 1355.6965, 1513.8556, 1609.7865, 1795.9370, 2018.9972, 2031.0509, 2036.0195, 2036.0195, 2234.1211, 2241.0771, 2301.2473, 2499.3525, 2597.2859, 2823.3140, 2923.3491

9. gi|125553404 **Mass:** 48242 **Score:** 248 **Expect:** 9.6e-020 **Queries matched:** 10

hypothetical protein OsI_21072 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
864.5004	863.4931	863.4752	0.0179	369	-	375	0	---	LLDFTQK
993.4539	992.4466	992.4464	0.0002	152	-	159	0	---	HAFGDQYR
993.4539	992.4466	992.4464	0.0002	152	-	159	0	24	HAFGDQYR
1355.6965	1354.6892	1354.6840	0.0052	319	-	331	0	---	TIEAEAAHGTVTR
1496.8447	1495.8374	1495.8333	0.0041	139	-	151	0	---	LVPGWTKPICIGR
1496.8447	1495.8374	1495.8333	0.0041	139	-	151	0	61	LVPGWTKPICIGR
1773.9766	1772.9693	1772.9606	0.0087	120	-	134	1	---	NILNGTVFREPIICK
1773.9766	1772.9693	1772.9606	0.0087	120	-	134	1	30	NILNGTVFREPIICK
1797.8894	1796.8821	1796.8693	0.0129	339	-	355	0	88	GGETSTNSIASIFAWTR
1797.8894	1796.8821	1796.8693	0.0129	339	-	355	0	---	GGETSTNSIASIFAWTR

No match to: 713.3889, 768.4931, 825.1118, 845.0977, 854.0434, 930.9944, 1098.0043, 1325.7952, 1513.8556, 1609.7865, 1795.9370, 1935.1006, 2018.9972, 2031.0509, 2036.0195, 2036.0195, 2234.1211, 2241.0771, 2290.1631, 2301.2473, 2499.3525, 2597.2859, 2823.3140, 2923.3491

10. gi|226500532 **Mass:** 46536 **Score:** 243 **Expect:** 3e-019 **Queries matched:** 10

hypothetical protein LOC100274592 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1355.6965	1354.6892	1354.6840	0.0052	302	-	314	0	---	TIEAEAAHGTVTR
1496.8447	1495.8374	1495.8333	0.0041	122	-	134	0	---	LVPGWTKPICIGR
1496.8447	1495.8374	1495.8333	0.0041	122	-	134	0	61	LVPGWTKPICIGR
1773.9766	1772.9693	1772.9606	0.0087	103	-	117	1	---	NIINGTVFREPIICK
1773.9766	1772.9693	1772.9606	0.0087	103	-	117	1	30	NIINGTVFREPIICK
1795.9370	1794.9297	1794.9125	0.0173	302	-	317	1	---	TIEAEAAHGTVTRHFR
1797.8894	1796.8821	1796.8693	0.0129	322	-	338	0	88	GGETSTNSIASIFAWTR
1797.8894	1796.8821	1796.8693	0.0129	322	-	338	0	---	GGETSTNSIASIFAWTR
2290.1631	2289.1558	2289.1501	0.0057	318	-	338	1	---	VHQKGGETSTNSIASIFAWTR
2597.2859	2596.2786	2596.2301	0.0485	8	-	29	1	---	VSNPIVEMDGDEMTRVFWQSIK + Oxidation (M)

No match to: 713.3889, 768.4931, 825.1118, 845.0977, 854.0434, 864.5004, 930.9944, 993.4539, 993.4539, 1098.0043, 1325.7952, 1513.8556, 1609.7865, 1935.1006, 2018.9972, 2031.0509, 2036.0195, 2036.0195, 2234.1211, 2241.0771, 2301.2473, 2499.3525, 2823.3140, 2923.3491

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 34

Protein View

Match to: **gi|219363507** Score: **279** Expect: **7.6e-023**
hypothetical protein LOC100217128 [Zea mays]

Nominal mass (M_r): **46411**; Calculated pI value: **6.58**
NCBI BLAST search of gi|219363507 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Zea mays
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|194697804 from Zea mays

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **23%**

Matched peptides shown in **Bold Red**

```
     1 MAFEKIKVSN PIVEMDGDEM TRVFWQSIKD KLIFPFLDLD IKYYDLGILH
    51 RDATDDKVTV EAAEATLKYN VAIKCATITP DETRVKEFNL KHMWKSPNGT
   101 IRNIINGTVF REPIICKNVP RLVPGWTKPI CIGRHAFGDQ YRATDAVLKG
   151 PGKLKLVFEG KEEQIDLEVF NFTGAGGVAL SMYNTDESIR AFAAASMTTA
   201 YEKKWPLYLS TKNTILKKYD GRFKDIFQEV YEADWKSKFE AAGIWYEHRL
   251 IDDMVAYALK SEGGYVWACK NYDGDVQSDF LAQGFGSLGL MTSVLVCPDG
   301 KTIEAEAAHG TVTRHFRVHQ KGGETSTNSI ASIFAWTRGL AHRAKLDDNA
   351 RLLDFALKLE AACVGAVESG KMTKDLALLV HGSSKVTRSH YLNTEEFIDA
   401 VATELRSRLG AN
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
8 - 29	2597.2859	2596.2786	2596.2301	0.0485	1	**VSNPIVEMDGDEMTRVFWQSIK** Oxidation (M) (No match)
103 - 117	1773.9766	1772.9693	1772.9606	0.0087	1	**NIINGTVFREPIICK** (No match)
103 - 117	1773.9766	1772.9693	1772.9606	0.0087	1	**NIINGTVFREPIICK** (Ions score 30)
122 - 134	1496.8447	1495.8374	1495.8333	0.0041	0	**LVPGWTKPICIGR** (No match)
122 - 134	1496.8447	1495.8374	1495.8333	0.0041	0	**LVPGWTKPICIGR** (Ions score 61)
135 - 142	993.4539	992.4466	992.4464	0.0002	0	**HAFGDQYR** (No match)
135 - 142	993.4539	992.4466	992.4464	0.0002	0	**HAFGDQYR** (Ions score 24)
302 - 314	1355.6965	1354.6892	1354.6840	0.0052	0	**TIEAEAAHGTVTR** (No match)
302 - 317	1795.9370	1794.9297	1794.9125	0.0173	1	**TIEAEAAHGTVTRHFR** (No match)
318 - 338	2290.1631	2289.1558	2289.1501	0.0057	1	**VHQKGGETSTNSIASIFAWTR** (No match)
322 - 338	1797.8894	1796.8821	1796.8693	0.0129	0	**GGETSTNSIASIFAWTR** (Ions score 88)
322 - 338	1797.8894	1796.8821	1796.8693	0.0129	0	**GGETSTNSIASIFAWTR** (No match)

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	Accession	Mass	Score	Description
1.	gi|4582787	36465	144	adenosine kinase [Zea mays]
2.	gi|194693574	37539	131	unknown [Zea mays]
3.	gi|51949800	37820	95	adenosine kinase isoform 1S [Nicotiana tabacum]
4.	gi|157356410	23206	49	unnamed protein product [Vitis vinifera]
5.	gi|215766747	14633	45	unnamed protein product [Oryza sativa Japonica Group]

Results List

1. gi|4582787 **Mass:** 36465 **Score:** 144 **Expect:** 2.4e-009 **Queries matched:** 9

adenosine kinase [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1027.6412	1026.6339	1026.6477	-0.0138	267	275	0	---	TFPVILLPK
1284.7811	1283.7738	1283.7852	-0.0114	267	277	1	---	TFPVILLPKEK
1424.7104	1423.7031	1423.7129	-0.0098	120	132	0	---	SLIANLSAANCYK
1679.8254	1678.8181	1678.8274	-0.0093	44	59	0	---	SNVEYIAGGATQNSIR
1679.8254	1678.8181	1678.8274	-0.0093	44	59	0	90	SNVEYIAGGATQNSIR
1835.9419	1834.9346	1834.9689	-0.0343	133	147	1	---	SEHLKRPENWALVEK
1835.9419	1834.9346	1834.9689	-0.0343	133	147	1	---	SEHLKRPENWALVEK
2009.1188	2008.1115	2008.1203	-0.0088	247	266	1	---	IAVITQGADPVVVAEDGKVK
2407.2100	2406.2027	2406.2682	-0.0654	1	22	1	---	GNPLLDISAVVDDAFLTKYDIK

No match to: 700.4064, 705.4153, 706.4159, 713.4158, 724.4982, 734.4885, 748.4456, 750.5007, 768.5281, 817.4893, 1133.6895, 1181.6285, 1197.6211, 1279.7637, 1334.8794, 1434.8983, 1448.9122, 1523.7798, 1540.7914, 1562.9437, 1618.0626, 1620.8188, 1732.1007, 1748.9111, 1773.8889, 1933.0112, 2061.1099, 2088.9768, 2166.2161, 2261.1279, 2293.1785, 2418.2239, 2498.1829, 2498.1829, 2512.0852, 2512.0852, 2526.0977, 2544.2825, 2544.2825, 2727.2776, 2752.4912, 3018.8137, 3252.4871, 3274.9487, 3485.6846

2. gi|194693574 **Mass:** 37539 **Score:** 131 **Expect:** 4.8e-008 **Queries matched:** 8

unknown [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1027.6412	1026.6339	1026.6477	-0.0138	278	286	0	---	TFPVILLPK
1284.7811	1283.7738	1283.7852	-0.0114	278	288	1	---	TFPVILLPKEK
1424.7104	1423.7031	1423.7129	-0.0098	131	143	0	---	SLIANLSAANCYK
1679.8254	1678.8181	1678.8274	-0.0093	55	70	0	---	SNVEYIAGGATQNSIR
1679.8254	1678.8181	1678.8274	-0.0093	55	70	0	90	SNVEYIAGGATQNSIR
1835.9419	1834.9346	1834.9689	-0.0343	144	158	1	---	SEHLKRPENWALVEK
1835.9419	1834.9346	1834.9689	-0.0343	144	158	1	---	SEHLKRPENWALVEK
2009.1188	2008.1115	2008.1203	-0.0088	258	277	1	---	IAVITQGADPVVVAEDGKVK

No match to: 700.4064, 705.4153, 706.4159, 713.4158, 724.4982, 734.4885, 748.4456, 750.5007, 768.5281, 817.4893, 1133.6895, 1181.6285, 1197.6211, 1279.7637, 1334.8794, 1434.8983, 1448.9122, 1523.7798, 1540.7914, 1562.9437, 1618.0626, 1620.8188, 1732.1007, 1748.9111, 1773.8889, 1933.0112, 2061.1099, 2088.9768, 2166.2161, 2261.1279, 2293.1785, 2407.2100, 2418.2239, 2498.1829, 2498.1829, 2512.0852, 2512.0852, 2526.0977, 2544.2825, 2544.2825, 2727.2776, 2752.4912, 3018.8137, 3252.4871, 3274.9487, 3485.6846

3. gi|51949800 **Mass:** 37820 **Score:** 95 **Expect:** 0.0002 **Queries matched:** 2

adenosine kinase isoform 1S [Nicotiana tabacum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1679.8254	1678.8181	1678.8274	-0.0093	54	69	0	---	SNVEYIAGGATQNSIR
1679.8254	1678.8181	1678.8274	-0.0093	54	69	0	90	SNVEYIAGGATQNSIR

No match to: 700.4064, 705.4153, 706.4159, 713.4158, 724.4982, 734.4885, 748.4456, 750.5007, 768.5281, 817.4893, 1027.6412, 1133.6895, 1181.6285, 1197.6211, 1279.7637, 1284.7811, 1334.8794, 1424.7104, 1434.8983, 1448.9122, 1523.7798, 1540.7914, 1562.9437, 1618.0626, 1620.8188, 1732.1007, 1748.9111, 1773.8889, 1835.9419, 1835.9419, 1933.0112, 2009.1188, 2061.1099, 2088.9768, 2166.2161, 2261.1279, 2293.1785, 2407.2100, 2418.2239, 2498.1829, 2498.1829, 2512.0852, 2512.0852, 2526.0977, 2544.2825, 2544.2825, 2727.2776, 2752.4912, 3018.8137, 3252.4871, 3274.9487, 3485.6846

4. gi|157356410 **Mass:** 23206 **Score:** 49 **Expect:** 8 **Queries matched:** 8

unnamed protein product [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1181.6285	1180.6212	1180.6604	-0.0392	153	162	0	---	IINPAFHLEK
1284.7811	1283.7738	1283.7178	0.0560	80	89	0	---	VLPFHFHFIK
1523.7798	1522.7725	1522.7310	0.0415	37	49	1	---	CLREQGLAGNSYR
1679.8254	1678.8181	1678.8245	-0.0063	50	63	1	---	LLHGDFKEMSMMLK
1679.8254	1678.8181	1678.8245	-0.0063	50	63	1	---	LLHGDFKEMSMMLK
2293.1785	2292.1712	2292.2088	-0.0376	3	22	0	---	HSSVAISFGFLTVLISCLWR
2544.2825	2543.2752	2543.3318	-0.0566	174	195	1	---	QTHFASQVTVKLLTCAQVFTHK
2544.2825	2543.2752	2543.3318	-0.0566	174	195	1	---	QTHFASQVTVKLLTCAQVFTHK

No match to: 700.4064, 705.4153, 706.4159, 713.4158, 724.4982, 734.4885, 748.4456, 750.5007, 768.5281, 817.4893, 1027.6412, 1133.6895, 1197.6211, 1279.7637, 1334.8794, 1424.7104, 1434.8983, 1448.9122, 1540.7914, 1562.9437, 1618.0626, 1620.8188, 1732.1007, 1748.9111, 1773.8889, 1835.9419, 1835.9419, 1933.0112, 2009.1188, 2061.1099, 2088.9768, 2166.2161, 2261.1279, 2407.2100, 2418.2239, 2498.1829, 2498.1829, 2512.0852, 2512.0852, 2526.0977, 2727.2776, 2752.4912, 3018.8137, 3252.4871, 3274.9487, 3485.6846

5. gi|215766747 **Mass:** 14633 **Score:** 45 **Expect:** 20 **Queries matched:** 7

unnamed protein product [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1835.9419	1834.9346	1834.8936	0.0410	70	84	0	3	SSVHFLNFQVSMFHR
1835.9419	1834.9346	1834.8936	0.0410	70	84	0	---	SSVHFLNFQVSMFHR
2261.1279	2260.1206	2260.1060	0.0146	99	117	0	---	DFFVMSTVGVDMIFITWPR
2293.1785	2292.1712	2292.0958	0.0754	99	117	0	---	DFFVMSTVGVDMIFITWPR + 2 Oxidation (M)
2498.1829	2497.1756	2497.2437	-0.0680	64	84	1	---	QPPSPRSSVHFLNFQVSMFHR
2498.1829	2497.1756	2497.2437	-0.0680	64	84	1	---	QPPSPRSSVHFLNFQVSMFHR

2727.2776 2726.2703 2726.3388 -0.0685 96 - 117 1 --- FFRDFFVMSTVGVDMIFITWPR + Oxidation (M)

No match to: 700.4064, 705.4153, 706.4159, 713.4158, 724.4982, 734.4885, 748.4456, 750.5007, 768.5281, 817.4893, 1027.6412, 1133.6895, 1181.6285, 1197.6211, 1279.7637, 1284.7811, 1334.8794, 1424.7104, 1434.8983, 1448.9122, 1523.7798, 1540.7914, 1562.9437, 1618.0626, 1620.8188, 1679.8254, 1679.8254, 1732.1007, 1748.9111, 1773.8889, 1933.0112, 2009.1188, 2061.1099, 2088.9768, 2166.2161, 2407.2100, 2418.2239, 2512.0852, 2512.0852, 2526.0977, 2544.2825, 2544.2825, 2752.4912, 3018.8137, 3252.4871, 3274.9487, 3485.6846

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 54

Protein View

Match to: **gi|4582787** Score: **144** Expect: **2.4e-009**
adenosine kinase [Zea mays]

Nominal mass (M_r): **36465**; Calculated pI value: **5.23**
NCBI BLAST search of gi|4582787 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Zea mays

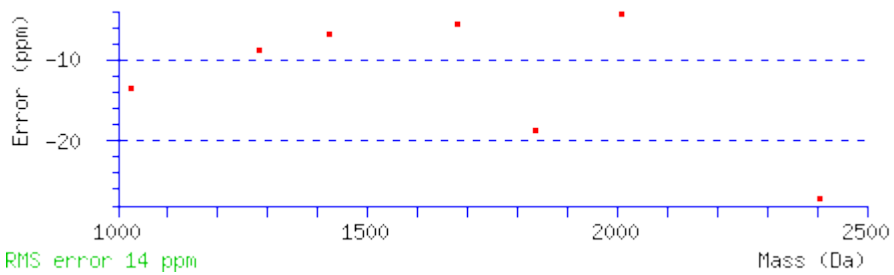
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **29%**

Matched peptides shown in **Bold Red**

```
    1 GNPLLDISAV VDDAFLTKYD IKLNNAILAE EKHLPMYDEL ASKSNVEYIA
   51 GGATQNSIRV AQWMLQTPGA TSYMGCIGKD KFGEEMKKNA QAAGVTAHYY
  101 EDETAPTGTC AVCVVGGERS LIANLSAANC YKSEHLKRPE NWALVEKAKY
  151 IYIAGFFLTV SPDSIQLVAE HAAANNKVFL MNLSAPFICE FFRDAQEKVL
  201 PYADYIFGNE TEAKIFAKVR GWETENIEEI ALKISQLPLA SGKQKRIAVI
  251 TQGADPVVVA EDGKVKTFPV ILLPKEKLVD TNGAGDAFVG GFLSQLVLGK
  301 GIEDCVRAGC YAANVIIQRP GCTYPEKPDF N
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
1 - 22	2407.2100	2406.2027	2406.2682	-0.0654	1	GNPLLDISAVVDDAFLTKYDIK (No match)
44 - 59	1679.8254	1678.8181	1678.8274	-0.0093	0	SNVEYIAGGATQNSIR (No match)
44 - 59	1679.8254	1678.8181	1678.8274	-0.0093	0	SNVEYIAGGATQNSIR (Ions score 90)
120 - 132	1424.7104	1423.7031	1423.7129	-0.0098	0	SLIANLSAANCYK (No match)
133 - 147	1835.9419	1834.9346	1834.9689	-0.0343	1	SEHLKRPENWALVEK (No match)
133 - 147	1835.9419	1834.9346	1834.9689	-0.0343	1	SEHLKRPENWALVEK (No match)
247 - 266	2009.1188	2008.1115	2008.1203	-0.0088	1	IAVITQGADPVVVAEDGKVK (No match)
267 - 275	1027.6412	1026.6339	1026.6477	-0.0138	0	TFPVILLPK (No match)
267 - 277	1284.7811	1283.7738	1283.7852	-0.0114	1	TFPVILLPKEK (No match)



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	Accession	Mass	Score	Description
1.	gi|129916	42153	526	RecName: Full=Phosphoglycerate kinase, cytosolic
2.	gi|28172913	31359	479	cytosolic 3-phosphoglycerate kinase [Hordeum vulgare subsp. vulgare]
3.	gi|28172905	31372	479	cytosolic 3-phosphoglycerate kinase [Triticum urartu]
4.	gi|226509797	42470	428	hypothetical protein LOC100274579 [Zea mays]
5.	gi|148906147	49267	386	unknown [Picea sitchensis]
6.	gi|116787582	53019	384	unknown [Picea sitchensis]
7.	gi|28172907	31321	377	cytosolic 3-phosphoglycerate kinase [Aegilops tauschii subsp. tauschii]
8.	gi|28172915	31663	328	cytosolic 3-phosphoglycerate kinase [Zea mays]
9.	gi|115469436	42310	262	Os06g0668200 [Oryza sativa (japonica cultivar-group)]
10.	gi|115444481	42196	110	Os02g0169300 [Oryza sativa (japonica cultivar-group)]

Results List

1. gi|129916 **Mass:** 42153 **Score:** 526 **Expect:** 1.5e-047 **Queries matched:** 17

RecName: Full=Phosphoglycerate kinase, cytosolic

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1074.6268	1073.6195	1073.6232	-0.0037	192	202	0	---	KPFAAIVGGSK
1190.7333	1189.7260	1189.7295	-0.0034	59	69	0	---	VILASHLGRPK
1190.7333	1189.7260	1189.7295	-0.0034	59	69	0	66	VILASHLGRPK
1446.8817	1445.8744	1445.8830	-0.0086	56	69	1	---	GAKVILASHLGRPK
1493.8259	1492.8186	1492.8224	-0.0037	166	178	0	---	FLRPSVAGFLMQK
1509.8083	1508.8010	1508.8173	-0.0163	166	178	0	61	FLRPSVAGFLMQK + Oxidation (M)
1509.8083	1508.8010	1508.8173	-0.0163	166	178	0	---	FLRPSVAGFLMQK + Oxidation (M)
1673.0125	1672.0052	1672.0147	-0.0095	59	74	1	---	VILASHLGRPKGVTPK
1919.9529	1918.9456	1918.9536	-0.0080	138	155	0	137	LASVADLYVNDAFGTAHR
1919.9529	1918.9456	1918.9536	-0.0080	138	155	0	---	LASVADLYVNDAFGTAHR
1999.9877	1998.9804	1998.9858	-0.0054	24	41	1	---	ADLNVPLDDAQKITDDTR
2048.0525	2047.0452	2047.0486	-0.0034	137	155	1	---	KLASVADLYVNDAFGTAHR
2048.0525	2047.0452	2047.0486	-0.0034	137	155	1	156	KLASVADLYVNDAFGTAHR
2430.2915	2429.2842	2429.2069	0.0774	84	105	0	---	LSELLGLEVVMAPDCIGEEVEK
2475.3206	2474.3133	2474.3103	0.0030	156	178	1	---	AHASTEGVTKFLRPSVAGFLMQK
2863.5044	2862.4971	2862.5465	-0.0494	166	191	1	---	FLRPSVAGFLMQKELDYLVGAVANPK
2879.5137	2878.5064	2878.5414	-0.0350	166	191	1	---	FLRPSVAGFLMQKELDYLVGAVANPK + Oxidation (M)

No match to: 768.5344, 965.5887, 1056.6549, 1056.6549, 1072.6469, 1135.5530, 1184.6486, 1198.5607, 1218.7054, 1359.8188, 1615.9658, 1629.0007, 1721.9082, 1735.0033, 1773.8186, 1813.9727, 1885.1591, 1901.9154, 2078.2683, 2193.1025, 2269.1738, 2371.2629, 2384.2725, 2400.2759, 2404.1797, 2445.3525, 2492.3059, 2515.3169, 2570.4106, 2785.4995, 2788.6926

2. gi|28172913 **Mass:** 31359 **Score:** 479 **Expect:** 7.6e-043 **Queries matched:** 14

cytosolic 3-phosphoglycerate kinase [Hordeum vulgare subsp. vulgare]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1056.6549	1055.6476	1055.6491	-0.0015	1	9	0	47	FSLKPLVPR
1056.6549	1055.6476	1055.6491	-0.0015	1	9	0	---	FSLKPLVPR
1074.6268	1073.6195	1073.6232	-0.0037	118	128	0	---	KPFAAIVGGSK
1493.8259	1492.8186	1492.8224	-0.0037	92	104	0	---	FLRPSVAGFLMQK
1509.8083	1508.8010	1508.8173	-0.0163	92	104	0	61	FLRPSVAGFLMQK + Oxidation (M)
1509.8083	1508.8010	1508.8173	-0.0163	92	104	0	---	FLRPSVAGFLMQK + Oxidation (M)
1919.9529	1918.9456	1918.9536	-0.0080	64	81	0	137	LASVADLYVNDAFGTAHR
1919.9529	1918.9456	1918.9536	-0.0080	64	81	0	---	LASVADLYVNDAFGTAHR
2048.0525	2047.0452	2047.0486	-0.0034	63	81	1	---	KLASVADLYVNDAFGTAHR
2048.0525	2047.0452	2047.0486	-0.0034	63	81	1	156	KLASVADLYVNDAFGTAHR
2445.3525	2444.3452	2444.2178	0.1275	10	31	0	---	LSELLGLEVVMAPDCIGQEVEK + Oxidation (M)
2475.3206	2474.3133	2474.3103	0.0030	82	104	1	---	AHASTEGVTKFLRPSVAGFLMQK
2863.5044	2862.4971	2862.5465	-0.0494	92	117	1	---	FLRPSVAGFLMQKELDYLVGAVANPK
2879.5137	2878.5064	2878.5414	-0.0350	92	117	1	---	FLRPSVAGFLMQKELDYLVGAVANPK + Oxidation (M)

No match to: 768.5344, 965.5887, 1072.6469, 1135.5530, 1184.6486, 1190.7333, 1190.7333, 1198.5607, 1218.7054, 1359.8188, 1446.8817, 1615.9658, 1629.0007, 1673.0125, 1721.9082, 1735.0033, 1773.8186, 1813.9727, 1885.1591, 1901.9154, 1999.9877, 2078.2683, 2193.1025, 2269.1738, 2371.2629, 2384.2725, 2400.2759, 2404.1797, 2430.2915, 2492.3059, 2515.3169, 2570.4106, 2785.4995, 2788.6926

3. gi|28172905 **Mass:** 31372 **Score:** 479 **Expect:** 7.6e-043 **Queries matched:** 14

cytosolic 3-phosphoglycerate kinase [Triticum urartu]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1056.6549	1055.6476	1055.6491	-0.0015	1	9	0	47	FSLKPLVPR
1056.6549	1055.6476	1055.6491	-0.0015	1	9	0	---	FSLKPLVPR
1074.6268	1073.6195	1073.6232	-0.0037	118	128	0	---	KPFAAIVGGSK
1493.8259	1492.8186	1492.8224	-0.0037	92	104	0	---	FLRPSVAGFLMQK
1509.8083	1508.8010	1508.8173	-0.0163	92	104	0	61	FLRPSVAGFLMQK + Oxidation (M)
1509.8083	1508.8010	1508.8173	-0.0163	92	104	0	---	FLRPSVAGFLMQK + Oxidation (M)
1919.9529	1918.9456	1918.9536	-0.0080	64	81	0	137	LASVADLYVNDAFGTAHR
1919.9529	1918.9456	1918.9536	-0.0080	64	81	0	---	LASVADLYVNDAFGTAHR
2048.0525	2047.0452	2047.0486	-0.0034	63	81	1	---	KLASVADLYVNDAFGTAHR
2048.0525	2047.0452	2047.0486	-0.0034	63	81	1	156	KLASVADLYVNDAFGTAHR
2430.2915	2429.2842	2429.2069	0.0774	10	31	0	---	LSELLGLEVVMAPDCIGEEVEK
2475.3206	2474.3133	2474.3103	0.0030	82	104	1	---	AHASTEGVTKFLRPSVAGFLMQK
2863.5044	2862.4971	2862.5465	-0.0494	92	117	1	---	FLRPSVAGFLMQKELDYLVGAVANPK
2879.5137	2878.5064	2878.5414	-0.0350	92	117	1	---	FLRPSVAGFLMQKELDYLVGAVANPK + Oxidation (M)

No match to: 768.5344, 965.5887, 1072.6469, 1135.5530, 1184.6486, 1190.7333, 1190.7333, 1198.5607, 1218.7054, 1359.8188, 1446.8817, 1615.9658, 1629.0007, 1673.0125, 1721.9082, 1735.0033, 1773.8186, 1813.9727, 1885.1591, 1901.9154, 1999.9877, 2078.2683, 2193.1025, 2269.1738, 2371.2629, 2384.2725, 2400.2759, 2404.1797, 2445.3525,

2492.3059, 2515.3169, 2570.4106, 2785.4995, 2788.6926

4. gi|226509797 **Mass:** 42470 **Score:** 428 **Expect:** 9.6e-038 **Queries matched:** 12

hypothetical protein LOC100274579 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1072.6469	1071.6396	1071.6440	-0.0044	75	83	0	---	YSLKPLVPR
1074.6268	1073.6195	1073.6232	-0.0037	192	202	0	---	KPFAAIVGGSK
1190.7333	1189.7260	1189.7295	-0.0034	59	69	0	---	VILASHLGRPK
1190.7333	1189.7260	1189.7295	-0.0034	59	69	0	66	VILASHLGRPK
1446.8817	1445.8744	1445.8830	-0.0086	56	69	1	---	GAKVILASHLGRPK
1673.0125	1672.0052	1672.0147	-0.0095	59	74	1	---	VILASHLGRPKGVTPK
1735.0033	1733.9960	1734.0039	-0.0078	106	122	0	---	LAAALPEGGVLLLENVR
1919.9529	1918.9456	1918.9536	-0.0080	138	155	0	137	LASVADLYVNDAFGTAHR
1919.9529	1918.9456	1918.9536	-0.0080	138	155	0	---	LASVADLYVNDAFGTAHR
1999.9877	1998.9804	1998.9858	-0.0054	24	41	1	---	ADLNVPLDDAQKITDDTR
2048.0525	2047.0452	2047.0486	-0.0034	137	155	1	---	KLASVADLYVNDAFGTAHR
2048.0525	2047.0452	2047.0486	-0.0034	137	155	1	156	KLASVADLYVNDAFGTAHR

No match to: 768.5344, 965.5887, 1056.6549, 1056.6549, 1135.5530, 1184.6486, 1198.5607, 1218.7054, 1359.8188, 1493.8259, 1509.8083, 1509.8083, 1615.9658, 1629.0007, 1721.9082, 1773.8186, 1813.9727, 1885.1591, 1901.9154, 2078.2683, 2193.1025, 2269.1738, 2371.2629, 2384.2725, 2400.2759, 2404.1797, 2430.2915, 2445.3525, 2475.3206, 2492.3059, 2515.3169, 2570.4106, 2785.4995, 2788.6926, 2863.5044, 2879.5137

5. gi|148906147 **Mass:** 49267 **Score:** 386 **Expect:** 1.5e-033 **Queries matched:** 8

unknown [Picea sitchensis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1072.6469	1071.6396	1071.6440	-0.0044	176	184	0	---	YSLKPLVPR
1190.7333	1189.7260	1189.7295	-0.0034	160	170	0	---	VILASHLGRPK
1190.7333	1189.7260	1189.7295	-0.0034	160	170	0	66	VILASHLGRPK
1673.0125	1672.0052	1672.0147	-0.0095	160	175	1	---	VILASHLGRPKGVTPK
1919.9529	1918.9456	1918.9536	-0.0080	239	256	0	137	LASVADLYVNDAFGTAHR
1919.9529	1918.9456	1918.9536	-0.0080	239	256	0	---	LASVADLYVNDAFGTAHR
2048.0525	2047.0452	2047.0486	-0.0034	238	256	1	---	KLASVADLYVNDAFGTAHR
2048.0525	2047.0452	2047.0486	-0.0034	238	256	1	156	KLASVADLYVNDAFGTAHR

No match to: 768.5344, 965.5887, 1056.6549, 1056.6549, 1074.6268, 1135.5530, 1184.6486, 1198.5607, 1218.7054, 1359.8188, 1446.8817, 1493.8259, 1509.8083, 1509.8083, 1615.9658, 1629.0007, 1721.9082, 1735.0033, 1773.8186, 1813.9727, 1885.1591, 1901.9154, 1999.9877, 2078.2683, 2193.1025, 2269.1738, 2371.2629, 2384.2725, 2400.2759, 2404.1797, 2430.2915, 2445.3525, 2475.3206, 2492.3059, 2515.3169, 2570.4106, 2785.4995, 2788.6926, 2863.5044, 2879.5137

6. gi|116787582 **Mass:** 53019 **Score:** 384 **Expect:** 2.4e-033 **Queries matched:** 8

unknown [Picea sitchensis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1072.6469	1071.6396	1071.6440	-0.0044	176	184	0	---	YSLKPLVPR

1190.7333	1189.7260	1189.7295	-0.0034	160 - 170	0	---	VILASHLGRPK
1190.7333	1189.7260	1189.7295	-0.0034	160 - 170	0	66	VILASHLGRPK
1673.0125	1672.0052	1672.0147	-0.0095	160 - 175	1	---	VILASHLGRPKGVTPK
1919.9529	1918.9456	1918.9536	-0.0080	239 - 256	0	137	LASVADLYVNDAFGTAHR
1919.9529	1918.9456	1918.9536	-0.0080	239 - 256	0	---	LASVADLYVNDAFGTAHR
2048.0525	2047.0452	2047.0486	-0.0034	238 - 256	1	---	KLASVADLYVNDAFGTAHR
2048.0525	2047.0452	2047.0486	-0.0034	238 - 256	1	156	KLASVADLYVNDAFGTAHR

No match to: 768.5344, 965.5887, 1056.6549, 1056.6549, 1074.6268, 1135.5530, 1184.6486, 1198.5607, 1218.7054, 1359.8188, 1446.8817, 1493.8259, 1509.8083, 1509.8083, 1615.9658, 1629.0007, 1721.9082, 1735.0033, 1773.8186, 1813.9727, 1885.1591, 1901.9154, 1999.9877, 2078.2683, 2193.1025, 2269.1738, 2371.2629, 2384.2725, 2400.2759, 2404.1797, 2430.2915, 2445.3525, 2475.3206, 2492.3059, 2515.3169, 2570.4106, 2785.4995, 2788.6926, 2863.5044, 2879.5137

7. gi|28172907 **Mass:** 31321 **Score:** 377 **Expect:** 1.2e-032 **Queries matched:** 8

cytosolic 3-phosphoglycerate kinase [Aegilops tauschii subsp. tauschii]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1056.6549	1055.6476	1055.6491	-0.0015	1 -	9	0	47	FSLKPLVPR
1056.6549	1055.6476	1055.6491	-0.0015	1 -	9	0	---	FSLKPLVPR
1074.6268	1073.6195	1073.6232	-0.0037	118 -	128	0	---	KPFAAIVGGSK
1919.9529	1918.9456	1918.9536	-0.0080	64 -	81	0	137	LASVADLYVNDAFGTAHR
1919.9529	1918.9456	1918.9536	-0.0080	64 -	81	0	---	LASVADLYVNDAFGTAHR
2048.0525	2047.0452	2047.0486	-0.0034	63 -	81	1	---	KLASVADLYVNDAFGTAHR
2048.0525	2047.0452	2047.0486	-0.0034	63 -	81	1	156	KLASVADLYVNDAFGTAHR
2430.2915	2429.2842	2429.2069	0.0774	10 -	31	0	---	LSELLGLEVVMAPDCIGEEVEK

No match to: 768.5344, 965.5887, 1072.6469, 1135.5530, 1184.6486, 1190.7333, 1190.7333, 1198.5607, 1218.7054, 1359.8188, 1446.8817, 1493.8259, 1509.8083, 1509.8083, 1615.9658, 1629.0007, 1673.0125, 1721.9082, 1735.0033, 1773.8186, 1813.9727, 1885.1591, 1901.9154, 1999.9877, 2078.2683, 2193.1025, 2269.1738, 2371.2629, 2384.2725, 2400.2759, 2404.1797, 2445.3525, 2475.3206, 2492.3059, 2515.3169, 2570.4106, 2785.4995, 2788.6926, 2863.5044, 2879.5137

8. gi|28172915 **Mass:** 31663 **Score:** 328 **Expect:** 9.6e-028 **Queries matched:** 7

cytosolic 3-phosphoglycerate kinase [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1072.6469	1071.6396	1071.6440	-0.0044	1 -	9	0	---	YSLKPLVPR
1074.6268	1073.6195	1073.6232	-0.0037	118 -	128	0	---	KPFAAIVGGSK
1735.0033	1733.9960	1734.0039	-0.0078	32 -	48	0	---	LAAALPEGGVLLLENVR
1919.9529	1918.9456	1918.9536	-0.0080	64 -	81	0	137	LASVADLYVNDAFGTAHR
1919.9529	1918.9456	1918.9536	-0.0080	64 -	81	0	---	LASVADLYVNDAFGTAHR
2048.0525	2047.0452	2047.0486	-0.0034	63 -	81	1	---	KLASVADLYVNDAFGTAHR
2048.0525	2047.0452	2047.0486	-0.0034	63 -	81	1	156	KLASVADLYVNDAFGTAHR

No match to: 768.5344, 965.5887, 1056.6549, 1056.6549, 1135.5530, 1184.6486, 1190.7333, 1190.7333, 1198.5607, 1218.7054, 1359.8188, 1446.8817, 1493.8259, 1509.8083, 1509.8083, 1615.9658, 1629.0007, 1673.0125, 1721.9082, 1773.8186, 1813.9727, 1885.1591, 1901.9154, 1999.9877, 2078.2683, 2193.1025, 2269.1738, 2371.2629, 2384.2725,

2400.2759, 2404.1797, 2430.2915, 2445.3525, 2475.3206, 2492.3059, 2515.3169, 2570.4106, 2785.4995, 2788.6926, 2863.5044, 2879.5137

9. gi|115469436 **Mass:** 42310 **Score:** 262 **Expect:** 3.8e-021 **Queries matched:** 11

Os06g0668200 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1072.6469	1071.6396	1071.6440	-0.0044	75 -	83	0	---	YSLKPLVPR
1074.6268	1073.6195	1073.6232	-0.0037	192 -	202	0	---	KPFAAIVGGSK
1190.7333	1189.7260	1189.7295	-0.0034	59 -	69	0	---	VILASHLGRPK
1190.7333	1189.7260	1189.7295	-0.0034	59 -	69	0	66	VILASHLGRPK
1446.8817	1445.8744	1445.8830	-0.0086	56 -	69	1	---	GAKVILASHLGRPK
1509.8083	1508.8010	1508.8173	-0.0163	166 -	178	0	---	YLRPSVAGFLMQK
1509.8083	1508.8010	1508.8173	-0.0163	166 -	178	0	---	YLRPSVAGFLMQK
1673.0125	1672.0052	1672.0147	-0.0095	59 -	74	1	---	VILASHLGRPKGVTPK
1919.9529	1918.9456	1918.9536	-0.0080	138 -	155	0	137	LASVADLYVNDAFGTAHR
1919.9529	1918.9456	1918.9536	-0.0080	138 -	155	0	---	LASVADLYVNDAFGTAHR
2879.5137	2878.5064	2878.5414	-0.0350	166 -	191	1	---	YLRPSVAGFLMQKELDYLVGAVANPK

No match to: 768.5344, 965.5887, 1056.6549, 1056.6549, 1135.5530, 1184.6486, 1198.5607, 1218.7054, 1359.8188, 1493.8259, 1615.9658, 1629.0007, 1721.9082, 1735.0033, 1773.8186, 1813.9727, 1885.1591, 1901.9154, 1999.9877, 2048.0525, 2048.0525, 2078.2683, 2193.1025, 2269.1738, 2371.2629, 2384.2725, 2400.2759, 2404.1797, 2430.2915, 2445.3525, 2475.3206, 2492.3059, 2515.3169, 2570.4106, 2785.4995, 2788.6926, 2863.5044

10. gi|115444481 **Mass:** 42196 **Score:** 110 **Expect:** 6.1e-006 **Queries matched:** 8

Os02g0169300 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1072.6469	1071.6396	1071.6440	-0.0044	75 -	83	0	---	YSLKPLVPR
1074.6268	1073.6195	1073.6232	-0.0037	192 -	202	0	---	KPFAAIVGGSK
1190.7333	1189.7260	1189.7295	-0.0034	59 -	69	0	---	VILASHLGRPK
1190.7333	1189.7260	1189.7295	-0.0034	59 -	69	0	66	VILASHLGRPK
1446.8817	1445.8744	1445.8830	-0.0086	56 -	69	1	---	GAKVILASHLGRPK
1673.0125	1672.0052	1672.0147	-0.0095	59 -	74	1	---	VILASHLGRPKGVTPK
1735.0033	1733.9960	1734.0039	-0.0078	106 -	122	0	---	LAAALPEGGVLLLENVR
1999.9877	1998.9804	1998.9858	-0.0054	24 -	41	1	---	ADLNVPLDDAQKITDDTR

No match to: 768.5344, 965.5887, 1056.6549, 1056.6549, 1135.5530, 1184.6486, 1198.5607, 1218.7054, 1359.8188, 1493.8259, 1509.8083, 1509.8083, 1615.9658, 1629.0007, 1721.9082, 1773.8186, 1813.9727, 1885.1591, 1901.9154, 1919.9529, 1919.9529, 2048.0525, 2048.0525, 2078.2683, 2193.1025, 2269.1738, 2371.2629, 2384.2725, 2400.2759, 2404.1797, 2430.2915, 2445.3525, 2475.3206, 2492.3059, 2515.3169, 2570.4106, 2785.4995, 2788.6926, 2863.5044, 2879.5137

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 48

Protein View

Match to: **gi|129916** Score: **526** Expect: **1.5e-047**
RecName: Full=Phosphoglycerate kinase, cytosolic

Nominal mass (M_r): **42153**; Calculated pI value: **5.64**
NCBI BLAST search of gi|129916 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Triticum aestivum
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|21835 from Triticum aestivum

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **31%**

Matched peptides shown in **Bold Red**

```
     1 MATKRSVGTL GEADLKGKKV FVRADLNVPL DDAQKITDDT RIRASIPTIK
    51 YLLEKGAKVI LASHLGRPKG VTPKFSLKPL VARLSELLGL EVVMAPDCIG
   101 EEVEKLAAAL PDGGVLLLEN VRFYKEEEKN DPEFAKKLAS VADLYVNDAF
   151 GTAHRAHAST EGVTKFLRPS VAGFLMQKEL DYLVGAVANP KKPFAAIVGG
   201 SKVSSKIGVI ESLLAKVDIL ILGGGMIFTF YKAQGLAVGK SLVEEDKLEL
   251 ATSLIETAKS KGVKLLLPTD VVVADKFAAD AESKIVPATA IPDGWMGLDV
   301 GPDSIKTFAE ALDTTKTVIW NGPMGVFEFE KFAAGTDAIA KQLAELTGKG
   351 VTTIIGGGDS VAAVEKAGLA DKMSHISTGG GASLELLEGK PLPGVLALDE
   401 A
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
24 - 41	1999.9877	1998.9804	1998.9858	-0.0054	1	**ADLNVPLDDAQKITDDTR** (No match)
56 - 69	1446.8817	1445.8744	1445.8830	-0.0086	1	**GAKVILASHLGRPK** (No match)
59 - 69	1190.7333	1189.7260	1189.7295	-0.0034	0	**VILASHLGRPK** (No match)
59 - 69	1190.7333	1189.7260	1189.7295	-0.0034	0	**VILASHLGRPK** (Ions score 66)
59 - 74	1673.0125	1672.0052	1672.0147	-0.0095	1	**VILASHLGRPKGVTPK** (No match)
84 - 105	2430.2915	2429.2842	2429.2069	0.0774	0	**LSELLGLEVVMAPDCIGEEVEK** (No match)
137 - 155	2048.0525	2047.0452	2047.0486	-0.0034	1	**KLASVADLYVNDAFGTAHR** (No match)
137 - 155	2048.0525	2047.0452	2047.0486	-0.0034	1	**KLASVADLYVNDAFGTAHR** (Ions score 156)
138 - 155	1919.9529	1918.9456	1918.9536	-0.0080	0	**LASVADLYVNDAFGTAHR** (Ions score 137)
138 - 155	1919.9529	1918.9456	1918.9536	-0.0080	0	**LASVADLYVNDAFGTAHR** (No match)
156 - 178	2475.3206	2474.3133	2474.3103	0.0030	1	**AHASTEGVTKFLRPSVAGFLMQK** (No match)
166 - 178	1493.8259	1492.8186	1492.8224	-0.0037	0	**FLRPSVAGFLMQK** (No match)
166 - 178	1509.8083	1508.8010	1508.8173	-0.0163	0	**FLRPSVAGFLMQK** Oxidation (M) (Ions score 61)
166 - 178	1509.8083	1508.8010	1508.8173	-0.0163	0	**FLRPSVAGFLMQK** Oxidation (M) (No match)
166 - 191	2863.5044	2862.4971	2862.5465	-0.0494	1	**FLRPSVAGFLMQKELDYLVGAVANPK** (No match)
166 - 191	2879.5137	2878.5064	2878.5414	-0.0350	1	**FLRPSVAGFLMQKELDYLVGAVANPK** Oxidation (M) (No match)
192 - 202	1074.6268	1073.6195	1073.6232	-0.0037	0	**KPFAAIVGGSK** (No match)

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	Accession	Mass	Score	Description
1.	gi|129916	42153	355	RecName: Full=Phosphoglycerate kinase, cytosolic
2.	gi|28172913	31359	328	cytosolic 3-phosphoglycerate kinase [Hordeum vulgare subsp. vulgare]
3.	gi|28172905	31372	328	cytosolic 3-phosphoglycerate kinase [Triticum urartu]
4.	gi|226509797	42470	270	hypothetical protein LOC100274579 [Zea mays]
5.	gi|148906147	49267	256	unknown [Picea sitchensis]
6.	gi|116787582	53019	255	unknown [Picea sitchensis]
7.	gi|28172907	31321	245	cytosolic 3-phosphoglycerate kinase [Aegilops tauschii subsp. tauschii]
8.	gi|115469436	42310	244	Os06g0668200 [Oryza sativa (japonica cultivar-group)]
9.	gi|28172915	31663	174	cytosolic 3-phosphoglycerate kinase [Zea mays]
10.	gi|225464999	42510	99	PREDICTED: hypothetical protein [Vitis vinifera]

Results List

1. gi|129916 **Mass:** 42153 **Score:** 355 **Expect:** 1.9e-030 **Queries matched:** 11

RecName: Full=Phosphoglycerate kinase, cytosolic

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1190.7489	1189.7416	1189.7295	0.0122	59	69	0	---	VILASHLGRPK
1190.7489	1189.7416	1189.7295	0.0122	59	69	0	74	VILASHLGRPK
1493.8593	1492.8520	1492.8224	0.0297	166	178	0	---	FLRPSVAGFLMQK
1493.8593	1492.8520	1492.8224	0.0297	166	178	0	(43)	FLRPSVAGFLMQK
1509.8480	1508.8407	1508.8173	0.0234	166	178	0	64	FLRPSVAGFLMQK + Oxidation (M)
1509.8480	1508.8407	1508.8173	0.0234	166	178	0	---	FLRPSVAGFLMQK + Oxidation (M)
1920.0026	1918.9953	1918.9536	0.0417	138	155	0	---	LASVADLYVNDAFGTAHR
1920.0026	1918.9953	1918.9536	0.0417	138	155	0	143	LASVADLYVNDAFGTAHR
2000.0443	1999.0370	1998.9858	0.0512	24	41	1	---	ADLNVPLDDAQKITDDTR
2048.1079	2047.1006	2047.0486	0.0520	137	155	1	---	KLASVADLYVNDAFGTAHR
2089.1775	2088.1702	2088.1201	0.0501	241	259	1	---	SLVEEDKLELATSLIETAK

No match to: 1056.6686, 1056.6686, 1735.0465, 1814.0109, 1886.2118, 1901.9751, 2269.2424, 2372.3413

2. gi|28172913 **Mass:** 31359 **Score:** 328 **Expect:** 9.6e-028 **Queries matched:** 10

cytosolic 3-phosphoglycerate kinase [Hordeum vulgare subsp. vulgare]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1056.6686	1055.6613	1055.6491	0.0122	1	9	0	57	FSLKPLVPR
1056.6686	1055.6613	1055.6491	0.0122	1	9	0	---	FSLKPLVPR
1493.8593	1492.8520	1492.8224	0.0297	92	104	0	---	FLRPSVAGFLMQK
1493.8593	1492.8520	1492.8224	0.0297	92	104	0	(43)	FLRPSVAGFLMQK
1509.8480	1508.8407	1508.8173	0.0234	92	104	0	64	FLRPSVAGFLMQK + Oxidation (M)

1509.8480	1508.8407	1508.8173	0.0234	92 - 104	0	---	FLRPSVAGFLMQK + Oxidation (M)
1920.0026	1918.9953	1918.9536	0.0417	64 - 81	0	---	LASVADLYVNDAFGTAHR
1920.0026	1918.9953	1918.9536	0.0417	64 - 81	0	143	LASVADLYVNDAFGTAHR
2048.1079	2047.1006	2047.0486	0.0520	63 - 81	1	---	KLASVADLYVNDAFGTAHR
2089.1775	2088.1702	2088.1201	0.0501	167 - 185	1	---	SLVEEDKLELATSLIETAK

No match to: 1190.7489, 1190.7489, 1735.0465, 1814.0109, 1886.2118, 1901.9751, 2000.0443, 2269.2424, 2372.3413

3. gi|28172905 **Mass:** 31372 **Score:** 328 **Expect:** 9.6e-028 **Queries matched:** 10

cytosolic 3-phosphoglycerate kinase [Triticum urartu]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1056.6686	1055.6613	1055.6491	0.0122	1 -	9	0	57	FSLKPLVPR
1056.6686	1055.6613	1055.6491	0.0122	1 -	9	0	---	FSLKPLVPR
1493.8593	1492.8520	1492.8224	0.0297	92 -	104	0	---	FLRPSVAGFLMQK
1493.8593	1492.8520	1492.8224	0.0297	92 -	104	0	(43)	FLRPSVAGFLMQK
1509.8480	1508.8407	1508.8173	0.0234	92 -	104	0	64	FLRPSVAGFLMQK + Oxidation (M)
1509.8480	1508.8407	1508.8173	0.0234	92 -	104	0	---	FLRPSVAGFLMQK + Oxidation (M)
1920.0026	1918.9953	1918.9536	0.0417	64 -	81	0	---	LASVADLYVNDAFGTAHR
1920.0026	1918.9953	1918.9536	0.0417	64 -	81	0	143	LASVADLYVNDAFGTAHR
2048.1079	2047.1006	2047.0486	0.0520	63 -	81	1	---	KLASVADLYVNDAFGTAHR
2089.1775	2088.1702	2088.1201	0.0501	167 -	185	1	---	SLVEEDKLELATSLIETAK

No match to: 1190.7489, 1190.7489, 1735.0465, 1814.0109, 1886.2118, 1901.9751, 2000.0443, 2269.2424, 2372.3413

4. gi|226509797 **Mass:** 42470 **Score:** 270 **Expect:** 6.1e-022 **Queries matched:** 7

hypothetical protein LOC100274579 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1190.7489	1189.7416	1189.7295	0.0122	59 -	69	0	---	VILASHLGRPK
1190.7489	1189.7416	1189.7295	0.0122	59 -	69	0	74	VILASHLGRPK
1735.0465	1734.0392	1734.0039	0.0354	106 -	122	0	---	LAAALPEGGVLLLENVR
1920.0026	1918.9953	1918.9536	0.0417	138 -	155	0	---	LASVADLYVNDAFGTAHR
1920.0026	1918.9953	1918.9536	0.0417	138 -	155	0	143	LASVADLYVNDAFGTAHR
2000.0443	1999.0370	1998.9858	0.0512	24 -	41	1	---	ADLNVPLDDAQKITDDTR
2048.1079	2047.1006	2047.0486	0.0520	137 -	155	1	---	KLASVADLYVNDAFGTAHR

No match to: 1056.6686, 1056.6686, 1493.8593, 1493.8593, 1509.8480, 1509.8480, 1814.0109, 1886.2118, 1901.9751, 2089.1775, 2269.2424, 2372.3413

5. gi|148906147 **Mass:** 49267 **Score:** 256 **Expect:** 1.5e-020 **Queries matched:** 6

unknown [Picea sitchensis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1190.7489	1189.7416	1189.7295	0.0122	160 -	170	0	---	VILASHLGRPK
1190.7489	1189.7416	1189.7295	0.0122	160 -	170	0	74	VILASHLGRPK
1920.0026	1918.9953	1918.9536	0.0417	239 -	256	0	---	LASVADLYVNDAFGTAHR
1920.0026	1918.9953	1918.9536	0.0417	239 -	256	0	143	LASVADLYVNDAFGTAHR

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
2048.1079	2047.1006	2047.0486	0.0520	238	-	256	1	---	KLASVADLYVNDAFGTAHR
2372.3413	2371.3340	2371.2052	0.1288	433	-	456	1	---	AGLAEKMSHISTGGGASLELLEGK + Oxidation (M)

No match to: 1056.6686, 1056.6686, 1493.8593, 1493.8593, 1509.8480, 1509.8480, 1735.0465, 1814.0109, 1886.2118, 1901.9751, 2000.0443, 2089.1775, 2269.2424

6. gi|116787582 **Mass:** 53019 **Score:** 255 **Expect:** 1.9e-020 **Queries matched:** 6

unknown [Picea sitchensis]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1190.7489	1189.7416	1189.7295	0.0122	160	-	170	0	---	VILASHLGRPK
1190.7489	1189.7416	1189.7295	0.0122	160	-	170	0	74	VILASHLGRPK
1920.0026	1918.9953	1918.9536	0.0417	239	-	256	0	---	LASVADLYVNDAFGTAHR
1920.0026	1918.9953	1918.9536	0.0417	239	-	256	0	143	LASVADLYVNDAFGTAHR
2048.1079	2047.1006	2047.0486	0.0520	238	-	256	1	---	KLASVADLYVNDAFGTAHR
2372.3413	2371.3340	2371.2052	0.1288	468	-	491	1	---	AGLAEKMSHISTGGGASLELLEGK + Oxidation (M)

No match to: 1056.6686, 1056.6686, 1493.8593, 1493.8593, 1509.8480, 1509.8480, 1735.0465, 1814.0109, 1886.2118, 1901.9751, 2000.0443, 2089.1775, 2269.2424

7. gi|28172907 **Mass:** 31321 **Score:** 245 **Expect:** 1.9e-019 **Queries matched:** 6

cytosolic 3-phosphoglycerate kinase [Aegilops tauschii subsp. tauschii]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1056.6686	1055.6613	1055.6491	0.0122	1	-	9	0	57	FSLKPLVPR
1056.6686	1055.6613	1055.6491	0.0122	1	-	9	0	---	FSLKPLVPR
1920.0026	1918.9953	1918.9536	0.0417	64	-	81	0	---	LASVADLYVNDAFGTAHR
1920.0026	1918.9953	1918.9536	0.0417	64	-	81	0	143	LASVADLYVNDAFGTAHR
2048.1079	2047.1006	2047.0486	0.0520	63	-	81	1	---	KLASVADLYVNDAFGTAHR
2089.1775	2088.1702	2088.1201	0.0501	167	-	185	1	---	SLVEEDKLELATSLIETAK

No match to: 1190.7489, 1190.7489, 1493.8593, 1493.8593, 1509.8480, 1509.8480, 1735.0465, 1814.0109, 1886.2118, 1901.9751, 2000.0443, 2269.2424, 2372.3413

8. gi|115469436 **Mass:** 42310 **Score:** 244 **Expect:** 2.4e-019 **Queries matched:** 6

Os06g0668200 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1190.7489	1189.7416	1189.7295	0.0122	59	-	69	0	---	VILASHLGRPK
1190.7489	1189.7416	1189.7295	0.0122	59	-	69	0	74	VILASHLGRPK
1509.8480	1508.8407	1508.8173	0.0234	166	-	178	0	---	YLRPSVAGFLMQK
1509.8480	1508.8407	1508.8173	0.0234	166	-	178	0	---	YLRPSVAGFLMQK
1920.0026	1918.9953	1918.9536	0.0417	138	-	155	0	---	LASVADLYVNDAFGTAHR
1920.0026	1918.9953	1918.9536	0.0417	138	-	155	0	143	LASVADLYVNDAFGTAHR

No match to: 1056.6686, 1056.6686, 1493.8593, 1493.8593, 1735.0465, 1814.0109, 1886.2118, 1901.9751, 2000.0443, 2048.1079, 2089.1775, 2269.2424, 2372.3413

9. gi|28172915 **Mass:** 31663 **Score:** 174 **Expect:** 2.4e-012 **Queries matched:** 4

cytosolic 3-phosphoglycerate kinase [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1735.0465	1734.0392	1734.0039	0.0354	32 -	48	0	---	LAAALPEGGVLLLENVR
1920.0026	1918.9953	1918.9536	0.0417	64 -	81	0	---	LASVADLYVNDAFGTAHR
1920.0026	1918.9953	1918.9536	0.0417	64 -	81	0	143	LASVADLYVNDAFGTAHR
2048.1079	2047.1006	2047.0486	0.0520	63 -	81	1	---	KLASVADLYVNDAFGTAHR

No match to: 1056.6686, 1056.6686, 1190.7489, 1190.7489, 1493.8593, 1493.8593, 1509.8480, 1509.8480, 1814.0109, 1886.2118, 1901.9751, 2000.0443, 2089.1775, 2269.2424, 2372.3413

10. gi|225464999 **Mass:** 42510 **Score:** 99 **Expect:** 7.6e-005 **Queries matched:** 5

PREDICTED: hypothetical protein [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1190.7489	1189.7416	1189.7295	0.0122	59 -	69	0	---	VILASHLGRPK
1190.7489	1189.7416	1189.7295	0.0122	59 -	69	0	74	VILASHLGRPK
1509.8480	1508.8407	1508.8813	-0.0406	262 -	276	0	---	GVSLLLPADVVIADK
1509.8480	1508.8407	1508.8813	-0.0406	262 -	276	0	---	GVSLLLPADVVIADK
2048.1079	2047.1006	2047.1512	-0.0506	51 -	69	1	---	YLMGHGAKVILASHLGRPK

No match to: 1056.6686, 1056.6686, 1493.8593, 1493.8593, 1735.0465, 1814.0109, 1886.2118, 1901.9751, 1920.0026, 1920.0026, 2000.0443, 2089.1775, 2269.2424, 2372.3413

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 19

Protein View

Match to: **gi|129916** Score: **355** Expect: **1.9e-030**
RecName: Full=Phosphoglycerate kinase, cytosolic

Nominal mass (M_r): **42153**; Calculated pI value: **5.64**
NCBI BLAST search of gi|129916 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Triticum aestivum
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|21835 from Triticum aestivum

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **19%**

Matched peptides shown in **Bold Red**

```
   1 MATKRSVGTL GEADLKGKKV FVRADLNVPL DDAQKITDDT RIRASIPTIK
  51 YLLEKGAKVI LASHLGRPKG VTPKFSLKPL VARLSELLGL EVVMAPDCIG
 101 EEVEKLAAAL PDGGVLLLEN VRFYKEEEKN DPEFAKKLAS VADLYVNDAF
 151 GTAHRAHAST EGVTKFLRPS VAGFLMQKEL DYLVGAVANP KKPFAAIVGG
 201 SKVSSKIGVI ESLLAKVDIL ILGGGMIFTF YKAQGLAVGK SLVEEDKLEL
 251 ATSLIETAKS KGVKLLLPTD VVVADKFAAD AESKIVPATA IPDGWMGLDV
 301 GPDSIKTFAE ALDTTKTVIW NGPMGVFEFE KFAAGTDAIA KQLAELTGKG
 351 VTTIIGGGDS VAAVEKAGLA DKMSHISTGG GASLELLEGK PLPGVLALDE
 401 A
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
24 - 41	2000.0443	1999.0370	1998.9858	0.0512	1	ADLNVPLDDAQKITDDTR	(No match)
59 - 69	1190.7489	1189.7416	1189.7295	0.0122	0	VILASHLGRPK	(No match)
59 - 69	1190.7489	1189.7416	1189.7295	0.0122	0	VILASHLGRPK	(Ions score 74)
137 - 155	2048.1079	2047.1006	2047.0486	0.0520	1	KLASVADLYVNDAFGTAHR	(No match)
138 - 155	1920.0026	1918.9953	1918.9536	0.0417	0	LASVADLYVNDAFGTAHR	(No match)
138 - 155	1920.0026	1918.9953	1918.9536	0.0417	0	LASVADLYVNDAFGTAHR	(Ions score 143)
166 - 178	1493.8593	1492.8520	1492.8224	0.0297	0	FLRPSVAGFLMQK	(No match)
166 - 178	1493.8593	1492.8520	1492.8224	0.0297	0	FLRPSVAGFLMQK	(Ions score 43)
166 - 178	1509.8480	1508.8407	1508.8173	0.0234	0	FLRPSVAGFLMQK	Oxidation (M) (Ions score 64)
166 - 178	1509.8480	1508.8407	1508.8173	0.0234	0	FLRPSVAGFLMQK	Oxidation (M) (No match)
241 - 259	2089.1775	2088.1702	2088.1201	0.0501	1	SLVEEDKLELATSLIETAK	(No match)

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	Accession	Mass	Score	Description
1.	gi|129916	42153	416	RecName: Full=Phosphoglycerate kinase, cytosolic
2.	gi|226509797	42470	383	hypothetical protein LOC100274579 [Zea mays]
3.	gi|28172913	31359	370	cytosolic 3-phosphoglycerate kinase [Hordeum vulgare subsp. vulgare]
4.	gi|28172905	31372	370	cytosolic 3-phosphoglycerate kinase [Triticum urartu]
5.	gi|28172907	31321	341	cytosolic 3-phosphoglycerate kinase [Aegilops tauschii subsp. tauschii]
6.	gi|148906147	49267	336	unknown [Picea sitchensis]
7.	gi|116787582	53019	335	unknown [Picea sitchensis]
8.	gi|28172915	31663	292	cytosolic 3-phosphoglycerate kinase [Zea mays]
9.	gi|115469436	42310	242	Os06g0668200 [Oryza sativa (japonica cultivar-group)]
10.	gi|115444481	42196	95	Os02g0169300 [Oryza sativa (japonica cultivar-group)]

Results List

1. gi|129916 **Mass:** 42153 **Score:** 416 **Expect:** 1.5e-036 **Queries matched:** 14

RecName: Full=Phosphoglycerate kinase, cytosolic

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1074.6298	1073.6225	1073.6232	-0.0007	192	202	0	---	KPFAAIVGGSK
1190.7456	1189.7383	1189.7295	0.0089	59	69	0	51	VILASHLGRPK
1190.7456	1189.7383	1189.7295	0.0089	59	69	0	---	VILASHLGRPK
1446.9026	1445.8953	1445.8830	0.0123	56	69	1	---	GAKVILASHLGRPK
1493.8335	1492.8262	1492.8224	0.0039	166	178	0	---	FLRPSVAGFLMQK
1509.8301	1508.8228	1508.8173	0.0055	166	178	0	---	FLRPSVAGFLMQK + Oxidation (M)
1673.0326	1672.0253	1672.0147	0.0106	59	74	1	---	VILASHLGRPKGVTPK
1919.9730	1918.9657	1918.9536	0.0121	138	155	0	130	LASVADLYVNDAFGTAHR
1919.9730	1918.9657	1918.9536	0.0121	138	155	0	---	LASVADLYVNDAFGTAHR
2000.0024	1998.9951	1998.9858	0.0093	24	41	1	---	ADLNVPLDDAQKITDDTR
2048.0701	2047.0628	2047.0486	0.0142	137	155	1	---	KLASVADLYVNDAFGTAHR
2048.0701	2047.0628	2047.0486	0.0142	137	155	1	129	KLASVADLYVNDAFGTAHR
2089.1379	2088.1306	2088.1201	0.0105	241	259	1	---	SLVEEDKLELATSLIETAK
2879.5291	2878.5218	2878.5414	-0.0196	166	191	1	---	FLRPSVAGFLMQKELDYLVGAVANPK + Oxidation (M)

No match to: 768.5340, 1056.6653, 1056.6653, 1359.8193, 1615.9823, 1629.0262, 1735.0209, 1773.8484, 1813.9908, 1885.1748, 1901.9360, 1918.1177, 2269.1921, 2269.1921, 2289.2744, 2371.2925, 2384.3118, 2515.3347, 2570.4302, 2788.7300, 2808.3503

2. gi|226509797 **Mass:** 42470 **Score:** 383 **Expect:** 3e-033 **Queries matched:** 11

hypothetical protein LOC100274579 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1074.6298	1073.6225	1073.6232	-0.0007	192	202	0	---	KPFAAIVGGSK

1190.7456	1189.7383	1189.7295	0.0089	59 - 69	0	51	VILASHLGRPK
1190.7456	1189.7383	1189.7295	0.0089	59 - 69	0	---	VILASHLGRPK
1446.9026	1445.8953	1445.8830	0.0123	56 - 69	1	---	GAKVILASHLGRPK
1673.0326	1672.0253	1672.0147	0.0106	59 - 74	1	---	VILASHLGRPKGVTPK
1735.0209	1734.0136	1734.0039	0.0098	106 - 122	0	---	LAAALPEGGVLLLENVR
1919.9730	1918.9657	1918.9536	0.0121	138 - 155	0	130	LASVADLYVNDAFGTAHR
1919.9730	1918.9657	1918.9536	0.0121	138 - 155	0	---	LASVADLYVNDAFGTAHR
2000.0024	1998.9951	1998.9858	0.0093	24 - 41	1	---	ADLNVPLDDAQKITDDTR
2048.0701	2047.0628	2047.0486	0.0142	137 - 155	1	---	KLASVADLYVNDAFGTAHR
2048.0701	2047.0628	2047.0486	0.0142	137 - 155	1	129	KLASVADLYVNDAFGTAHR

No match to: 768.5340, 1056.6653, 1056.6653, 1359.8193, 1493.8335, 1509.8301, 1615.9823, 1629.0262, 1773.8484, 1813.9908, 1885.1748, 1901.9360, 1918.1177, 2089.1379, 2269.1921, 2269.1921, 2289.2744, 2371.2925, 2384.3118, 2515.3347, 2570.4302, 2788.7300, 2808.3503, 2879.5291

3. gi|28172913 **Mass:** 31359 **Score:** 370 **Expect:** 6.1e-032 **Queries matched:** 11

cytosolic 3-phosphoglycerate kinase [Hordeum vulgare subsp. vulgare]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1056.6653	1055.6580	1055.6491	0.0089	1 -	9	0	38	FSLKPLVPR
1056.6653	1055.6580	1055.6491	0.0089	1 -	9	0	---	FSLKPLVPR
1074.6298	1073.6225	1073.6232	-0.0007	118 -	128	0	---	KPFAAIVGGSK
1493.8335	1492.8262	1492.8224	0.0039	92 -	104	0	---	FLRPSVAGFLMQK
1509.8301	1508.8228	1508.8173	0.0055	92 -	104	0	---	FLRPSVAGFLMQK + Oxidation (M)
1919.9730	1918.9657	1918.9536	0.0121	64 -	81	0	130	LASVADLYVNDAFGTAHR
1919.9730	1918.9657	1918.9536	0.0121	64 -	81	0	---	LASVADLYVNDAFGTAHR
2048.0701	2047.0628	2047.0486	0.0142	63 -	81	1	---	KLASVADLYVNDAFGTAHR
2048.0701	2047.0628	2047.0486	0.0142	63 -	81	1	129	KLASVADLYVNDAFGTAHR
2089.1379	2088.1306	2088.1201	0.0105	167 -	185	1	---	SLVEEDKLELATSLIETAK
2879.5291	2878.5218	2878.5414	-0.0196	92 -	117	1	---	FLRPSVAGFLMQKELDYLVGAVANPK + Oxidation (M)

No match to: 768.5340, 1190.7456, 1190.7456, 1359.8193, 1446.9026, 1615.9823, 1629.0262, 1673.0326, 1735.0209, 1773.8484, 1813.9908, 1885.1748, 1901.9360, 1918.1177, 2000.0024, 2269.1921, 2269.1921, 2289.2744, 2371.2925, 2384.3118, 2515.3347, 2570.4302, 2788.7300, 2808.3503

4. gi|28172905 **Mass:** 31372 **Score:** 370 **Expect:** 6.1e-032 **Queries matched:** 11

cytosolic 3-phosphoglycerate kinase [Triticum urartu]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1056.6653	1055.6580	1055.6491	0.0089	1 -	9	0	38	FSLKPLVPR
1056.6653	1055.6580	1055.6491	0.0089	1 -	9	0	---	FSLKPLVPR
1074.6298	1073.6225	1073.6232	-0.0007	118 -	128	0	---	KPFAAIVGGSK
1493.8335	1492.8262	1492.8224	0.0039	92 -	104	0	---	FLRPSVAGFLMQK
1509.8301	1508.8228	1508.8173	0.0055	92 -	104	0	---	FLRPSVAGFLMQK + Oxidation (M)
1919.9730	1918.9657	1918.9536	0.0121	64 -	81	0	130	LASVADLYVNDAFGTAHR
1919.9730	1918.9657	1918.9536	0.0121	64 -	81	0	---	LASVADLYVNDAFGTAHR

2048.0701	2047.0628	2047.0486	0.0142	63 - 81	1	---	KLASVADLYVNDAFGTAHR
2048.0701	2047.0628	2047.0486	0.0142	63 - 81	1	129	KLASVADLYVNDAFGTAHR
2089.1379	2088.1306	2088.1201	0.0105	167 - 185	1	---	SLVEEDKLELATSLIETAK
2879.5291	2878.5218	2878.5414	-0.0196	92 - 117	1	---	FLRPSVAGFLMQKELDYLVGAVANPK + Oxidation (M)

No match to: 768.5340, 1190.7456, 1190.7456, 1359.8193, 1446.9026, 1615.9823, 1629.0262, 1673.0326, 1735.0209, 1773.8484, 1813.9908, 1885.1748, 1901.9360, 1918.1177, 2000.0024, 2269.1921, 2269.1921, 2289.2744, 2371.2925, 2384.3118, 2515.3347, 2570.4302, 2788.7300, 2808.3503

5. gi|28172907 **Mass:** 31321 **Score:** 341 **Expect:** 4.8e-029 **Queries matched:** 8

cytosolic 3-phosphoglycerate kinase [Aegilops tauschii subsp. tauschii]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1056.6653	1055.6580	1055.6491	0.0089	1 -	9	0	38	FSLKPLVPR
1056.6653	1055.6580	1055.6491	0.0089	1 -	9	0	---	FSLKPLVPR
1074.6298	1073.6225	1073.6232	-0.0007	118 -	128	0	---	KPFAAIVGGSK
1919.9730	1918.9657	1918.9536	0.0121	64 -	81	0	130	LASVADLYVNDAFGTAHR
1919.9730	1918.9657	1918.9536	0.0121	64 -	81	0	---	LASVADLYVNDAFGTAHR
2048.0701	2047.0628	2047.0486	0.0142	63 -	81	1	---	KLASVADLYVNDAFGTAHR
2048.0701	2047.0628	2047.0486	0.0142	63 -	81	1	129	KLASVADLYVNDAFGTAHR
2089.1379	2088.1306	2088.1201	0.0105	167 -	185	1	---	SLVEEDKLELATSLIETAK

No match to: 768.5340, 1190.7456, 1190.7456, 1359.8193, 1446.9026, 1493.8335, 1509.8301, 1615.9823, 1629.0262, 1673.0326, 1735.0209, 1773.8484, 1813.9908, 1885.1748, 1901.9360, 1918.1177, 2000.0024, 2269.1921, 2269.1921, 2289.2744, 2371.2925, 2384.3118, 2515.3347, 2570.4302, 2788.7300, 2808.3503, 2879.5291

6. gi|148906147 **Mass:** 49267 **Score:** 336 **Expect:** 1.5e-028 **Queries matched:** 7

unknown [Picea sitchensis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1190.7456	1189.7383	1189.7295	0.0089	160 -	170	0	51	VILASHLGRPK
1190.7456	1189.7383	1189.7295	0.0089	160 -	170	0	---	VILASHLGRPK
1673.0326	1672.0253	1672.0147	0.0106	160 -	175	1	---	VILASHLGRPKGVTPK
1919.9730	1918.9657	1918.9536	0.0121	239 -	256	0	130	LASVADLYVNDAFGTAHR
1919.9730	1918.9657	1918.9536	0.0121	239 -	256	0	---	LASVADLYVNDAFGTAHR
2048.0701	2047.0628	2047.0486	0.0142	238 -	256	1	---	KLASVADLYVNDAFGTAHR
2048.0701	2047.0628	2047.0486	0.0142	238 -	256	1	129	KLASVADLYVNDAFGTAHR

No match to: 768.5340, 1056.6653, 1056.6653, 1074.6298, 1359.8193, 1446.9026, 1493.8335, 1509.8301, 1615.9823, 1629.0262, 1735.0209, 1773.8484, 1813.9908, 1885.1748, 1901.9360, 1918.1177, 2000.0024, 2089.1379, 2269.1921, 2269.1921, 2289.2744, 2371.2925, 2384.3118, 2515.3347, 2570.4302, 2788.7300, 2808.3503, 2879.5291

7. gi|116787582 **Mass:** 53019 **Score:** 335 **Expect:** 1.9e-028 **Queries matched:** 7

unknown [Picea sitchensis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1190.7456	1189.7383	1189.7295	0.0089	160 -	170	0	51	VILASHLGRPK
1190.7456	1189.7383	1189.7295	0.0089	160 -	170	0	---	VILASHLGRPK

1673.0326	1672.0253	1672.0147	0.0106	160 - 175	1	---	VILASHLGRPKGVTPK
1919.9730	1918.9657	1918.9536	0.0121	239 - 256	0	130	LASVADLYVNDAFGTAHR
1919.9730	1918.9657	1918.9536	0.0121	239 - 256	0	---	LASVADLYVNDAFGTAHR
2048.0701	2047.0628	2047.0486	0.0142	238 - 256	1	---	KLASVADLYVNDAFGTAHR
2048.0701	2047.0628	2047.0486	0.0142	238 - 256	1	129	KLASVADLYVNDAFGTAHR

No match to: 768.5340, 1056.6653, 1056.6653, 1074.6298, 1359.8193, 1446.9026, 1493.8335, 1509.8301, 1615.9823, 1629.0262, 1735.0209, 1773.8484, 1813.9908, 1885.1748, 1901.9360, 1918.1177, 2000.0024, 2089.1379, 2269.1921, 2269.1921, 2289.2744, 2371.2925, 2384.3118, 2515.3347, 2570.4302, 2788.7300, 2808.3503, 2879.5291

8. gi|28172915 **Mass:** 31663 **Score:** 292 **Expect:** 3.8e-024 **Queries matched:** 6

cytosolic 3-phosphoglycerate kinase [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1074.6298	1073.6225	1073.6232	-0.0007	118 -	128	0	---	KPFAAIVGGSK
1735.0209	1734.0136	1734.0039	0.0098	32 -	48	0	---	LAAALPEGGVLLLENVR
1919.9730	1918.9657	1918.9536	0.0121	64 -	81	0	130	LASVADLYVNDAFGTAHR
1919.9730	1918.9657	1918.9536	0.0121	64 -	81	0	---	LASVADLYVNDAFGTAHR
2048.0701	2047.0628	2047.0486	0.0142	63 -	81	1	---	KLASVADLYVNDAFGTAHR
2048.0701	2047.0628	2047.0486	0.0142	63 -	81	1	129	KLASVADLYVNDAFGTAHR

No match to: 768.5340, 1056.6653, 1056.6653, 1190.7456, 1190.7456, 1359.8193, 1446.9026, 1493.8335, 1509.8301, 1615.9823, 1629.0262, 1673.0326, 1773.8484, 1813.9908, 1885.1748, 1901.9360, 1918.1177, 2000.0024, 2089.1379, 2269.1921, 2269.1921, 2289.2744, 2371.2925, 2384.3118, 2515.3347, 2570.4302, 2788.7300, 2808.3503, 2879.5291

9. gi|115469436 **Mass:** 42310 **Score:** 242 **Expect:** 3.8e-019 **Queries matched:** 9

Os06g0668200 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1074.6298	1073.6225	1073.6232	-0.0007	192 -	202	0	---	KPFAAIVGGSK
1190.7456	1189.7383	1189.7295	0.0089	59 -	69	0	51	VILASHLGRPK
1190.7456	1189.7383	1189.7295	0.0089	59 -	69	0	---	VILASHLGRPK
1446.9026	1445.8953	1445.8830	0.0123	56 -	69	1	---	GAKVILASHLGRPK
1509.8301	1508.8228	1508.8173	0.0055	166 -	178	0	---	YLRPSVAGFLMQK
1673.0326	1672.0253	1672.0147	0.0106	59 -	74	1	---	VILASHLGRPKGVTPK
1919.9730	1918.9657	1918.9536	0.0121	138 -	155	0	130	LASVADLYVNDAFGTAHR
1919.9730	1918.9657	1918.9536	0.0121	138 -	155	0	---	LASVADLYVNDAFGTAHR
2879.5291	2878.5218	2878.5414	-0.0196	166 -	191	1	---	YLRPSVAGFLMQKELDYLVGAVANPK

No match to: 768.5340, 1056.6653, 1056.6653, 1359.8193, 1493.8335, 1615.9823, 1629.0262, 1735.0209, 1773.8484, 1813.9908, 1885.1748, 1901.9360, 1918.1177, 2000.0024, 2048.0701, 2048.0701, 2089.1379, 2269.1921, 2269.1921, 2289.2744, 2371.2925, 2384.3118, 2515.3347, 2570.4302, 2788.7300, 2808.3503

10. gi|115444481 **Mass:** 42196 **Score:** 95 **Expect:** 0.00018 **Queries matched:** 7

Os02g0169300 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1074.6298	1073.6225	1073.6232	-0.0007	192 -	202	0	---	KPFAAIVGGSK

1190.7456	1189.7383	1189.7295	0.0089	59 - 69	0	51	VILASHLGRPK
1190.7456	1189.7383	1189.7295	0.0089	59 - 69	0	---	VILASHLGRPK
1446.9026	1445.8953	1445.8830	0.0123	56 - 69	1	---	GAKVILASHLGRPK
1673.0326	1672.0253	1672.0147	0.0106	59 - 74	1	---	VILASHLGRPKGVTPK
1735.0209	1734.0136	1734.0039	0.0098	106 - 122	0	---	LAAALPEGGVLLLENVR
2000.0024	1998.9951	1998.9858	0.0093	24 - 41	1	---	ADLNVPLDDAQKITDDTR

No match to: 768.5340, 1056.6653, 1056.6653, 1359.8193, 1493.8335, 1509.8301, 1615.9823, 1629.0262, 1773.8484, 1813.9908, 1885.1748, 1901.9360, 1918.1177, 1919.9730, 1919.9730, 2048.0701, 2048.0701, 2089.1379, 2269.1921, 2269.1921, 2289.2744, 2371.2925, 2384.3118, 2515.3347, 2570.4302, 2788.7300, 2808.3503, 2879.5291

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 35

Protein View

Match to: **gi|129916** Score: **416** Expect: **1.5e-036**
RecName: Full=Phosphoglycerate kinase, cytosolic

Nominal mass (M_r): **42153**; Calculated pI value: **5.64**
NCBI BLAST search of gi|129916 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Triticum aestivum
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|21835 from Triticum aestivum

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **27%**

Matched peptides shown in **Bold Red**

```
   1 MATKRSVGTL GEADLKGKKV FVRADLNVPL DDAQKITDDT RIRASIPTIK
  51 YLLEKGAKVI LASHLGRPKG VTPKFSLKPL VARLSELLGL EVVMAPDCIG
 101 EEVEKLAAAL PDGGVLLLEN VRFYKEEEKN DPEFAKKLAS VADLYVNDAF
 151 GTAHRAHAST EGVTKFLRPS VAGFLMQKEL DYLVGAVANP KKPFAAIVGG
 201 SKVSSKIGVI ESLLAKVDIL ILGGGMIFTF YKAQGLAVGK SLVEEDKLEL
 251 ATSLIETAKS KGVKLLLPTD VVVADKFAAD AESKIVPATA IPDGWMGLDV
 301 GPDSIKTFAE ALDTTKTVIW NGPMGVFEFE KFAAGTDAIA KQLAELTGKG
 351 VTTIIGGGDS VAAVEKAGLA DKMSHISTGG GASLELLEGK PLPGVLALDE
 401 A
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
24 - 41	2000.0024	1998.9951	1998.9858	0.0093	1	**ADLNVPLDDAQKITDDTR** (No match)
56 - 69	1446.9026	1445.8953	1445.8830	0.0123	1	**GAKVILASHLGRPK** (No match)
59 - 69	1190.7456	1189.7383	1189.7295	0.0089	0	**VILASHLGRPK** (Ions score 51)
59 - 69	1190.7456	1189.7383	1189.7295	0.0089	0	**VILASHLGRPK** (No match)
59 - 74	1673.0326	1672.0253	1672.0147	0.0106	1	**VILASHLGRPKGVTPK** (No match)
137 - 155	2048.0701	2047.0628	2047.0486	0.0142	1	**KLASVADLYVNDAFGTAHR** (No match)
137 - 155	2048.0701	2047.0628	2047.0486	0.0142	1	**KLASVADLYVNDAFGTAHR** (Ions score 129)
138 - 155	1919.9730	1918.9657	1918.9536	0.0121	0	**LASVADLYVNDAFGTAHR** (Ions score 130)
138 - 155	1919.9730	1918.9657	1918.9536	0.0121	0	**LASVADLYVNDAFGTAHR** (No match)
166 - 178	1493.8335	1492.8262	1492.8224	0.0039	0	**FLRPSVAGFLMQK** (No match)
166 - 178	1509.8301	1508.8228	1508.8173	0.0055	0	**FLRPSVAGFLMQK** Oxidation (M) (No match)
166 - 191	2879.5291	2878.5218	2878.5414	-0.0196	1	**FLRPSVAGFLMQKELDYLVGAVANPK** Oxidation (M) (No match)
192 - 202	1074.6298	1073.6225	1073.6232	-0.0007	0	**KPFAAIVGGSK** (No match)
241 - 259	2089.1379	2088.1306	2088.1201	0.0105	1	**SLVEEDKLELATSLIETAK** (No match)

Spot 57

Index

	Accession	Mass	Score	Description
1.	gi|76573373	33722	234	succinyl-CoA ligase beta subunit-like protein [Solanum tuberosum]
2.	gi|27803873	45154	229	succinyl CoA ligase beta subunit [Lycopersicon esculentum]
3.	gi|83284007	45625	229	succinyl CoA ligase beta subunit-like protein [Solanum tuberosum]
4.	gi|146215968	45538	131	succinyl-CoA ligase beta subunit [Caragana jubata]
5.	gi|115488132	22542	53	Os12g0272100 [Oryza sativa (japonica cultivar-group)]
6.	gi|224084233	13187	52	predicted protein [Populus trichocarpa]
7.	gi|125555376	13948	49	hypothetical protein OsI_23016 [Oryza sativa Indica Group]
8.	gi|168045131	154678	48	predicted protein [Physcomitrella patens subsp. patens]
9.	gi|115441223	20850	47	Os01g0864000 [Oryza sativa (japonica cultivar-group)]
10.	gi|89179423	98557	45	hypothetical protein 20.t00010 [Asparagus officinalis]

Results List

1. gi|76573373 **Mass:** 33722 **Score:** 234 **Expect:** 2.4e-018 **Queries matched:** 5

succinyl-CoA ligase beta subunit-like protein [Solanum tuberosum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1198.5455	1197.5382	1197.5414	-0.0032	141	150	0	---	LNFDDNAAYR
1198.5455	1197.5382	1197.5414	-0.0032	141	150	0	92	LNFDDNAAYR
1454.6985	1453.6912	1453.6949	-0.0037	141	152	1	---	LNFDDNAAYRQK
1866.9397	1865.9324	1865.9271	0.0053	134	150	1	119	LVAADAKLNFDDNAAYR
1866.9397	1865.9324	1865.9271	0.0053	134	150	1	---	LVAADAKLNFDDNAAYR

No match to: 768.5286, 801.4528, 802.4584, 987.5643, 1004.5873, 1046.5718, 1234.7466, 1251.7679, 1503.8102, 1588.7675, 1604.7607, 2094.1184, 2260.1458, 2372.2190, 2388.2175, 2432.3662, 2432.3662, 2449.3843, 2449.3843, 2500.2781, 2513.3630, 2513.3630, 2516.3364

2. gi|27803873 **Mass:** 45154 **Score:** 229 **Expect:** 7.6e-018 **Queries matched:** 5

succinyl CoA ligase beta subunit [Lycopersicon esculentum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1198.5455	1197.5382	1197.5414	-0.0032	247	256	0	---	LNFDDNAAYR
1198.5455	1197.5382	1197.5414	-0.0032	247	256	0	92	LNFDDNAAYR
1454.6985	1453.6912	1453.6949	-0.0037	247	258	1	---	LNFDDNAAYRQK
1866.9397	1865.9324	1865.9271	0.0053	240	256	1	119	LVAADAKLNFDDNAAYR
1866.9397	1865.9324	1865.9271	0.0053	240	256	1	---	LVAADAKLNFDDNAAYR

No match to: 768.5286, 801.4528, 802.4584, 987.5643, 1004.5873, 1046.5718, 1234.7466, 1251.7679, 1503.8102, 1588.7675, 1604.7607, 2094.1184, 2260.1458, 2372.2190, 2388.2175, 2432.3662, 2432.3662, 2449.3843, 2449.3843, 2500.2781, 2513.3630, 2513.3630, 2516.3364

3. gi|83284007 **Mass:** 45625 **Score:** 229 **Expect:** 7.6e-018 **Queries matched:** 5

succinyl CoA ligase beta subunit-like protein [Solanum tuberosum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1198.5455	1197.5382	1197.5414	-0.0032	251	260	0	---	LNFDDNAAYR
1198.5455	1197.5382	1197.5414	-0.0032	251	260	0	92	LNFDDNAAYR
1454.6985	1453.6912	1453.6949	-0.0037	251	262	1	---	LNFDDNAAYRQK
1866.9397	1865.9324	1865.9271	0.0053	244	260	1	119	LVAADAKLNFDDNAAYR
1866.9397	1865.9324	1865.9271	0.0053	244	260	1	---	LVAADAKLNFDDNAAYR

No match to: 768.5286, 801.4528, 802.4584, 987.5643, 1004.5873, 1046.5718, 1234.7466, 1251.7679, 1503.8102, 1588.7675, 1604.7607, 2094.1184, 2260.1458, 2372.2190, 2388.2175, 2432.3662, 2432.3662, 2449.3843, 2449.3843, 2500.2781, 2513.3630, 2513.3630, 2516.3364

4. gi|146215968 **Mass:** 45538 **Score:** 131 **Expect:** 4.8e-008 **Queries matched:** 6

succinyl-CoA ligase beta subunit [Caragana jubata]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1198.5455	1197.5382	1197.5414	-0.0032	251	260	0	---	LNFDDNAAYR
1198.5455	1197.5382	1197.5414	-0.0032	251	260	0	92	LNFDDNAAYR
1454.6985	1453.6912	1453.6949	-0.0037	251	262	1	---	LNFDDNAAYRQK
1503.8102	1502.8029	1502.8530	-0.0501	346	359	0	---	VEAILVNIFGGIMK
1604.7607	1603.7534	1603.8317	-0.0783	64	77	1	---	DVFANQNEVVVKSR
2260.1458	2259.1385	2259.2547	-0.1162	339	359	1	---	ILTADDKVEAILVNIFGGIMK

No match to: 768.5286, 801.4528, 802.4584, 987.5643, 1004.5873, 1046.5718, 1234.7466, 1251.7679, 1588.7675, 1866.9397, 1866.9397, 2094.1184, 2372.2190, 2388.2175, 2432.3662, 2432.3662, 2449.3843, 2449.3843, 2500.2781, 2513.3630, 2513.3630, 2516.3364

5. gi|115488132 **Mass:** 22542 **Score:** 53 **Expect:** 3 **Queries matched:** 5

Os12g0272100 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1866.9397	1865.9324	1865.9172	0.0152	121	136	1	---	YEHRSNFVPPPPSPSR
1866.9397	1865.9324	1865.9172	0.0152	121	136	1	---	YEHRSNFVPPPPSPSR
2260.1458	2259.1385	2259.1681	-0.0296	138	159	0	---	QGLNIGTSAAFMQVTSSVVPPR
2432.3662	2431.3589	2431.2641	0.0948	138	160	1	---	QGLNIGTSAAFMQVTSSVVPPRR + Oxidation (M)
2432.3662	2431.3589	2431.2641	0.0948	137	159	1	8	RQGLNIGTSAAFMQVTSSVVPPR + Oxidation (M)

No match to: 768.5286, 801.4528, 802.4584, 987.5643, 1004.5873, 1046.5718, 1198.5455, 1198.5455, 1234.7466, 1251.7679, 1454.6985, 1503.8102, 1588.7675, 1604.7607, 2094.1184, 2372.2190, 2388.2175, 2449.3843, 2449.3843, 2500.2781, 2513.3630, 2513.3630, 2516.3364

6. gi|224084233 **Mass:** 13187 **Score:** 52 **Expect:** 3.6 **Queries matched:** 5

predicted protein [Populus trichocarpa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1604.7607	1603.7534	1603.8205	-0.0671	23	36	1	---	APQSFSENEKLNLK
2372.2190	2371.2117	2371.1114	0.1004	84	105	0	---	AFQALAASSLDQENMASAYQQK
2388.2175	2387.2102	2387.1063	0.1040	84	105	0	---	AFQALAASSLDQENMASAYQQK + Oxidation (M)

2500.2781	2499.2708	2499.2063	0.0645	83 - 105	1	---	KAFQALAASSLDQENMASAYQQK
2516.3364	2515.3291	2515.3007	0.0285	1 - 22	1	---	MGHFLLSFIYPSPKTMSFVVSK

No match to: 768.5286, 801.4528, 802.4584, 987.5643, 1004.5873, 1046.5718, 1198.5455, 1198.5455, 1234.7466, 1251.7679, 1454.6985, 1503.8102, 1588.7675, 1866.9397, 1866.9397, 2094.1184, 2260.1458, 2432.3662, 2432.3662, 2449.3843, 2449.3843, 2513.3630, 2513.3630

7. gi|125555376 **Mass:** 13948 **Score:** 49 **Expect:** 8.6 **Queries matched:** 5

hypothetical protein OsI_23016 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
768.5286	767.5213	767.5017	0.0196	27 -	33	1	---	LVVPGRK
801.4528	800.4455	800.4252	0.0203	74 -	81	1	---	ERGGLGGR
802.4584	801.4511	801.4245	0.0266	58 -	64	1	---	GWQAKGR
987.5643	986.5570	986.5005	0.0566	76 -	87	1	---	GGLGGRGGSGGR
1604.7607	1603.7534	1603.7338	0.0196	46 -	62	1	---	STGDGSGGPGSRGWQAK

No match to: 1004.5873, 1046.5718, 1198.5455, 1198.5455, 1234.7466, 1251.7679, 1454.6985, 1503.8102, 1588.7675, 1866.9397, 1866.9397, 2094.1184, 2260.1458, 2372.2190, 2388.2175, 2432.3662, 2432.3662, 2449.3843, 2449.3843, 2500.2781, 2513.3630, 2513.3630, 2516.3364

8. gi|168045131 **Mass:** 154678 **Score:** 48 **Expect:** 11 **Queries matched:** 10

predicted protein [Physcomitrella patens subsp. patens]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
768.5286	767.5213	767.5269	-0.0055	999 -	1005	0	---	GIKPLIK
802.4584	801.4511	801.4232	0.0279	988 -	995	0	---	SIGPSVDK
987.5643	986.5570	986.5508	0.0062	884 -	892	1	---	LGDLNARTK
1004.5873	1003.5800	1003.5670	0.0130	829 -	836	1	---	MMNKVLLR
1198.5455	1197.5382	1197.6142	-0.0760	1130 -	1138	1	---	ETKWEHIQK
1198.5455	1197.5382	1197.6142	-0.0760	1130 -	1138	1	---	ETKWEHIQK
1251.7679	1250.7606	1250.6982	0.0624	256 -	266	1	---	YVSSIQVARTK
1503.8102	1502.8029	1502.7075	0.0955	893 -	905	0	---	EGSFETLMFLASR + Oxidation (M)
2500.2781	2499.2708	2499.2315	0.0393	1358 -	1380	1	---	SSSRQILSQFLPLGSVSEMYSPS
2516.3364	2515.3291	2515.3362	-0.0070	319 -	340	0	---	VEVSLRPLYGPIASLYDIYGYK

No match to: 801.4528, 1046.5718, 1234.7466, 1454.6985, 1588.7675, 1604.7607, 1866.9397, 1866.9397, 2094.1184, 2260.1458, 2372.2190, 2388.2175, 2432.3662, 2432.3662, 2449.3843, 2449.3843, 2513.3630, 2513.3630

9. gi|115441223 **Mass:** 20850 **Score:** 47 **Expect:** 12 **Queries matched:** 5

Os01g0864000 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1604.7607	1603.7534	1603.8253	-0.0718	188 -	201	1	---	DATMHAILLNRVNH
2388.2175	2387.2102	2387.1955	0.0148	1 -	21	1	---	QAQVAQRLLHVDDHGVHGHDR
2449.3843	2448.3770	2448.5056	-0.1286	163 -	184	1	---	LRRPLDSQRPLLPAVPLPVLAK
2449.3843	2448.3770	2448.5056	-0.1286	163 -	184	1	---	LRRPLDSQRPLLPAVPLPVLAK
2500.2781	2499.2708	2499.1332	0.1376	46 -	75	1	---	GAGGGAAGAGAAGDEAEAEAAASAAEAGRR

No match to: 768.5286, 801.4528, 802.4584, 987.5643, 1004.5873, 1046.5718, 1198.5455, 1198.5455, 1234.7466, 1251.7679, 1454.6985, 1503.8102, 1588.7675, 1866.9397, 1866.9397, 2094.1184, 2260.1458, 2372.2190, 2432.3662, 2432.3662, 2513.3630, 2513.3630, 2516.3364

10. gi|89179423 **Mass:** 98557 **Score:** 45 **Expect:** 19 **Queries matched:** 8

hypothetical protein 20.t00010 [Asparagus officinalis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
987.5643	986.5570	986.5145	0.0426	211	219	1	---	ESGSVQPKR
1503.8102	1502.8029	1502.8317	-0.0288	441	453	1	---	TRTGAIRPVNYQK
1588.7675	1587.7602	1587.8580	-0.0977	322	335	1	---	VSSQVSDLRELLSR
2094.1184	2093.1111	2093.0462	0.0649	390	408	1	---	KTAEAEYPQVTINMIGQGK + Oxidation (M)
2260.1458	2259.1385	2259.1681	-0.0296	496	514	0	---	VDEHHVMLQAQQETLLQLK
2388.2175	2387.2102	2387.2695	-0.0593	73	95	1	---	ALSFGQELKLALLAEDPTSASAR
2432.3662	2431.3589	2431.2641	0.0948	495	514	1	---	RVDEHHVMLQAQQETLLQLK + Oxidation (M)
2432.3662	2431.3589	2431.2641	0.0948	495	514	1	---	RVDEHHVMLQAQQETLLQLK + Oxidation (M)

No match to: 768.5286, 801.4528, 802.4584, 1004.5873, 1046.5718, 1198.5455, 1198.5455, 1234.7466, 1251.7679, 1454.6985, 1604.7607, 1866.9397, 1866.9397, 2372.2190, 2449.3843, 2449.3843, 2500.2781, 2513.3630, 2513.3630, 2516.3364

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 28

Protein View

Match to: **gi|76573373** Score: **234** Expect: **2.4e-018**
succinyl-CoA ligase beta subunit-like protein [Solanum tuberosum]

Nominal mass (M_r): **33722**; Calculated pI value: **4.87**
NCBI BLAST search of gi|76573373 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Solanum tuberosum

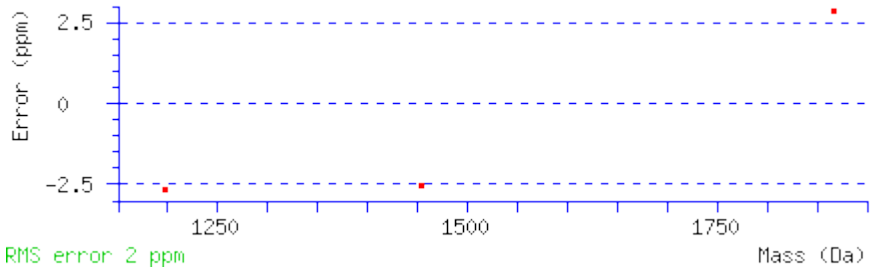
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **6%**

Matched peptides shown in **Bold Red**

```
    1 MLGQMLVTKQ TGAQGKVVSK VYLCEKMSLV NEMYFSIILD RATAGPLIIA
   51 CRKGGTSIED LAEKFPDMII KVPIDVFKGI SDEDAAKVVD GLAPKVADRN
  101 DSIEQVKKLY NLFCETDCTM LEINPLAETS DNKLVAADAK LNFDDNAAYR
  151 QKEIFSLRDS SQEDPREVAA AKADLNYIGL DGEIGCMVNG AGLAMATMDI
  201 IKLHGGTPAN FLDVGGNATE GQVVEAFKIL TADEKVKAIL VNIFGGIMKC
  251 DVIASGIVNA AKQVQLKVPV IVRLEGTNVE QGKRILKESG MKLITAEDLD
  301 DAAEKAVKAL A
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
134 - 150	1866.9397	1865.9324	1865.9271	0.0053	1	LVAADAKLNFDDNAAYR	(Ions score 119)
134 - 150	1866.9397	1865.9324	1865.9271	0.0053	1	LVAADAKLNFDDNAAYR	(No match)
141 - 150	1198.5455	1197.5382	1197.5414	-0.0032	0	LNFDDNAAYR	(No match)
141 - 150	1198.5455	1197.5382	1197.5414	-0.0032	0	LNFDDNAAYR	(Ions score 92)
141 - 152	1454.6985	1453.6912	1453.6949	-0.0037	1	LNFDDNAAYRQK	(No match)



Spot 58

Index

	Accession	Mass	Score	Description
1.	gi|125583637	46268	87	hypothetical protein OsJ_08330 [Oryza sativa Japonica Group]
2.	gi|115448599	48315	76	Os02g0741200 [Oryza sativa (japonica cultivar-group)]
3.	gi|224081931	63298	61	predicted protein [Populus trichocarpa]
4.	gi|152003254	55286	59	(S)-N-methylcoclaurine-3'-hydroxylase [Coptis chinensis]
5.	gi|222618186	104658	54	hypothetical protein OsJ_01275 [Oryza sativa Japonica Group]
6.	gi|218187788	14410	51	hypothetical protein OsI_00973 [Oryza sativa Indica Group]
7.	gi|116056879	49571	48	unnamed protein product [Ostreococcus tauri]
8.	gi|9971208	55032	48	(S)-N-methylcoclaurine-3'-hydroxylase [Coptis japonica]
9.	gi|157359830	2817	48	unnamed protein product [Vitis vinifera]
10.	gi|224123468	10262	44	predicted protein [Populus trichocarpa]

Results List

1. gi|125583637 **Mass:** 46268 **Score:** 87 **Expect:** 0.0014 **Queries matched:** 8

hypothetical protein OsJ_08330 [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
875.5130	874.5057	874.5024	0.0033	381	387	1	---	RTQPFVK
1267.6949	1266.6876	1266.7407	-0.0531	59	73	0	---	AIVAGAAVAGAAVAR
1329.6777	1328.6704	1328.6870	-0.0166	150	162	0	---	QMANPTTAAGVLR
1345.6866	1344.6793	1344.6819	-0.0026	150	162	0	---	QMANPTTAAGVLR + Oxidation (M)
1470.6659	1469.6586	1469.6609	-0.0023	126	137	0	42	LSPDYYAQTCPR
1470.6659	1469.6586	1469.6609	-0.0023	126	137	0	---	LSPDYYAQTCPR
1826.8331	1825.8258	1825.8417	-0.0159	126	140	1	---	LSPDYYAQTCPRAER
1826.8331	1825.8258	1825.8417	-0.0159	126	140	1	10	LSPDYYAQTCPRAER

No match to: 768.5347, 801.4731, 929.5572, 986.5854, 1187.6769, 1308.6554, 1312.6703, 1328.6448, 1378.6145, 1378.6145, 1486.6553, 1523.7795, 1534.7015, 1813.0037, 1813.0037, 1825.8046, 1828.9818, 1841.7904, 1857.7968, 1911.9114, 1941.1030, 1957.0912, 2256.0757, 2256.0757, 2357.2041, 2572.3315

2. gi|115448599 **Mass:** 48315 **Score:** 76 **Expect:** 0.015 **Queries matched:** 7

Os02g0741200 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
875.5130	874.5057	874.5024	0.0033	397	403	1	---	RTQPFVK
1329.6777	1328.6704	1328.6870	-0.0166	166	178	0	---	QMANPTTAAGVLR
1345.6866	1344.6793	1344.6819	-0.0026	166	178	0	---	QMANPTTAAGVLR + Oxidation (M)
1470.6659	1469.6586	1469.6609	-0.0023	142	153	0	42	LSPDYYAQTCPR
1470.6659	1469.6586	1469.6609	-0.0023	142	153	0	---	LSPDYYAQTCPR
1826.8331	1825.8258	1825.8417	-0.0159	142	156	1	---	LSPDYYAQTCPRAER
1826.8331	1825.8258	1825.8417	-0.0159	142	156	1	10	LSPDYYAQTCPRAER

No match to: 768.5347, 801.4731, 929.5572, 986.5854, 1187.6769, 1267.6949, 1308.6554, 1312.6703, 1328.6448, 1378.6145, 1378.6145, 1486.6553, 1523.7795, 1534.7015, 1813.0037, 1813.0037, 1825.8046, 1828.9818, 1841.7904, 1857.7968, 1911.9114, 1941.1030, 1957.0912, 2256.0757, 2256.0757, 2357.2041, 2572.3315

3. gi|224081931 **Mass:** 63298 **Score:** 61 **Expect:** 0.52 **Queries matched:** 11

predicted protein [Populus trichocarpa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
875.5130	874.5057	874.4773	0.0285	424	431	1	---	GRVYGAPR
1312.6703	1311.6630	1311.6419	0.0212	22	33	1	---	STSSKSFQTPSR
1329.6777	1328.6704	1328.6217	0.0488	393	403	1	---	MEMISKYGTNR
1345.6866	1344.6793	1344.6166	0.0628	393	403	1	---	MEMISKYGTNR + Oxidation (M)
1470.6659	1469.6586	1469.7150	-0.0564	38	50	0	---	GSTFQQPVYQTSK
1470.6659	1469.6586	1469.6674	-0.0088	244	255	0	---	YSFPEEDESIVR
1486.6553	1485.6480	1485.7207	-0.0726	387	398	1	---	VVENYKMEMISK + Oxidation (M)
1826.8331	1825.8258	1825.8635	-0.0376	359	374	0	---	EPPWDDVFSALHQSAK
1826.8331	1825.8258	1825.8958	-0.0700	35	50	1	---	NNKGSTFQQPVYQTSK
2256.0757	2255.0684	2255.0382	0.0303	244	261	1	---	YSFPEEDESIVRNIWEDK
2256.0757	2255.0684	2255.0382	0.0303	244	261	1	---	YSFPEEDESIVRNIWEDK

No match to: 768.5347, 801.4731, 929.5572, 986.5854, 1187.6769, 1267.6949, 1308.6554, 1328.6448, 1378.6145, 1378.6145, 1523.7795, 1534.7015, 1813.0037, 1813.0037, 1825.8046, 1828.9818, 1841.7904, 1857.7968, 1911.9114, 1941.1030, 1957.0912, 2357.2041, 2572.3315

4. gi|152003254 **Mass:** 55286 **Score:** 59 **Expect:** 0.86 **Queries matched:** 10

(S)-N-methylcoclaurine-3'-hydroxylase [Coptis chinensis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
875.5130	874.5057	874.4759	0.0298	158	165	1	---	SKEGEVVK
1378.6145	1377.6072	1377.6676	-0.0604	412	424	0	---	GNDFELIPFGGGR
1378.6145	1377.6072	1377.6676	-0.0604	412	424	0	---	GNDFELIPFGGGR
1534.7015	1533.6942	1533.7687	-0.0745	412	425	1	---	GNDFELIPFGGGRR
1813.0037	1811.9964	1811.8909	0.1055	360	374	1	---	RALETCTVMNYTIPK + Oxidation (M)
1813.0037	1811.9964	1811.8909	0.1055	360	374	1	---	RALETCTVMNYTIPK + Oxidation (M)
1857.7968	1856.7895	1856.9057	-0.1161	388	402	1	---	DPKTWDDPLNFKPER
2256.0757	2255.0684	2255.1949	-0.1265	330	348	1	1	ESDLPHLPYLQAFVKETLR
2256.0757	2255.0684	2255.1949	-0.1265	330	348	1	---	ESDLPHLPYLQAFVKETLR
2572.3315	2571.3242	2571.2281	0.0961	391	411	1	---	TWDDPLNFKPERFLSSDVDYK

No match to: 768.5347, 801.4731, 929.5572, 986.5854, 1187.6769, 1267.6949, 1308.6554, 1312.6703, 1328.6448, 1329.6777, 1345.6866, 1470.6659, 1470.6659, 1486.6553, 1523.7795, 1825.8046, 1826.8331, 1826.8331, 1828.9818, 1841.7904, 1911.9114, 1941.1030, 1957.0912, 2357.2041

5. gi|222618186 **Mass:** 104658 **Score:** 54 **Expect:** 2.4 **Queries matched:** 11

hypothetical protein OsJ_01275 [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide

801.4731	800.4658	800.4392	0.0267	361 - 367	0	---	DGLLVER
875.5130	874.5057	874.5024	0.0033	732 - 739	0	---	NVIFAVGR
929.5572	928.5499	928.5090	0.0410	880 - 887	1	---	DGRLAELR
986.5854	985.5781	985.5133	0.0648	376 - 383	1	---	WYKHGAPK
1328.6448	1327.6375	1327.6480	-0.0105	110 - 121	1	---	HGRASISSQEEK
1378.6145	1377.6072	1377.5520	0.0553	889 - 901	0	---	GADGCGGGWEWAR
1378.6145	1377.6072	1377.5520	0.0553	889 - 901	0	---	GADGCGGGWEWAR
1534.7015	1533.6942	1533.6531	0.0412	888 - 901	1	---	RGADGCGGGWEWAR
1841.7904	1840.7831	1840.8825	-0.0993	576 - 590	1	---	SIDINFHMRVMHADR
1857.7968	1856.7895	1856.8774	-0.0878	576 - 590	1	---	SIDINFHMRVMHADR + Oxidation (M)
2357.2041	2356.1968	2356.3365	-0.1397	255 - 275	1	---	KLFLSITNGSLVEVTELQPLR

No match to: 768.5347, 1187.6769, 1267.6949, 1308.6554, 1312.6703, 1329.6777, 1345.6866, 1470.6659, 1470.6659, 1486.6553, 1523.7795, 1813.0037, 1813.0037, 1825.8046, 1826.8331, 1826.8331, 1828.9818, 1911.9114, 1941.1030, 1957.0912, 2256.0757, 2256.0757, 2572.3315

6. gi|218187788 **Mass:** 14410 **Score:** 51 **Expect:** 5.2 **Queries matched:** 5

hypothetical protein OsI_00973 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
801.4731	800.4658	800.4140	0.0518	75 -	81	0	---	VNAVNER
929.5572	928.5499	928.5090	0.0410	74 -	81	1	---	KVNAVNER
1267.6949	1266.6876	1266.6945	-0.0069	49 -	58	1	---	HARYQLVQPR
1312.6703	1311.6630	1311.6531	0.0099	5 -	16	1	---	ELDAANTSHAKR
2572.3315	2571.3242	2571.3002	0.0240	104 -	128	1	---	VKTYAGAVDPLPESMPTQAAVTPGR + Oxidation (M)

No match to: 768.5347, 875.5130, 986.5854, 1187.6769, 1308.6554, 1328.6448, 1329.6777, 1345.6866, 1378.6145, 1378.6145, 1470.6659, 1470.6659, 1486.6553, 1523.7795, 1534.7015, 1813.0037, 1813.0037, 1825.8046, 1826.8331, 1826.8331, 1828.9818, 1841.7904, 1857.7968, 1911.9114, 1941.1030, 1957.0912, 2256.0757, 2256.0757, 2357.2041

7. gi|116056879 **Mass:** 49571 **Score:** 48 **Expect:** 8.8 **Queries matched:** 9

unnamed protein product [Ostreococcus tauri]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
875.5130	874.5057	874.4760	0.0298	130 -	137	0	---	SVQELTAK
1312.6703	1311.6630	1311.7510	-0.0879	138 -	149	1	---	NGALVKELEALR
1329.6777	1328.6704	1328.6935	-0.0231	169 -	179	1	---	NVELAEEIEKR
1378.6145	1377.6072	1377.6749	-0.0676	296 -	308	0	---	GVQDAPGNLQSHR
1378.6145	1377.6072	1377.6749	-0.0676	296 -	308	0	5	GVQDAPGNLQSHR
1534.7015	1533.6942	1533.7760	-0.0817	296 -	309	1	---	GVQDAPGNLQSHRR
1813.0037	1811.9964	1811.8835	0.1129	150 -	166	1	---	HELEDGKMAISGLDAAR
1813.0037	1811.9964	1811.8835	0.1129	150 -	166	1	---	HELEDGKMAISGLDAAR
1828.9818	1827.9745	1827.8784	0.0961	150 -	166	1	---	HELEDGKMAISGLDAAR + Oxidation (M)

No match to: 768.5347, 801.4731, 929.5572, 986.5854, 1187.6769, 1267.6949, 1308.6554, 1328.6448, 1345.6866, 1470.6659, 1470.6659, 1486.6553, 1523.7795, 1825.8046, 1826.8331, 1826.8331, 1841.7904, 1857.7968, 1911.9114, 1941.1030, 1957.0912, 2256.0757, 2256.0757, 2357.2041, 2572.3315

8. gi|9971208 **Mass:** 55032 **Score:** 48 **Expect:** 9.2 **Queries matched:** 9

(S)-N-methylcoclaurine-3'-hydroxylase [Coptis japonica]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1378.6145	1377.6072	1377.6676	-0.0604	412 -	424	0	---	GNDFELIPFGGGR
1378.6145	1377.6072	1377.6676	-0.0604	412 -	424	0	---	GNDFELIPFGGGR
1534.7015	1533.6942	1533.7687	-0.0745	412 -	425	1	---	GNDFELIPFGGGRR
1813.0037	1811.9964	1811.8909	0.1055	360 -	374	1	---	RALETCTVMNYTIPK + Oxidation (M)
1813.0037	1811.9964	1811.8909	0.1055	360 -	374	1	---	RALETCTVMNYTIPK + Oxidation (M)
1857.7968	1856.7895	1856.9057	-0.1161	388 -	402	1	---	DPKTWDDPLNFKPER
2256.0757	2255.0684	2255.1949	-0.1265	330 -	348	1	1	ESDLPHLPYLQAFVKETLR
2256.0757	2255.0684	2255.1949	-0.1265	330 -	348	1	---	ESDLPHLPYLQAFVKETLR
2572.3315	2571.3242	2571.2281	0.0961	391 -	411	1	---	TWDDPLNFKPERFLSSDVDYK

No match to: 768.5347, 801.4731, 875.5130, 929.5572, 986.5854, 1187.6769, 1267.6949, 1308.6554, 1312.6703, 1328.6448, 1329.6777, 1345.6866, 1470.6659, 1470.6659, 1486.6553, 1523.7795, 1825.8046, 1826.8331, 1826.8331, 1828.9818, 1841.7904, 1911.9114, 1941.1030, 1957.0912, 2357.2041

9. gi|157359830 **Mass:** 2817 **Score:** 48 **Expect:** 11 **Queries matched:** 3

unnamed protein product [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
986.5854	985.5781	985.5920	-0.0138	2 -	11	0	---	LATGLLVGSR
1328.6448	1327.6375	1327.7149	-0.0774	15 -	25	0	---	WNPVRPVQPVH
1523.7795	1522.7722	1522.8289	-0.0567	1 -	14	1	---	MLATGLLVGSRFSR + Oxidation (M)

No match to: 768.5347, 801.4731, 875.5130, 929.5572, 1187.6769, 1267.6949, 1308.6554, 1312.6703, 1329.6777, 1345.6866, 1378.6145, 1378.6145, 1470.6659, 1470.6659, 1486.6553, 1534.7015, 1813.0037, 1813.0037, 1825.8046, 1826.8331, 1826.8331, 1828.9818, 1841.7904, 1857.7968, 1911.9114, 1941.1030, 1957.0912, 2256.0757, 2256.0757, 2357.2041, 2572.3315

10. gi|224123468 **Mass:** 10262 **Score:** 44 **Expect:** 23 **Queries matched:** 5

predicted protein [Populus trichocarpa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
986.5854	985.5781	985.5556	0.0226	28 -	36	1	---	NNGLAIEKK
1187.6769	1186.6696	1186.6808	-0.0112	58 -	67	1	---	IEIVLEKSEK
1911.9114	1910.9041	1910.8567	0.0474	68 -	85	0	---	FDSLMNAVSSAPEEEAAK + Oxidation (M)
2256.0757	2255.0684	2255.0263	0.0422	65 -	85	1	---	SEKFDSLMNAVSSAPEEEAAK + Oxidation (M)
2256.0757	2255.0684	2255.0263	0.0422	65 -	85	1	---	SEKFDSLMNAVSSAPEEEAAK + Oxidation (M)

No match to: 768.5347, 801.4731, 875.5130, 929.5572, 1267.6949, 1308.6554, 1312.6703, 1328.6448, 1329.6777, 1345.6866, 1378.6145, 1378.6145, 1470.6659, 1470.6659, 1486.6553, 1523.7795, 1534.7015, 1813.0037, 1813.0037, 1825.8046, 1826.8331, 1826.8331, 1828.9818, 1841.7904, 1857.7968, 1941.1030, 1957.0912, 2357.2041, 2572.3315

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 34

Protein View

Match to: **gi|125583637** Score: **87** Expect: **0.0014**
hypothetical protein OsJ_08330 [Oryza sativa Japonica Group]

Nominal mass (M_r): **46268**; Calculated pI value: **6.25**
NCBI BLAST search of gi|125583637 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Oryza sativa Japonica Group

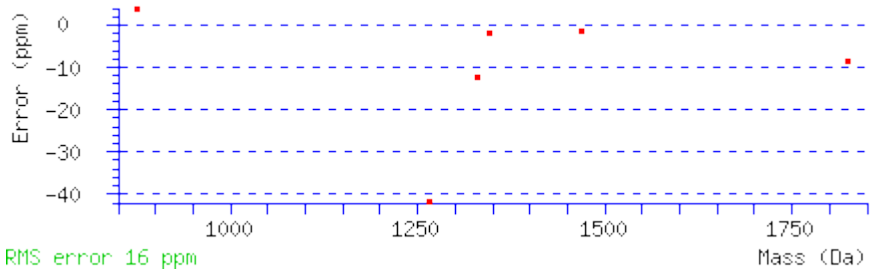
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **11%**

Matched peptides shown in **Bold Red**

```
     1 MRPSFLLLLV VFAGVLAGGA RAGPPLAGEN LPGQLLPGEK PPGQPLPGAA
    51 VAGATVARAI VAGAAVAGAA VARAIVAGAA FGQSLPGQPL PGQPLVGEKP
   101 PGQPLVPGQP LVGEKPPGQP LGGDKLSPDY YAQTCPRAER IVAEVVQSKQ
   151 MANPTTAAGV LRLFFHDCFV SGCDASVLVA ATAFEKSEQS AEINHSLPGD
   201 AFDAVVRAKL ALELECPEVV SCADILALAA RVLITMTGGP RYPISFGRKD
   251 SLTSSPTAPD KEMPQSNFTM DQVIKLFQDK GFTVQEMVAL SGGHTLGFSH
   301 CKEFAQRIYD YQGKPGNVDP TMNPVLSKGL QTACKEYLKD PTIAAFNDVM
   351 TPGKFDNMYF VNLERGLGLL ATDEEMWSDK RTQPFVKLYA SNPTAFFDDF
   401 SRAIDKLSLF GVKTGAAGEI RRRCDTYNHG PMPK
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
59 - 73	1267.6949	1266.6876	1266.7407	-0.0531	0	**AIVAGAAVAGAAVAR** (No match)
126 - 137	1470.6659	1469.6586	1469.6609	-0.0023	0	**LSPDYYAQTCPR** (Ions score 42)
126 - 137	1470.6659	1469.6586	1469.6609	-0.0023	0	**LSPDYYAQTCPR** (No match)
126 - 140	1826.8331	1825.8258	1825.8417	-0.0159	1	**LSPDYYAQTCPRAER** (No match)
126 - 140	1826.8331	1825.8258	1825.8417	-0.0159	1	**LSPDYYAQTCPRAER** (Ions score 10)
150 - 162	1329.6777	1328.6704	1328.6870	-0.0166	0	**QMANPTTAAGVLR** (No match)
150 - 162	1345.6866	1344.6793	1344.6819	-0.0026	0	**QMANPTTAAGVLR** Oxidation (M) (No match)
381 - 387	875.5130	874.5057	874.5024	0.0033	1	**RTQPFVK** (No match)



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	Accession	Mass	Score	Description
1.	gi|5419990	25028	380	putative fructose-bisphosphate aldolase [Phleum pratense]
2.	gi|218157	39151	290	cytoplasmic aldolase [Oryza sativa Japonica Group]
3.	gi|110288655	39137	289	Fructose-bisphosphate aldolase, cytoplasmic isozyme, putative, expressed [Oryza sativa (japonic
4.	gi|125548604	39099	289	hypothetical protein OsI_16195 [Oryza sativa Indica Group]
5.	gi|2213867	38362	233	fructose-biphosphate aldolase [Mesembryanthemum crystallinum]

Results List

1. gi|5419990 **Mass:** 25028 **Score:** 380 **Expect:** 6e-033 **Queries matched:** 12

putative fructose-bisphosphate aldolase [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
707.3981	706.3908	706.3914	-0.0006	8	12	1	---	FAKWR
829.3873	828.3800	828.3766	0.0035	1	7	0	---	YYEAGAR
932.5661	931.5588	931.5603	-0.0014	187	194	1	---	AQKAFLVR
1175.5872	1174.5799	1174.5770	0.0029	1	10	1	---	YYEAGARFAK
1371.7255	1370.7182	1370.7135	0.0048	157	167	0	---	KPWFLSFSFGR
1646.7933	1645.7860	1645.7843	0.0017	65	78	0	---	CAYVTEVVLAACYK
1842.0037	1840.9964	1840.9987	-0.0023	153	167	1	---	LQTKKPWFLSFSFGR
2108.0693	2107.0620	2107.0657	-0.0037	17	36	0	132	IGPNEPSQLSIDQNAQGLAR
2108.0693	2107.0620	2107.0657	-0.0037	17	36	0	---	IGPNEPSQLSIDQNAQGLAR
2519.3511	2518.3438	2518.3503	-0.0064	13	36	1	138	AVLKIGPNEPSQLSIDQNAQGLAR
2519.3511	2518.3438	2518.3503	-0.0064	13	36	1	---	AVLKIGPNEPSQLSIDQNAQGLAR
2706.3247	2705.3174	2705.3143	0.0031	197	223	1	---	ANSEATLGTYKGDATLGEGASESLHVK

No match to: 713.4079, 724.4917, 750.5140, 768.5206, 838.5289, 886.9874, 1118.6782, 1171.5227, 1188.5472, 1279.7628, 1334.8818, 1346.7317, 1346.7317, 1448.9081, 1474.8251, 1474.8251, 1488.8026, 1517.7474, 1603.7975, 1616.7971, 1645.2821, 1646.2751, 1662.8142, 1662.8142, 1845.0188, 1973.1145, 2003.0433, 2146.1096, 2190.1541, 2429.1951, 2461.3135, 2473.3079, 2771.3965, 2977.4219, 2995.4661, 3060.6577

2. gi|218157 **Mass:** 39151 **Score:** 290 **Expect:** 6e-024 **Queries matched:** 11

cytoplasmic aldolase [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
707.3981	706.3908	706.3914	-0.0006	140	144	1	---	FAKWR
829.3873	828.3800	828.3766	0.0035	133	139	0	---	YYEAGAR
1175.5872	1174.5799	1174.5770	0.0029	133	142	1	---	YYEAGARFAK
1346.7317	1345.7244	1345.7241	0.0003	238	249	0	83	VAPEVIAEYTVR
1346.7317	1345.7244	1345.7241	0.0003	238	249	0	---	VAPEVIAEYTVR
1474.8251	1473.8178	1473.8190	-0.0012	237	249	1	109	KVAPEVIAEYTVR

1474.8251	1473.8178	1473.8190	-0.0012	237 - 249	1	---	KVAPEVIAEYTVR
1488.8026	1487.7953	1487.7943	0.0010	25 - 39	1	---	GILAADESTGTIGKR
1662.8142	1661.8069	1661.8121	-0.0051	40 - 53	1	38	FASINVENVEDNRR
1662.8142	1661.8069	1661.8121	-0.0051	40 - 53	1	---	FASINVENVEDNRR
1845.0188	1844.0115	1844.0155	-0.0040	238 - 253	1	---	VAPEVIAEYTVRTLQR

No match to: 713.4079, 724.4917, 750.5140, 768.5206, 838.5289, 886.9874, 932.5661, 1118.6782, 1171.5227, 1188.5472, 1279.7628, 1334.8818, 1371.7255, 1448.9081, 1517.7474, 1603.7975, 1616.7971, 1645.2821, 1646.2751, 1646.7933, 1842.0037, 1973.1145, 2003.0433, 2108.0693, 2108.0693, 2146.1096, 2190.1541, 2429.1951, 2461.3135, 2473.3079, 2519.3511, 2519.3511, 2706.3247, 2771.3965, 2977.4219, 2995.4661, 3060.6577

3. gi|110288655 **Mass:** 39137 **Score:** 289 **Expect:** 7.6e-024 **Queries matched:** 11

Fructose-bisphosphate aldolase, cytoplasmic isozyme, putative, expressed [Oryza sativa (japonica cu

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
707.3981	706.3908	706.3914	-0.0006	140 - 144	1	---	FAKWR
829.3873	828.3800	828.3766	0.0035	133 - 139	0	---	YYEAGAR
1175.5872	1174.5799	1174.5770	0.0029	133 - 142	1	---	YYEAGARFAK
1346.7317	1345.7244	1345.7241	0.0003	238 - 249	0	83	VAPEVIAEYTVR
1346.7317	1345.7244	1345.7241	0.0003	238 - 249	0	---	VAPEVIAEYTVR
1474.8251	1473.8178	1473.8190	-0.0012	237 - 249	1	109	KVAPEVIAEYTVR
1474.8251	1473.8178	1473.8190	-0.0012	237 - 249	1	---	KVAPEVIAEYTVR
1488.8026	1487.7953	1487.7943	0.0010	25 - 39	1	---	GILAADESTGTIGKR
1662.8142	1661.8069	1661.8121	-0.0051	40 - 53	1	38	FASINVENVEDNRR
1662.8142	1661.8069	1661.8121	-0.0051	40 - 53	1	---	FASINVENVEDNRR
1845.0188	1844.0115	1844.0155	-0.0040	238 - 253	1	---	VAPEVIAEYTVRTLQR

No match to: 713.4079, 724.4917, 750.5140, 768.5206, 838.5289, 886.9874, 932.5661, 1118.6782, 1171.5227, 1188.5472, 1279.7628, 1334.8818, 1371.7255, 1448.9081, 1517.7474, 1603.7975, 1616.7971, 1645.2821, 1646.2751, 1646.7933, 1842.0037, 1973.1145, 2003.0433, 2108.0693, 2108.0693, 2146.1096, 2190.1541, 2429.1951, 2461.3135, 2473.3079, 2519.3511, 2519.3511, 2706.3247, 2771.3965, 2977.4219, 2995.4661, 3060.6577

4. gi|125548604 **Mass:** 39099 **Score:** 289 **Expect:** 7.6e-024 **Queries matched:** 11

hypothetical protein OsI_16195 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
707.3981	706.3908	706.3914	-0.0006	140 - 144	1	---	FAKWR
829.3873	828.3800	828.3766	0.0035	133 - 139	0	---	YYEAGAR
1175.5872	1174.5799	1174.5770	0.0029	133 - 142	1	---	YYEAGARFAK
1346.7317	1345.7244	1345.7241	0.0003	238 - 249	0	83	VAPEVIAEYTVR
1346.7317	1345.7244	1345.7241	0.0003	238 - 249	0	---	VAPEVIAEYTVR
1474.8251	1473.8178	1473.8190	-0.0012	237 - 249	1	109	KVAPEVIAEYTVR
1474.8251	1473.8178	1473.8190	-0.0012	237 - 249	1	---	KVAPEVIAEYTVR
1488.8026	1487.7953	1487.7943	0.0010	25 - 39	1	---	GILAADESTGTIGKR
1662.8142	1661.8069	1661.8121	-0.0051	40 - 53	1	38	FASINVENVEDNRR
1662.8142	1661.8069	1661.8121	-0.0051	40 - 53	1	---	FASINVENVEDNRR

1845.0188	1844.0115	1844.0155	-0.0040	238 - 253	1	---	VAPEVIAEYTVRTLQR

No match to: 713.4079, 724.4917, 750.5140, 768.5206, 838.5289, 886.9874, 932.5661, 1118.6782, 1171.5227, 1188.5472, 1279.7628, 1334.8818, 1371.7255, 1448.9081, 1517.7474, 1603.7975, 1616.7971, 1645.2821, 1646.2751, 1646.7933, 1842.0037, 1973.1145, 2003.0433, 2108.0693, 2108.0693, 2146.1096, 2190.1541, 2429.1951, 2461.3135, 2473.3079, 2519.3511, 2519.3511, 2706.3247, 2771.3965, 2977.4219, 2995.4661, 3060.6577

5. gi|2213867 **Mass:** 38362 **Score:** 233 **Expect:** 3e-018 **Queries matched:** 8

fructose-biphosphate aldolase [Mesembryanthemum crystallinum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
707.3981	706.3908	706.3914	-0.0006	140 -	144	1	---	FAKWR
1346.7317	1345.7244	1345.7241	0.0003	238 -	249	0	83	VAPEVIAEYTVR
1346.7317	1345.7244	1345.7241	0.0003	238 -	249	0	---	VAPEVIAEYTVR
1474.8251	1473.8178	1473.8190	-0.0012	237 -	249	1	109	KVAPEVIAEYTVR
1474.8251	1473.8178	1473.8190	-0.0012	237 -	249	1	---	KVAPEVIAEYTVR
1488.8026	1487.7953	1487.7943	0.0010	25 -	39	1	---	GILAADESTGTIGKR
1603.7975	1602.7902	1602.8365	-0.0462	312 -	325	1	---	EENVEKAQAVFLAR
1646.7933	1645.7860	1645.7695	0.0165	337 -	353	0	---	YQGGAGGADASESLHVK

No match to: 713.4079, 724.4917, 750.5140, 768.5206, 829.3873, 838.5289, 886.9874, 932.5661, 1118.6782, 1171.5227, 1175.5872, 1188.5472, 1279.7628, 1334.8818, 1371.7255, 1448.9081, 1517.7474, 1616.7971, 1645.2821, 1646.2751, 1662.8142, 1662.8142, 1842.0037, 1845.0188, 1973.1145, 2003.0433, 2108.0693, 2108.0693, 2146.1096, 2190.1541, 2429.1951, 2461.3135, 2473.3079, 2519.3511, 2519.3511, 2706.3247, 2771.3965, 2977.4219, 2995.4661, 3060.6577

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 48

Protein View

Match to: **gi|5419990** Score: **380** Expect: **6e-033**
putative fructose-bisphosphate aldolase [Phleum pratense]

Nominal mass (M_r): **25028**; Calculated pI value: **7.79**
NCBI BLAST search of gi|5419990 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **44%**

Matched peptides shown in **Bold Red**

```
    1 YYEAGARFAK WRAVLKIGPN EPSQLSIDQN AQGLARYAII CQENGLVPIV
   51 EPEILVDGPH DIDRCAYVTE VVLAACYKAL NDQHVLLEGS LLKPNMVTPG
  101 SDAKKVAPRE SLAEYTVRTL QRTVPPAVPA IVFLSGGQSE EEATVNLNAM
  151 NKLQTKKPWF LSFSFGRALQ QSTLKAWSGK EENVGKAQKA FLVRCKANSE
  201 ATLGTYKGDA TLGEGASESL HVKDYKY
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
1 - 7	829.3873	828.3800	828.3766	0.0035	0	YYEAGAR	(No match)
1 - 10	1175.5872	1174.5799	1174.5770	0.0029	1	YYEAGARFAK	(No match)
8 - 12	707.3981	706.3908	706.3914	-0.0006	1	FAKWR	(No match)
13 - 36	2519.3511	2518.3438	2518.3503	-0.0064	1	AVLKIGPNEPSQLSIDQNAQGLAR	(Ions score 138)
13 - 36	2519.3511	2518.3438	2518.3503	-0.0064	1	AVLKIGPNEPSQLSIDQNAQGLAR	(No match)
17 - 36	2108.0693	2107.0620	2107.0657	-0.0037	0	IGPNEPSQLSIDQNAQGLAR	(Ions score 132)
17 - 36	2108.0693	2107.0620	2107.0657	-0.0037	0	IGPNEPSQLSIDQNAQGLAR	(No match)
65 - 78	1646.7933	1645.7860	1645.7843	0.0017	0	CAYVTEVVLAACYK	(No match)
153 - 167	1842.0037	1840.9964	1840.9987	-0.0023	1	LQTKKPWFLSFSFGR	(No match)
157 - 167	1371.7255	1370.7182	1370.7135	0.0048	0	KPWFLSFSFGR	(No match)
187 - 194	932.5661	931.5588	931.5603	-0.0014	1	AQKAFLVR	(No match)
197 - 223	2706.3247	2705.3174	2705.3143	0.0031	1	ANSEATLGTYKGDATLGEGASESLHVK	(No match)

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	Accession	Mass	Score	Description
1.	gi|5419990	25028	98	putative fructose-bisphosphate aldolase [Phleum pratense]
2.	gi|218157	39151	61	cytoplasmic aldolase [Oryza sativa Japonica Group]
3.	gi|110288655	39137	60	Fructose-bisphosphate aldolase, cytoplasmic isozyme, putative, expressed [Oryza sativa (japoni
4.	gi|125548604	39099	60	hypothetical protein OsI_16195 [Oryza sativa Indica Group]
5.	gi|157349664	18221	43	unnamed protein product [Vitis vinifera]
6.	gi|149193337	65309	41	putative NPR1 [Brassica napus]
7.	gi|222618457	32488	40	hypothetical protein OsJ_01802 [Oryza sativa Japonica Group]
8.	gi|147859008	18390	38	hypothetical protein [Vitis vinifera]
9.	gi|157346056	5290	36	unnamed protein product [Vitis vinifera]
10.	gi|121582261	41341	36	flavanone 3-hydroxylase [Iris x hollandica]

Results List

1. gi|5419990 **Mass:** 25028 **Score:** 98 **Expect:** 8.9e-005 **Queries matched:** 8

putative fructose-bisphosphate aldolase [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
707.4003	706.3930	706.3914	0.0016	8	12	1	---	FAKWR
829.3848	828.3775	828.3766	0.0010	1	7	0	---	YYEAGAR
1371.7256	1370.7183	1370.7135	0.0049	157	167	0	---	KPWFLSFSFGR
1371.7256	1370.7183	1370.7135	0.0049	157	167	0	---	KPWFLSFSFGR
1842.0159	1841.0086	1840.9987	0.0099	153	167	1	---	LQTKKPWFLSFSFGR
2108.0776	2107.0703	2107.0657	0.0046	17	36	0	---	IGPNEPSQLSIDQNAQGLAR
2108.0776	2107.0703	2107.0657	0.0046	17	36	0	37	IGPNEPSQLSIDQNAQGLAR
2519.3645	2518.3572	2518.3503	0.0070	13	36	1	---	AVLKIGPNEPSQLSIDQNAQGLAR

No match to: 713.4089, 734.4876, 736.4933, 750.5179, 768.5250, 848.5140, 864.5357, 886.9847, 1259.7633, 1279.7665, 1334.8848, 1346.7340, 1346.7340, 1404.6797, 1405.1611, 1448.9095, 1474.8293, 1474.8293, 1618.0731, 1629.7556, 1662.8214, 1662.8214, 1732.0967, 2016.2816, 2146.1113, 2462.3171, 2850.3660, 3350.6162, 3810.8176

2. gi|218157 **Mass:** 39151 **Score:** 61 **Expect:** 0.45 **Queries matched:** 8

cytoplasmic aldolase [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
707.4003	706.3930	706.3914	0.0016	140	144	1	---	FAKWR
829.3848	828.3775	828.3766	0.0010	133	139	0	---	YYEAGAR
1346.7340	1345.7267	1345.7241	0.0026	238	249	0	9	VAPEVIAEYTVR
1346.7340	1345.7267	1345.7241	0.0026	238	249	0	---	VAPEVIAEYTVR
1474.8293	1473.8220	1473.8190	0.0030	237	249	1	---	KVAPEVIAEYTVR
1474.8293	1473.8220	1473.8190	0.0030	237	249	1	---	KVAPEVIAEYTVR
1662.8214	1661.8141	1661.8121	0.0021	40	53	1	18	FASINVENVEDNRR

1662.8214	1661.8141	1661.8121	0.0021	40 - 53	1	---	FASINVENVEDNRR

No match to: 713.4089, 734.4876, 736.4933, 750.5179, 768.5250, 848.5140, 864.5357, 886.9847, 1259.7633, 1279.7665, 1334.8848, 1371.7256, 1371.7256, 1404.6797, 1405.1611, 1448.9095, 1618.0731, 1629.7556, 1732.0967, 1842.0159, 2016.2816, 2108.0776, 2108.0776, 2146.1113, 2462.3171, 2519.3645, 2850.3660, 3350.6162, 3810.8176

3. gi|110288655 **Mass:** 39137 **Score:** 60 **Expect:** 0.55 **Queries matched:** 8

Fructose-bisphosphate aldolase, cytoplasmic isozyme, putative, expressed [Oryza sativa (japonica cu

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
707.4003	706.3930	706.3914	0.0016	140 -	144	1	---	FAKWR
829.3848	828.3775	828.3766	0.0010	133 -	139	0	---	YYEAGAR
1346.7340	1345.7267	1345.7241	0.0026	238 -	249	0	9	VAPEVIAEYTVR
1346.7340	1345.7267	1345.7241	0.0026	238 -	249	0	---	VAPEVIAEYTVR
1474.8293	1473.8220	1473.8190	0.0030	237 -	249	1	---	KVAPEVIAEYTVR
1474.8293	1473.8220	1473.8190	0.0030	237 -	249	1	---	KVAPEVIAEYTVR
1662.8214	1661.8141	1661.8121	0.0021	40 -	53	1	18	FASINVENVEDNRR
1662.8214	1661.8141	1661.8121	0.0021	40 -	53	1	---	FASINVENVEDNRR

No match to: 713.4089, 734.4876, 736.4933, 750.5179, 768.5250, 848.5140, 864.5357, 886.9847, 1259.7633, 1279.7665, 1334.8848, 1371.7256, 1371.7256, 1404.6797, 1405.1611, 1448.9095, 1618.0731, 1629.7556, 1732.0967, 1842.0159, 2016.2816, 2108.0776, 2108.0776, 2146.1113, 2462.3171, 2519.3645, 2850.3660, 3350.6162, 3810.8176

4. gi|125548604 **Mass:** 39099 **Score:** 60 **Expect:** 0.55 **Queries matched:** 8

hypothetical protein OsI_16195 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
707.4003	706.3930	706.3914	0.0016	140 -	144	1	---	FAKWR
829.3848	828.3775	828.3766	0.0010	133 -	139	0	---	YYEAGAR
1346.7340	1345.7267	1345.7241	0.0026	238 -	249	0	9	VAPEVIAEYTVR
1346.7340	1345.7267	1345.7241	0.0026	238 -	249	0	---	VAPEVIAEYTVR
1474.8293	1473.8220	1473.8190	0.0030	237 -	249	1	---	KVAPEVIAEYTVR
1474.8293	1473.8220	1473.8190	0.0030	237 -	249	1	---	KVAPEVIAEYTVR
1662.8214	1661.8141	1661.8121	0.0021	40 -	53	1	18	FASINVENVEDNRR
1662.8214	1661.8141	1661.8121	0.0021	40 -	53	1	---	FASINVENVEDNRR

No match to: 713.4089, 734.4876, 736.4933, 750.5179, 768.5250, 848.5140, 864.5357, 886.9847, 1259.7633, 1279.7665, 1334.8848, 1371.7256, 1371.7256, 1404.6797, 1405.1611, 1448.9095, 1618.0731, 1629.7556, 1732.0967, 1842.0159, 2016.2816, 2108.0776, 2108.0776, 2146.1113, 2462.3171, 2519.3645, 2850.3660, 3350.6162, 3810.8176

5. gi|157349664 **Mass:** 18221 **Score:** 43 **Expect:** 34 **Queries matched:** 6

unnamed protein product [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1346.7340	1345.7267	1345.7857	-0.0589	119 -	130	0	9	LLIVPSDITFTK
1346.7340	1345.7267	1345.7857	-0.0589	119 -	130	0	---	LLIVPSDITFTK
1474.8293	1473.8220	1473.8806	-0.0586	119 -	131	1	---	LLIVPSDITFTKK
1474.8293	1473.8220	1473.8806	-0.0586	119 -	131	1	---	LLIVPSDITFTKK

2108.0776	2107.0703	2107.0234	0.0469	94 - 112	1	---	ISPEEDSVIWKGGGHGHFR
2108.0776	2107.0703	2107.0234	0.0469	94 - 112	1	6	ISPEEDSVIWKGGGHGHFR

No match to: 707.4003, 713.4089, 734.4876, 736.4933, 750.5179, 768.5250, 829.3848, 848.5140, 864.5357, 886.9847, 1259.7633, 1279.7665, 1334.8848, 1371.7256, 1371.7256, 1404.6797, 1405.1611, 1448.9095, 1618.0731, 1629.7556, 1662.8214, 1662.8214, 1732.0967, 1842.0159, 2016.2816, 2146.1113, 2462.3171, 2519.3645, 2850.3660, 3350.6162, 3810.8176

6. gi|149193337 **Mass:** 65309 **Score:** 41 **Expect:** 54 **Queries matched:** 7

putative NPR1 [Brassica napus]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1259.7633	1258.7560	1258.7206	0.0354	195 -	205	0	---	VMIEDTLVVLK
1474.8293	1473.8220	1473.7510	0.0710	77 -	88	1	---	EVSFHRCILSAR
1474.8293	1473.8220	1473.7510	0.0710	77 -	88	1	---	EVSFHRCILSAR
1662.8214	1661.8141	1661.8559	-0.0417	472 -	485	1	19	FVEMHQSRLTALSK + Oxidation (M)
1662.8214	1661.8141	1661.8559	-0.0417	472 -	485	1	---	FVEMHQSRLTALSK + Oxidation (M)
2108.0776	2107.0703	2107.0149	0.0554	403 -	421	0	---	EPFPEDVFPSLAVAADEFK
2108.0776	2107.0703	2107.0149	0.0554	403 -	421	0	---	EPFPEDVFPSLAVAADEFK

No match to: 707.4003, 713.4089, 734.4876, 736.4933, 750.5179, 768.5250, 829.3848, 848.5140, 864.5357, 886.9847, 1279.7665, 1334.8848, 1346.7340, 1346.7340, 1371.7256, 1371.7256, 1404.6797, 1405.1611, 1448.9095, 1618.0731, 1629.7556, 1732.0967, 1842.0159, 2016.2816, 2146.1113, 2462.3171, 2519.3645, 2850.3660, 3350.6162, 3810.8176

7. gi|222618457 **Mass:** 32488 **Score:** 40 **Expect:** 56 **Queries matched:** 8

hypothetical protein OsJ_01802 [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1279.7665	1278.7592	1278.7257	0.0335	213 -	223	0	---	FVTIDLLTMVK
1346.7340	1345.7267	1345.7275	-0.0008	108 -	119	1	---	TMPVTLTVKDNK
1346.7340	1345.7267	1345.7275	-0.0008	108 -	119	1	---	TMPVTLTVKDNK
1371.7256	1370.7183	1370.7670	-0.0487	123 -	133	1	---	QAEHLRYLTIK
1371.7256	1370.7183	1370.7670	-0.0487	123 -	133	1	---	QAEHLRYLTIK
1662.8214	1661.8141	1661.8095	0.0046	63 -	80	0	---	GAAVAAAAGGGVFMHYGR
1662.8214	1661.8141	1661.8095	0.0046	63 -	80	0	---	GAAVAAAAGGGVFMHYGR
3350.6162	3349.6089	3349.5006	0.1083	87 -	116	1	---	TPADYDMEDGDEVSFFPDGTRTMPVTLTVK + Oxidation (M)

No match to: 707.4003, 713.4089, 734.4876, 736.4933, 750.5179, 768.5250, 829.3848, 848.5140, 864.5357, 886.9847, 1259.7633, 1334.8848, 1404.6797, 1405.1611, 1448.9095, 1474.8293, 1474.8293, 1618.0731, 1629.7556, 1732.0967, 1842.0159, 2016.2816, 2108.0776, 2108.0776, 2146.1113, 2462.3171, 2519.3645, 2850.3660, 3810.8176

8. gi|147859008 **Mass:** 18390 **Score:** 38 **Expect:** 98 **Queries matched:** 4

hypothetical protein [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1346.7340	1345.7267	1345.6612	0.0655	45 -	56	0	---	VITEDAIEVDDK
1346.7340	1345.7267	1345.6612	0.0655	45 -	56	0	---	VITEDAIEVDDK
1662.8214	1661.8141	1661.8810	-0.0669	1 -	15	0	25	MVSGLINANPVIYQK + Oxidation (M)
1662.8214	1661.8141	1661.8810	-0.0669	1 -	15	0	---	MVSGLINANPVIYQK + Oxidation (M)

No match to: 707.4003, 713.4089, 734.4876, 736.4933, 750.5179, 768.5250, 829.3848, 848.5140, 864.5357, 886.9847, 1259.7633, 1279.7665, 1334.8848, 1371.7256, 1371.7256, 1404.6797, 1405.1611, 1448.9095, 1474.8293, 1474.8293, 1618.0731, 1629.7556, 1732.0967, 1842.0159, 2016.2816, 2108.0776, 2108.0776, 2146.1113, 2462.3171, 2519.3645, 2850.3660, 3350.6162, 3810.8176

9. gi|157346056 **Mass:** 5290 **Score:** 36 **Expect:** 1.4e+002 **Queries matched:** 2

unnamed protein product [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1662.8214	1661.8141	1661.8810	-0.0669	1 -	15	0	25	MVSGLINANPVIYQK + Oxidation (M)
1662.8214	1661.8141	1661.8810	-0.0669	1 -	15	0	---	MVSGLINANPVIYQK + Oxidation (M)

No match to: 707.4003, 713.4089, 734.4876, 736.4933, 750.5179, 768.5250, 829.3848, 848.5140, 864.5357, 886.9847, 1259.7633, 1279.7665, 1334.8848, 1346.7340, 1346.7340, 1371.7256, 1371.7256, 1404.6797, 1405.1611, 1448.9095, 1474.8293, 1474.8293, 1618.0731, 1629.7556, 1732.0967, 1842.0159, 2016.2816, 2108.0776, 2108.0776, 2146.1113, 2462.3171, 2519.3645, 2850.3660, 3350.6162, 3810.8176

10. gi|121582261 **Mass:** 41341 **Score:** 36 **Expect:** 1.6e+002 **Queries matched:** 6

flavanone 3-hydroxylase [Iris x hollandica]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1371.7256	1370.7183	1370.6574	0.0610	169 -	179	1	---	YSEKLMELACK
1371.7256	1370.7183	1370.6574	0.0610	169 -	179	1	---	YSEKLMELACK
1662.8214	1661.8141	1661.8736	-0.0595	351 -	365	1	3	LHENAKVEEAVAQPK
1662.8214	1661.8141	1661.8736	-0.0595	351 -	365	1	---	LHENAKVEEAVAQPK
2462.3171	2461.3098	2461.3288	-0.0190	225 -	247	1	---	RHTDPGTITLLLQDQVGGLQATK
3350.6162	3349.6089	3349.6955	-0.0866	248 -	278	1	---	DGGKTWFTVQPIQGSLVVNLGDHAHFLSNGR

No match to: 707.4003, 713.4089, 734.4876, 736.4933, 750.5179, 768.5250, 829.3848, 848.5140, 864.5357, 886.9847, 1259.7633, 1279.7665, 1334.8848, 1346.7340, 1346.7340, 1404.6797, 1405.1611, 1448.9095, 1474.8293, 1474.8293, 1618.0731, 1629.7556, 1732.0967, 1842.0159, 2016.2816, 2108.0776, 2108.0776, 2146.1113, 2519.3645, 2850.3660, 3810.8176

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 37

Protein View

Match to: **gi|5419990** Score: **98** Expect: **8.9e-005**
putative fructose-bisphosphate aldolase [Phleum pratense]

Nominal mass (M_r): **25028**; Calculated pI value: **7.79**
NCBI BLAST search of gi|5419990 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

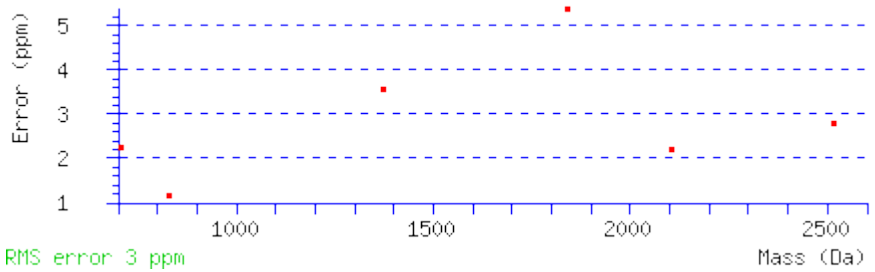
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **22%**

Matched peptides shown in **Bold Red**

```
    1 YYEAGARFAK WRAVLKIGPN EPSQLSIDQN AQGLARYAII CQENGLVPIV
   51 EPEILVDGPH DIDRCAYVTE VVLAACYKAL NDQHVLLEGS LLKPNMVTPG
  101 SDAKKVAPRE SLAEYTVRTL QRTVPPAVPA IVFLSGGQSE EEATVNLNAM
  151 NKLQTKKPWF LSFSFGRALQ QSTLKAWSGK EENVGKAQKA FLVRCKANSE
  201 ATLGTYKGDA TLGEGASESL HVKDYKY
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
1 - 7	829.3848	828.3775	828.3766	0.0010	0	YYEAGAR	(No match)
8 - 12	707.4003	706.3930	706.3914	0.0016	1	FAKWR	(No match)
13 - 36	2519.3645	2518.3572	2518.3503	0.0070	1	AVLKIGPNEPSQLSIDQNAQGLAR	(No match)
17 - 36	2108.0776	2107.0703	2107.0657	0.0046	0	IGPNEPSQLSIDQNAQGLAR	(No match)
17 - 36	2108.0776	2107.0703	2107.0657	0.0046	0	IGPNEPSQLSIDQNAQGLAR	(Ions score 37)
153 - 167	1842.0159	1841.0086	1840.9987	0.0099	1	LQTKKPWFLSFSFGR	(No match)
157 - 167	1371.7256	1370.7183	1370.7135	0.0049	0	KPWFLSFSFGR	(No match)
157 - 167	1371.7256	1370.7183	1370.7135	0.0049	0	KPWFLSFSFGR	(No match)



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Index

	Accession	Mass	Score	Description
1.	gi|51703306	36768	150	glyceraldehyde 3-phosphate dehydrogenase [Daucus carota]
2.	gi|1345501	36645	149	glycolytic glyceraldehyde 3-phosphate dehydrogenase [Antirrhinum majus]
3.	gi|120666	36776	149	RecName: Full=Glyceraldehyde-3-phosphate dehydrogenase, cytosolic
4.	gi|462137	37105	140	RecName: Full=Glyceraldehyde-3-phosphate dehydrogenase, cytosolic
5.	gi|58220789	20438	116	glyceraldehyde-3-phosphate dehydrogenase [Triticum monococcum]

Results List

1. gi|51703306 **Mass:** 36768 **Score:** 150 **Expect:** 6e-010 **Queries matched:** 10

glyceraldehyde 3-phosphate dehydrogenase [Daucus carota]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
746.3695	745.3622	745.3619	0.0003	197	202	1	---	DWRGGR
784.5114	783.5041	783.5078	-0.0037	14	20	1	---	IGRLVAR
1242.7340	1241.7267	1241.7244	0.0024	2	13	1	80	APIKIGINGFGR
1242.7340	1241.7267	1241.7244	0.0024	2	13	1	---	APIKIGINGFGR
1434.7511	1433.7438	1433.7514	-0.0075	203	217	0	---	AASFNIIPSSTGAAK
1704.9036	1703.8963	1703.8954	0.0009	200	217	1	9	GGRAASFNIIPSSTGAAK
1704.9036	1703.8963	1703.8954	0.0009	200	217	1	---	GGRAASFNIIPSSTGAAK
1725.8989	1724.8916	1724.8443	0.0474	129	143	1	---	DAPMFVVGVNEKEYK
1725.8989	1724.8916	1724.8443	0.0474	129	143	1	---	DAPMFVVGVNEKEYK
1775.8022	1774.7949	1774.7950	-0.0001	312	325	0	---	LVSWYDNEWGYSTR

No match to: 713.4083, 724.4948, 750.5090, 768.5217, 782.4802, 838.5283, 864.5340, 886.9839, 1225.7076, 1225.7076, 1247.6031, 1279.7625, 1334.8812, 1401.8324, 1401.8324, 1448.9139, 1493.8096, 1517.7535, 1562.9437, 1568.9214, 1618.0653, 1732.0951, 2187.0293, 2565.1860, 2664.3489

2. gi|1345501 **Mass:** 36645 **Score:** 149 **Expect:** 7.6e-010 **Queries matched:** 10

glycolytic glyceraldehyde 3-phosphate dehydrogenase [Antirrhinum majus]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
746.3695	745.3622	745.3619	0.0003	196	201	1	---	DWRGGR
784.5114	783.5041	783.5078	-0.0037	13	19	1	---	IGRLVAR
1242.7340	1241.7267	1241.7244	0.0024	1	12	1	80	APIKIGINGFGR
1242.7340	1241.7267	1241.7244	0.0024	1	12	1	---	APIKIGINGFGR
1434.7511	1433.7438	1433.7514	-0.0075	202	216	0	---	AASFNIIPSSTGAAK
1704.9036	1703.8963	1703.8954	0.0009	199	216	1	9	GGRAASFNIIPSSTGAAK
1704.9036	1703.8963	1703.8954	0.0009	199	216	1	---	GGRAASFNIIPSSTGAAK
1725.8989	1724.8916	1724.8443	0.0474	128	142	1	---	DAPMFVVGVNEKEYK
1725.8989	1724.8916	1724.8443	0.0474	128	142	1	---	DAPMFVVGVNEKEYK

1775.8022	1774.7949	1774.7950	-0.0001	311 - 324	0	---	LVSWYDNEWGYSTR

No match to: 713.4083, 724.4948, 750.5090, 768.5217, 782.4802, 838.5283, 864.5340, 886.9839, 1225.7076, 1225.7076, 1247.6031, 1279.7625, 1334.8812, 1401.8324, 1401.8324, 1448.9139, 1493.8096, 1517.7535, 1562.9437, 1568.9214, 1618.0653, 1732.0951, 2187.0293, 2565.1860, 2664.3489

3. gi|120666 **Mass:** 36776 **Score:** 149 **Expect:** 7.6e-010 **Queries matched:** 10

RecName: Full=Glyceraldehyde-3-phosphate dehydrogenase, cytosolic

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
746.3695	745.3622	745.3619	0.0003	197 -	202	1	---	DWRGGR
784.5114	783.5041	783.5078	-0.0037	14 -	20	1	---	IGRLVAR
1242.7340	1241.7267	1241.7244	0.0024	2 -	13	1	80	APIKIGINGFGR
1242.7340	1241.7267	1241.7244	0.0024	2 -	13	1	---	APIKIGINGFGR
1434.7511	1433.7438	1433.7514	-0.0075	203 -	217	0	---	AASFNIIPSSTGAAK
1704.9036	1703.8963	1703.8954	0.0009	200 -	217	1	9	GGRAASFNIIPSSTGAAK
1704.9036	1703.8963	1703.8954	0.0009	200 -	217	1	---	GGRAASFNIIPSSTGAAK
1725.8989	1724.8916	1724.8443	0.0474	129 -	143	1	---	DAPMFVVGVNEKEYK
1725.8989	1724.8916	1724.8443	0.0474	129 -	143	1	---	DAPMFVVGVNEKEYK
1775.8022	1774.7949	1774.7950	-0.0001	312 -	325	0	---	LVSWYDNEWGYSTR

No match to: 713.4083, 724.4948, 750.5090, 768.5217, 782.4802, 838.5283, 864.5340, 886.9839, 1225.7076, 1225.7076, 1247.6031, 1279.7625, 1334.8812, 1401.8324, 1401.8324, 1448.9139, 1493.8096, 1517.7535, 1562.9437, 1568.9214, 1618.0653, 1732.0951, 2187.0293, 2565.1860, 2664.3489

4. gi|462137 **Mass:** 37105 **Score:** 140 **Expect:** 6e-009 **Queries matched:** 8

RecName: Full=Glyceraldehyde-3-phosphate dehydrogenase, cytosolic

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
746.3695	745.3622	745.3619	0.0003	197 -	202	1	---	DWRGGR
784.5114	783.5041	783.5078	-0.0037	14 -	20	1	---	IGRLVAR
1242.7340	1241.7267	1241.7244	0.0024	2 -	13	1	80	APIKIGINGFGR
1242.7340	1241.7267	1241.7244	0.0024	2 -	13	1	---	APIKIGINGFGR
1434.7511	1433.7438	1433.7514	-0.0075	203 -	217	0	---	AASFNIIPSSTGAAK
1704.9036	1703.8963	1703.8954	0.0009	200 -	217	1	9	GGRAASFNIIPSSTGAAK
1704.9036	1703.8963	1703.8954	0.0009	200 -	217	1	---	GGRAASFNIIPSSTGAAK
1775.8022	1774.7949	1774.7950	-0.0001	312 -	325	0	---	LVSWYDNEWGYSTR

No match to: 713.4083, 724.4948, 750.5090, 768.5217, 782.4802, 838.5283, 864.5340, 886.9839, 1225.7076, 1225.7076, 1247.6031, 1279.7625, 1334.8812, 1401.8324, 1401.8324, 1448.9139, 1493.8096, 1517.7535, 1562.9437, 1568.9214, 1618.0653, 1725.8989, 1725.8989, 1732.0951, 2187.0293, 2565.1860, 2664.3489

5. gi|58220789 **Mass:** 20438 **Score:** 116 **Expect:** 1.5e-006 **Queries matched:** 5

glyceraldehyde-3-phosphate dehydrogenase [Triticum monococcum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
784.5114	783.5041	783.5078	-0.0037	14 -	20	1	---	IGRLVAR
1242.7340	1241.7267	1241.7244	0.0024	2 -	13	1	80	APIKIGINGFGR

1242.7340	1241.7267	1241.7244	0.0024	2 -	13	1	---	APIKIGINGFGR
1725.8989	1724.8916	1724.8919	-0.0003	68 -	82	1	15	TLLFGEKEVAVFGCR
1725.8989	1724.8916	1724.8919	-0.0003	68 -	82	1	---	TLLFGEKEVAVFGCR

No match to: 713.4083, 724.4948, 746.3695, 750.5090, 768.5217, 782.4802, 838.5283, 864.5340, 886.9839, 1225.7076, 1225.7076, 1247.6031, 1279.7625, 1334.8812, 1401.8324, 1401.8324, 1434.7511, 1448.9139, 1493.8096, 1517.7535, 1562.9437, 1568.9214, 1618.0653, 1704.9036, 1704.9036, 1732.0951, 1775.8022, 2187.0293, 2565.1860, 2664.3489

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 35

Protein View

Match to: **gi|51703306** Score: **150** Expect: **6e-010**
glyceraldehyde 3-phosphate dehydrogenase [Daucus carota]

Nominal mass (M_r): **36768;** Calculated pI value: **7.05**
NCBI BLAST search of gi|51703306 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Daucus carota

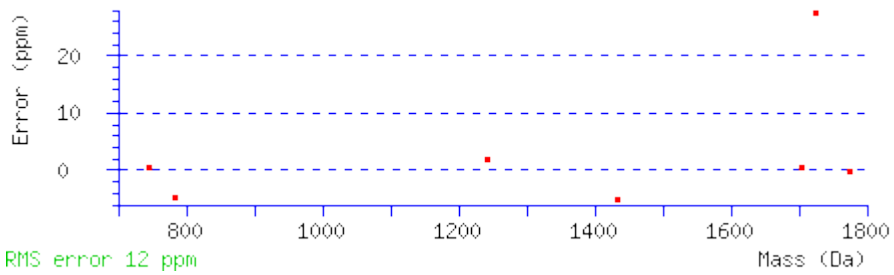
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **20%**

Matched peptides shown in **Bold Red**

```
   1 MAPIKIGING FGRIGRLVAR VALQRDDVEL VAVNDPFIST DYMTYMFKYD
  51 SVHGAWKHHE LKVKDEKTLL FGEKPVAVFG CRNPEEIPWA STGAEYIVES
 101 TGVFTDKDKA AAHLKGGAKK VIISAPSKDA PMFVVGVNEK EYKSDLHIVS
 151 NASCTTNCLA PLAKVINDRF GIVEGLMTTV HSITATQKTV DGPSAKDWRG
 201 GRAASFNIIP SSTGAAKAVG KVLPQLNGKL TGMSFRVPTV DVSVVDLTVR
 251 LEKKATYDQI KAAIKEESEG KLKGILGYTE DDVVSTDFVG DSRSSIFDAK
 301 AGIALNDNFV KLVSWYDNEW GYSTRVVDLI VHMASVQ
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
2 - 13	1242.7340	1241.7267	1241.7244	0.0024	1	APIKIGINGFGR	(Ions score 80)
2 - 13	1242.7340	1241.7267	1241.7244	0.0024	1	APIKIGINGFGR	(No match)
14 - 20	784.5114	783.5041	783.5078	-0.0037	1	IGRLVAR	(No match)
129 - 143	1725.8989	1724.8916	1724.8443	0.0474	1	DAPMFVVGVNEKEYK	(No match)
129 - 143	1725.8989	1724.8916	1724.8443	0.0474	1	DAPMFVVGVNEKEYK	(No match)
197 - 202	746.3695	745.3622	745.3619	0.0003	1	DWRGGR	(No match)
200 - 217	1704.9036	1703.8963	1703.8954	0.0009	1	GGRAASFNIIPSSTGAAK	(Ions score 9)
200 - 217	1704.9036	1703.8963	1703.8954	0.0009	1	GGRAASFNIIPSSTGAAK	(No match)
203 - 217	1434.7511	1433.7438	1433.7514	-0.0075	0	AASFNIIPSSTGAAK	(No match)
312 - 325	1775.8022	1774.7949	1774.7950	-0.0001	0	LVSWYDNEWGYSTR	(No match)



Spot 62

Index

	Accession	Mass	Score	Description
1.	gi|5419990	25028	441	putative fructose-bisphosphate aldolase [Phleum pratense]
2.	gi|218157	39151	300	cytoplasmic aldolase [Oryza sativa Japonica Group]
3.	gi|110288655	39137	299	Fructose-bisphosphate aldolase, cytoplasmic isozyme, putative, expressed [Oryza sativa (japonic
4.	gi|125548604	39099	299	hypothetical protein OsI_16195 [Oryza sativa Indica Group]
5.	gi|2213867	38362	231	fructose-biphosphate aldolase [Mesembryanthemum crystallinum]

Results List

1. gi|5419990 **Mass:** 25028 **Score:** 441 **Expect:** 4.8e-039 **Queries matched:** 16

putative fructose-bisphosphate aldolase [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
707.3954	706.3881	706.3914	-0.0033	8	12	1	---	FAKWR
772.4767	771.4694	771.4755	-0.0061	11	16	1	---	WRAVLK
829.3843	828.3770	828.3766	0.0005	1	7	0	---	YYEAGAR
932.5695	931.5622	931.5603	0.0020	187	194	1	---	AQKAFLVR
1175.5815	1174.5742	1174.5770	-0.0028	1	10	1	---	YYEAGARFAK
1371.7205	1370.7132	1370.7135	-0.0002	157	167	0	---	KPWFLSFSFGR
1842.0088	1841.0015	1840.9987	0.0028	153	167	1	---	LQTKKPWFLSFSFGR
2108.0740	2107.0667	2107.0657	0.0010	17	36	0	147	IGPNEPSQLSIDQNAQGLAR
2108.0740	2107.0667	2107.0657	0.0010	17	36	0	---	IGPNEPSQLSIDQNAQGLAR
2519.3608	2518.3535	2518.3503	0.0033	13	36	1	---	AVLKIGPNEPSQLSIDQNAQGLAR
2519.3608	2518.3535	2518.3503	0.0033	13	36	1	165	AVLKIGPNEPSQLSIDQNAQGLAR
2706.3369	2705.3296	2705.3143	0.0153	197	223	1	---	ANSEATLGTYKGDATLGEGASESLHVK
2747.4443	2746.4370	2746.4323	0.0047	79	104	0	---	ALNDQHVLLEGSLLKPNMVTPGSDAK
2763.4558	2762.4485	2762.4272	0.0213	79	104	0	---	ALNDQHVLLEGSLLKPNMVTPGSDAK + Oxidation (M)
2875.5435	2874.5362	2874.5272	0.0090	79	105	1	---	ALNDQHVLLEGSLLKPNMVTPGSDAKK
2891.5688	2890.5615	2890.5221	0.0394	79	105	1	---	ALNDQHVLLEGSLLKPNMVTPGSDAKK + Oxidation (M)

No match to: 713.4080, 723.3889, 739.3893, 768.5220, 778.4389, 831.9066, 832.4095, 886.9785, 925.5665, 1118.6896, 1171.5214, 1187.5255, 1188.5458, 1260.6650, 1279.7678, 1334.8820, 1346.7311, 1346.7311, 1448.9087, 1474.8262, 1474.8262, 1488.8027, 1517.7458, 1534.7495, 1603.8085, 1616.7977, 1629.7709, 1645.2863, 1646.2760, 1662.8171, 1662.8171, 1818.9146, 1845.0225, 1881.0026, 1973.1206, 2003.0432, 2052.1914, 2146.1162, 2190.1670, 2429.1943, 2461.3059, 2473.3098, 2589.3125, 2771.3987, 2977.4417, 2994.4683, 3059.6621, 3188.6580, 3350.8259

2. gi|218157 **Mass:** 39151 **Score:** 300 **Expect:** 6e-025 **Queries matched:** 12

cytoplasmic aldolase [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
707.3954	706.3881	706.3914	-0.0033	140	144	1	---	FAKWR

772.4767	771.4694	771.4755	-0.0061	143 - 148	1	---	WRAVLK
829.3843	828.3770	828.3766	0.0005	133 - 139	0	---	YYEAGAR
1175.5815	1174.5742	1174.5770	-0.0028	133 - 142	1	---	YYEAGARFAK
1346.7311	1345.7238	1345.7241	-0.0003	238 - 249	0	96	VAPEVIAEYTVR
1346.7311	1345.7238	1345.7241	-0.0003	238 - 249	0	---	VAPEVIAEYTVR
1474.8262	1473.8189	1473.8190	-0.0001	237 - 249	1	103	KVAPEVIAEYTVR
1474.8262	1473.8189	1473.8190	-0.0001	237 - 249	1	---	KVAPEVIAEYTVR
1488.8027	1487.7954	1487.7943	0.0011	25 - 39	1	---	GILAADESTGTIGKR
1662.8171	1661.8098	1661.8121	-0.0022	40 - 53	1	---	FASINVENVEDNRR
1662.8171	1661.8098	1661.8121	-0.0022	40 - 53	1	41	FASINVENVEDNRR
1845.0225	1844.0152	1844.0155	-0.0003	238 - 253	1	---	VAPEVIAEYTVRTLQR

No match to: 713.4080, 723.3889, 739.3893, 768.5220, 778.4389, 831.9066, 832.4095, 886.9785, 925.5665, 932.5695, 1118.6896, 1171.5214, 1187.5255, 1188.5458, 1260.6650, 1279.7678, 1334.8820, 1371.7205, 1448.9087, 1517.7458, 1534.7495, 1603.8085, 1616.7977, 1629.7709, 1645.2863, 1646.2760, 1818.9146, 1842.0088, 1881.0026, 1973.1206, 2003.0432, 2052.1914, 2108.0740, 2108.0740, 2146.1162, 2190.1670, 2429.1943, 2461.3059, 2473.3098, 2519.3608, 2519.3608, 2589.3125, 2706.3369, 2747.4443, 2763.4558, 2771.3987, 2875.5435, 2891.5688, 2977.4417, 2994.4683, 3059.6621, 3188.6580, 3350.8259

3. gi|110288655 **Mass:** 39137 **Score:** 299 **Expect:** 7.6e-025 **Queries matched:** 12

Fructose-bisphosphate aldolase, cytoplasmic isozyme, putative, expressed [Oryza sativa (japonica cu

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
707.3954	706.3881	706.3914	-0.0033	140 - 144	1	---	FAKWR
772.4767	771.4694	771.4755	-0.0061	143 - 148	1	---	WRAVLK
829.3843	828.3770	828.3766	0.0005	133 - 139	0	---	YYEAGAR
1175.5815	1174.5742	1174.5770	-0.0028	133 - 142	1	---	YYEAGARFAK
1346.7311	1345.7238	1345.7241	-0.0003	238 - 249	0	96	VAPEVIAEYTVR
1346.7311	1345.7238	1345.7241	-0.0003	238 - 249	0	---	VAPEVIAEYTVR
1474.8262	1473.8189	1473.8190	-0.0001	237 - 249	1	103	KVAPEVIAEYTVR
1474.8262	1473.8189	1473.8190	-0.0001	237 - 249	1	---	KVAPEVIAEYTVR
1488.8027	1487.7954	1487.7943	0.0011	25 - 39	1	---	GILAADESTGTIGKR
1662.8171	1661.8098	1661.8121	-0.0022	40 - 53	1	---	FASINVENVEDNRR
1662.8171	1661.8098	1661.8121	-0.0022	40 - 53	1	41	FASINVENVEDNRR
1845.0225	1844.0152	1844.0155	-0.0003	238 - 253	1	---	VAPEVIAEYTVRTLQR

No match to: 713.4080, 723.3889, 739.3893, 768.5220, 778.4389, 831.9066, 832.4095, 886.9785, 925.5665, 932.5695, 1118.6896, 1171.5214, 1187.5255, 1188.5458, 1260.6650, 1279.7678, 1334.8820, 1371.7205, 1448.9087, 1517.7458, 1534.7495, 1603.8085, 1616.7977, 1629.7709, 1645.2863, 1646.2760, 1818.9146, 1842.0088, 1881.0026, 1973.1206, 2003.0432, 2052.1914, 2108.0740, 2108.0740, 2146.1162, 2190.1670, 2429.1943, 2461.3059, 2473.3098, 2519.3608, 2519.3608, 2589.3125, 2706.3369, 2747.4443, 2763.4558, 2771.3987, 2875.5435, 2891.5688, 2977.4417, 2994.4683, 3059.6621, 3188.6580, 3350.8259

4. gi|125548604 **Mass:** 39099 **Score:** 299 **Expect:** 7.6e-025 **Queries matched:** 12

hypothetical protein OsI_16195 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide

707.3954	706.3881	706.3914	-0.0033	140 - 144	1	---	FAKWR
772.4767	771.4694	771.4755	-0.0061	143 - 148	1	---	WRAVLK
829.3843	828.3770	828.3766	0.0005	133 - 139	0	---	YYEAGAR
1175.5815	1174.5742	1174.5770	-0.0028	133 - 142	1	---	YYEAGARFAK
1346.7311	1345.7238	1345.7241	-0.0003	238 - 249	0	96	VAPEVIAEYTVR
1346.7311	1345.7238	1345.7241	-0.0003	238 - 249	0	---	VAPEVIAEYTVR
1474.8262	1473.8189	1473.8190	-0.0001	237 - 249	1	103	KVAPEVIAEYTVR
1474.8262	1473.8189	1473.8190	-0.0001	237 - 249	1	---	KVAPEVIAEYTVR
1488.8027	1487.7954	1487.7943	0.0011	25 - 39	1	---	GILAADESTGTIGKR
1662.8171	1661.8098	1661.8121	-0.0022	40 - 53	1	---	FASINVENVEDNRR
1662.8171	1661.8098	1661.8121	-0.0022	40 - 53	1	41	FASINVENVEDNRR
1845.0225	1844.0152	1844.0155	-0.0003	238 - 253	1	---	VAPEVIAEYTVRTLQR

No match to: 713.4080, 723.3889, 739.3893, 768.5220, 778.4389, 831.9066, 832.4095, 886.9785, 925.5665, 932.5695, 1118.6896, 1171.5214, 1187.5255, 1188.5458, 1260.6650, 1279.7678, 1334.8820, 1371.7205, 1448.9087, 1517.7458, 1534.7495, 1603.8085, 1616.7977, 1629.7709, 1645.2863, 1646.2760, 1818.9146, 1842.0088, 1881.0026, 1973.1206, 2003.0432, 2052.1914, 2108.0740, 2108.0740, 2146.1162, 2190.1670, 2429.1943, 2461.3059, 2473.3098, 2519.3608, 2519.3608, 2589.3125, 2706.3369, 2747.4443, 2763.4558, 2771.3987, 2875.5435, 2891.5688, 2977.4417, 2994.4683, 3059.6621, 3188.6580, 3350.8259

5. gi|2213867 **Mass:** 38362 **Score:** 231 **Expect:** 4.8e-018 **Queries matched:** 8

fructose-biphosphate aldolase [Mesembryanthemum crystallinum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
707.3954	706.3881	706.3914	-0.0033	140 - 144	1	---	FAKWR
772.4767	771.4694	771.4755	-0.0061	143 - 148	1	---	WRAVLK
1346.7311	1345.7238	1345.7241	-0.0003	238 - 249	0	96	VAPEVIAEYTVR
1346.7311	1345.7238	1345.7241	-0.0003	238 - 249	0	---	VAPEVIAEYTVR
1474.8262	1473.8189	1473.8190	-0.0001	237 - 249	1	103	KVAPEVIAEYTVR
1474.8262	1473.8189	1473.8190	-0.0001	237 - 249	1	---	KVAPEVIAEYTVR
1488.8027	1487.7954	1487.7943	0.0011	25 - 39	1	---	GILAADESTGTIGKR
1603.8085	1602.8012	1602.8365	-0.0352	312 - 325	1	---	EENVEKAQAVFLAR

No match to: 713.4080, 723.3889, 739.3893, 768.5220, 778.4389, 829.3843, 831.9066, 832.4095, 886.9785, 925.5665, 932.5695, 1118.6896, 1171.5214, 1175.5815, 1187.5255, 1188.5458, 1260.6650, 1279.7678, 1334.8820, 1371.7205, 1448.9087, 1517.7458, 1534.7495, 1616.7977, 1629.7709, 1645.2863, 1646.2760, 1662.8171, 1662.8171, 1818.9146, 1842.0088, 1845.0225, 1881.0026, 1973.1206, 2003.0432, 2052.1914, 2108.0740, 2108.0740, 2146.1162, 2190.1670, 2429.1943, 2461.3059, 2473.3098, 2519.3608, 2519.3608, 2589.3125, 2706.3369, 2747.4443, 2763.4558, 2771.3987, 2875.5435, 2891.5688, 2977.4417, 2994.4683, 3059.6621, 3188.6580, 3350.8259

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 65

Protein View

Match to: **gi|5419990** Score: **441** Expect: **4.8e-039**
putative fructose-bisphosphate aldolase [Phleum pratense]

Nominal mass (M_r): **25028**; Calculated pI value: **7.79**
NCBI BLAST search of gi|5419990 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **49%**

Matched peptides shown in **Bold Red**

```
  1 YYEAGARFAK WRAVLKIGPN EPSQLSIDQN AQGLARYAII CQENGLVPIV
 51 EPEILVDGPH DIDRCAYVTE VVLAACYKAL NDQHVLLEGS LLKPNMVTPG
101 SDAKKVAPRE SLAEYTVRTL QRTVPPAVPA IVFLSGGQSE EEATVNLNAM
151 NKLQTKKPWF LSFSFGRALQ QSTLKAWSGK EENVGKAQKA FLVRCKANSE
201 ATLGTYKGDA TLGEGASESL HVKDYKY
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
1 - 7	829.3843	828.3770	828.3766	0.0005	0	YYEAGAR (No match)
1 - 10	1175.5815	1174.5742	1174.5770	-0.0028	1	YYEAGARFAK (No match)
8 - 12	707.3954	706.3881	706.3914	-0.0033	1	FAKWR (No match)
11 - 16	772.4767	771.4694	771.4755	-0.0061	1	WRAVLK (No match)
13 - 36	2519.3608	2518.3535	2518.3503	0.0033	1	AVLKIGPNEPSQLSIDQNAQGLAR (No match)
13 - 36	2519.3608	2518.3535	2518.3503	0.0033	1	AVLKIGPNEPSQLSIDQNAQGLAR (Ions score 165)
17 - 36	2108.0740	2107.0667	2107.0657	0.0010	0	IGPNEPSQLSIDQNAQGLAR (Ions score 147)
17 - 36	2108.0740	2107.0667	2107.0657	0.0010	0	IGPNEPSQLSIDQNAQGLAR (No match)
79 - 104	2747.4443	2746.4370	2746.4323	0.0047	0	ALNDQHVLLEGSLLKPNMVTPGSDAK (No match)
79 - 104	2763.4558	2762.4485	2762.4272	0.0213	0	ALNDQHVLLEGSLLKPNMVTPGSDAK Oxidation (M) (No match)
79 - 105	2875.5435	2874.5362	2874.5272	0.0090	1	ALNDQHVLLEGSLLKPNMVTPGSDAKK (No match)
79 - 105	2891.5688	2890.5615	2890.5221	0.0394	1	ALNDQHVLLEGSLLKPNMVTPGSDAKK Oxidation (M) (No match)
153 - 167	1842.0088	1841.0015	1840.9987	0.0028	1	LQTKKPWFLSFSFGR (No match)
157 - 167	1371.7205	1370.7132	1370.7135	-0.0002	0	KPWFLSFSFGR (No match)
187 - 194	932.5695	931.5622	931.5603	0.0020	1	AQKAFLVR (No match)
197 - 223	2706.3369	2705.3296	2705.3143	0.0153	1	ANSEATLGTYKGDATLGEGASESLHVK (No match)

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	Accession	Mass	Score	Description
1.	gi|51703306	36768	222	glyceraldehyde 3-phosphate dehydrogenase [Daucus carota]
2.	gi|1345501	36645	221	glycolytic glyceraldehyde 3-phosphate dehydrogenase [Antirrhinum majus]
3.	gi|120666	36776	220	RecName: Full=Glyceraldehyde-3-phosphate dehydrogenase, cytosolic
4.	gi|120668	33443	206	RecName: Full=Glyceraldehyde-3-phosphate dehydrogenase, cytosolic
5.	gi|462137	37105	191	RecName: Full=Glyceraldehyde-3-phosphate dehydrogenase, cytosolic
6.	gi|148508784	36854	151	glyceraldehyde-3-phosphate dehydrogenase [Triticum aestivum]
7.	gi|115371630	36877	143	glyceraldehyde-3 phosphate dehydrogenase [Polygonum sibiricum]
8.	gi|120675	37015	134	RecName: Full=Glyceraldehyde-3-phosphate dehydrogenase, cytosolic
9.	gi|162458671	36656	133	cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC4 [Zea mays]
10.	gi|194707656	36613	133	unknown [Zea mays]

Results List

1. gi|51703306 **Mass:** 36768 **Score:** 222 **Expect:** 3.8e-017 **Queries matched:** 14

glyceraldehyde 3-phosphate dehydrogenase [Daucus carota]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
746.3664	745.3591	745.3619	-0.0028	197	202	1	---	DWRGGR
784.5105	783.5032	783.5078	-0.0046	14	20	1	---	IGRLVAR
833.4711	832.4638	832.4555	0.0084	6	13	0	---	IGINGFGR
1161.6272	1160.6199	1160.6189	0.0010	301	311	0	---	AGIALNDNFVK
1242.7374	1241.7301	1241.7244	0.0058	2	13	1	82	APIKIGINGFGR
1242.7374	1241.7301	1241.7244	0.0058	2	13	1	---	APIKIGINGFGR
1434.7560	1433.7487	1433.7514	-0.0026	203	217	0	---	AASFNIIPSSTGAAK
1704.9102	1703.9029	1703.8954	0.0075	200	217	1	---	GGRAASFNIIPSSTGAAK
1725.9106	1724.9033	1724.8443	0.0591	129	143	1	---	DAPMFVVGVNEKEYK
1725.9106	1724.9033	1724.8443	0.0591	129	143	1	---	DAPMFVVGVNEKEYK
1775.8123	1774.8050	1774.7950	0.0100	312	325	0	58	LVSWYDNEWGYSTR
1775.8123	1774.8050	1774.7950	0.0100	312	325	0	---	LVSWYDNEWGYSTR
1869.0740	1868.0667	1868.0618	0.0049	237	253	1	---	VPTVDVSVVDLTVRLEK
1910.0029	1908.9956	1908.9944	0.0012	294	311	1	---	SSIFDAKAGIALNDNFVK

No match to: 713.4005, 724.4910, 734.4893, 736.4972, 750.5109, 768.5142, 782.4717, 834.4753, 838.5221, 848.5233, 864.5333, 1007.6652, 1033.6917, 1225.7120, 1225.7120, 1247.6091, 1264.6997, 1279.7533, 1334.8765, 1336.6516, 1401.8431, 1448.9153, 1517.7506, 1562.9436, 1568.9407, 1618.0295, 1732.0928, 1749.8596, 1791.8119, 1807.8062, 2015.2837, 2143.0369, 2186.0339, 2186.0339, 2193.1377, 2230.2166, 2239.1445, 2299.4705, 2564.1958, 2632.3594, 2648.3667, 2662.4324, 2664.3718, 2665.3701, 2825.3167, 2908.4268, 2919.4272, 2923.3740, 3332.5688, 3349.6125, 3455.7031

2. gi|1345501 **Mass:** 36645 **Score:** 221 **Expect:** 4.8e-017 **Queries matched:** 14

glycolytic glyceraldehyde 3-phosphate dehydrogenase [Antirrhinum majus]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
746.3664	745.3591	745.3619	-0.0028	196	201	1	---	DWRGGR
784.5105	783.5032	783.5078	-0.0046	13	19	1	---	IGRLVAR
833.4711	832.4638	832.4555	0.0084	5	12	0	---	IGINGFGR
1161.6272	1160.6199	1160.6189	0.0010	300	310	0	---	AGIALNDNFVK
1242.7374	1241.7301	1241.7244	0.0058	1	12	1	82	APIKIGINGFGR
1242.7374	1241.7301	1241.7244	0.0058	1	12	1	---	APIKIGINGFGR
1434.7560	1433.7487	1433.7514	-0.0026	202	216	0	---	AASFNIIPSSTGAAK
1704.9102	1703.9029	1703.8954	0.0075	199	216	1	---	GGRAASFNIIPSSTGAAK
1725.9106	1724.9033	1724.8443	0.0591	128	142	1	---	DAPMFVVGVNEKEYK
1725.9106	1724.9033	1724.8443	0.0591	128	142	1	---	DAPMFVVGVNEKEYK
1775.8123	1774.8050	1774.7950	0.0100	311	324	0	58	LVSWYDNEWGYSTR
1775.8123	1774.8050	1774.7950	0.0100	311	324	0	---	LVSWYDNEWGYSTR
1869.0740	1868.0667	1868.0618	0.0049	236	252	1	---	VPTVDVSVVDLTVRLEK
1910.0029	1908.9956	1908.9944	0.0012	293	310	1	---	SSIFDAKAGIALNDNFVK

No match to: 713.4005, 724.4910, 734.4893, 736.4972, 750.5109, 768.5142, 782.4717, 834.4753, 838.5221, 848.5233, 864.5333, 1007.6652, 1033.6917, 1225.7120, 1225.7120, 1247.6091, 1264.6997, 1279.7533, 1334.8765, 1336.6516, 1401.8431, 1448.9153, 1517.7506, 1562.9436, 1568.9407, 1618.0295, 1732.0928, 1749.8596, 1791.8119, 1807.8062, 2015.2837, 2143.0369, 2186.0339, 2186.0339, 2193.1377, 2230.2166, 2239.1445, 2299.4705, 2564.1958, 2632.3594, 2648.3667, 2662.4324, 2664.3718, 2665.3701, 2825.3167, 2908.4268, 2919.4272, 2923.3740, 3332.5688, 3349.6125, 3455.7031

3. gi|120666 **Mass:** 36776 **Score:** 220 **Expect:** 6.1e-017 **Queries matched:** 14

RecName: Full=Glyceraldehyde-3-phosphate dehydrogenase, cytosolic

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
746.3664	745.3591	745.3619	-0.0028	197	202	1	---	DWRGGR
784.5105	783.5032	783.5078	-0.0046	14	20	1	---	IGRLVAR
833.4711	832.4638	832.4555	0.0084	6	13	0	---	IGINGFGR
1161.6272	1160.6199	1160.6189	0.0010	301	311	0	---	AGIALNDNFVK
1242.7374	1241.7301	1241.7244	0.0058	2	13	1	82	APIKIGINGFGR
1242.7374	1241.7301	1241.7244	0.0058	2	13	1	---	APIKIGINGFGR
1434.7560	1433.7487	1433.7514	-0.0026	203	217	0	---	AASFNIIPSSTGAAK
1704.9102	1703.9029	1703.8954	0.0075	200	217	1	---	GGRAASFNIIPSSTGAAK
1725.9106	1724.9033	1724.8443	0.0591	129	143	1	---	DAPMFVVGVNEKEYK
1725.9106	1724.9033	1724.8443	0.0591	129	143	1	---	DAPMFVVGVNEKEYK
1775.8123	1774.8050	1774.7950	0.0100	312	325	0	58	LVSWYDNEWGYSTR
1775.8123	1774.8050	1774.7950	0.0100	312	325	0	---	LVSWYDNEWGYSTR
1869.0740	1868.0667	1868.0618	0.0049	237	253	1	---	VPTVDVSVVDLTVRLEK
1910.0029	1908.9956	1908.9944	0.0012	294	311	1	---	SSIFDAKAGIALNDNFVK

No match to: 713.4005, 724.4910, 734.4893, 736.4972, 750.5109, 768.5142, 782.4717, 834.4753, 838.5221, 848.5233, 864.5333, 1007.6652, 1033.6917, 1225.7120, 1225.7120, 1247.6091, 1264.6997, 1279.7533, 1334.8765, 1336.6516,

1401.8431, 1448.9153, 1517.7506, 1562.9436, 1568.9407, 1618.0295, 1732.0928, 1749.8596, 1791.8119, 1807.8062, 2015.2837, 2143.0369, 2186.0339, 2186.0339, 2193.1377, 2230.2166, 2239.1445, 2299.4705, 2564.1958, 2632.3594, 2648.3667, 2662.4324, 2664.3718, 2665.3701, 2825.3167, 2908.4268, 2919.4272, 2923.3740, 3332.5688, 3349.6125, 3455.7031

4. gi|120668 **Mass:** 33443 **Score:** 206 **Expect:** 1.5e-015 **Queries matched:** 16

RecName: Full=Glyceraldehyde-3-phosphate dehydrogenase, cytosolic

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
746.3664	745.3591	745.3619	-0.0028	165	170	1	---	DWRGGR
1161.6272	1160.6199	1160.6189	0.0010	269	279	0	---	AGIALNDNFVK
1247.6091	1246.6018	1246.5942	0.0076	157	167	1	---	TVDGPSSKDWR
1434.7560	1433.7487	1433.7514	-0.0026	171	185	0	---	AASFNIIPSSTGAAK
1704.9102	1703.9029	1703.8954	0.0075	168	185	1	---	GGRAASFNIIPSSTGAAK
1725.9106	1724.9033	1724.8919	0.0114	36	50	1	---	TLLFGEKEVAVFGCR
1725.9106	1724.9033	1724.8919	0.0114	36	50	1	16	TLLFGEKEVAVFGCR
1775.8123	1774.8050	1774.7950	0.0100	280	293	0	58	LVSWYDNEWGYSTR
1775.8123	1774.8050	1774.7950	0.0100	280	293	0	---	LVSWYDNEWGYSTR
1910.0029	1908.9956	1908.9944	0.0012	262	279	1	---	SSIFDAKAGIALNDNFVK
2186.0339	2185.0266	2185.0174	0.0092	242	261	0	33	GILGYVDEDLVSTDFQGDSR
2186.0339	2185.0266	2185.0174	0.0092	242	261	0	---	GILGYVDEDLVSTDFQGDSR
2632.3594	2631.3521	2631.3512	0.0009	133	156	1	---	VINDRFGIVEGLMTTVHAMTATQK
2648.3667	2647.3594	2647.3461	0.0133	133	156	1	---	VINDRFGIVEGLMTTVHAMTATQK + Oxidation (M)
2664.3718	2663.3645	2663.3410	0.0235	133	156	1	---	VINDRFGIVEGLMTTVHAMTATQK + 2 Oxidation (M)
2923.3740	2922.3667	2922.3922	-0.0255	51	77	1	---	NPEEIPWAAAGAEYVVESTGVFTDKDK

No match to: 713.4005, 724.4910, 734.4893, 736.4972, 750.5109, 768.5142, 782.4717, 784.5105, 833.4711, 834.4753, 838.5221, 848.5233, 864.5333, 1007.6652, 1033.6917, 1225.7120, 1225.7120, 1242.7374, 1242.7374, 1264.6997, 1279.7533, 1334.8765, 1336.6516, 1401.8431, 1448.9153, 1517.7506, 1562.9436, 1568.9407, 1618.0295, 1732.0928, 1749.8596, 1791.8119, 1807.8062, 1869.0740, 2015.2837, 2143.0369, 2193.1377, 2230.2166, 2239.1445, 2299.4705, 2564.1958, 2662.4324, 2665.3701, 2825.3167, 2908.4268, 2919.4272, 3332.5688, 3349.6125, 3455.7031

5. gi|462137 **Mass:** 37105 **Score:** 191 **Expect:** 4.8e-014 **Queries matched:** 10

RecName: Full=Glyceraldehyde-3-phosphate dehydrogenase, cytosolic

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
746.3664	745.3591	745.3619	-0.0028	197	202	1	---	DWRGGR
784.5105	783.5032	783.5078	-0.0046	14	20	1	---	IGRLVAR
833.4711	832.4638	832.4555	0.0084	6	13	0	---	IGINGFGR
1242.7374	1241.7301	1241.7244	0.0058	2	13	1	82	APIKIGINGFGR
1242.7374	1241.7301	1241.7244	0.0058	2	13	1	---	APIKIGINGFGR
1434.7560	1433.7487	1433.7514	-0.0026	203	217	0	---	AASFNIIPSSTGAAK
1704.9102	1703.9029	1703.8954	0.0075	200	217	1	---	GGRAASFNIIPSSTGAAK
1749.8596	1748.8523	1748.8383	0.0141	49	62	1	---	YDSVHGQWKHHDIK
1775.8123	1774.8050	1774.7950	0.0100	312	325	0	58	LVSWYDNEWGYSTR

1775.8123	1774.8050	1774.7950	0.0100	312 - 325	0	---	LVSWYDNEWGYSTR

No match to: 713.4005, 724.4910, 734.4893, 736.4972, 750.5109, 768.5142, 782.4717, 834.4753, 838.5221, 848.5233, 864.5333, 1007.6652, 1033.6917, 1161.6272, 1225.7120, 1225.7120, 1247.6091, 1264.6997, 1279.7533, 1334.8765, 1336.6516, 1401.8431, 1448.9153, 1517.7506, 1562.9436, 1568.9407, 1618.0295, 1725.9106, 1725.9106, 1732.0928, 1791.8119, 1807.8062, 1869.0740, 1910.0029, 2015.2837, 2143.0369, 2186.0339, 2186.0339, 2193.1377, 2230.2166, 2239.1445, 2299.4705, 2564.1958, 2632.3594, 2648.3667, 2662.4324, 2664.3718, 2665.3701, 2825.3167, 2908.4268, 2919.4272, 2923.3740, 3332.5688, 3349.6125, 3455.7031

6. gi|148508784 **Mass:** 36854 **Score:** 151 **Expect:** 4.8e-010 **Queries matched:** 14

glyceraldehyde-3-phosphate dehydrogenase [Triticum aestivum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
746.3664	745.3591	745.3619	-0.0028	197 -	202	1	---	DWRGGR
784.5105	783.5032	783.5078	-0.0046	14 -	20	1	---	IGRLVAR
833.4711	832.4638	832.4555	0.0084	6 -	13	0	---	IGINGFGR
1247.6091	1246.6018	1246.5942	0.0076	189 -	199	1	---	TVDGPSSKDWR
1434.7560	1433.7487	1433.7514	-0.0026	203 -	217	0	---	AASFNIIPSSTGAAK
1704.9102	1703.9029	1703.8954	0.0075	200 -	217	1	---	GGRAASFNIIPSSTGAAK
1725.9106	1724.9033	1724.8919	0.0114	68 -	82	1	---	TLLFGEKEVAVFGCR
1725.9106	1724.9033	1724.8919	0.0114	68 -	82	1	16	TLLFGEKEVAVFGCR
1775.8123	1774.8050	1774.7950	0.0100	312 -	325	0	58	LVSWYDNEWGYSTR
1775.8123	1774.8050	1774.7950	0.0100	312 -	325	0	---	LVSWYDNEWGYSTR
2632.3594	2631.3521	2631.3512	0.0009	165 -	188	1	---	VINDRFGIVEGLMTTVHAMTATQK
2648.3667	2647.3594	2647.3461	0.0133	165 -	188	1	---	VINDRFGIVEGLMTTVHAMTATQK + Oxidation (M)
2664.3718	2663.3645	2663.3410	0.0235	165 -	188	1	---	VINDRFGIVEGLMTTVHAMTATQK + 2 Oxidation (M)
2923.3740	2922.3667	2922.3922	-0.0255	83 -	109	1	---	NPEEIPWAAAGAEYVVESTGVFTDKDK

No match to: 713.4005, 724.4910, 734.4893, 736.4972, 750.5109, 768.5142, 782.4717, 834.4753, 838.5221, 848.5233, 864.5333, 1007.6652, 1033.6917, 1161.6272, 1225.7120, 1225.7120, 1242.7374, 1242.7374, 1264.6997, 1279.7533, 1334.8765, 1336.6516, 1401.8431, 1448.9153, 1517.7506, 1562.9436, 1568.9407, 1618.0295, 1732.0928, 1749.8596, 1791.8119, 1807.8062, 1869.0740, 1910.0029, 2015.2837, 2143.0369, 2186.0339, 2186.0339, 2193.1377, 2230.2166, 2239.1445, 2299.4705, 2564.1958, 2662.4324, 2665.3701, 2825.3167, 2908.4268, 2919.4272, 3332.5688, 3349.6125, 3455.7031

7. gi|115371630 **Mass:** 36877 **Score:** 143 **Expect:** 3e-009 **Queries matched:** 13

glyceraldehyde-3 phosphate dehydrogenase [Polygonum sibiricum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
746.3664	745.3591	745.3619	-0.0028	197 -	202	1	---	DWRGGR
784.5105	783.5032	783.5078	-0.0046	14 -	20	1	---	IGRLVAR
833.4711	832.4638	832.4555	0.0084	6 -	13	0	---	IGINGFGR
1161.6272	1160.6199	1160.6189	0.0010	301 -	311	0	---	AGIALNDNFVK
1434.7560	1433.7487	1433.7514	-0.0026	203 -	217	0	---	AASFNIIPSSTGAAK
1704.9102	1703.9029	1703.8954	0.0075	200 -	217	1	---	GGRAASFNIIPSSTGAAK
1749.8596	1748.8523	1748.8383	0.0141	49 -	62	1	---	YDTVHGQWKHHDVK
1775.8123	1774.8050	1774.7950	0.0100	312 -	325	0	58	LVSWYDNEWGYSTR

1775.8123	1774.8050	1774.7950	0.0100	312 - 325	0	---	LVSWYDNEWGYSTR
1869.0740	1868.0667	1868.0618	0.0049	237 - 253	1	---	VPTVDVSVVDLTVRLEK
1910.0029	1908.9956	1908.9944	0.0012	294 - 311	1	---	SSIFDAKAGIALNDNFVK
2186.0339	2185.0266	2185.0174	0.0092	274 - 293	0	---	GILGYTDEDLVSTDFVGDNR
2186.0339	2185.0266	2185.0174	0.0092	274 - 293	0	---	GILGYTDEDLVSTDFVGDNR

No match to: 713.4005, 724.4910, 734.4893, 736.4972, 750.5109, 768.5142, 782.4717, 834.4753, 838.5221, 848.5233, 864.5333, 1007.6652, 1033.6917, 1225.7120, 1225.7120, 1242.7374, 1242.7374, 1247.6091, 1264.6997, 1279.7533, 1334.8765, 1336.6516, 1401.8431, 1448.9153, 1517.7506, 1562.9436, 1568.9407, 1618.0295, 1725.9106, 1725.9106, 1732.0928, 1791.8119, 1807.8062, 2015.2837, 2143.0369, 2193.1377, 2230.2166, 2239.1445, 2299.4705, 2564.1958, 2632.3594, 2648.3667, 2662.4324, 2664.3718, 2665.3701, 2825.3167, 2908.4268, 2919.4272, 2923.3740, 3332.5688, 3349.6125, 3455.7031

8. gi|120675 **Mass:** 37015 **Score:** 134 **Expect:** 2.4e-008 **Queries matched:** 12

RecName: Full=Glyceraldehyde-3-phosphate dehydrogenase, cytosolic

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
746.3664	745.3591	745.3619	-0.0028	199 - 204	1	---	DWRGGR
784.5105	783.5032	783.5078	-0.0046	16 - 22	1	---	IGRLVAR
833.4711	832.4638	832.4555	0.0084	8 - 15	0	---	IGINGFGR
1225.7120	1224.7047	1224.6900	0.0147	328 - 338	1	---	VVDLIIHMSKA
1225.7120	1224.7047	1224.6900	0.0147	328 - 338	1	---	VVDLIIHMSKA
1434.7560	1433.7487	1433.7514	-0.0026	205 - 219	0	---	AASFNIIPSSTGAAK
1704.9102	1703.9029	1703.8954	0.0075	202 - 219	1	---	GGRAASFNIIPSSTGAAK
1775.8123	1774.8050	1774.7950	0.0100	314 - 327	0	58	LVSWYDNEWGYSTR
1775.8123	1774.8050	1774.7950	0.0100	314 - 327	0	---	LVSWYDNEWGYSTR
1869.0740	1868.0667	1868.0618	0.0049	239 - 255	1	---	VPTVDVSVVDLTVRLEK
2923.3740	2922.3667	2922.3558	0.0109	85 - 111	1	---	NPEDIPWGEAGADFVVESTGVFTDKDK
3349.6125	3348.6052	3348.6773	-0.0721	23 - 50	1	---	VILQRNDVELVAVNDPFITTEYMTYMFK

No match to: 713.4005, 724.4910, 734.4893, 736.4972, 750.5109, 768.5142, 782.4717, 834.4753, 838.5221, 848.5233, 864.5333, 1007.6652, 1033.6917, 1161.6272, 1242.7374, 1242.7374, 1247.6091, 1264.6997, 1279.7533, 1334.8765, 1336.6516, 1401.8431, 1448.9153, 1517.7506, 1562.9436, 1568.9407, 1618.0295, 1725.9106, 1725.9106, 1732.0928, 1749.8596, 1791.8119, 1807.8062, 1910.0029, 2015.2837, 2143.0369, 2186.0339, 2186.0339, 2193.1377, 2230.2166, 2239.1445, 2299.4705, 2564.1958, 2632.3594, 2648.3667, 2662.4324, 2664.3718, 2665.3701, 2825.3167, 2908.4268, 2919.4272, 3332.5688, 3455.7031

9. gi|162458671 **Mass:** 36656 **Score:** 133 **Expect:** 3e-008 **Queries matched:** 11

cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC4 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
746.3664	745.3591	745.3619	-0.0028	197 - 202	1	---	DWRGGR
784.5105	783.5032	783.5078	-0.0046	14 - 20	1	---	IGRLVAR
833.4711	832.4638	832.4555	0.0084	6 - 13	0	---	IGINGFGR
1247.6091	1246.6018	1246.5942	0.0076	189 - 199	1	---	TVDGPSSKDWR
1434.7560	1433.7487	1433.7514	-0.0026	203 - 217	0	---	AASFNIIPSSTGAAK
1704.9102	1703.9029	1703.8954	0.0075	200 - 217	1	---	GGRAASFNIIPSSTGAAK

1725.9106	1724.9033	1724.8919	0.0114	68 - 82	1	---	TLLFGEKEVAVFGCR
1725.9106	1724.9033	1724.8919	0.0114	68 - 82	1	16	TLLFGEKEVAVFGCR
1775.8123	1774.8050	1774.7950	0.0100	312 - 325	0	58	LVSWYDNEWGYSTR
1775.8123	1774.8050	1774.7950	0.0100	312 - 325	0	---	LVSWYDNEWGYSTR
1869.0740	1868.0667	1868.0618	0.0049	237 - 253	1	---	VPTVDVSVVDLTVRLEK

No match to: 713.4005, 724.4910, 734.4893, 736.4972, 750.5109, 768.5142, 782.4717, 834.4753, 838.5221, 848.5233, 864.5333, 1007.6652, 1033.6917, 1161.6272, 1225.7120, 1225.7120, 1242.7374, 1242.7374, 1264.6997, 1279.7533, 1334.8765, 1336.6516, 1401.8431, 1448.9153, 1517.7506, 1562.9436, 1568.9407, 1618.0295, 1732.0928, 1749.8596, 1791.8119, 1807.8062, 1910.0029, 2015.2837, 2143.0369, 2186.0339, 2186.0339, 2193.1377, 2230.2166, 2239.1445, 2299.4705, 2564.1958, 2632.3594, 2648.3667, 2662.4324, 2664.3718, 2665.3701, 2825.3167, 2908.4268, 2919.4272, 2923.3740, 3332.5688, 3349.6125, 3455.7031

10. gi|194707656 **Mass:** 36613 **Score:** 133 **Expect:** 3e-008 **Queries matched:** 11

unknown [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
746.3664	745.3591	745.3619	-0.0028	197 - 202		1	---	DWRGGR
784.5105	783.5032	783.5078	-0.0046	14 - 20		1	---	IGRLVAR
833.4711	832.4638	832.4555	0.0084	6 - 13		0	---	IGINGFGR
1247.6091	1246.6018	1246.5942	0.0076	189 - 199		1	---	TVDGPSSKDWR
1434.7560	1433.7487	1433.7514	-0.0026	203 - 217		0	---	AASFNIIPSSTGAAK
1704.9102	1703.9029	1703.8954	0.0075	200 - 217		1	---	GGRAASFNIIPSSTGAAK
1725.9106	1724.9033	1724.8919	0.0114	68 - 82		1	---	TLLFGEKEVAVFGCR
1725.9106	1724.9033	1724.8919	0.0114	68 - 82		1	16	TLLFGEKEVAVFGCR
1775.8123	1774.8050	1774.7950	0.0100	312 - 325		0	58	LVSWYDNEWGYSTR
1775.8123	1774.8050	1774.7950	0.0100	312 - 325		0	---	LVSWYDNEWGYSTR
1869.0740	1868.0667	1868.0618	0.0049	237 - 253		1	---	VPTVDVSVVDLTVRLEK

No match to: 713.4005, 724.4910, 734.4893, 736.4972, 750.5109, 768.5142, 782.4717, 834.4753, 838.5221, 848.5233, 864.5333, 1007.6652, 1033.6917, 1161.6272, 1225.7120, 1225.7120, 1242.7374, 1242.7374, 1264.6997, 1279.7533, 1334.8765, 1336.6516, 1401.8431, 1448.9153, 1517.7506, 1562.9436, 1568.9407, 1618.0295, 1732.0928, 1749.8596, 1791.8119, 1807.8062, 1910.0029, 2015.2837, 2143.0369, 2186.0339, 2186.0339, 2193.1377, 2230.2166, 2239.1445, 2299.4705, 2564.1958, 2632.3594, 2648.3667, 2662.4324, 2664.3718, 2665.3701, 2825.3167, 2908.4268, 2919.4272, 2923.3740, 3332.5688, 3349.6125, 3455.7031

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 65

Protein View

Match to: **gi|51703306** Score: **222** Expect: **3.8e-017**
glyceraldehyde 3-phosphate dehydrogenase [Daucus carota]

Nominal mass (M_r): **36768**; Calculated pI value: **7.05**
NCBI BLAST search of gi|51703306 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Daucus carota

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **30%**

Matched peptides shown in **Bold Red**

```
     1 MAPIKIGING FGRIGRLVAR VALQRDDVEL VAVNDPFIST DYMTYMFKYD
    51 SVHGAWKHHE LKVKDEKTLL FGEKPVAVFG CRNPEEIPWA STGAEYIVES
   101 TGVFTDKDKA AAHLKGGAKK VIISAPSKDA PMFVVGVNEK EYKSDLHIVS
   151 NASCTTNCLA PLAKVINDRF GIVEGLMTTV HSITATQKTV DGPSAKDWRG
   201 GRAASFNIIP SSTGAAKAVG KVLPQLNGKL TGMSFRVPTV DVSVVDLTVR
   251 LEKKATYDQI KAAIKEESEG KLKGILGYTE DDVVSTDFVG DSRSSIFDAK
   301 AGIALNDNFV KLVSWYDNEW GYSTRVVDLI VHMASVQ
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
2 - 13	1242.7374	1241.7301	1241.7244	0.0058	1	APIKIGINGFGR	(Ions score 82)
2 - 13	1242.7374	1241.7301	1241.7244	0.0058	1	APIKIGINGFGR	(No match)
6 - 13	833.4711	832.4638	832.4555	0.0084	0	IGINGFGR	(No match)
14 - 20	784.5105	783.5032	783.5078	-0.0046	1	IGRLVAR	(No match)
129 - 143	1725.9106	1724.9033	1724.8443	0.0591	1	DAPMFVVGVNEKEYK	(No match)
129 - 143	1725.9106	1724.9033	1724.8443	0.0591	1	DAPMFVVGVNEKEYK	(No match)
197 - 202	746.3664	745.3591	745.3619	-0.0028	1	DWRGGR	(No match)
200 - 217	1704.9102	1703.9029	1703.8954	0.0075	1	GGRAASFNIIPSSTGAAK	(No match)
203 - 217	1434.7560	1433.7487	1433.7514	-0.0026	0	AASFNIIPSSTGAAK	(No match)
237 - 253	1869.0740	1868.0667	1868.0618	0.0049	1	VPTVDVSVVDLTVRLEK	(No match)
294 - 311	1910.0029	1908.9956	1908.9944	0.0012	1	SSIFDAKAGIALNDNFVK	(No match)
301 - 311	1161.6272	1160.6199	1160.6189	0.0010	0	AGIALNDNFVK	(No match)
312 - 325	1775.8123	1774.8050	1774.7950	0.0100	0	LVSWYDNEWGYSTR	(Ions score 58)
312 - 325	1775.8123	1774.8050	1774.7950	0.0100	0	LVSWYDNEWGYSTR	(No match)

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Index

	Accession	Mass	Score	Description
1.	gi|226502274	44631	87	hypothetical protein LOC100273946 [Zea mays]
2.	gi|125581161	27071	68	hypothetical protein OsJ_05753 [Oryza sativa Japonica Group]
3.	gi|2832691	39669	67	polygalacturonase-like protein [Arabidopsis thaliana]
4.	gi|218190250	40600	67	hypothetical protein OsI_06235 [Oryza sativa Indica Group]
5.	gi|224102769	44771	67	predicted protein [Populus trichocarpa]
6.	gi|15236790	45764	67	glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein [Arabidop
7.	gi|49388133	44519	67	putative exopolygalacturonase precursor [Oryza sativa Japonica Group]
8.	gi|115444829	47052	66	Os02g0196700 [Oryza sativa (japonica cultivar-group)]
9.	gi|15225803	76008	65	glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein [Arabidop
10.	gi|255566763	42374	42	Polygalacturonase precursor, putative [Ricinus communis]

Results List

1. gi|226502274 **Mass:** 44631 **Score:** 87 **Expect:** 0.0012 **Queries matched:** 4

hypothetical protein LOC100273946 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
734.4844	733.4771	733.4334	0.0438	307	313	1	---	SSLKATK
1353.6807	1352.6734	1352.6618	0.0116	260	273	0	60	CGPGHGISVGSLGR
1353.6807	1352.6734	1352.6618	0.0116	260	273	0	---	CGPGHGISVGSLGR
2565.1968	2564.1895	2564.3420	-0.1525	162	183	1	---	SYNCKILPNSLVLDFVTNAQIR

No match to: 713.3979, 768.5065, 864.5247, 1183.5016, 1183.5016, 1279.7466, 1336.6523, 1336.6523, 1448.8778, 1774.8444, 2922.3516, 3057.4939

2. gi|125581161 **Mass:** 27071 **Score:** 68 **Expect:** 0.088 **Queries matched:** 2

hypothetical protein OsJ_05753 [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1353.6807	1352.6734	1352.6618	0.0116	92	105	0	60	CGPGHGISVGSLGR
1353.6807	1352.6734	1352.6618	0.0116	92	105	0	---	CGPGHGISVGSLGR

No match to: 713.3979, 734.4844, 768.5065, 864.5247, 1183.5016, 1183.5016, 1279.7466, 1336.6523, 1336.6523, 1448.8778, 1774.8444, 2565.1968, 2922.3516, 3057.4939

3. gi|2832691 **Mass:** 39669 **Score:** 67 **Expect:** 0.12 **Queries matched:** 2

polygalacturonase-like protein [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1353.6807	1352.6734	1352.6618	0.0116	193	206	0	60	CGPGHGISVGSLGR
1353.6807	1352.6734	1352.6618	0.0116	193	206	0	---	CGPGHGISVGSLGR

No match to: 713.3979, 734.4844, 768.5065, 864.5247, 1183.5016, 1183.5016, 1279.7466, 1336.6523, 1336.6523, 1448.8778, 1774.8444, 2565.1968, 2922.3516, 3057.4939

4. gi|218190250 **Mass:** 40600 **Score:** 67 **Expect:** 0.12 **Queries matched:** 2

hypothetical protein OsI_06235 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1353.6807	1352.6734	1352.6618	0.0116	226 -	239	0	60	CGPGHGISVGSLGR
1353.6807	1352.6734	1352.6618	0.0116	226 -	239	0	---	CGPGHGISVGSLGR

No match to: 713.3979, 734.4844, 768.5065, 864.5247, 1183.5016, 1183.5016, 1279.7466, 1336.6523, 1336.6523, 1448.8778, 1774.8444, 2565.1968, 2922.3516, 3057.4939

5. gi|224102769 **Mass:** 44771 **Score:** 67 **Expect:** 0.13 **Queries matched:** 2

predicted protein [Populus trichocarpa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1353.6807	1352.6734	1352.6618	0.0116	252 -	265	0	60	CGPGHGISVGSLGR
1353.6807	1352.6734	1352.6618	0.0116	252 -	265	0	---	CGPGHGISVGSLGR

No match to: 713.3979, 734.4844, 768.5065, 864.5247, 1183.5016, 1183.5016, 1279.7466, 1336.6523, 1336.6523, 1448.8778, 1774.8444, 2565.1968, 2922.3516, 3057.4939

6. gi|15236790 **Mass:** 45764 **Score:** 67 **Expect:** 0.13 **Queries matched:** 2

glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein [Arabidopsis t

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1353.6807	1352.6734	1352.6618	0.0116	245 -	258	0	60	CGPGHGISVGSLGR
1353.6807	1352.6734	1352.6618	0.0116	245 -	258	0	---	CGPGHGISVGSLGR

No match to: 713.3979, 734.4844, 768.5065, 864.5247, 1183.5016, 1183.5016, 1279.7466, 1336.6523, 1336.6523, 1448.8778, 1774.8444, 2565.1968, 2922.3516, 3057.4939

7. gi|49388133 **Mass:** 44519 **Score:** 67 **Expect:** 0.13 **Queries matched:** 2

putative exopolygalacturonase precursor [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1353.6807	1352.6734	1352.6618	0.0116	264 -	277	0	60	CGPGHGISVGSLGR
1353.6807	1352.6734	1352.6618	0.0116	264 -	277	0	---	CGPGHGISVGSLGR

No match to: 713.3979, 734.4844, 768.5065, 864.5247, 1183.5016, 1183.5016, 1279.7466, 1336.6523, 1336.6523, 1448.8778, 1774.8444, 2565.1968, 2922.3516, 3057.4939

8. gi|115444829 **Mass:** 47052 **Score:** 66 **Expect:** 0.14 **Queries matched:** 2

Os02g0196700 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1353.6807	1352.6734	1352.6618	0.0116	291 -	304	0	60	CGPGHGISVGSLGR
1353.6807	1352.6734	1352.6618	0.0116	291 -	304	0	---	CGPGHGISVGSLGR

No match to: 713.3979, 734.4844, 768.5065, 864.5247, 1183.5016, 1183.5016, 1279.7466, 1336.6523, 1336.6523, 1448.8778, 1774.8444, 2565.1968, 2922.3516, 3057.4939

9. gi|15225803 **Mass:** 76008 **Score:** 65 **Expect:** 0.18 **Queries matched:** 2

glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein [Arabidopsis t

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1353.6807	1352.6734	1352.6618	0.0116	243 -	256	0	60	CGPGHGISVGSLGR
1353.6807	1352.6734	1352.6618	0.0116	243 -	256	0	---	CGPGHGISVGSLGR

No match to: 713.3979, 734.4844, 768.5065, 864.5247, 1183.5016, 1183.5016, 1279.7466, 1336.6523, 1336.6523, 1448.8778, 1774.8444, 2565.1968, 2922.3516, 3057.4939

10. gi|255566763 **Mass:** 42374 **Score:** 42 **Expect:** 37 **Queries matched:** 3

Polygalacturonase precursor, putative [Ricinus communis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1279.7466	1278.7393	1278.6615	0.0779	377 -	387	1	---	RIGHVRPDGCL
1353.6807	1352.6734	1352.6870	-0.0136	232 -	245	0	26	CGPGHGISIGSLAK
1353.6807	1352.6734	1352.6870	-0.0136	232 -	245	0	---	CGPGHGISIGSLAK

No match to: 713.3979, 734.4844, 768.5065, 864.5247, 1183.5016, 1183.5016, 1336.6523, 1336.6523, 1448.8778, 1774.8444, 2565.1968, 2922.3516, 3057.4939

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 16

Protein View

Match to: **gi|226502274** Score: **87** Expect: **0.0012**
hypothetical protein LOC100273946 [Zea mays]

Nominal mass (M_r): **44631**; Calculated pI value: **8.96**
NCBI BLAST search of gi|226502274 against nr
Unformatted sequence string for pasting into other applications
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|194706004 from Zea mays

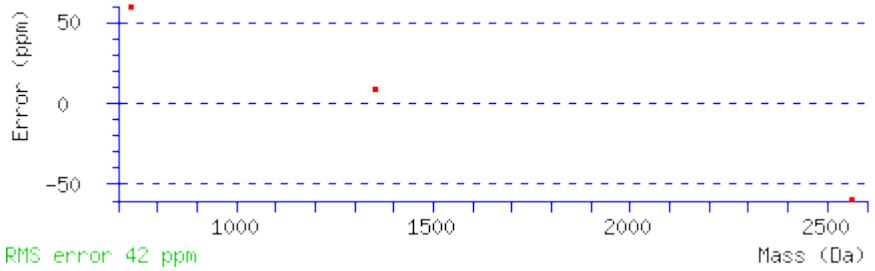
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **10%**

Matched peptides shown in **Bold Red**

```
   1 MAFISSAAMK AAVAALLVFA AVSPAARAVA AEAEAKAKAV GGAPSVPAGS
  51 LDIAQLGAKG DGKSDSTPMV LKAWKHACEA TGQQKIVIPK GNYLTGALDL
 101 VGPCKSSIII RLDGNLLGTG DLNAYKRNWI EIQNVDNLSI NGHGTIDGQG
 151 ALVWNKNECQ RSYNCKILPN SLVLDFVTNA QIRGITLLNS KFFHMNIFGS
 201 KNVVIDKVTI KAPGNSPNTD GIHIGDSSNV TISGTTIAVG DDCVSIGPGS
 251 KTIRVKGVKC GPGHGISVGS LGRYKDEKDV EDVKVTGCTL AGTTNGLRIK
 301 SYEDSKSSLK ATKFLYQDVT MDNVSYPIII DQKYCPNNIC VKSGASKVAV
 351 NDVVFKNIHG TSNTPEAITL NCANNLPCQG VQLINVDIKY NRSDNKTMSV
 401 CKNAIGKSIG MAKELACV
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
162 - 183	2565.1968	2564.1895	2564.3420	-0.1525	1	SYNCKILPNSLVLDFVTNAQIR	(No match)
260 - 273	1353.6807	1352.6734	1352.6618	0.0116	0	CGPGHGISVGSLGR	(Ions score 60)
260 - 273	1353.6807	1352.6734	1352.6618	0.0116	0	CGPGHGISVGSLGR	(No match)
307 - 313	734.4844	733.4771	733.4334	0.0438	1	SSLKATK	(No match)



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Index

	Accession	Mass	Score	Description
1.	gi|218190250	40600	124	hypothetical protein OsI_06235 [Oryza sativa Indica Group]
2.	gi|49388133	44519	123	putative exopolygalacturonase precursor [Oryza sativa Japonica Group]
3.	gi|115444829	47052	123	Os02g0196700 [Oryza sativa (japonica cultivar-group)]
4.	gi|222849203	44771	123	predicted protein [Populus trichocarpa]
5.	gi|125581161	27071	117	hypothetical protein OsJ_05753 [Oryza sativa Japonica Group]

Results List

1. gi|218190250 **Mass:** 40600 **Score:** 124 **Expect:** 2.4e-007 **Queries matched:** 3

hypothetical protein OsI_06235 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1353.6660	1352.6587	1352.6618	-0.0031	226	239	0	---	CGPGHGISVGSLGR
1353.6660	1352.6587	1352.6618	-0.0031	226	239	0	109	CGPGHGISVGSLGR
1903.9612	1902.9539	1903.0414	-0.0875	133	149	0	---	ILPNSLVIDYSTNVTVR

No match to: 713.4079, 724.4963, 768.5212, 838.5328, 881.2689, 886.9876, 1183.4987, 1183.4987, 1336.6459, 1336.6459, 1352.6399, 1726.9327, 1774.8638, 1774.8638, 2139.0852, 2139.0852, 2689.3809

2. gi|49388133 **Mass:** 44519 **Score:** 123 **Expect:** 3e-007 **Queries matched:** 3

putative exopolygalacturonase precursor [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1353.6660	1352.6587	1352.6618	-0.0031	264	277	0	---	CGPGHGISVGSLGR
1353.6660	1352.6587	1352.6618	-0.0031	264	277	0	109	CGPGHGISVGSLGR
1903.9612	1902.9539	1903.0414	-0.0875	171	187	0	---	ILPNSLVIDYSTNVTVR

No match to: 713.4079, 724.4963, 768.5212, 838.5328, 881.2689, 886.9876, 1183.4987, 1183.4987, 1336.6459, 1336.6459, 1352.6399, 1726.9327, 1774.8638, 1774.8638, 2139.0852, 2139.0852, 2689.3809

3. gi|115444829 **Mass:** 47052 **Score:** 123 **Expect:** 3e-007 **Queries matched:** 3

Os02g0196700 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1353.6660	1352.6587	1352.6618	-0.0031	291	304	0	---	CGPGHGISVGSLGR
1353.6660	1352.6587	1352.6618	-0.0031	291	304	0	109	CGPGHGISVGSLGR
1903.9612	1902.9539	1903.0414	-0.0875	198	214	0	---	ILPNSLVIDYSTNVTVR

No match to: 713.4079, 724.4963, 768.5212, 838.5328, 881.2689, 886.9876, 1183.4987, 1183.4987, 1336.6459, 1336.6459, 1352.6399, 1726.9327, 1774.8638, 1774.8638, 2139.0852, 2139.0852, 2689.3809

4. gi|222849203 **Mass:** 44771 **Score:** 123 **Expect:** 3e-007 **Queries matched:** 3

predicted protein [Populus trichocarpa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1352.6399	1351.6326	1351.6772	-0.0445	56 -	67	1	---	TDDSKAFIAAWK
1353.6660	1352.6587	1352.6618	-0.0031	252 -	265	0	---	CGPGHGISVGSLGR
1353.6660	1352.6587	1352.6618	-0.0031	252 -	265	0	109	CGPGHGISVGSLGR

No match to: 713.4079, 724.4963, 768.5212, 838.5328, 881.2689, 886.9876, 1183.4987, 1183.4987, 1336.6459, 1336.6459, 1726.9327, 1774.8638, 1774.8638, 1903.9612, 2139.0852, 2139.0852, 2689.3809

5. gi|125581161 **Mass:** 27071 **Score:** 117 **Expect:** 1.2e-006 **Queries matched:** 2

hypothetical protein OsJ_05753 [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1353.6660	1352.6587	1352.6618	-0.0031	92 -	105	0	---	CGPGHGISVGSLGR
1353.6660	1352.6587	1352.6618	-0.0031	92 -	105	0	109	CGPGHGISVGSLGR

No match to: 713.4079, 724.4963, 768.5212, 838.5328, 881.2689, 886.9876, 1183.4987, 1183.4987, 1336.6459, 1336.6459, 1352.6399, 1726.9327, 1774.8638, 1774.8638, 1903.9612, 2139.0852, 2139.0852, 2689.3809

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 20

Protein View

Match to: **gi|218190250** Score: **124** Expect: **2.4e-007**
hypothetical protein OsI_06235 [Oryza sativa Indica Group]

Nominal mass (M_r): **40600**; Calculated pI value: **7.92**
NCBI BLAST search of gi|218190250 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Oryza sativa Indica Group

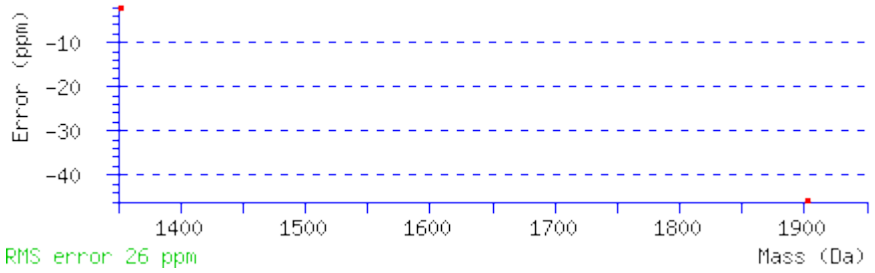
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **8%**

Matched peptides shown in **Bold Red**

```
   1 MVSSTRRTTS SLSATTAAAI AAAAAALMVS VAFATAQYTP ATSAAPGAAA
  51 AGAAAPYTPG AAGAAPSGPC TSSIILRLDG NLLGTGDLNA YKTNWIEVEH
 101 VDNFAINGHG IIDGQGPLVW THNQCNKNYN CKILPNSLVI DYSTNVTVRG
 151 ITLKNSKFFH LNIYESKNVV IDKVTITSPG DSPNTDGIHV GDSTNITISS
 201 TTIAAGDDCI SIGPGTKMVR VNGVRCGPGH GISVGSLGRY KDEKDVEDII
 251 VTNCTIKGTT NGLRIKSYED SKSQLRATKF LYDGITMDNV SYPIIIDQKY
 301 CPNNICSASG TSKVAVTDIV FKNIVGTSAT PEAVTLNCAN NLPCQGIQLH
 351 NVDLKYAGQG NTTLSVCKNV AGKSSNVAKE LACV
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
133 - 149	1903.9612	1902.9539	1903.0414	-0.0875	0	ILPNSLVIDYSTNVTVR	(No match)
226 - 239	1353.6660	1352.6587	1352.6618	-0.0031	0	CGPGHGISVGSLGR	(No match)
226 - 239	1353.6660	1352.6587	1352.6618	-0.0031	0	CGPGHGISVGSLGR	(Ions score 109)



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	Accession	Mass	Score	Description
1.	gi|125527658	92956	148	hypothetical protein OsI_03688 [Oryza sativa Indica Group]
2.	gi|115439863	92910	138	Os01g0742200 [Oryza sativa (japonica cultivar-group)]
3.	gi|157348808	56769	50	unnamed protein product [Vitis vinifera]
4.	gi|10798636	16323	50	elongation factor 2 [Nicotiana tabacum]
5.	gi|194700054	32946	49	unknown [Zea mays]

Results List

1. gi|125527658 **Mass:** 92956 **Score:** 148 **Expect:** 9.6e-010 **Queries matched:** 12

hypothetical protein OsI_03688 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
852.4524	851.4451	851.4362	0.0090	576	582	1	---	SPNKHNR
1152.6400	1151.6327	1151.6120	0.0207	394	404	1	---	VFSGRVATGMK
1330.7771	1329.7698	1329.7768	-0.0070	711	722	0	---	VIYAAQLTAKPR
1330.7771	1329.7698	1329.7768	-0.0070	711	722	0	43	VIYAAQLTAKPR
1486.8771	1485.8698	1485.8779	-0.0081	710	722	1	50	RVIYAAQLTAKPR
1486.8771	1485.8698	1485.8779	-0.0081	710	722	1	---	RVIYAAQLTAKPR
1650.8243	1649.8170	1649.8300	-0.0130	615	628	1	---	ILSEEFGWDKDLAK
2116.0632	2115.0559	2115.0571	-0.0011	751	768	0	---	GHVFEEMQRPGTPLYNIK
2132.0557	2131.0484	2131.0520	-0.0035	751	768	0	10	GHVFEEMQRPGTPLYNIK + Oxidation (M)
2132.0557	2131.0484	2131.0520	-0.0035	751	768	0	---	GHVFEEMQRPGTPLYNIK + Oxidation (M)
2288.1555	2287.1482	2287.1531	-0.0049	750	768	1	---	RGHVFEEMQRPGTPLYNIK + Oxidation (M)
2728.3945	2727.3872	2727.3472	0.0401	583	606	1	---	LYMEARPMEEGLPEAINEGRIGPR

No match to: 713.4143, 724.4999, 743.9482, 744.4532, 768.5270, 838.5302, 864.5374, 886.9824, 955.5328, 1053.5331, 1111.6255, 1279.7725, 1305.6713, 1320.5829, 1350.6790, 1459.7474, 1470.3124, 1687.9594, 1770.9344, 1770.9344, 1866.9231, 1995.0167, 2069.6809, 2151.1140, 2279.2065, 2304.1301, 2304.1301, 2383.9539, 2490.2427, 2885.6758, 3039.7012

2. gi|115439863 **Mass:** 92910 **Score:** 138 **Expect:** 9.6e-009 **Queries matched:** 11

Os01g0742200 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
852.4524	851.4451	851.4362	0.0090	576	582	1	---	SPNKHNR
1152.6400	1151.6327	1151.6120	0.0207	394	404	1	---	VFSGRVATGMK
1330.7771	1329.7698	1329.7768	-0.0070	711	722	0	---	VIYAAQLTAKPR
1330.7771	1329.7698	1329.7768	-0.0070	711	722	0	43	VIYAAQLTAKPR
1486.8771	1485.8698	1485.8779	-0.0081	710	722	1	50	RVIYAAQLTAKPR
1486.8771	1485.8698	1485.8779	-0.0081	710	722	1	---	RVIYAAQLTAKPR

1650.8243	1649.8170	1649.8300	-0.0130	615 - 628	1	---	ILSEEFGWDKDLAK
2116.0632	2115.0559	2115.0571	-0.0011	751 - 768	0	---	GHVFEEMQRPGTPLYNIK
2132.0557	2131.0484	2131.0520	-0.0035	751 - 768	0	10	GHVFEEMQRPGTPLYNIK + Oxidation (M)
2132.0557	2131.0484	2131.0520	-0.0035	751 - 768	0	---	GHVFEEMQRPGTPLYNIK + Oxidation (M)
2288.1555	2287.1482	2287.1531	-0.0049	750 - 768	1	---	RGHVFEEMQRPGTPLYNIK + Oxidation (M)

No match to: 713.4143, 724.4999, 743.9482, 744.4532, 768.5270, 838.5302, 864.5374, 886.9824, 955.5328, 1053.5331, 1111.6255, 1279.7725, 1305.6713, 1320.5829, 1350.6790, 1459.7474, 1470.3124, 1687.9594, 1770.9344, 1770.9344, 1866.9231, 1995.0167, 2069.6809, 2151.1140, 2279.2065, 2304.1301, 2304.1301, 2383.9539, 2490.2427, 2728.3945, 2885.6758, 3039.7012

3. gi|157348808 **Mass:** 56769 **Score:** 50 **Expect:** 5.6 **Queries matched:** 9

unnamed protein product [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
852.4524	851.4451	851.4362	0.0090	245 - 251	1	---	SPNKHNR
955.5328	954.5255	954.5246	0.0009	367 - 376	0	---	GGGQVIPTAR
1111.6255	1110.6182	1110.6257	-0.0075	367 - 377	1	---	GGGQVIPTARR
1459.7474	1458.7401	1458.7652	-0.0251	74 - 86	1	---	VRIMGPNYVPGEK
1650.8243	1649.8170	1649.8300	-0.0130	284 - 297	1	---	ILSEEFGWDKDLAK
2116.0632	2115.0559	2115.0571	-0.0011	418 - 435	0	---	GHVFEEMQRPGTPLYNIK
2132.0557	2131.0484	2131.0520	-0.0035	418 - 435	0	10	GHVFEEMQRPGTPLYNIK + Oxidation (M)
2132.0557	2131.0484	2131.0520	-0.0035	418 - 435	0	---	GHVFEEMQRPGTPLYNIK + Oxidation (M)
2288.1555	2287.1482	2287.1531	-0.0049	417 - 435	1	---	RGHVFEEMQRPGTPLYNIK + Oxidation (M)

No match to: 713.4143, 724.4999, 743.9482, 744.4532, 768.5270, 838.5302, 864.5374, 886.9824, 1053.5331, 1152.6400, 1279.7725, 1305.6713, 1320.5829, 1330.7771, 1330.7771, 1350.6790, 1470.3124, 1486.8771, 1486.8771, 1687.9594, 1770.9344, 1770.9344, 1866.9231, 1995.0167, 2069.6809, 2151.1140, 2279.2065, 2304.1301, 2304.1301, 2383.9539, 2490.2427, 2728.3945, 2885.6758, 3039.7012

4. gi|10798636 **Mass:** 16323 **Score:** 50 **Expect:** 5.9 **Queries matched:** 6

elongation factor 2 [Nicotiana tabacum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
955.5328	954.5255	954.5246	0.0009	6 - 15	0	---	GGGQVIPTAR
1111.6255	1110.6182	1110.6257	-0.0075	6 - 16	1	---	GGGQVIPTARR
2116.0632	2115.0559	2115.0571	-0.0011	57 - 74	0	---	GHVFEEMQRPGTPLYNIK
2132.0557	2131.0484	2131.0520	-0.0035	57 - 74	0	10	GHVFEEMQRPGTPLYNIK + Oxidation (M)
2132.0557	2131.0484	2131.0520	-0.0035	57 - 74	0	---	GHVFEEMQRPGTPLYNIK + Oxidation (M)
2288.1555	2287.1482	2287.1531	-0.0049	56 - 74	1	---	RGHVFEEMQRPGTPLYNIK + Oxidation (M)

No match to: 713.4143, 724.4999, 743.9482, 744.4532, 768.5270, 838.5302, 852.4524, 864.5374, 886.9824, 1053.5331, 1152.6400, 1279.7725, 1305.6713, 1320.5829, 1330.7771, 1330.7771, 1350.6790, 1459.7474, 1470.3124, 1486.8771, 1486.8771, 1650.8243, 1687.9594, 1770.9344, 1770.9344, 1866.9231, 1995.0167, 2069.6809, 2151.1140, 2279.2065, 2304.1301, 2304.1301, 2383.9539, 2490.2427, 2728.3945, 2885.6758, 3039.7012

5. gi|194700054 **Mass:** 32946 **Score:** 49 **Expect:** 8.5 **Queries matched:** 7

unknown [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
852.4524	851.4451	851.4362	0.0090	31	37	1	---	SPNKHNR
955.5328	954.5255	954.5246	0.0009	153	162	0	---	GGGQVIPTAR
1111.6255	1110.6182	1110.6257	-0.0075	153	163	1	---	GGGQVIPTARR
2116.0632	2115.0559	2115.0571	-0.0011	204	221	0	---	GHVFEEMQRPGTPLYNIK
2132.0557	2131.0484	2131.0520	-0.0035	204	221	0	10	GHVFEEMQRPGTPLYNIK + Oxidation (M)
2132.0557	2131.0484	2131.0520	-0.0035	204	221	0	---	GHVFEEMQRPGTPLYNIK + Oxidation (M)
2288.1555	2287.1482	2287.1531	-0.0049	203	221	1	---	RGHVFEEMQRPGTPLYNIK + Oxidation (M)

No match to: 713.4143, 724.4999, 743.9482, 744.4532, 768.5270, 838.5302, 864.5374, 886.9824, 1053.5331, 1152.6400, 1279.7725, 1305.6713, 1320.5829, 1330.7771, 1330.7771, 1350.6790, 1459.7474, 1470.3124, 1486.8771, 1486.8771, 1650.8243, 1687.9594, 1770.9344, 1770.9344, 1866.9231, 1995.0167, 2069.6809, 2151.1140, 2279.2065, 2304.1301, 2304.1301, 2383.9539, 2490.2427, 2728.3945, 2885.6758, 3039.7012

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 43

Protein View

Match to: **gi|125527658** Score: **148** Expect: **9.6e-010**
hypothetical protein OsI_03688 [Oryza sativa Indica Group]

Nominal mass (M_r): **92956**; Calculated pI value: **6.15**
NCBI BLAST search of gi|125527658 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Oryza sativa Indica Group

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **10%**

Matched peptides shown in **Bold Red**

```
   1 MVKFTVEEMR RIMDKKHNIR NMSVVAHVDH GKSTLTDSLV AAAGIIAQDV
  51 AGDVRMTDSR ADEAERGITI KSTGISLYYE MSDESLKSYK GDRDGNEYLI
 101 NLIDSPGHVD FSSEVTAALR ITDGALVVVD CIEGVCVQTE TVLRQALGER
 151 IRPVLTVNKM DRCFLELQVG GEEAYQTFSR VIENANVIMA TYEDALLGDV
 201 QVYPEKGTVA FSAGLHGWAF TLSNFAKMYA SEFGVDESKM MERLWGENYF
 251 DPTTKKWTIK HTGSDTCKRG FIQFCYEPIR QIINTCMNDQ KDKLLPMLQK
 301 LGVTMKDLTG KALMKRVMQT WLPASNALLE MMIYHLPSPA KAQRYRVENL
 351 YEGPLDDIYA SAIRNCDPEG PLMLYVSKMI PASDKGRFYA FGRVFSGRVA
 401 TGMKVRIMGP NYAPGQKKDL YVKNVQRTVI WMGKKQESVE DVPCGNTVAM
 451 VGLDQFITKN ATLTNEKEVD ACPIKAMKFS VSPVVRIAVQ CKVASDLSKL
 501 VEGLKRLAKS DPMVLCTVEE SGEHIIAGAG ELHLEICLKD LQEDFMGGAE
 551 ITVSPPVVSF RETVLEKSCR TVMSKSPNKH NRLYMEARPM EEGLPEAINE
 601 GRIGPRDDPK VRSKILSEEF GWDKDLAKKI WCFGPETTGP NIVVDMCKGV
 651 QYLNEIKDSV VAGFQWASKE GALAEENMRG RGICFEVCDV ILHSDAIHRG
 701 GGQIIPTARR VIYAAQLTAK PRLLEPVYLV EIQAPENALG GIYSVLNQKR
 751 GHVFEEMQRP GTPLYNIKAY LPVIESFGFT STLRAATSGQ AFPLFVFDHW
 801 EMLSVDPLEP GTRQLTLSWI SARGRV
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
394 - 404	1152.6400	1151.6327	1151.6120	0.0207	1	**VFSGRVATGMK** (No match)
576 - 582	852.4524	851.4451	851.4362	0.0090	1	**SPNKHNR** (No match)
583 - 606	2728.3945	2727.3872	2727.3472	0.0401	1	**LYMEARPMEEGLPEAINEGRIGPR** (No match)
615 - 628	1650.8243	1649.8170	1649.8300	-0.0130	1	**ILSEEFGWDKDLAK** (No match)
710 - 722	1486.8771	1485.8698	1485.8779	-0.0081	1	**RVIYAAQLTAKPR** (Ions score 50)
710 - 722	1486.8771	1485.8698	1485.8779	-0.0081	1	**RVIYAAQLTAKPR** (No match)
711 - 722	1330.7771	1329.7698	1329.7768	-0.0070	0	**VIYAAQLTAKPR** (No match)
711 - 722	1330.7771	1329.7698	1329.7768	-0.0070	0	**VIYAAQLTAKPR** (Ions score 43)
750 - 768	2288.1555	2287.1482	2287.1531	-0.0049	1	**RGHVFEEMQRPGTPLYNIK** Oxidation (M) (No match)
751 - 768	2116.0632	2115.0559	2115.0571	-0.0011	0	**GHVFEEMQRPGTPLYNIK** (No match)
751 - 768	2132.0557	2131.0484	2131.0520	-0.0035	0	**GHVFEEMQRPGTPLYNIK** Oxidation (M) (Ions score 10)
751 - 768	2132.0557	2131.0484	2131.0520	-0.0035	0	**GHVFEEMQRPGTPLYNIK** Oxidation (M) (No match)

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	Accession	Mass	Score	Description
1.	gi|5419990	25028	288	putative fructose-bisphosphate aldolase [Phleum pratense]
2.	gi|218157	39151	166	cytoplasmic aldolase [Oryza sativa Japonica Group]
3.	gi|110288655	39137	165	Fructose-bisphosphate aldolase, cytoplasmic isozyme, putative, expressed [Oryza sativa (japoni
4.	gi|125548604	39099	165	hypothetical protein OsI_16195 [Oryza sativa Indica Group]
5.	gi|2213867	38362	151	fructose-biphosphate aldolase [Mesembryanthemum crystallinum]
6.	gi|77999255	38812	63	unknown [Solanum tuberosum]
7.	gi|14484932	22651	62	fructose-1,6-bisphosphate aldolase [Lycopersicon esculentum]
8.	gi|195647936	10427	58	hypothetical protein [Zea mays]
9.	gi|87241376	19965	56	IMP dehydrogenase/GMP reductase, related [Medicago truncatula]
10.	gi|226501498	74401	55	hypothetical protein LOC100279342 [Zea mays]

Results List

1. gi|5419990 **Mass:** 25028 **Score:** 288 **Expect:** 9.6e-024 **Queries matched:** 12

putative fructose-bisphosphate aldolase [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
707.3941	706.3868	706.3914	-0.0046	8	12	1	---	FAKWR
829.3837	828.3764	828.3766	-0.0001	1	7	0	---	YYEAGAR
932.5704	931.5631	931.5603	0.0029	187	194	1	---	AQKAFLVR
1371.7285	1370.7212	1370.7135	0.0078	157	167	0	49	KPWFLSFSFGR
1371.7285	1370.7212	1370.7135	0.0078	157	167	0	---	KPWFLSFSFGR
1842.0175	1841.0102	1840.9987	0.0115	153	167	1	---	LQTKKPWFLSFSFGR
2108.0801	2107.0728	2107.0657	0.0071	17	36	0	98	IGPNEPSQLSIDQNAQGLAR
2108.0801	2107.0728	2107.0657	0.0071	17	36	0	---	IGPNEPSQLSIDQNAQGLAR
2519.3623	2518.3550	2518.3503	0.0048	13	36	1	---	AVLKIGPNEPSQLSIDQNAQGLAR
2519.3623	2518.3550	2518.3503	0.0048	13	36	1	54	AVLKIGPNEPSQLSIDQNAQGLAR
2763.4409	2762.4336	2762.4272	0.0064	79	104	0	---	ALNDQHVLLEGSLLKPNMVTPGSDAK + Oxidation (M)
2891.5393	2890.5320	2890.5221	0.0099	79	105	1	---	ALNDQHVLLEGSLLKPNMVTPGSDAKK + Oxidation (M)

No match to: 713.3993, 734.4901, 750.5125, 768.5131, 782.4778, 848.5271, 881.2793, 1133.7045, 1171.5286, 1188.5547, 1279.7615, 1291.6660, 1305.6913, 1334.8771, 1346.7351, 1346.7351, 1357.6692, 1444.7163, 1448.9102, 1474.8335, 1474.8335, 1515.7523, 1562.9409, 1603.8252, 1629.7651, 1647.7928, 1662.8282, 1732.0938, 1774.0338, 1845.0260, 1941.0308, 1973.1165, 2052.1912, 2146.1272, 2190.1741, 2240.1384, 2320.1719, 2342.1069, 2429.1943, 2473.3154, 2565.1975, 2613.2000, 2630.2371, 2749.4507, 2771.3960, 2824.3115, 2923.3582, 3189.6284, 3462.8738

2. gi|218157 **Mass:** 39151 **Score:** 166 **Expect:** 1.5e-011 **Queries matched:** 8

cytoplasmic aldolase [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
707.3941	706.3868	706.3914	-0.0046	140	144	1	---	FAKWR

829.3837	828.3764	828.3766	-0.0001	133 - 139	0	---	YYEAGAR
1346.7351	1345.7278	1345.7241	0.0037	238 - 249	0	58	VAPEVIAEYTVR
1346.7351	1345.7278	1345.7241	0.0037	238 - 249	0	---	VAPEVIAEYTVR
1474.8335	1473.8262	1473.8190	0.0072	237 - 249	1	---	KVAPEVIAEYTVR
1474.8335	1473.8262	1473.8190	0.0072	237 - 249	1	75	KVAPEVIAEYTVR
1662.8282	1661.8209	1661.8121	0.0089	40 - 53	1	---	FASINVENVEDNRR
1845.0260	1844.0187	1844.0155	0.0032	238 - 253	1	---	VAPEVIAEYTVRTLQR

No match to: 713.3993, 734.4901, 750.5125, 768.5131, 782.4778, 848.5271, 881.2793, 932.5704, 1133.7045, 1171.5286, 1188.5547, 1279.7615, 1291.6660, 1305.6913, 1334.8771, 1357.6692, 1371.7285, 1371.7285, 1444.7163, 1448.9102, 1515.7523, 1562.9409, 1603.8252, 1629.7651, 1647.7928, 1732.0938, 1774.0338, 1842.0175, 1941.0308, 1973.1165, 2052.1912, 2108.0801, 2108.0801, 2146.1272, 2190.1741, 2240.1384, 2320.1719, 2342.1069, 2429.1943, 2473.3154, 2519.3623, 2519.3623, 2565.1975, 2613.2000, 2630.2371, 2749.4507, 2763.4409, 2771.3960, 2824.3115, 2891.5393, 2923.3582, 3189.6284, 3462.8738

3. gi|110288655 **Mass:** 39137 **Score:** 165 **Expect:** 1.9e-011 **Queries matched:** 8

Fructose-bisphosphate aldolase, cytoplasmic isozyme, putative, expressed [Oryza sativa (japonica cu

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
707.3941	706.3868	706.3914	-0.0046	140 - 144	1	---	FAKWR
829.3837	828.3764	828.3766	-0.0001	133 - 139	0	---	YYEAGAR
1346.7351	1345.7278	1345.7241	0.0037	238 - 249	0	58	VAPEVIAEYTVR
1346.7351	1345.7278	1345.7241	0.0037	238 - 249	0	---	VAPEVIAEYTVR
1474.8335	1473.8262	1473.8190	0.0072	237 - 249	1	---	KVAPEVIAEYTVR
1474.8335	1473.8262	1473.8190	0.0072	237 - 249	1	75	KVAPEVIAEYTVR
1662.8282	1661.8209	1661.8121	0.0089	40 - 53	1	---	FASINVENVEDNRR
1845.0260	1844.0187	1844.0155	0.0032	238 - 253	1	---	VAPEVIAEYTVRTLQR

No match to: 713.3993, 734.4901, 750.5125, 768.5131, 782.4778, 848.5271, 881.2793, 932.5704, 1133.7045, 1171.5286, 1188.5547, 1279.7615, 1291.6660, 1305.6913, 1334.8771, 1357.6692, 1371.7285, 1371.7285, 1444.7163, 1448.9102, 1515.7523, 1562.9409, 1603.8252, 1629.7651, 1647.7928, 1732.0938, 1774.0338, 1842.0175, 1941.0308, 1973.1165, 2052.1912, 2108.0801, 2108.0801, 2146.1272, 2190.1741, 2240.1384, 2320.1719, 2342.1069, 2429.1943, 2473.3154, 2519.3623, 2519.3623, 2565.1975, 2613.2000, 2630.2371, 2749.4507, 2763.4409, 2771.3960, 2824.3115, 2891.5393, 2923.3582, 3189.6284, 3462.8738

4. gi|125548604 **Mass:** 39099 **Score:** 165 **Expect:** 1.9e-011 **Queries matched:** 8

hypothetical protein OsI_16195 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
707.3941	706.3868	706.3914	-0.0046	140 - 144	1	---	FAKWR
829.3837	828.3764	828.3766	-0.0001	133 - 139	0	---	YYEAGAR
1346.7351	1345.7278	1345.7241	0.0037	238 - 249	0	58	VAPEVIAEYTVR
1346.7351	1345.7278	1345.7241	0.0037	238 - 249	0	---	VAPEVIAEYTVR
1474.8335	1473.8262	1473.8190	0.0072	237 - 249	1	---	KVAPEVIAEYTVR
1474.8335	1473.8262	1473.8190	0.0072	237 - 249	1	75	KVAPEVIAEYTVR
1662.8282	1661.8209	1661.8121	0.0089	40 - 53	1	---	FASINVENVEDNRR
1845.0260	1844.0187	1844.0155	0.0032	238 - 253	1	---	VAPEVIAEYTVRTLQR

No match to: 713.3993, 734.4901, 750.5125, 768.5131, 782.4778, 848.5271, 881.2793, 932.5704, 1133.7045, 1171.5286, 1188.5547, 1279.7615, 1291.6660, 1305.6913, 1334.8771, 1357.6692, 1371.7285, 1371.7285, 1444.7163, 1448.9102, 1515.7523, 1562.9409, 1603.8252, 1629.7651, 1647.7928, 1732.0938, 1774.0338, 1842.0175, 1941.0308, 1973.1165, 2052.1912, 2108.0801, 2108.0801, 2146.1272, 2190.1741, 2240.1384, 2320.1719, 2342.1069, 2429.1943, 2473.3154, 2519.3623, 2519.3623, 2565.1975, 2613.2000, 2630.2371, 2749.4507, 2763.4409, 2771.3960, 2824.3115, 2891.5393, 2923.3582, 3189.6284, 3462.8738

5. gi|2213867 **Mass:** 38362 **Score:** 151 **Expect:** 4.8e-010 **Queries matched:** 6

fructose-biphosphate aldolase [Mesembryanthemum crystallinum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
707.3941	706.3868	706.3914	-0.0046	140 -	144	1	---	FAKWR
1346.7351	1345.7278	1345.7241	0.0037	238 -	249	0	58	VAPEVIAEYTVR
1346.7351	1345.7278	1345.7241	0.0037	238 -	249	0	---	VAPEVIAEYTVR
1474.8335	1473.8262	1473.8190	0.0072	237 -	249	1	---	KVAPEVIAEYTVR
1474.8335	1473.8262	1473.8190	0.0072	237 -	249	1	75	KVAPEVIAEYTVR
1603.8252	1602.8179	1602.8365	-0.0185	312 -	325	1	---	EENVEKAQAVFLAR

No match to: 713.3993, 734.4901, 750.5125, 768.5131, 782.4778, 829.3837, 848.5271, 881.2793, 932.5704, 1133.7045, 1171.5286, 1188.5547, 1279.7615, 1291.6660, 1305.6913, 1334.8771, 1357.6692, 1371.7285, 1371.7285, 1444.7163, 1448.9102, 1515.7523, 1562.9409, 1629.7651, 1647.7928, 1662.8282, 1732.0938, 1774.0338, 1842.0175, 1845.0260, 1941.0308, 1973.1165, 2052.1912, 2108.0801, 2108.0801, 2146.1272, 2190.1741, 2240.1384, 2320.1719, 2342.1069, 2429.1943, 2473.3154, 2519.3623, 2519.3623, 2565.1975, 2613.2000, 2630.2371, 2749.4507, 2763.4409, 2771.3960, 2824.3115, 2891.5393, 2923.3582, 3189.6284, 3462.8738

6. gi|77999255 **Mass:** 38812 **Score:** 63 **Expect:** 0.33 **Queries matched:** 3

unknown [Solanum tuberosum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
707.3941	706.3868	706.3914	-0.0046	140 -	144	1	---	FAKWR
1346.7351	1345.7278	1345.7241	0.0037	238 -	249	0	58	VAPEVIAEYTVR
1346.7351	1345.7278	1345.7241	0.0037	238 -	249	0	---	VAPEVIAEYTVR

No match to: 713.3993, 734.4901, 750.5125, 768.5131, 782.4778, 829.3837, 848.5271, 881.2793, 932.5704, 1133.7045, 1171.5286, 1188.5547, 1279.7615, 1291.6660, 1305.6913, 1334.8771, 1357.6692, 1371.7285, 1371.7285, 1444.7163, 1448.9102, 1474.8335, 1474.8335, 1515.7523, 1562.9409, 1603.8252, 1629.7651, 1647.7928, 1662.8282, 1732.0938, 1774.0338, 1842.0175, 1845.0260, 1941.0308, 1973.1165, 2052.1912, 2108.0801, 2108.0801, 2146.1272, 2190.1741, 2240.1384, 2320.1719, 2342.1069, 2429.1943, 2473.3154, 2519.3623, 2519.3623, 2565.1975, 2613.2000, 2630.2371, 2749.4507, 2763.4409, 2771.3960, 2824.3115, 2891.5393, 2923.3582, 3189.6284, 3462.8738

7. gi|14484932 **Mass:** 22651 **Score:** 62 **Expect:** 0.37 **Queries matched:** 2

fructose-1,6-bisphosphate aldolase [Lycopersicon esculentum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1346.7351	1345.7278	1345.7241	0.0037	88 -	99	0	58	VAPEVIAEYTVR
1346.7351	1345.7278	1345.7241	0.0037	88 -	99	0	---	VAPEVIAEYTVR

No match to: 707.3941, 713.3993, 734.4901, 750.5125, 768.5131, 782.4778, 829.3837, 848.5271, 881.2793, 932.5704, 1133.7045, 1171.5286, 1188.5547, 1279.7615, 1291.6660, 1305.6913, 1334.8771, 1357.6692, 1371.7285, 1371.7285, 1444.7163, 1448.9102, 1474.8335, 1474.8335, 1515.7523, 1562.9409, 1603.8252, 1629.7651, 1647.7928, 1662.8282, 1732.0938, 1774.0338, 1842.0175, 1845.0260, 1941.0308, 1973.1165, 2052.1912, 2108.0801, 2108.0801, 2146.1272,

2190.1741, 2240.1384, 2320.1719, 2342.1069, 2429.1943, 2473.3154, 2519.3623, 2519.3623, 2565.1975, 2613.2000, 2630.2371, 2749.4507, 2763.4409, 2771.3960, 2824.3115, 2891.5393, 2923.3582, 3189.6284, 3462.8738

8. gi|195647936 **Mass:** 10427 **Score:** 58 **Expect:** 1.1 **Queries matched:** 5

hypothetical protein [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1842.0175	1841.0102	1841.0563	-0.0460	2	16	1	---	IVNQQVVNIWYIPKK
1845.0260	1844.0187	1844.0018	0.0169	1	15	0	---	MIVNQQVVNIWYIPK
1973.1165	1972.1092	1972.0968	0.0125	1	16	1	---	MIVNQQVVNIWYIPKK
2473.3154	2472.3081	2472.1597	0.1485	69	88	1	---	IQLESEAREVNPFFNPEYQY
2565.1975	2564.1902	2564.2102	-0.0200	17	39	1	---	DESSRPDDVISAAQRYIEQNGSK

No match to: 707.3941, 713.3993, 734.4901, 750.5125, 768.5131, 782.4778, 829.3837, 848.5271, 881.2793, 932.5704, 1133.7045, 1171.5286, 1188.5547, 1279.7615, 1291.6660, 1305.6913, 1334.8771, 1346.7351, 1346.7351, 1357.6692, 1371.7285, 1371.7285, 1444.7163, 1448.9102, 1474.8335, 1474.8335, 1515.7523, 1562.9409, 1603.8252, 1629.7651, 1647.7928, 1662.8282, 1732.0938, 1774.0338, 1941.0308, 2052.1912, 2108.0801, 2108.0801, 2146.1272, 2190.1741, 2240.1384, 2320.1719, 2342.1069, 2429.1943, 2519.3623, 2519.3623, 2613.2000, 2630.2371, 2749.4507, 2763.4409, 2771.3960, 2824.3115, 2891.5393, 2923.3582, 3189.6284, 3462.8738

9. gi|87241376 **Mass:** 19965 **Score:** 56 **Expect:** 1.5 **Queries matched:** 7

IMP dehydrogenase/GMP reductase, related [Medicago truncatula]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1291.6660	1290.6587	1290.7044	-0.0457	143	154	0	---	IGSTGRPALTYR
1305.6913	1304.6840	1304.6724	0.0116	80	91	0	---	QIIPPDEGSPPR
2519.3623	2518.3550	2518.3042	0.0509	38	58	1	---	EMLAPVLIDPIAGFYLDWRQR + Oxidation (M)
2519.3623	2518.3550	2518.3042	0.0509	38	58	1	---	EMLAPVLIDPIAGFYLDWRQR + Oxidation (M)
2630.2371	2629.2298	2629.2219	0.0079	59	79	1	---	CGRPWQHEPGYMAWYAKVTHR
2923.3582	2922.3509	2922.4834	-0.1325	80	105	1	---	QIIPPDEGSPPRLANVEQIIEEEHGR
3189.6284	3188.6211	3188.5944	0.0267	106	133	1	---	EIPDTLTIIRDVVQVADNVVAMQEEMTK + 2 Oxidation (M)

No match to: 707.3941, 713.3993, 734.4901, 750.5125, 768.5131, 782.4778, 829.3837, 848.5271, 881.2793, 932.5704, 1133.7045, 1171.5286, 1188.5547, 1279.7615, 1334.8771, 1346.7351, 1346.7351, 1357.6692, 1371.7285, 1371.7285, 1444.7163, 1448.9102, 1474.8335, 1474.8335, 1515.7523, 1562.9409, 1603.8252, 1629.7651, 1647.7928, 1662.8282, 1732.0938, 1774.0338, 1842.0175, 1845.0260, 1941.0308, 1973.1165, 2052.1912, 2108.0801, 2108.0801, 2146.1272, 2190.1741, 2240.1384, 2320.1719, 2342.1069, 2429.1943, 2473.3154, 2565.1975, 2613.2000, 2749.4507, 2763.4409, 2771.3960, 2824.3115, 2891.5393, 3462.8738

10. gi|226501498 **Mass:** 74401 **Score:** 55 **Expect:** 2.1 **Queries matched:** 10

hypothetical protein LOC100279342 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
713.3993	712.3920	712.3867	0.0053	559	564	0	---	DNLPVR
829.3837	828.3764	828.3799	-0.0035	220	225	1	---	ERYSMK + Oxidation (M)
1346.7351	1345.7278	1345.6890	0.0388	517	529	0	9	NPSAPVHVFGGHK
1346.7351	1345.7278	1345.6890	0.0388	517	529	0	---	NPSAPVHVFGGHK
1474.8335	1473.8262	1473.7840	0.0422	517	530	1	---	NPSAPVHVFGGHKK

1474.8335	1473.8262	1473.7840	0.0422	517 - 530	1	6	NPSAPVHVFGGHKK
2473.3154	2472.3081	2472.2495	0.0586	531 - 553	1	---	AVSYVKFLSNNELASASTDSTLR
2749.4507	2748.4434	2748.2887	0.1548	377 - 400	0	---	VFEFSTVVNEPSDVHCPVVEMATR
2763.4409	2762.4336	2762.3189	0.1147	163 - 184	0	---	QMEQQESETNMQILLVFLHCLR + Oxidation (M)
2891.5393	2890.5320	2890.4139	0.1181	163 - 185	1	---	QMEQQESETNMQILLVFLHCLRK + Oxidation (M)

No match to: 707.3941, 734.4901, 750.5125, 768.5131, 782.4778, 848.5271, 881.2793, 932.5704, 1133.7045, 1171.5286, 1188.5547, 1279.7615, 1291.6660, 1305.6913, 1334.8771, 1357.6692, 1371.7285, 1371.7285, 1444.7163, 1448.9102, 1515.7523, 1562.9409, 1603.8252, 1629.7651, 1647.7928, 1662.8282, 1732.0938, 1774.0338, 1842.0175, 1845.0260, 1941.0308, 1973.1165, 2052.1912, 2108.0801, 2108.0801, 2146.1272, 2190.1741, 2240.1384, 2320.1719, 2342.1069, 2429.1943, 2519.3623, 2519.3623, 2565.1975, 2613.2000, 2630.2371, 2771.3960, 2824.3115, 2923.3582, 3189.6284, 3462.8738

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 61

Protein View

Match to: **gi|5419990** Score: **288** Expect: **9.6e-024**
putative fructose-bisphosphate aldolase [Phleum pratense]

Nominal mass (M_r): **25028**; Calculated pI value: **7.79**
NCBI BLAST search of gi|5419990 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **37%**

Matched peptides shown in **Bold Red**

```
    1 YYEAGARFAK WRAVLKIGPN EPSQLSIDQN AQGLARYAII CQENGLVPIV
   51 EPEILVDGPH DIDRCAYVTE VVLAACYKAL NDQHVLLEGS LLKPNMVTPG
  101 SDAKKVAPRE SLAEYTVRTL QRTVPPAVPA IVFLSGGQSE EEATVNLNAM
  151 NKLQTKKPWF LSFSFGRALQ QSTLKAWSGK EENVGKAQKA FLVRCKANSE
  201 ATLGTYKGDA TLGEGASESL HVKDYKY
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
1 - 7	829.3837	828.3764	828.3766	-0.0001	0	**YYEAGAR** (No match)
8 - 12	707.3941	706.3868	706.3914	-0.0046	1	**FAKWR** (No match)
13 - 36	2519.3623	2518.3550	2518.3503	0.0048	1	**AVLKIGPNEPSQLSIDQNAQGLAR** (No match)
13 - 36	2519.3623	2518.3550	2518.3503	0.0048	1	**AVLKIGPNEPSQLSIDQNAQGLAR** (Ions score 54)
17 - 36	2108.0801	2107.0728	2107.0657	0.0071	0	**IGPNEPSQLSIDQNAQGLAR** (Ions score 98)
17 - 36	2108.0801	2107.0728	2107.0657	0.0071	0	**IGPNEPSQLSIDQNAQGLAR** (No match)
79 - 104	2763.4409	2762.4336	2762.4272	0.0064	0	**ALNDQHVLLEGSLLKPNMVTPGSDAK** Oxidation (M) (No match)
79 - 105	2891.5393	2890.5320	2890.5221	0.0099	1	**ALNDQHVLLEGSLLKPNMVTPGSDAKK** Oxidation (M) (No match)
153 - 167	1842.0175	1841.0102	1840.9987	0.0115	1	**LQTKKPWFLSFSFGR** (No match)
157 - 167	1371.7285	1370.7212	1370.7135	0.0078	0	**KPWFLSFSFGR** (Ions score 49)
157 - 167	1371.7285	1370.7212	1370.7135	0.0078	0	**KPWFLSFSFGR** (No match)
187 - 194	932.5704	931.5631	931.5603	0.0029	1	**AQKAFLVR** (No match)

Spot 68

Index

	Accession	Mass	Score	Description
1.	gi|5419990	25028	304	putative fructose-bisphosphate aldolase [Phleum pratense]
2.	gi|218157	39151	166	cytoplasmic aldolase [Oryza sativa Japonica Group]
3.	gi|110288655	39137	165	Fructose-bisphosphate aldolase, cytoplasmic isozyme, putative, expressed [Oryza sativa (japoni
4.	gi|125548604	39099	165	hypothetical protein OsI_16195 [Oryza sativa Indica Group]
5.	gi|2213867	38362	134	fructose-biphosphate aldolase [Mesembryanthemum crystallinum]
6.	gi|115479777	50061	58	Os09g0479800 [Oryza sativa (japonica cultivar-group)]
7.	gi|222641784	50052	58	hypothetical protein OsJ_29767 [Oryza sativa Japonica Group]
8.	gi|147839169	70010	58	hypothetical protein [Vitis vinifera]
9.	gi|14484932	22651	57	fructose-1,6-bisphosphate aldolase [Lycopersicon esculentum]
10.	gi|157349664	18221	56	unnamed protein product [Vitis vinifera]

Results List

1. gi|5419990 **Mass:** 25028 **Score:** 304 **Expect:** 2.4e-025 **Queries matched:** 9

putative fructose-bisphosphate aldolase [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
829.3907	828.3834	828.3766	0.0069	1	7	0	---	YYEAGAR
932.5709	931.5636	931.5603	0.0034	187	194	1	---	AQKAFLVR
1371.7278	1370.7205	1370.7135	0.0071	157	167	0	---	KPWFLSFSFGR
1371.7278	1370.7205	1370.7135	0.0071	157	167	0	38	KPWFLSFSFGR
1842.0314	1841.0241	1840.9987	0.0254	153	167	1	---	LQTKKPWFLSFSFGR
2108.0754	2107.0681	2107.0657	0.0024	17	36	0	---	IGPNEPSQLSIDQNAQGLAR
2108.0754	2107.0681	2107.0657	0.0024	17	36	0	96	IGPNEPSQLSIDQNAQGLAR
2519.3623	2518.3550	2518.3503	0.0048	13	36	1	97	AVLKIGPNEPSQLSIDQNAQGLAR
2519.3623	2518.3550	2518.3503	0.0048	13	36	1	---	AVLKIGPNEPSQLSIDQNAQGLAR

No match to: 713.4023, 734.4853, 768.5165, 864.5162, 1171.5214, 1188.5532, 1346.7358, 1346.7358, 1474.8311, 1474.8311, 1515.7418, 1662.8289, 1845.0332, 1941.0146, 1973.1277, 2631.2415

2. gi|218157 **Mass:** 39151 **Score:** 166 **Expect:** 1.5e-011 **Queries matched:** 7

cytoplasmic aldolase [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
829.3907	828.3834	828.3766	0.0069	133	139	0	---	YYEAGAR
1346.7358	1345.7285	1345.7241	0.0044	238	249	0	50	VAPEVIAEYTVR
1346.7358	1345.7285	1345.7241	0.0044	238	249	0	---	VAPEVIAEYTVR
1474.8311	1473.8238	1473.8190	0.0048	237	249	1	71	KVAPEVIAEYTVR
1474.8311	1473.8238	1473.8190	0.0048	237	249	1	---	KVAPEVIAEYTVR
1662.8289	1661.8216	1661.8121	0.0096	40	53	1	---	FASINVENVEDNRR
1845.0332	1844.0259	1844.0155	0.0104	238	253	1	---	VAPEVIAEYTVRTLQR

No match to: 713.4023, 734.4853, 768.5165, 864.5162, 932.5709, 1171.5214, 1188.5532, 1371.7278, 1371.7278, 1515.7418, 1842.0314, 1941.0146, 1973.1277, 2108.0754, 2108.0754, 2519.3623, 2519.3623, 2631.2415

3. gi|110288655 **Mass:** 39137 **Score:** 165 **Expect:** 1.9e-011 **Queries matched:** 7

Fructose-bisphosphate aldolase, cytoplasmic isozyme, putative, expressed [Oryza sativa (japonica cu

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
829.3907	828.3834	828.3766	0.0069	133	139	0	---	YYEAGAR
1346.7358	1345.7285	1345.7241	0.0044	238	249	0	50	VAPEVIAEYTVR
1346.7358	1345.7285	1345.7241	0.0044	238	249	0	---	VAPEVIAEYTVR
1474.8311	1473.8238	1473.8190	0.0048	237	249	1	71	KVAPEVIAEYTVR
1474.8311	1473.8238	1473.8190	0.0048	237	249	1	---	KVAPEVIAEYTVR
1662.8289	1661.8216	1661.8121	0.0096	40	53	1	---	FASINVENVEDNRR
1845.0332	1844.0259	1844.0155	0.0104	238	253	1	---	VAPEVIAEYTVRTLQR

No match to: 713.4023, 734.4853, 768.5165, 864.5162, 932.5709, 1171.5214, 1188.5532, 1371.7278, 1371.7278, 1515.7418, 1842.0314, 1941.0146, 1973.1277, 2108.0754, 2108.0754, 2519.3623, 2519.3623, 2631.2415

4. gi|125548604 **Mass:** 39099 **Score:** 165 **Expect:** 1.9e-011 **Queries matched:** 7

hypothetical protein OsI_16195 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
829.3907	828.3834	828.3766	0.0069	133	139	0	---	YYEAGAR
1346.7358	1345.7285	1345.7241	0.0044	238	249	0	50	VAPEVIAEYTVR
1346.7358	1345.7285	1345.7241	0.0044	238	249	0	---	VAPEVIAEYTVR
1474.8311	1473.8238	1473.8190	0.0048	237	249	1	71	KVAPEVIAEYTVR
1474.8311	1473.8238	1473.8190	0.0048	237	249	1	---	KVAPEVIAEYTVR
1662.8289	1661.8216	1661.8121	0.0096	40	53	1	---	FASINVENVEDNRR
1845.0332	1844.0259	1844.0155	0.0104	238	253	1	---	VAPEVIAEYTVRTLQR

No match to: 713.4023, 734.4853, 768.5165, 864.5162, 932.5709, 1171.5214, 1188.5532, 1371.7278, 1371.7278, 1515.7418, 1842.0314, 1941.0146, 1973.1277, 2108.0754, 2108.0754, 2519.3623, 2519.3623, 2631.2415

5. gi|2213867 **Mass:** 38362 **Score:** 134 **Expect:** 2.4e-008 **Queries matched:** 4

fructose-biphosphate aldolase [Mesembryanthemum crystallinum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1346.7358	1345.7285	1345.7241	0.0044	238	249	0	50	VAPEVIAEYTVR
1346.7358	1345.7285	1345.7241	0.0044	238	249	0	---	VAPEVIAEYTVR
1474.8311	1473.8238	1473.8190	0.0048	237	249	1	71	KVAPEVIAEYTVR
1474.8311	1473.8238	1473.8190	0.0048	237	249	1	---	KVAPEVIAEYTVR

No match to: 713.4023, 734.4853, 768.5165, 829.3907, 864.5162, 932.5709, 1171.5214, 1188.5532, 1371.7278, 1371.7278, 1515.7418, 1662.8289, 1842.0314, 1845.0332, 1941.0146, 1973.1277, 2108.0754, 2108.0754, 2519.3623, 2519.3623, 2631.2415

6. gi|115479777 **Mass:** 50061 **Score:** 58 **Expect:** 0.96 **Queries matched:** 8

Os09g0479800 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1171.5214	1170.5141	1170.5743	-0.0602	377 -	385	0	---	YIDPTYMIR
1188.5532	1187.5459	1187.5782	-0.0322	218 -	228	0	---	TVDNDVGVVDR
1371.7278	1370.7205	1370.7094	0.0111	295 -	306	1	---	GAGGLFDFLYRR
1371.7278	1370.7205	1370.7094	0.0111	295 -	306	1	---	GAGGLFDFLYRR
1474.8311	1473.8238	1473.8667	-0.0429	17 -	31	0	16	LPTLAGAAIPNPIAR
1474.8311	1473.8238	1473.8667	-0.0429	17 -	31	0	---	LPTLAGAAIPNPIAR
2108.0754	2107.0681	2107.1636	-0.0955	208 -	228	1	---	LAVAVAGIPKTVDNDVGVVDR
2108.0754	2107.0681	2107.1636	-0.0955	208 -	228	1	---	LAVAVAGIPKTVDNDVGVVDR

No match to: 713.4023, 734.4853, 768.5165, 829.3907, 864.5162, 932.5709, 1346.7358, 1346.7358, 1515.7418, 1662.8289, 1842.0314, 1845.0332, 1941.0146, 1973.1277, 2519.3623, 2519.3623, 2631.2415

7. gi|222641784 **Mass:** 50052 **Score:** 58 **Expect:** 0.96 **Queries matched:** 8

hypothetical protein OsJ_29767 [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1171.5214	1170.5141	1170.5743	-0.0602	377 -	385	0	---	YIDPTYMIR
1188.5532	1187.5459	1187.5782	-0.0322	218 -	228	0	---	TVDNDVGVVDR
1371.7278	1370.7205	1370.7094	0.0111	295 -	306	1	---	GAGGLFDFLYRR
1371.7278	1370.7205	1370.7094	0.0111	295 -	306	1	---	GAGGLFDFLYRR
1474.8311	1473.8238	1473.8667	-0.0429	17 -	31	0	16	LPTLAGAAIPNPIAR
1474.8311	1473.8238	1473.8667	-0.0429	17 -	31	0	---	LPTLAGAAIPNPIAR
2108.0754	2107.0681	2107.1636	-0.0955	208 -	228	1	---	LAVAVAGIPKTVDNDVGVVDR
2108.0754	2107.0681	2107.1636	-0.0955	208 -	228	1	---	LAVAVAGIPKTVDNDVGVVDR

No match to: 713.4023, 734.4853, 768.5165, 829.3907, 864.5162, 932.5709, 1346.7358, 1346.7358, 1515.7418, 1662.8289, 1842.0314, 1845.0332, 1941.0146, 1973.1277, 2519.3623, 2519.3623, 2631.2415

8. gi|147839169 **Mass:** 70010 **Score:** 58 **Expect:** 1 **Queries matched:** 6

hypothetical protein [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1346.7358	1345.7285	1345.7857	-0.0571	560 -	571	0	16	LLIVPSDITFTK
1474.8311	1473.8238	1473.8806	-0.0568	560 -	572	1	8	LLIVPSDITFTKK
1515.7418	1514.7345	1514.7591	-0.0246	258 -	269	1	---	AYDSINWKFLMK
1662.8289	1661.8216	1661.8988	-0.0771	209 -	223	1	---	VLDKVVSTDQNAFVK
2108.0754	2107.0681	2107.0234	0.0447	535 -	553	1	---	ISPEEDSVIWKGGGHGHFR
2108.0754	2107.0681	2107.0234	0.0447	535 -	553	1	---	ISPEEDSVIWKGGGHGHFR

No match to: 713.4023, 734.4853, 768.5165, 829.3907, 864.5162, 932.5709, 1171.5214, 1188.5532, 1346.7358, 1371.7278, 1371.7278, 1474.8311, 1842.0314, 1845.0332, 1941.0146, 1973.1277, 2519.3623, 2519.3623, 2631.2415

9. gi|14484932 **Mass:** 22651 **Score:** 57 **Expect:** 1.2 **Queries matched:** 2

fructose-1,6-bisphosphate aldolase [Lycopersicon esculentum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1346.7358	1345.7285	1345.7241	0.0044	88 -	99	0	50	VAPEVIAEYTVR

1346.7358	1345.7285	1345.7241	0.0044	88 - 99	0	---	VAPEVIAEYTVR

No match to: 713.4023, 734.4853, 768.5165, 829.3907, 864.5162, 932.5709, 1171.5214, 1188.5532, 1371.7278, 1371.7278, 1474.8311, 1474.8311, 1515.7418, 1662.8289, 1842.0314, 1845.0332, 1941.0146, 1973.1277, 2108.0754, 2108.0754, 2519.3623, 2519.3623, 2631.2415

10. gi|157349664 **Mass:** 18221 **Score:** 56 **Expect:** 1.5 **Queries matched:** 6

unnamed protein product [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1346.7358	1345.7285	1345.7857	-0.0571	119 -	130	0	16	LLIVPSDITFTK
1346.7358	1345.7285	1345.7857	-0.0571	119 -	130	0	---	LLIVPSDITFTK
1474.8311	1473.8238	1473.8806	-0.0568	119 -	131	1	8	LLIVPSDITFTKK
1474.8311	1473.8238	1473.8806	-0.0568	119 -	131	1	---	LLIVPSDITFTKK
2108.0754	2107.0681	2107.0234	0.0447	94 -	112	1	---	ISPEEDSVIWKGGGHGHFR
2108.0754	2107.0681	2107.0234	0.0447	94 -	112	1	---	ISPEEDSVIWKGGGHGHFR

No match to: 713.4023, 734.4853, 768.5165, 829.3907, 864.5162, 932.5709, 1171.5214, 1188.5532, 1371.7278, 1371.7278, 1515.7418, 1662.8289, 1842.0314, 1845.0332, 1941.0146, 1973.1277, 2519.3623, 2519.3623, 2631.2415

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 25

Protein View

Match to: **gi|5419990** Score: **304** Expect: **2.4e-025**
putative fructose-bisphosphate aldolase [Phleum pratense]

Nominal mass (M_r): **25028**; Calculated pI value: **7.79**
NCBI BLAST search of gi|5419990 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

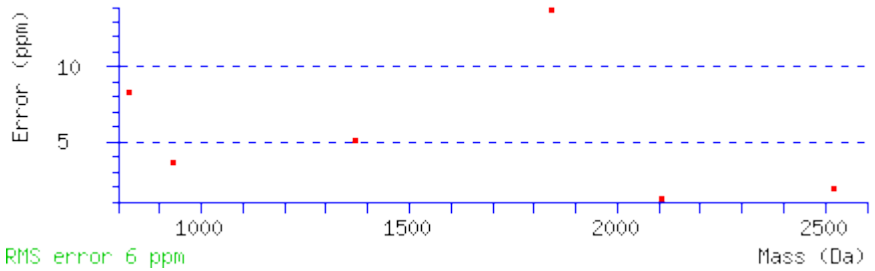
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **23%**

Matched peptides shown in **Bold Red**

```
    1 YYEAGARFAK WRAVLKIGPN EPSQLSIDQN AQGLARYAII CQENGLVPIV
   51 EPEILVDGPH DIDRCAYVTE VVLAACYKAL NDQHVLLEGS LLKPNMVTPG
  101 SDAKKVAPRE SLAEYTVRTL QRTVPPAVPA IVFLSGGQSE EEATVNLNAM
  151 NKLQTKKPWF LSFSFGRALQ QSTLKAWSGK EENVGKAQKA FLVRCKANSE
  201 ATLGTYKGDA TLGEGASESL HVKDYKY
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
1 - 7	829.3907	828.3834	828.3766	0.0069	0	YYEAGAR	(No match)
13 - 36	2519.3623	2518.3550	2518.3503	0.0048	1	AVLKIGPNEPSQLSIDQNAQGLAR	(Ions score 97)
13 - 36	2519.3623	2518.3550	2518.3503	0.0048	1	AVLKIGPNEPSQLSIDQNAQGLAR	(No match)
17 - 36	2108.0754	2107.0681	2107.0657	0.0024	0	IGPNEPSQLSIDQNAQGLAR	(No match)
17 - 36	2108.0754	2107.0681	2107.0657	0.0024	0	IGPNEPSQLSIDQNAQGLAR	(Ions score 96)
153 - 167	1842.0314	1841.0241	1840.9987	0.0254	1	LQTKKPWFLSFSFGR	(No match)
157 - 167	1371.7278	1370.7205	1370.7135	0.0071	0	KPWFLSFSFGR	(No match)
157 - 167	1371.7278	1370.7205	1370.7135	0.0071	0	KPWFLSFSFGR	(Ions score 38)
187 - 194	932.5709	931.5636	931.5603	0.0034	1	AQKAFLVR	(No match)



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	Accession	Mass	Score	Description
1.	gi|4826572	42579	156	polygalacturonase [Phleum pratense]
2.	gi|15241898	47040	41	F-box family protein [Arabidopsis thaliana]
3.	gi|222868850	18717	39	predicted protein [Populus trichocarpa]
4.	gi|66932629	8565	39	isocitrate dehydrogenase [Saltugilia latimeri]
5.	gi|115474109	21023	37	Os07g0681400 [Oryza sativa (japonica cultivar-group)]
6.	gi|195655533	12999	37	hypothetical protein [Zea mays]
7.	gi|168009401	18535	37	predicted protein [Physcomitrella patens subsp. patens]
8.	gi|194700084	18190	36	unknown [Zea mays]
9.	gi|222845076	23801	36	extra response regulator [Populus trichocarpa]
10.	gi|15233780	12153	36	unknown protein [Arabidopsis thaliana]

Results List

1. gi|4826572 **Mass:** 42579 **Score:** 156 **Expect:** 1.5e-010 **Queries matched:** 13

polygalacturonase [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1032.5339	1031.5266	1031.5222	0.0044	101	108	0	---	ANWIEIMR
1048.5227	1047.5154	1047.5171	-0.0017	101	108	0	---	ANWIEIMR + Oxidation (M)
1120.5583	1119.5510	1119.5495	0.0016	126	135	1	---	AVWGKNSCAK
1323.6937	1322.6864	1322.6805	0.0059	99	108	1	---	YKANWIEIMR
1323.6937	1322.6864	1322.6805	0.0059	99	108	1	47	YKANWIEIMR
1339.6830	1338.6757	1338.6754	0.0003	99	108	1	(14)	YKANWIEIMR + Oxidation (M)
1339.6830	1338.6757	1338.6754	0.0003	99	108	1	---	YKANWIEIMR + Oxidation (M)
1388.6163	1387.6090	1387.6053	0.0038	166	175	0	62	FFHMNIYECK
1388.6163	1387.6090	1387.6053	0.0038	166	175	0	---	FFHMNIYECK
1404.6113	1403.6040	1403.6002	0.0039	166	175	0	(45)	FFHMNIYECK + Oxidation (M)
1404.6113	1403.6040	1403.6002	0.0039	166	175	0	---	FFHMNIYECK + Oxidation (M)
2384.2666	2383.2593	2383.1980	0.0613	288	307	1	---	LTYENVKMEDVGYPIIIDQK + Oxidation (M)
2781.4067	2780.3994	2780.3828	0.0167	176	203	1	---	GVTVKDVTITAPGDSPNTDGIHIGDSSK

No match to: 713.4099, 734.4896, 736.4969, 750.5195, 768.5248, 855.0323, 864.5381, 886.9855, 1064.5226, 1080.5109, 1277.2297, 1279.7607, 1334.8937, 1355.6840, 1371.6823, 1448.9275, 1516.8561, 1553.8110, 1618.0729, 1732.1044, 1758.0616, 1902.2831, 2096.1563, 2157.9590, 2168.1357, 2296.2388, 2296.2388, 2318.1865, 2923.4119, 2985.4805, 3688.8682

2. gi|15241898 **Mass:** 47040 **Score:** 41 **Expect:** 50 **Queries matched:** 8

F-box family protein [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1032.5339	1031.5266	1031.5399	-0.0133	100	108	0	---	SWVEVAVSR

1120.5583	1119.5510	1119.5939	-0.0429	36 - 43	0	---	FLWMWLPK
1323.6937	1322.6864	1322.7459	-0.0594	67 - 77	1	---	DFIAKNLPLHR
1323.6937	1322.6864	1322.7459	-0.0594	67 - 77	1	---	DFIAKNLPLHR
1404.6113	1403.6040	1403.5629	0.0411	372 - 381	0	---	WYYSEEQEDR
1404.6113	1403.6040	1403.5629	0.0411	372 - 381	0	---	WYYSEEQEDR
1516.8561	1515.8488	1515.7854	0.0634	1 - 14	0	---	MAEISGLPDDLLVK + Oxidation (M)
2384.2666	2383.2593	2383.3436	-0.0843	1 - 22	1	---	MAEISGLPDDLLVKILAFLPTK

No match to: 713.4099, 734.4896, 736.4969, 750.5195, 768.5248, 855.0323, 864.5381, 886.9855, 1048.5227, 1064.5226, 1080.5109, 1277.2297, 1279.7607, 1334.8937, 1339.6830, 1339.6830, 1355.6840, 1371.6823, 1388.6163, 1388.6163, 1448.9275, 1553.8110, 1618.0729, 1732.1044, 1758.0616, 1902.2831, 2096.1563, 2157.9590, 2168.1357, 2296.2388, 2296.2388, 2318.1865, 2781.4067, 2923.4119, 2985.4805, 3688.8682

3. gi|222868850 **Mass:** 18717 **Score:** 39 **Expect:** 71 **Queries matched:** 5

predicted protein [Populus trichocarpa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1355.6840	1354.6767	1354.7204	-0.0437	99 - 110		1	---	AEAQSINPEIRK
1404.6113	1403.6040	1403.6503	-0.0463	137 - 149		0	---	SGTFPLCDGSHVK
1404.6113	1403.6040	1403.6503	-0.0463	137 - 149		0	---	SGTFPLCDGSHVK
2318.1865	2317.1792	2317.1770	0.0023	52 - 73		1	---	ATRLLIMSMTVASTSTASASFR + Oxidation (M)
2384.2666	2383.2593	2383.1763	0.0831	55 - 76		1	---	LLIMSMTVASTSTASASFRYSK + 2 Oxidation (M)

No match to: 713.4099, 734.4896, 736.4969, 750.5195, 768.5248, 855.0323, 864.5381, 886.9855, 1032.5339, 1048.5227, 1064.5226, 1080.5109, 1120.5583, 1277.2297, 1279.7607, 1323.6937, 1323.6937, 1334.8937, 1339.6830, 1339.6830, 1371.6823, 1388.6163, 1388.6163, 1448.9275, 1516.8561, 1553.8110, 1618.0729, 1732.1044, 1758.0616, 1902.2831, 2096.1563, 2157.9590, 2168.1357, 2296.2388, 2296.2388, 2781.4067, 2923.4119, 2985.4805, 3688.8682

4. gi|66932629 **Mass:** 8565 **Score:** 39 **Expect:** 71 **Queries matched:** 3

isocitrate dehydrogenase [Saltugilia latimeri]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1355.6840	1354.6767	1354.6840	-0.0073	30 - 42		0	---	TIEAEAAHGTVTR
2318.1865	2317.1792	2317.1563	0.0230	50 - 71		1	---	GGETSTNSIASIFAWSRGLAHR
2985.4805	2984.4732	2984.3895	0.0837	1 - 29		0	---	DGDAQSDFLAQGFGSLGLMTSVLVCPDGK

No match to: 713.4099, 734.4896, 736.4969, 750.5195, 768.5248, 855.0323, 864.5381, 886.9855, 1032.5339, 1048.5227, 1064.5226, 1080.5109, 1120.5583, 1277.2297, 1279.7607, 1323.6937, 1323.6937, 1334.8937, 1339.6830, 1339.6830, 1371.6823, 1388.6163, 1388.6163, 1404.6113, 1404.6113, 1448.9275, 1516.8561, 1553.8110, 1618.0729, 1732.1044, 1758.0616, 1902.2831, 2096.1563, 2157.9590, 2168.1357, 2296.2388, 2296.2388, 2384.2666, 2781.4067, 2923.4119, 3688.8682

5. gi|115474109 **Mass:** 21023 **Score:** 37 **Expect:** 1.1e+002 **Queries matched:** 4

Os07g0681400 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1371.6823	1370.6750	1370.6102	0.0648	175 - 186		1	---	DSDGRVDFGEFK
2168.1357	2167.1284	2167.0684	0.0600	133 - 152		0	---	VFDVDGDGFISASELQEVLK
2296.2388	2295.2315	2295.1566	0.0749	2 - 22		0	---	EGEQQQQQQQSVAAVRPSLGK

2296.2388	2295.2315	2295.1633	0.0682	133 - 153	1	---	VFDVDGDGFISASELQEVLKK	

No match to: 713.4099, 734.4896, 736.4969, 750.5195, 768.5248, 855.0323, 864.5381, 886.9855, 1032.5339, 1048.5227, 1064.5226, 1080.5109, 1120.5583, 1277.2297, 1279.7607, 1323.6937, 1323.6937, 1334.8937, 1339.6830, 1339.6830, 1355.6840, 1388.6163, 1388.6163, 1404.6113, 1404.6113, 1448.9275, 1516.8561, 1553.8110, 1618.0729, 1732.1044, 1758.0616, 1902.2831, 2096.1563, 2157.9590, 2318.1865, 2384.2666, 2781.4067, 2923.4119, 2985.4805, 3688.8682

6. gi|195655533 **Mass:** 12999 **Score:** 37 **Expect:** 1.2e+002 **Queries matched:** 3

hypothetical protein [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1553.8110	1552.8037	1552.7568	0.0469	29 -	42	1	---	FASQACRATAPFAR
2781.4067	2780.3994	2780.3751	0.0243	1 -	25	1	---	MDAAAVLDAFSAAPRHQLRPAAWCR
3688.8682	3687.8609	3687.7084	0.1526	36 -	71	1	---	ATAPFARTDWQAACAILASNSTGGHDASSNTQPASR

No match to: 713.4099, 734.4896, 736.4969, 750.5195, 768.5248, 855.0323, 864.5381, 886.9855, 1032.5339, 1048.5227, 1064.5226, 1080.5109, 1120.5583, 1277.2297, 1279.7607, 1323.6937, 1323.6937, 1334.8937, 1339.6830, 1339.6830, 1355.6840, 1371.6823, 1388.6163, 1388.6163, 1404.6113, 1404.6113, 1448.9275, 1516.8561, 1618.0729, 1732.1044, 1758.0616, 1902.2831, 2096.1563, 2157.9590, 2168.1357, 2296.2388, 2296.2388, 2318.1865, 2384.2666, 2923.4119, 2985.4805

7. gi|168009401 **Mass:** 18535 **Score:** 37 **Expect:** 1.3e+002 **Queries matched:** 7

predicted protein [Physcomitrella patens subsp. patens]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1080.5109	1079.5036	1079.5222	-0.0186	58 -	66	0	---	WVGFVADMR
1323.6937	1322.6864	1322.6553	0.0311	56 -	66	1	---	SRWVGFVADMR
1323.6937	1322.6864	1322.6553	0.0311	56 -	66	1	---	SRWVGFVADMR
1339.6830	1338.6757	1338.6502	0.0255	56 -	66	1	---	SRWVGFVADMR + Oxidation (M)
1339.6830	1338.6757	1338.6502	0.0255	56 -	66	1	---	SRWVGFVADMR + Oxidation (M)
1355.6840	1354.6767	1354.6741	0.0026	2 -	13	0	---	EQWGPRPATTGR
2384.2666	2383.2593	2383.1815	0.0779	1 -	22	1	---	MEQWGPRPATTGRTGTSGPLQR

No match to: 713.4099, 734.4896, 736.4969, 750.5195, 768.5248, 855.0323, 864.5381, 886.9855, 1032.5339, 1048.5227, 1064.5226, 1120.5583, 1277.2297, 1279.7607, 1334.8937, 1371.6823, 1388.6163, 1388.6163, 1404.6113, 1404.6113, 1448.9275, 1516.8561, 1553.8110, 1618.0729, 1732.1044, 1758.0616, 1902.2831, 2096.1563, 2157.9590, 2168.1357, 2296.2388, 2296.2388, 2318.1865, 2781.4067, 2923.4119, 2985.4805, 3688.8682

8. gi|194700084 **Mass:** 18190 **Score:** 36 **Expect:** 1.4e+002 **Queries matched:** 4

unknown [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
713.4099	712.4026	712.4231	-0.0205	86 -	91	0	---	QLSLPR
1553.8110	1552.8037	1552.7860	0.0177	2 -	13	1	---	PRLEFVYHMFSK
2157.9590	2156.9517	2156.9475	0.0042	14 -	31	1	---	MCEPVVDPAMVSRCATYR + Oxidation (M)
2168.1357	2167.1284	2167.0336	0.0948	27 -	46	1	---	CATYRASPSGSLCLVPAMAR

No match to: 734.4896, 736.4969, 750.5195, 768.5248, 855.0323, 864.5381, 886.9855, 1032.5339, 1048.5227, 1064.5226, 1080.5109, 1120.5583, 1277.2297, 1279.7607, 1323.6937, 1323.6937, 1334.8937, 1339.6830, 1339.6830, 1355.6840, 1371.6823, 1388.6163, 1388.6163, 1404.6113, 1404.6113, 1448.9275, 1516.8561, 1618.0729, 1732.1044,

1758.0616, 1902.2831, 2096.1563, 2296.2388, 2296.2388, 2318.1865, 2384.2666, 2781.4067, 2923.4119, 2985.4805, 3688.8682

9. gi|222845076 **Mass:** 23801 **Score:** 36 **Expect:** 1.5e+002 **Queries matched:** 5

extra response regulator [Populus trichocarpa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1032.5339	1031.5266	1031.5763	-0.0497	188	196	1	---	GSSINKWIK
1080.5109	1079.5036	1079.5182	-0.0145	23	31	1	---	CIANFDGKR
1120.5583	1119.5510	1119.5560	-0.0049	32	41	0	---	QVFDNAIGEK
1516.8561	1515.8488	1515.8483	0.0006	197	209	1	---	KPLNLEKIAAIFC
2781.4067	2780.3994	2780.3587	0.0408	133	157	0	---	EAVYLHLGGASFDIILMDSQMPVMK + Oxidation (M)

No match to: 713.4099, 734.4896, 736.4969, 750.5195, 768.5248, 855.0323, 864.5381, 886.9855, 1048.5227, 1064.5226, 1277.2297, 1279.7607, 1323.6937, 1323.6937, 1334.8937, 1339.6830, 1339.6830, 1355.6840, 1371.6823, 1388.6163, 1388.6163, 1404.6113, 1404.6113, 1448.9275, 1553.8110, 1618.0729, 1732.1044, 1758.0616, 1902.2831, 2096.1563, 2157.9590, 2168.1357, 2296.2388, 2296.2388, 2318.1865, 2384.2666, 2923.4119, 2985.4805, 3688.8682

10. gi|15233780 **Mass:** 12153 **Score:** 36 **Expect:** 1.6e+002 **Queries matched:** 3

unknown protein [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
2157.9590	2156.9517	2156.8633	0.0885	1	20	1	---	MGSNTCGGCGERAVSNEAER + Oxidation (M)
2384.2666	2383.2593	2383.3070	-0.0477	13	34	1	---	AVSNEAERSIIQDIVTAVIVTR
2923.4119	2922.4046	2922.5088	-0.1041	36	61	0	---	EDIYLTGYEILMGLLYGLGALVYATR + Oxidation (M)

No match to: 713.4099, 734.4896, 736.4969, 750.5195, 768.5248, 855.0323, 864.5381, 886.9855, 1032.5339, 1048.5227, 1064.5226, 1080.5109, 1120.5583, 1277.2297, 1279.7607, 1323.6937, 1323.6937, 1334.8937, 1339.6830, 1339.6830, 1355.6840, 1371.6823, 1388.6163, 1388.6163, 1404.6113, 1404.6113, 1448.9275, 1516.8561, 1553.8110, 1618.0729, 1732.1044, 1758.0616, 1902.2831, 2096.1563, 2168.1357, 2296.2388, 2296.2388, 2318.1865, 2781.4067, 2985.4805, 3688.8682

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 44

Protein View

Match to: **gi|4826572** Score: **156** Expect: **1.5e-010**
polygalacturonase [Phleum pratense]

Nominal mass (M_r): **42579**; Calculated pI value: **7.83**
NCBI BLAST search of gi|4826572 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **19%**

Matched peptides shown in **Bold Red**

```
   1 GKKEEKKEEK KESGDAASGA DGTYDITKLG AKPDGKTDCT KEVEEAWASA
  51 CGGTGKNTIV IPKGDFLTGP LNFTGPCKGD SVTIKLDGNL LSSNDLAKYK
 101 ANWIEIMRIK KLTITGKGTL DGQGKAVWGK NSCAKNYNCK ILPNTLVLDF
 151 CDDALIEGIT LLNAKFFHMN IYECKGVTVK DVTITAPGDS PNTDGIHIGD
 201 SSKVTITDTT IGTGDDCISI GPGSTGLNIT GVTCGPGHGI SVGSLGRYKD
 251 EKDVTDITVK NCVLKKSTNG LRIKSYEDAK SPLTASKLTY ENVKMEDVGY
 301 PIIIDQKYCP NKICTSKGDS ARVTVKDVTF RNITGTSSTP EAVSLLCSDK
 351 QPCNGVTMND VKIEYSGTNN KTMAVCTNAK VTAKGVSEAN TCAA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
99 - 108	1323.6937	1322.6864	1322.6805	0.0059	1	**YKANWIEIMR** (No match)
99 - 108	1323.6937	1322.6864	1322.6805	0.0059	1	**YKANWIEIMR** (Ions score 47)
99 - 108	1339.6830	1338.6757	1338.6754	0.0003	1	**YKANWIEIMR** Oxidation (M) (Ions score 14)
99 - 108	1339.6830	1338.6757	1338.6754	0.0003	1	**YKANWIEIMR** Oxidation (M) (No match)
101 - 108	1032.5339	1031.5266	1031.5222	0.0044	0	**ANWIEIMR** (No match)
101 - 108	1048.5227	1047.5154	1047.5171	-0.0017	0	**ANWIEIMR** Oxidation (M) (No match)
126 - 135	1120.5583	1119.5510	1119.5495	0.0016	1	**AVWGKNSCAK** (No match)
166 - 175	1388.6163	1387.6090	1387.6053	0.0038	0	**FFHMNIYECK** (Ions score 62)
166 - 175	1388.6163	1387.6090	1387.6053	0.0038	0	**FFHMNIYECK** (No match)
166 - 175	1404.6113	1403.6040	1403.6002	0.0039	0	**FFHMNIYECK** Oxidation (M) (Ions score 45)
166 - 175	1404.6113	1403.6040	1403.6002	0.0039	0	**FFHMNIYECK** Oxidation (M) (No match)
176 - 203	2781.4067	2780.3994	2780.3828	0.0167	1	**GVTVKDVTITAPGDSPNTDGIHIGDSSK** (No match)
288 - 307	2384.2666	2383.2593	2383.1980	0.0613	1	**LTYENVKMEDVGYPIIIDQK** Oxidation (M) (No match)

Spot 70

Index

	Accession	Mass	Score	Description
1.	gi|29500897	28269	457	phl p5a allergen precursor [Phleum pratense]
2.	gi|13430402	27795	402	group V allergen Phl p 5 precursor [Phleum pratense]
3.	gi|398830	31083	395	Phlp5 [Phleum pratense]
4.	gi|3135503	27692	388	major allergen Phl p 5 [Phleum pratense]
5.	gi|3135501	27586	388	major allergen Phl p 5 [Phleum pratense]
6.	gi|3135499	27658	388	major allergen Phl p 5 [Phleum pratense]
7.	gi|1092249	28713	356	major allergen Phl p Va
8.	gi|2851456	28513	356	RecName: Full=Pollen allergen Phl p 5a; AltName: Full=Allergen Phl p Va; AltName: Allergen=Phl
9.	gi|422005	26530	346	PHLP5A protein - common timothy (fragment)
10.	gi|3309039	31010	292	group V allergen Phl p 5.0103 precursor [Phleum pratense]

Results List

1. gi|29500897 **Mass:** 28269 **Score:** 457 **Expect:** 1.2e-040 **Queries matched:** 21

phl p5a allergen precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1058.6166	1057.6093	1057.6171	-0.0078	209	218	0	---	FIPALEAAVK
1071.5627	1070.5554	1070.5648	-0.0093	233	241	0	---	YTVFETALK
1105.5510	1104.5437	1104.5451	-0.0013	76	86	0	---	AFAEGLSGEPK
1155.6233	1154.6160	1154.6335	-0.0175	101	110	1	---	LDAAYKLAYK
1199.6604	1198.6531	1198.6597	-0.0066	233	242	1	62	YTVFETALKK
1199.6604	1198.6531	1198.6597	-0.0066	233	242	1	---	YTVFETALKK
1213.6168	1212.6095	1212.6138	-0.0043	64	75	0	---	TFVATFGAASNK
1295.7467	1294.7394	1294.7496	-0.0101	153	164	0	---	VIPAGELQVIEK
1419.7385	1418.7312	1418.7405	-0.0093	219	232	0	---	QAYAATVATAPEVK
1471.7408	1470.7335	1470.7354	-0.0019	121	133	0	33	YDAYVATLSEALR
1471.7408	1470.7335	1470.7354	-0.0019	121	133	0	---	YDAYVATLSEALR
1541.8418	1540.8345	1540.8361	-0.0016	48	63	1	---	AALAAAAGVPPADKYR
1541.8418	1540.8345	1540.8361	-0.0016	48	63	1	38	AALAAAAGVPPADKYR
1927.0927	1926.0854	1926.0825	0.0029	153	170	1	---	VIPAGELQVIEKVDAAFK
1975.1217	1974.1144	1974.1149	-0.0004	134	152	0	68	IIAGTLEVHAVKPAAEEVK
1975.1217	1974.1144	1974.1149	-0.0004	134	152	0	---	IIAGTLEVHAVKPAAEEVK
2173.1680	2172.1607	2172.1102	0.0506	198	218	1	---	ASTGGAYESYKFIPALEAAVK
2300.1602	2299.1529	2299.1483	0.0046	64	86	1	---	TFVATFGAASNKAFAEGLSGEPK
2427.2070	2426.1997	2426.1964	0.0033	111	133	1	---	TAEGATPEAKYDAYVATLSEALR
2427.2070	2426.1997	2426.1964	0.0033	111	133	1	77	TAEGATPEAKYDAYVATLSEALR
2737.4165	2736.4092	2736.3870	0.0222	171	197	1	---	VAATAANAAPANDKFTVFEAAFNNAIK

No match to: 713.4105, 724.4937, 734.4936, 736.5001, 741.4404, 750.5166, 768.5229, 782.4922, 864.5334, 1033.6946, 1119.5645, 1149.5895, 1279.7640, 1305.6899, 1309.7368, 1334.8815, 1448.9127, 1538.7968, 1549.7990, 1559.8430, 1572.8557, 1618.0624, 1707.7743, 1726.9674, 1732.0964, 1920.0383, 1944.0811, 1964.0356, 2172.1907, 2273.2717, 2314.1819, 2444.3047, 2683.4487, 2825.3157, 2832.3706, 2849.3831, 2902.4856, 2965.4460, 2982.4219, 3443.8538, 3809.9648

2. gi|13430402 **Mass:** 27795 **Score:** 402 **Expect:** 3.8e-035 **Queries matched:** 19

group V allergen Phl p 5 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1058.6166	1057.6093	1057.6171	-0.0078	200	209	0	---	FIPALEAAVK
1071.5627	1070.5554	1070.5648	-0.0093	224	232	0	---	YTVFETALK
1105.5510	1104.5437	1104.5451	-0.0013	67	77	0	---	AFAEGLSGEPK
1155.6233	1154.6160	1154.6335	-0.0175	92	101	1	---	LDAAYKLAYK
1199.6604	1198.6531	1198.6597	-0.0066	224	233	1	62	YTVFETALKK
1199.6604	1198.6531	1198.6597	-0.0066	224	233	1	---	YTVFETALKK
1213.6168	1212.6095	1212.6138	-0.0043	55	66	0	---	TFVATFGAASNK
1279.7640	1278.7567	1278.6931	0.0636	41	52	0	---	SERPAIVPPADK
1295.7467	1294.7394	1294.7496	-0.0101	144	155	0	---	VIPAGELQVIEK
1419.7385	1418.7312	1418.7405	-0.0093	210	223	0	---	QAYAATVATAPEVK
1471.7408	1470.7335	1470.7354	-0.0019	112	124	0	33	YDAYVATLSEALR
1471.7408	1470.7335	1470.7354	-0.0019	112	124	0	---	YDAYVATLSEALR
1927.0927	1926.0854	1926.0825	0.0029	144	161	1	---	VIPAGELQVIEKVDAAFK
1975.1217	1974.1144	1974.1149	-0.0004	125	143	0	68	IIAGTLEVHAVKPAAEEVK
1975.1217	1974.1144	1974.1149	-0.0004	125	143	0	---	IIAGTLEVHAVKPAAEEVK
2300.1602	2299.1529	2299.1483	0.0046	55	77	1	---	TFVATFGAASNKAFAEGLSGEPK
2427.2070	2426.1997	2426.1964	0.0033	102	124	1	---	TAEGATPEAKYDAYVATLSEALR
2427.2070	2426.1997	2426.1964	0.0033	102	124	1	77	TAEGATPEAKYDAYVATLSEALR
2737.4165	2736.4092	2736.3870	0.0222	162	188	1	---	VAATAANAAPANDKFTVFEAAFNNAIK

No match to: 713.4105, 724.4937, 734.4936, 736.5001, 741.4404, 750.5166, 768.5229, 782.4922, 864.5334, 1033.6946, 1119.5645, 1149.5895, 1305.6899, 1309.7368, 1334.8815, 1448.9127, 1538.7968, 1541.8418, 1541.8418, 1549.7990, 1559.8430, 1572.8557, 1618.0624, 1707.7743, 1726.9674, 1732.0964, 1920.0383, 1944.0811, 1964.0356, 2172.1907, 2173.1680, 2273.2717, 2314.1819, 2444.3047, 2683.4487, 2825.3157, 2832.3706, 2849.3831, 2902.4856, 2965.4460, 2982.4219, 3443.8538, 3809.9648

3. gi|398830 **Mass:** 31083 **Score:** 395 **Expect:** 1.9e-034 **Queries matched:** 19

Phlp5 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1058.6166	1057.6093	1057.6171	-0.0078	237	246	0	---	FIPALEAAVK
1071.5627	1070.5554	1070.5648	-0.0093	261	269	0	---	YTVFETALK
1105.5510	1104.5437	1104.5451	-0.0013	104	114	0	---	AFAEGLSGEPK
1155.6233	1154.6160	1154.6335	-0.0175	129	138	1	---	LDAAYKLAYK
1199.6604	1198.6531	1198.6597	-0.0066	261	270	1	62	YTVFETALKK
1199.6604	1198.6531	1198.6597	-0.0066	261	270	1	---	YTVFETALKK

1213.6168	1212.6095	1212.6138	-0.0043	92 - 103	0	---	TFVATFGAASNK
1295.7467	1294.7394	1294.7496	-0.0101	181 - 192	0	---	VIPAGELQVIEK
1419.7385	1418.7312	1418.7405	-0.0093	247 - 260	0	---	QAYAATVATAPEVK
1471.7408	1470.7335	1470.7354	-0.0019	149 - 161	0	33	YDAYVATLSEALR
1471.7408	1470.7335	1470.7354	-0.0019	149 - 161	0	---	YDAYVATLSEALR
1572.8557	1571.8484	1571.8419	0.0065	76 - 91	1	---	AALAAAAGVQPADKYR
1927.0927	1926.0854	1926.0825	0.0029	181 - 198	1	---	VIPAGELQVIEKVDAAFK
1975.1217	1974.1144	1974.1149	-0.0004	162 - 180	0	68	IIAGTLEVHAVKPAAEEVK
1975.1217	1974.1144	1974.1149	-0.0004	162 - 180	0	---	IIAGTLEVHAVKPAAEEVK
2173.1680	2172.1607	2172.1102	0.0506	226 - 246	1	---	ASTGGAYESYKFIPALEAAVK
2300.1602	2299.1529	2299.1483	0.0046	92 - 114	1	---	TFVATFGAASNKAFAEGLSGEPK
2427.2070	2426.1997	2426.1964	0.0033	139 - 161	1	---	TAEGATPEAKYDAYVATLSEALR
2427.2070	2426.1997	2426.1964	0.0033	139 - 161	1	77	TAEGATPEAKYDAYVATLSEALR

No match to: 713.4105, 724.4937, 734.4936, 736.5001, 741.4404, 750.5166, 768.5229, 782.4922, 864.5334, 1033.6946, 1119.5645, 1149.5895, 1279.7640, 1305.6899, 1309.7368, 1334.8815, 1448.9127, 1538.7968, 1541.8418, 1541.8418, 1549.7990, 1559.8430, 1618.0624, 1707.7743, 1726.9674, 1732.0964, 1920.0383, 1944.0811, 1964.0356, 2172.1907, 2273.2717, 2314.1819, 2444.3047, 2683.4487, 2737.4165, 2825.3157, 2832.3706, 2849.3831, 2902.4856, 2965.4460, 2982.4219, 3443.8538, 3809.9648

4. gi|3135503 **Mass:** 27692 **Score:** 388 **Expect:** 9.6e-034 **Queries matched:** 18

major allergen Phl p 5 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1058.6166	1057.6093	1057.6171	-0.0078	201 - 210	0	---	FIPALEAAVK
1071.5627	1070.5554	1070.5648	-0.0093	225 - 233	0	---	YTVFETALK
1119.5645	1118.5572	1118.5607	-0.0035	68 - 78	0	---	AFAEGLSAEPK
1155.6233	1154.6160	1154.6335	-0.0175	93 - 102	1	---	LDAAYKLAYK
1199.6604	1198.6531	1198.6597	-0.0066	225 - 234	1	62	YTVFETALKK
1199.6604	1198.6531	1198.6597	-0.0066	225 - 234	1	---	YTVFETALKK
1213.6168	1212.6095	1212.6138	-0.0043	56 - 67	0	---	TFVATFGAASNK
1295.7467	1294.7394	1294.7496	-0.0101	145 - 156	0	---	VIPAGELQVIEK
1419.7385	1418.7312	1418.7405	-0.0093	211 - 224	0	---	QAYAATVATAPEVK
1471.7408	1470.7335	1470.7354	-0.0019	113 - 125	0	33	YDAYVATLSEALR
1471.7408	1470.7335	1470.7354	-0.0019	113 - 125	0	---	YDAYVATLSEALR
1975.1217	1974.1144	1974.1149	-0.0004	126 - 144	0	68	IIAGTLEVHAVKPAAEEVK
1975.1217	1974.1144	1974.1149	-0.0004	126 - 144	0	---	IIAGTLEVHAVKPAAEEVK
2173.1680	2172.1607	2172.1102	0.0506	190 - 210	1	---	ASTGGAYESYKFIPALEAAVK
2314.1819	2313.1746	2313.1640	0.0106	56 - 78	1	---	TFVATFGAASNKAFAEGLSAEPK
2427.2070	2426.1997	2426.1964	0.0033	103 - 125	1	---	TAEGATPEAKYDAYVATLSEALR
2427.2070	2426.1997	2426.1964	0.0033	103 - 125	1	77	TAEGATPEAKYDAYVATLSEALR
2737.4165	2736.4092	2736.3870	0.0222	163 - 189	1	---	VAATAANAAPANDKFTVFEAAFNNAIK

No match to: 713.4105, 724.4937, 734.4936, 736.5001, 741.4404, 750.5166, 768.5229, 782.4922, 864.5334, 1033.6946, 1105.5510, 1149.5895, 1279.7640, 1305.6899, 1309.7368, 1334.8815, 1448.9127, 1538.7968, 1541.8418, 1541.8418,

1549.7990, 1559.8430, 1572.8557, 1618.0624, 1707.7743, 1726.9674, 1732.0964, 1920.0383, 1927.0927, 1944.0811, 1964.0356, 2172.1907, 2273.2717, 2300.1602, 2444.3047, 2683.4487, 2825.3157, 2832.3706, 2849.3831, 2902.4856, 2965.4460, 2982.4219, 3443.8538, 3809.9648

5. gi|3135501 **Mass:** 27586 **Score:** 388 **Expect:** 9.6e-034 **Queries matched:** 18

major allergen Phl p 5 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1058.6166	1057.6093	1057.6171	-0.0078	201	210	0	---	FIPALEAAVK
1071.5627	1070.5554	1070.5648	-0.0093	225	233	0	---	YTVFETALK
1119.5645	1118.5572	1118.5607	-0.0035	68	78	0	---	AFAEGLSAEPK
1155.6233	1154.6160	1154.6335	-0.0175	93	102	1	---	LDAAYKLAYK
1199.6604	1198.6531	1198.6597	-0.0066	225	234	1	62	YTVFETALKK
1199.6604	1198.6531	1198.6597	-0.0066	225	234	1	---	YTVFETALKK
1213.6168	1212.6095	1212.6138	-0.0043	56	67	0	---	TFVATFGAASNK
1295.7467	1294.7394	1294.7496	-0.0101	145	156	0	---	VIPAGELQVIEK
1419.7385	1418.7312	1418.7405	-0.0093	211	224	0	---	QAYAATVATAPEVK
1471.7408	1470.7335	1470.7354	-0.0019	113	125	0	33	YDAYVATLSEALR
1471.7408	1470.7335	1470.7354	-0.0019	113	125	0	---	YDAYVATLSEALR
1975.1217	1974.1144	1974.1149	-0.0004	126	144	0	68	IIAGTLEVHAVKPAAEEVK
1975.1217	1974.1144	1974.1149	-0.0004	126	144	0	---	IIAGTLEVHAVKPAAEEVK
2173.1680	2172.1607	2172.1102	0.0506	190	210	1	---	ASTGGAYESYKFIPALEAAVK
2314.1819	2313.1746	2313.1640	0.0106	56	78	1	---	TFVATFGAASNKAFAEGLSAEPK
2427.2070	2426.1997	2426.1964	0.0033	103	125	1	---	TAEGATPEAKYDAYVATLSEALR
2427.2070	2426.1997	2426.1964	0.0033	103	125	1	77	TAEGATPEAKYDAYVATLSEALR
2737.4165	2736.4092	2736.3870	0.0222	163	189	1	---	VAATAANAAPANDKFTVFEAAFNNAIK

No match to: 713.4105, 724.4937, 734.4936, 736.5001, 741.4404, 750.5166, 768.5229, 782.4922, 864.5334, 1033.6946, 1105.5510, 1149.5895, 1279.7640, 1305.6899, 1309.7368, 1334.8815, 1448.9127, 1538.7968, 1541.8418, 1541.8418, 1549.7990, 1559.8430, 1572.8557, 1618.0624, 1707.7743, 1726.9674, 1732.0964, 1920.0383, 1927.0927, 1944.0811, 1964.0356, 2172.1907, 2273.2717, 2300.1602, 2444.3047, 2683.4487, 2825.3157, 2832.3706, 2849.3831, 2902.4856, 2965.4460, 2982.4219, 3443.8538, 3809.9648

6. gi|3135499 **Mass:** 27658 **Score:** 388 **Expect:** 9.6e-034 **Queries matched:** 18

major allergen Phl p 5 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1058.6166	1057.6093	1057.6171	-0.0078	201	210	0	---	FIPALEAAVK
1071.5627	1070.5554	1070.5648	-0.0093	225	233	0	---	YTVFETALK
1119.5645	1118.5572	1118.5607	-0.0035	68	78	0	---	AFAEGLSAEPK
1155.6233	1154.6160	1154.6335	-0.0175	93	102	1	---	LDAAYKLAYK
1199.6604	1198.6531	1198.6597	-0.0066	225	234	1	62	YTVFETALKK
1199.6604	1198.6531	1198.6597	-0.0066	225	234	1	---	YTVFETALKK
1213.6168	1212.6095	1212.6138	-0.0043	56	67	0	---	TFVATFGAASNK
1295.7467	1294.7394	1294.7496	-0.0101	145	156	0	---	VIPAGELQVIEK

1419.7385	1418.7312	1418.7405	-0.0093	211 - 224	0	---	QAYAATVATAPEVK
1471.7408	1470.7335	1470.7354	-0.0019	113 - 125	0	33	YDAYVATLSEALR
1471.7408	1470.7335	1470.7354	-0.0019	113 - 125	0	---	YDAYVATLSEALR
1975.1217	1974.1144	1974.1149	-0.0004	126 - 144	0	68	IIAGTLEVHAVKPAAEEVK
1975.1217	1974.1144	1974.1149	-0.0004	126 - 144	0	---	IIAGTLEVHAVKPAAEEVK
2173.1680	2172.1607	2172.1102	0.0506	190 - 210	1	---	ASTGGAYESYKFIPALEAAVK
2314.1819	2313.1746	2313.1640	0.0106	56 - 78	1	---	TFVATFGAASNKAFAEGLSAEPK
2427.2070	2426.1997	2426.1964	0.0033	103 - 125	1	---	TAEGATPEAKYDAYVATLSEALR
2427.2070	2426.1997	2426.1964	0.0033	103 - 125	1	77	TAEGATPEAKYDAYVATLSEALR
2737.4165	2736.4092	2736.3870	0.0222	163 - 189	1	---	VAATAANAAPANDKFTVFEAAFNNAIK

No match to: 713.4105, 724.4937, 734.4936, 736.5001, 741.4404, 750.5166, 768.5229, 782.4922, 864.5334, 1033.6946, 1105.5510, 1149.5895, 1279.7640, 1305.6899, 1309.7368, 1334.8815, 1448.9127, 1538.7968, 1541.8418, 1541.8418, 1549.7990, 1559.8430, 1572.8557, 1618.0624, 1707.7743, 1726.9674, 1732.0964, 1920.0383, 1927.0927, 1944.0811, 1964.0356, 2172.1907, 2273.2717, 2300.1602, 2444.3047, 2683.4487, 2825.3157, 2832.3706, 2849.3831, 2902.4856, 2965.4460, 2982.4219, 3443.8538, 3809.9648

7. gi|1092249 **Mass:** 28713 **Score:** 356 **Expect:** 1.5e-030 **Queries matched:** 16

major allergen Phl p Va

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1058.6166	1057.6093	1057.6171	-0.0078	211 - 220	0	---	FIPALEAAVK
1071.5627	1070.5554	1070.5648	-0.0093	235 - 243	0	---	YTVFETALK
1105.5510	1104.5437	1104.5451	-0.0013	78 - 88	0	---	AFAEGLSGEPK
1155.6233	1154.6160	1154.6335	-0.0175	103 - 112	1	---	LDAAYKLAYK
1199.6604	1198.6531	1198.6597	-0.0066	235 - 244	1	62	YTVFETALKK
1199.6604	1198.6531	1198.6597	-0.0066	235 - 244	1	---	YTVFETALKK
1295.7467	1294.7394	1294.7496	-0.0101	155 - 166	0	---	VIPAGELQVIEK
1419.7385	1418.7312	1418.7405	-0.0093	221 - 234	0	---	QAYAATVATAPEVK
1471.7408	1470.7335	1470.7354	-0.0019	123 - 135	0	33	YDAYVATLSEALR
1471.7408	1470.7335	1470.7354	-0.0019	123 - 135	0	---	YDAYVATLSEALR
1927.0927	1926.0854	1926.0825	0.0029	155 - 172	1	---	VIPAGELQVIEKVDAAFK
1975.1217	1974.1144	1974.1149	-0.0004	136 - 154	0	68	IIAGTLEVHAVKPAAEEVK
1975.1217	1974.1144	1974.1149	-0.0004	136 - 154	0	---	IIAGTLEVHAVKPAAEEVK
2173.1680	2172.1607	2172.1102	0.0506	200 - 220	1	---	ASTGGAYESYKFIPALEAAVK
2427.2070	2426.1997	2426.1964	0.0033	113 - 135	1	---	TAEGATPEAKYDAYVATLSEALR
2427.2070	2426.1997	2426.1964	0.0033	113 - 135	1	77	TAEGATPEAKYDAYVATLSEALR

No match to: 713.4105, 724.4937, 734.4936, 736.5001, 741.4404, 750.5166, 768.5229, 782.4922, 864.5334, 1033.6946, 1119.5645, 1149.5895, 1213.6168, 1279.7640, 1305.6899, 1309.7368, 1334.8815, 1448.9127, 1538.7968, 1541.8418, 1541.8418, 1549.7990, 1559.8430, 1572.8557, 1618.0624, 1707.7743, 1726.9674, 1732.0964, 1920.0383, 1944.0811, 1964.0356, 2172.1907, 2273.2717, 2300.1602, 2314.1819, 2444.3047, 2683.4487, 2737.4165, 2825.3157, 2832.3706, 2849.3831, 2902.4856, 2965.4460, 2982.4219, 3443.8538, 3809.9648

8. gi|2851456 **Mass:** 28513 **Score:** 356 **Expect:** 1.5e-030 **Queries matched:** 16

RecName: Full=Pollen allergen Phl p 5a; AltName: Full=Allergen Phl p Va; AltName: Allergen=Phl p 5a

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1058.6166	1057.6093	1057.6171	-0.0078	211	220	0	---	FIPALEAAVK
1071.5627	1070.5554	1070.5648	-0.0093	235	243	0	---	YTVFETALK
1105.5510	1104.5437	1104.5451	-0.0013	78	88	0	---	AFAEGLSGEPK
1155.6233	1154.6160	1154.6335	-0.0175	103	112	1	---	LDAAYKLAYK
1199.6604	1198.6531	1198.6597	-0.0066	235	244	1	62	YTVFETALKK
1199.6604	1198.6531	1198.6597	-0.0066	235	244	1	---	YTVFETALKK
1295.7467	1294.7394	1294.7496	-0.0101	155	166	0	---	VIPAGELQVIEK
1419.7385	1418.7312	1418.7405	-0.0093	221	234	0	---	QAYAATVATAPEVK
1471.7408	1470.7335	1470.7354	-0.0019	123	135	0	33	YDAYVATLSEALR
1471.7408	1470.7335	1470.7354	-0.0019	123	135	0	---	YDAYVATLSEALR
1927.0927	1926.0854	1926.0825	0.0029	155	172	1	---	VIPAGELQVIEKVDAAFK
1975.1217	1974.1144	1974.1149	-0.0004	136	154	0	68	IIAGTLEVHAVKPAAEEVK
1975.1217	1974.1144	1974.1149	-0.0004	136	154	0	---	IIAGTLEVHAVKPAAEEVK
2173.1680	2172.1607	2172.1102	0.0506	200	220	1	---	ASTGGAYESYKFIPALEAAVK
2427.2070	2426.1997	2426.1964	0.0033	113	135	1	---	TAEGATPEAKYDAYVATLSEALR
2427.2070	2426.1997	2426.1964	0.0033	113	135	1	77	TAEGATPEAKYDAYVATLSEALR

No match to: 713.4105, 724.4937, 734.4936, 736.5001, 741.4404, 750.5166, 768.5229, 782.4922, 864.5334, 1033.6946, 1119.5645, 1149.5895, 1213.6168, 1279.7640, 1305.6899, 1309.7368, 1334.8815, 1448.9127, 1538.7968, 1541.8418, 1541.8418, 1549.7990, 1559.8430, 1572.8557, 1618.0624, 1707.7743, 1726.9674, 1732.0964, 1920.0383, 1944.0811, 1964.0356, 2172.1907, 2273.2717, 2300.1602, 2314.1819, 2444.3047, 2683.4487, 2737.4165, 2825.3157, 2832.3706, 2849.3831, 2902.4856, 2965.4460, 2982.4219, 3443.8538, 3809.9648

9. gi|422005 **Mass:** 26530 **Score:** 346 **Expect:** 1.5e-029 **Queries matched:** 15

PHLP5A protein - common timothy (fragment)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1058.6166	1057.6093	1057.6171	-0.0078	183	192	0	---	FIPALEAAVK
1071.5627	1070.5554	1070.5648	-0.0093	207	215	0	---	YTVFETALK
1105.5510	1104.5437	1104.5451	-0.0013	50	60	0	---	AFAEGLSGEPK
1155.6233	1154.6160	1154.6335	-0.0175	75	84	1	---	LDAAYKLAYK
1199.6604	1198.6531	1198.6597	-0.0066	207	216	1	62	YTVFETALKK
1199.6604	1198.6531	1198.6597	-0.0066	207	216	1	---	YTVFETALKK
1309.7368	1308.7295	1308.7652	-0.0357	127	138	0	---	VIPAAELQVIEK
1419.7385	1418.7312	1418.7405	-0.0093	193	206	0	---	QAYAATVATAPEVK
1471.7408	1470.7335	1470.7354	-0.0019	95	107	0	33	YDAYVATLSEALR
1471.7408	1470.7335	1470.7354	-0.0019	95	107	0	---	YDAYVATLSEALR
1975.1217	1974.1144	1974.1149	-0.0004	108	126	0	68	IIAGTLEVHAVKPAAEEVK
1975.1217	1974.1144	1974.1149	-0.0004	108	126	0	---	IIAGTLEVHAVKPAAEEVK
2173.1680	2172.1607	2172.1102	0.0506	172	192	1	---	ASTGGAYESYKFIPALEAAVK
2427.2070	2426.1997	2426.1964	0.0033	85	107	1	---	TAEGATPEAKYDAYVATLSEALR
2427.2070	2426.1997	2426.1964	0.0033	85	107	1	77	TAEGATPEAKYDAYVATLSEALR

No match to: 713.4105, 724.4937, 734.4936, 736.5001, 741.4404, 750.5166, 768.5229, 782.4922, 864.5334, 1033.6946, 1119.5645, 1149.5895, 1213.6168, 1279.7640, 1295.7467, 1305.6899, 1334.8815, 1448.9127, 1538.7968, 1541.8418, 1541.8418, 1549.7990, 1559.8430, 1572.8557, 1618.0624, 1707.7743, 1726.9674, 1732.0964, 1920.0383, 1927.0927, 1944.0811, 1964.0356, 2172.1907, 2273.2717, 2300.1602, 2314.1819, 2444.3047, 2683.4487, 2737.4165, 2825.3157, 2832.3706, 2849.3831, 2902.4856, 2965.4460, 2982.4219, 3443.8538, 3809.9648

10. gi|3309039 **Mass:** 31010 **Score:** 292 **Expect:** 3.8e-024 **Queries matched:** 16

group V allergen Phl p 5.0103 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1058.6166	1057.6093	1057.6171	-0.0078	237	246	0	---	FIPALEAAVK
1071.5627	1070.5554	1070.5648	-0.0093	261	269	0	---	YTVFETALK
1105.5510	1104.5437	1104.5451	-0.0013	104	114	0	---	AFAEGLSGEPK
1155.6233	1154.6160	1154.6335	-0.0175	129	138	1	---	LDAAYKLAYK
1199.6604	1198.6531	1198.6597	-0.0066	261	270	1	62	YTVFETALKK
1199.6604	1198.6531	1198.6597	-0.0066	261	270	1	---	YTVFETALKK
1213.6168	1212.6095	1212.6138	-0.0043	92	103	0	---	TFVATFGAASNK
1295.7467	1294.7394	1294.7496	-0.0101	181	192	0	---	VIPAGELQVIEK
1419.7385	1418.7312	1418.7405	-0.0093	247	260	0	---	QAYAATVATAPEVK
1541.8418	1540.8345	1540.8361	-0.0016	76	91	1	---	AALAAAAGVPPADKYR
1541.8418	1540.8345	1540.8361	-0.0016	76	91	1	38	AALAAAAGVPPADKYR
1927.0927	1926.0854	1926.0825	0.0029	181	198	1	---	VIPAGELQVIEKVDAAFK
1975.1217	1974.1144	1974.1149	-0.0004	162	180	0	68	IIAGTLEVHAVKPAAEEVK
1975.1217	1974.1144	1974.1149	-0.0004	162	180	0	---	IIAGTLEVHAVKPAAEEVK
2173.1680	2172.1607	2172.1102	0.0506	226	246	1	---	ASTGGAYESYKFIPALEAAVK
2300.1602	2299.1529	2299.1483	0.0046	92	114	1	---	TFVATFGAASNKAFAEGLSGEPK

No match to: 713.4105, 724.4937, 734.4936, 736.5001, 741.4404, 750.5166, 768.5229, 782.4922, 864.5334, 1033.6946, 1119.5645, 1149.5895, 1279.7640, 1305.6899, 1309.7368, 1334.8815, 1448.9127, 1471.7408, 1471.7408, 1538.7968, 1549.7990, 1559.8430, 1572.8557, 1618.0624, 1707.7743, 1726.9674, 1732.0964, 1920.0383, 1944.0811, 1964.0356, 2172.1907, 2273.2717, 2314.1819, 2427.2070, 2427.2070, 2444.3047, 2683.4487, 2737.4165, 2825.3157, 2832.3706, 2849.3831, 2902.4856, 2965.4460, 2982.4219, 3443.8538, 3809.9648

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 62

Protein View

Match to: **gi|29500897** Score: **457** Expect: **1.2e-040**
phl p5a allergen precursor [Phleum pratense]

Nominal mass (M_r): **28269**; Calculated pI value: **7.94**
NCBI BLAST search of gi|29500897 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **63%**

Matched peptides shown in **Bold Red**

```
    1 ADLGYGPATP AAPAAGYTPA APAGAEPAGK ATTEEQKLIE KINAGFKAAL
   51 AAAAGVPPAD KYRTFVATFG AASNKAFAEG LSGEPKGAAE SSSKAALTSK
  101 LDAAYKLAYK TAEGATPEAK YDAYVATLSE ALRIIAGTLE VHAVKPAAEE
  151 VKVIPAGELQ VIEKVDAAFK VAATAANAAP ANDKFTVFEA AFNNAIKAST
  201 GGAYESYKFI PALEAAVKQA YAATVATAPE VKYTVFETAL KKAITAMSEA
  251 QKAAKPAAAA TATATSAVGA ATGAATAATG GYKV
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
48 - 63	1541.8418	1540.8345	1540.8361	-0.0016	1	AALAAAAGVPPADKYR (No match)
48 - 63	1541.8418	1540.8345	1540.8361	-0.0016	1	AALAAAAGVPPADKYR (Ions score 38)
64 - 75	1213.6168	1212.6095	1212.6138	-0.0043	0	TFVATFGAASNK (No match)
64 - 86	2300.1602	2299.1529	2299.1483	0.0046	1	TFVATFGAASNKAFAEGLSGEPK (No match)
76 - 86	1105.5510	1104.5437	1104.5451	-0.0013	0	AFAEGLSGEPK (No match)
101 - 110	1155.6233	1154.6160	1154.6335	-0.0175	1	LDAAYKLAYK (No match)
111 - 133	2427.2070	2426.1997	2426.1964	0.0033	1	TAEGATPEAKYDAYVATLSEALR (No match)
111 - 133	2427.2070	2426.1997	2426.1964	0.0033	1	TAEGATPEAKYDAYVATLSEALR (Ions score 77)
121 - 133	1471.7408	1470.7335	1470.7354	-0.0019	0	YDAYVATLSEALR (Ions score 33)
121 - 133	1471.7408	1470.7335	1470.7354	-0.0019	0	YDAYVATLSEALR (No match)
134 - 152	1975.1217	1974.1144	1974.1149	-0.0004	0	IIAGTLEVHAVKPAAEEVK (Ions score 68)
134 - 152	1975.1217	1974.1144	1974.1149	-0.0004	0	IIAGTLEVHAVKPAAEEVK (No match)
153 - 164	1295.7467	1294.7394	1294.7496	-0.0101	0	VIPAGELQVIEK (No match)
153 - 170	1927.0927	1926.0854	1926.0825	0.0029	1	VIPAGELQVIEKVDAAFK (No match)
171 - 197	2737.4165	2736.4092	2736.3870	0.0222	1	VAATAANAAPANDKFTVFEAAFNNAIK (No match)
198 - 218	2173.1680	2172.1607	2172.1102	0.0506	1	ASTGGAYESYKFIPALEAAVK (No match)
209 - 218	1058.6166	1057.6093	1057.6171	-0.0078	0	FIPALEAAVK (No match)

219 - 232	1419.7385	1418.7312	1418.7405	-0.0093	0	**QAYAATVATAPEVK** (No match)
233 - 241	1071.5627	1070.5554	1070.5648	-0.0093	0	**YTVFETALK** (No match)
233 - 242	1199.6604	1198.6531	1198.6597	-0.0066	1	**YTVFETALKK** (Ions score 62)
233 - 242	1199.6604	1198.6531	1198.6597	-0.0066	1	**YTVFETALKK** (No match)

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	Accession	Mass	Score	Description
1.	gi|28373838	26611	350	Chain A, Crystal Structure Of Phl P 1, A Major Timothy Grass Pollen Allergen
2.	gi|1171008	28838	346	RecName: Full=Pollen allergen Phl p 1; AltName: Full=Allergen Phl p I; AltName: Allergen=Phl p
3.	gi|168314	27685	280	pollen allergen
4.	gi|6599300	28742	277	pollen allergen [Lolium perenne]
5.	gi|126385	28819	268	RecName: Full=Pollen allergen Lol p 1; AltName: Full=Allergen Lol p I; AltName: Full=Allergen R
6.	gi|168316	28807	268	pollen allergen
7.	gi|33149333	26532	241	group 1 allergen Dac g 1.01 precursor [Dactylis glomerata]
8.	gi|33149335	28849	235	group 1 allergen Dac g 1.02 precursor [Dactylis glomerata]
9.	gi|2498576	29448	170	RecName: Full=Major pollen allergen Pha a 1; AltName: Full=Allergen Pha a I; AltName: Allergen=
10.	gi|3860384	28728	165	major group I allergen Hol l 1 [Holcus lanatus]

Results List

1. gi|28373838 **Mass:** 26611 **Score:** 350 **Expect:** 6.1e-030 **Queries matched:** 16

Chain A, Crystal Structure Of Phl P 1, A Major Timothy Grass Pollen Allergen

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
890.5134	889.5061	889.5021	0.0040	206	213	0	---	LTGPFTVR
1004.4999	1003.4926	1003.4875	0.0051	192	199	0	18	ESWGAIWR
1004.4999	1003.4926	1003.4875	0.0051	192	199	0	---	ESWGAIWR
1057.4432	1056.4359	1056.4368	-0.0009	69	77	0	---	GCGSCFEIK
1149.5961	1148.5888	1148.5825	0.0063	127	136	0	---	SAGELELQFR
1149.5961	1148.5888	1148.5825	0.0063	127	136	0	68	SAGELELQFR
1288.7083	1287.7010	1287.7186	-0.0176	155	166	0	---	GSNPNYLALLVK
1305.6948	1304.6875	1304.6836	0.0039	127	137	1	46	SAGELELQFRR
1305.6948	1304.6875	1304.6836	0.0039	127	137	1	---	SAGELELQFRR
1349.6854	1348.6781	1348.6775	0.0006	24	36	0	46	STWYGKPTGAGPK
1349.6854	1348.6781	1348.6775	0.0006	24	36	0	---	STWYGKPTGAGPK
1357.6124	1356.6051	1356.5914	0.0137	66	77	1	---	SGRGCGSCFEIK
1418.7783	1417.7710	1417.7677	0.0033	125	136	1	---	LRSAGELELQFR
1559.8518	1558.8445	1558.8355	0.0091	200	213	1	67	IDTPDKLTGPFTVR
1559.8518	1558.8445	1558.8355	0.0091	200	213	1	---	IDTPDKLTGPFTVR
1720.8896	1719.8823	1719.8678	0.0145	167	182	1	---	YVNGDGDVVAVDIKEK

No match to: 713.4060, 724.4935, 734.4916, 750.5144, 768.5228, 782.4718, 792.6006, 864.5260, 881.2831, 917.5641, 973.5466, 1020.4987, 1135.5895, 1264.7098, 1289.1426, 1291.6821, 1327.6780, 1371.6848, 1448.9104, 1471.7566, 1541.8538, 1557.8572, 1571.8873, 1572.8862, 1574.8828, 1732.1042, 1805.9023, 1932.0055, 1976.1290, 2050.0862, 2102.1243, 2231.2161, 2300.1614, 2427.2021, 2565.1973, 2663.3765, 2825.3235, 2921.3728, 3091.3887, 3092.4260, 3107.4170, 3349.5967

2. gi|1171008 **Mass:** 28838 **Score:** 346 **Expect:** 1.5e-029 **Queries matched:** 16

RecName: Full=Pollen allergen Phl p 1; AltName: Full=Allergen Phl p I; AltName: Allergen=Phl p 1; F

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
890.5134	889.5061	889.5021	0.0040	228	235	0	---	LTGPFTVR
1004.4999	1003.4926	1003.4875	0.0051	214	221	0	18	ESWGAIWR
1004.4999	1003.4926	1003.4875	0.0051	214	221	0	---	ESWGAIWR
1057.4432	1056.4359	1056.4368	-0.0009	91	99	0	---	GCGSCFEIK
1149.5961	1148.5888	1148.5825	0.0063	149	158	0	---	SAGELELQFR
1149.5961	1148.5888	1148.5825	0.0063	149	158	0	68	SAGELELQFR
1288.7083	1287.7010	1287.7186	-0.0176	177	188	0	---	GSNPNYLALLVK
1305.6948	1304.6875	1304.6836	0.0039	149	159	1	46	SAGELELQFRR
1305.6948	1304.6875	1304.6836	0.0039	149	159	1	---	SAGELELQFRR
1349.6854	1348.6781	1348.6775	0.0006	46	58	0	46	STWYGKPTGAGPK
1349.6854	1348.6781	1348.6775	0.0006	46	58	0	---	STWYGKPTGAGPK
1357.6124	1356.6051	1356.5914	0.0137	88	99	1	---	SGRGCGSCFEIK
1418.7783	1417.7710	1417.7677	0.0033	147	158	1	---	LRSAGELELQFR
1559.8518	1558.8445	1558.8355	0.0091	222	235	1	67	IDTPDKLTGPFTVR
1559.8518	1558.8445	1558.8355	0.0091	222	235	1	---	IDTPDKLTGPFTVR
1720.8896	1719.8823	1719.8678	0.0145	189	204	1	---	YVNGDGDVVAVDIKEK

No match to: 713.4060, 724.4935, 734.4916, 750.5144, 768.5228, 782.4718, 792.6006, 864.5260, 881.2831, 917.5641, 973.5466, 1020.4987, 1135.5895, 1264.7098, 1289.1426, 1291.6821, 1327.6780, 1371.6848, 1448.9104, 1471.7566, 1541.8538, 1557.8572, 1571.8873, 1572.8862, 1574.8828, 1732.1042, 1805.9023, 1932.0055, 1976.1290, 2050.0862, 2102.1243, 2231.2161, 2300.1614, 2427.2021, 2565.1973, 2663.3765, 2825.3235, 2921.3728, 3091.3887, 3092.4260, 3107.4170, 3349.5967

3. gi|168314 **Mass:** 27685 **Score:** 280 **Expect:** 6.1e-023 **Queries matched:** 11

pollen allergen

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
890.5134	889.5061	889.5021	0.0040	217	224	0	---	LTGPFTVR
1057.4432	1056.4359	1056.4368	-0.0009	80	88	0	---	GCGSCFEIK
1149.5961	1148.5888	1148.5825	0.0063	138	147	0	---	SAGELELQFR
1149.5961	1148.5888	1148.5825	0.0063	138	147	0	68	SAGELELQFR
1288.7083	1287.7010	1287.7186	-0.0176	166	177	0	---	GSNPNYLAILVK
1305.6948	1304.6875	1304.6836	0.0039	138	148	1	46	SAGELELQFRR
1305.6948	1304.6875	1304.6836	0.0039	138	148	1	---	SAGELELQFRR
1349.6854	1348.6781	1348.6775	0.0006	35	47	0	46	STWYGKPTGAGPK
1349.6854	1348.6781	1348.6775	0.0006	35	47	0	---	STWYGKPTGAGPK
1559.8518	1558.8445	1558.8355	0.0091	211	224	1	67	IDTPDKLTGPFTVR
1559.8518	1558.8445	1558.8355	0.0091	211	224	1	---	IDTPDKLTGPFTVR

No match to: 713.4060, 724.4935, 734.4916, 750.5144, 768.5228, 782.4718, 792.6006, 864.5260, 881.2831, 917.5641, 973.5466, 1004.4999, 1004.4999, 1020.4987, 1135.5895, 1264.7098, 1289.1426, 1291.6821, 1327.6780, 1357.6124, 1371.6848, 1418.7783, 1448.9104, 1471.7566, 1541.8538, 1557.8572, 1571.8873, 1572.8862, 1574.8828, 1720.8896,

1732.1042, 1805.9023, 1932.0055, 1976.1290, 2050.0862, 2102.1243, 2231.2161, 2300.1614, 2427.2021, 2565.1973, 2663.3765, 2825.3235, 2921.3728, 3091.3887, 3092.4260, 3107.4170, 3349.5967

4. gi|6599300 **Mass:** 28742 **Score:** 277 **Expect:** 1.2e-022 **Queries matched:** 11

pollen allergen [Lolium perenne]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
890.5134	889.5061	889.5021	0.0040	228	235	0	---	LTGPFTVR
1057.4432	1056.4359	1056.4368	-0.0009	91	99	0	---	GCGSCFEIK
1149.5961	1148.5888	1148.5825	0.0063	149	158	0	---	SAGELELQFR
1149.5961	1148.5888	1148.5825	0.0063	149	158	0	68	SAGELELQFR
1305.6948	1304.6875	1304.6836	0.0039	149	159	1	46	SAGELELQFRR
1305.6948	1304.6875	1304.6836	0.0039	149	159	1	---	SAGELELQFRR
1349.6854	1348.6781	1348.6775	0.0006	46	58	0	46	STWYGKPTGAGPK
1349.6854	1348.6781	1348.6775	0.0006	46	58	0	---	STWYGKPTGAGPK
1418.7783	1417.7710	1417.7677	0.0033	147	158	1	---	LRSAGELELQFR
1559.8518	1558.8445	1558.8355	0.0091	222	235	1	67	IDTPDKLTGPFTVR
1559.8518	1558.8445	1558.8355	0.0091	222	235	1	---	IDTPDKLTGPFTVR

No match to: 713.4060, 724.4935, 734.4916, 750.5144, 768.5228, 782.4718, 792.6006, 864.5260, 881.2831, 917.5641, 973.5466, 1004.4999, 1004.4999, 1020.4987, 1135.5895, 1264.7098, 1288.7083, 1289.1426, 1291.6821, 1327.6780, 1357.6124, 1371.6848, 1448.9104, 1471.7566, 1541.8538, 1557.8572, 1571.8873, 1572.8862, 1574.8828, 1720.8896, 1732.1042, 1805.9023, 1932.0055, 1976.1290, 2050.0862, 2102.1243, 2231.2161, 2300.1614, 2427.2021, 2565.1973, 2663.3765, 2825.3235, 2921.3728, 3091.3887, 3092.4260, 3107.4170, 3349.5967

5. gi|126385 **Mass:** 28819 **Score:** 268 **Expect:** 9.6e-022 **Queries matched:** 10

RecName: Full=Pollen allergen Lol p 1; AltName: Full=Allergen Lol p I; AltName: Full=Allergen R7; A

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
890.5134	889.5061	889.5021	0.0040	228	235	0	---	LTGPFTVR
1057.4432	1056.4359	1056.4368	-0.0009	91	99	0	---	GCGSCFEIK
1149.5961	1148.5888	1148.5825	0.0063	149	158	0	---	SAGELELQFR
1149.5961	1148.5888	1148.5825	0.0063	149	158	0	68	SAGELELQFR
1305.6948	1304.6875	1304.6836	0.0039	149	159	1	46	SAGELELQFRR
1305.6948	1304.6875	1304.6836	0.0039	149	159	1	---	SAGELELQFRR
1349.6854	1348.6781	1348.6775	0.0006	46	58	0	46	STWYGKPTGAGPK
1349.6854	1348.6781	1348.6775	0.0006	46	58	0	---	STWYGKPTGAGPK
1559.8518	1558.8445	1558.8355	0.0091	222	235	1	67	IDTPDKLTGPFTVR
1559.8518	1558.8445	1558.8355	0.0091	222	235	1	---	IDTPDKLTGPFTVR

No match to: 713.4060, 724.4935, 734.4916, 750.5144, 768.5228, 782.4718, 792.6006, 864.5260, 881.2831, 917.5641, 973.5466, 1004.4999, 1004.4999, 1020.4987, 1135.5895, 1264.7098, 1288.7083, 1289.1426, 1291.6821, 1327.6780, 1357.6124, 1371.6848, 1418.7783, 1448.9104, 1471.7566, 1541.8538, 1557.8572, 1571.8873, 1572.8862, 1574.8828, 1720.8896, 1732.1042, 1805.9023, 1932.0055, 1976.1290, 2050.0862, 2102.1243, 2231.2161, 2300.1614, 2427.2021, 2565.1973, 2663.3765, 2825.3235, 2921.3728, 3091.3887, 3092.4260, 3107.4170, 3349.5967

6. gi|168316 **Mass:** 28807 **Score:** 268 **Expect:** 9.6e-022 **Queries matched:** 10

pollen allergen

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
890.5134	889.5061	889.5021	0.0040	228	235	0	---	LTGPFTVR
1057.4432	1056.4359	1056.4368	-0.0009	91	99	0	---	GCGSCFEIK
1149.5961	1148.5888	1148.5825	0.0063	149	158	0	---	SAGELELQFR
1149.5961	1148.5888	1148.5825	0.0063	149	158	0	68	SAGELELQFR
1305.6948	1304.6875	1304.6836	0.0039	149	159	1	46	SAGELELQFRR
1305.6948	1304.6875	1304.6836	0.0039	149	159	1	---	SAGELELQFRR
1349.6854	1348.6781	1348.6775	0.0006	46	58	0	46	STWYGKPTGAGPK
1349.6854	1348.6781	1348.6775	0.0006	46	58	0	---	STWYGKPTGAGPK
1559.8518	1558.8445	1558.8355	0.0091	222	235	1	67	IDTPDKLTGPFTVR
1559.8518	1558.8445	1558.8355	0.0091	222	235	1	---	IDTPDKLTGPFTVR

No match to: 713.4060, 724.4935, 734.4916, 750.5144, 768.5228, 782.4718, 792.6006, 864.5260, 881.2831, 917.5641, 973.5466, 1004.4999, 1004.4999, 1020.4987, 1135.5895, 1264.7098, 1288.7083, 1289.1426, 1291.6821, 1327.6780, 1357.6124, 1371.6848, 1418.7783, 1448.9104, 1471.7566, 1541.8538, 1557.8572, 1571.8873, 1572.8862, 1574.8828, 1720.8896, 1732.1042, 1805.9023, 1932.0055, 1976.1290, 2050.0862, 2102.1243, 2231.2161, 2300.1614, 2427.2021, 2565.1973, 2663.3765, 2825.3235, 2921.3728, 3091.3887, 3092.4260, 3107.4170, 3349.5967

7. gi|33149333 **Mass:** 26532 **Score:** 241 **Expect:** 4.8e-019 **Queries matched:** 12

group 1 allergen Dac g 1.01 precursor [Dactylis glomerata]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
890.5134	889.5061	889.5021	0.0040	205	212	0	---	LTGPFTVR
1004.4999	1003.4926	1003.4875	0.0051	191	198	0	18	ESWGAIWR
1004.4999	1003.4926	1003.4875	0.0051	191	198	0	---	ESWGAIWR
1057.4432	1056.4359	1056.4368	-0.0009	68	76	0	---	GCGSCFEIK
1149.5961	1148.5888	1148.5825	0.0063	126	135	0	---	SAGELELQFR
1149.5961	1148.5888	1148.5825	0.0063	126	135	0	68	SAGELELQFR
1288.7083	1287.7010	1287.7186	-0.0176	154	165	0	---	GSNPNYLALLVK
1305.6948	1304.6875	1304.6836	0.0039	126	136	1	46	SAGELELQFRR
1305.6948	1304.6875	1304.6836	0.0039	126	136	1	---	SAGELELQFRR
1349.6854	1348.6781	1348.6775	0.0006	23	35	0	46	STWYGKPTGAGPK
1349.6854	1348.6781	1348.6775	0.0006	23	35	0	---	STWYGKPTGAGPK
1418.7783	1417.7710	1417.7677	0.0033	124	135	1	---	LRSAGELELQFR

No match to: 713.4060, 724.4935, 734.4916, 750.5144, 768.5228, 782.4718, 792.6006, 864.5260, 881.2831, 917.5641, 973.5466, 1020.4987, 1135.5895, 1264.7098, 1289.1426, 1291.6821, 1327.6780, 1357.6124, 1371.6848, 1448.9104, 1471.7566, 1541.8538, 1557.8572, 1559.8518, 1559.8518, 1571.8873, 1572.8862, 1574.8828, 1720.8896, 1732.1042, 1805.9023, 1932.0055, 1976.1290, 2050.0862, 2102.1243, 2231.2161, 2300.1614, 2427.2021, 2565.1973, 2663.3765, 2825.3235, 2921.3728, 3091.3887, 3092.4260, 3107.4170, 3349.5967

8. gi|33149335 **Mass:** 28849 **Score:** 235 **Expect:** 1.9e-018 **Queries matched:** 12

group 1 allergen Dac g 1.02 precursor [Dactylis glomerata]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
890.5134	889.5061	889.5021	0.0040	229	236	0	---	LTGPFTVR

1004.4999	1003.4926	1003.4875	0.0051	215 - 222	0	18	ESWGAIWR
1004.4999	1003.4926	1003.4875	0.0051	215 - 222	0	---	ESWGAIWR
1057.4432	1056.4359	1056.4368	-0.0009	92 - 100	0	---	GCGSCFEIK
1149.5961	1148.5888	1148.5825	0.0063	150 - 159	0	---	SAGELELQFR
1149.5961	1148.5888	1148.5825	0.0063	150 - 159	0	68	SAGELELQFR
1288.7083	1287.7010	1287.7186	-0.0176	178 - 189	0	---	GSNPNYLALLVK
1305.6948	1304.6875	1304.6836	0.0039	150 - 160	1	46	SAGELELQFRR
1305.6948	1304.6875	1304.6836	0.0039	150 - 160	1	---	SAGELELQFRR
1349.6854	1348.6781	1348.6775	0.0006	47 - 59	0	46	STWYGKPTGAGPK
1349.6854	1348.6781	1348.6775	0.0006	47 - 59	0	---	STWYGKPTGAGPK
1418.7783	1417.7710	1417.7677	0.0033	148 - 159	1	---	LRSAGELELQFR

No match to: 713.4060, 724.4935, 734.4916, 750.5144, 768.5228, 782.4718, 792.6006, 864.5260, 881.2831, 917.5641, 973.5466, 1020.4987, 1135.5895, 1264.7098, 1289.1426, 1291.6821, 1327.6780, 1357.6124, 1371.6848, 1448.9104, 1471.7566, 1541.8538, 1557.8572, 1559.8518, 1559.8518, 1571.8873, 1572.8862, 1574.8828, 1720.8896, 1732.1042, 1805.9023, 1932.0055, 1976.1290, 2050.0862, 2102.1243, 2231.2161, 2300.1614, 2427.2021, 2565.1973, 2663.3765, 2825.3235, 2921.3728, 3091.3887, 3092.4260, 3107.4170, 3349.5967

9. gi|2498576 **Mass:** 29448 **Score:** 170 **Expect:** 6.1e-012 **Queries matched:** 9

RecName: Full=Major pollen allergen Pha a 1; AltName: Full=Allergen Pha a I; AltName: Allergen=Pha

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
890.5134	889.5061	889.5021	0.0040	234 - 241	0	---	LTGPFTVR
1004.4999	1003.4926	1003.4875	0.0051	220 - 227	0	18	ESWGAIWR
1004.4999	1003.4926	1003.4875	0.0051	220 - 227	0	---	ESWGAIWR
1057.4432	1056.4359	1056.4368	-0.0009	97 - 105	0	---	GCGSCFELK
1288.7083	1287.7010	1287.7186	-0.0176	183 - 194	0	---	GSNPNYLALLVK
1349.6854	1348.6781	1348.6775	0.0006	52 - 64	0	46	STWYGKPTGAGPK
1349.6854	1348.6781	1348.6775	0.0006	52 - 64	0	---	STWYGKPTGAGPK
1559.8518	1558.8445	1558.8355	0.0091	228 - 241	1	67	IDTPDKLTGPFTVR
1559.8518	1558.8445	1558.8355	0.0091	228 - 241	1	---	IDTPDKLTGPFTVR

No match to: 713.4060, 724.4935, 734.4916, 750.5144, 768.5228, 782.4718, 792.6006, 864.5260, 881.2831, 917.5641, 973.5466, 1020.4987, 1135.5895, 1149.5961, 1149.5961, 1264.7098, 1289.1426, 1291.6821, 1305.6948, 1305.6948, 1327.6780, 1357.6124, 1371.6848, 1418.7783, 1448.9104, 1471.7566, 1541.8538, 1557.8572, 1571.8873, 1572.8862, 1574.8828, 1720.8896, 1732.1042, 1805.9023, 1932.0055, 1976.1290, 2050.0862, 2102.1243, 2231.2161, 2300.1614, 2427.2021, 2565.1973, 2663.3765, 2825.3235, 2921.3728, 3091.3887, 3092.4260, 3107.4170, 3349.5967

10. gi|3860384 **Mass:** 28728 **Score:** 165 **Expect:** 1.9e-011 **Queries matched:** 9

major group I allergen Hol l 1 [Holcus lanatus]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
890.5134	889.5061	889.5021	0.0040	228 - 235	0	---	LTGPFTVR
1057.4432	1056.4359	1056.4368	-0.0009	91 - 99	0	---	GCGSCFEIK
1149.5961	1148.5888	1148.6189	-0.0301	149 - 158	1	---	SAGELELKFR
1149.5961	1148.5888	1148.6189	-0.0301	149 - 158	1	68	SAGELELKFR
1288.7083	1287.7010	1287.7186	-0.0176	177 - 188	0	---	GSNPNYLALLVK

1349.6854	1348.6781	1348.6775	0.0006	46 - 58	0	46	STWYGKPTGAGPK
1349.6854	1348.6781	1348.6775	0.0006	46 - 58	0	---	STWYGKPTGAGPK
1357.6124	1356.6051	1356.5914	0.0137	88 - 99	1	---	SGRGCGSCFEIK
1371.6848	1370.6775	1370.6717	0.0058	244 - 255	0	---	VEAEDVIPEGWK

No match to: 713.4060, 724.4935, 734.4916, 750.5144, 768.5228, 782.4718, 792.6006, 864.5260, 881.2831, 917.5641, 973.5466, 1004.4999, 1004.4999, 1020.4987, 1135.5895, 1264.7098, 1289.1426, 1291.6821, 1305.6948, 1305.6948, 1327.6780, 1418.7783, 1448.9104, 1471.7566, 1541.8538, 1557.8572, 1559.8518, 1559.8518, 1571.8873, 1572.8862, 1574.8828, 1720.8896, 1732.1042, 1805.9023, 1932.0055, 1976.1290, 2050.0862, 2102.1243, 2231.2161, 2300.1614, 2427.2021, 2565.1973, 2663.3765, 2825.3235, 2921.3728, 3091.3887, 3092.4260, 3107.4170, 3349.5967

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 58

Protein View

Match to: **gi|28373838** Score: **350** Expect: **6.1e-030**
Chain A, Crystal Structure Of Phl P 1, A Major Timothy Grass Pollen Allergen

Nominal mass (M_r): **26611**; Calculated pI value: **6.17**
NCBI BLAST search of gi|28373838 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|28373839 from Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **36%**

Matched peptides shown in **Bold Red**

```
   1 AIPKVPPGPN ITATYGDKWL DAKSTWYGKP TGAGPKDNGG ACGYKDVDKP
  51 PFSGMTGCGN TPIFKSGRGC GSCFEIKCTK PEACSGEPVV VHITDDNEEP
 101 IAPYHFDLSG HAFGAMAKKG DEQKLRSAGE LELQFRRVKC KYPEGTKVTF
 151 HVEKGSNPNY LALLVKYVNG DGDVVAVDIK EKGKDKWIEL KESWGAIWRI
 201 DTPDKLTGPF TVRYTTEGGT KTEAEDVIPE GWKADTSYES K
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
24 - 36	1349.6854	1348.6781	1348.6775	0.0006	0	STWYGKPTGAGPK	(Ions score 46)
24 - 36	1349.6854	1348.6781	1348.6775	0.0006	0	STWYGKPTGAGPK	(No match)
66 - 77	1357.6124	1356.6051	1356.5914	0.0137	1	SGRGCGSCFEIK	(No match)
69 - 77	1057.4432	1056.4359	1056.4368	-0.0009	0	GCGSCFEIK	(No match)
125 - 136	1418.7783	1417.7710	1417.7677	0.0033	1	LRSAGELELQFR	(No match)
127 - 136	1149.5961	1148.5888	1148.5825	0.0063	0	SAGELELQFR	(No match)
127 - 136	1149.5961	1148.5888	1148.5825	0.0063	0	SAGELELQFR	(Ions score 68)
127 - 137	1305.6948	1304.6875	1304.6836	0.0039	1	SAGELELQFRR	(Ions score 46)
127 - 137	1305.6948	1304.6875	1304.6836	0.0039	1	SAGELELQFRR	(No match)
155 - 166	1288.7083	1287.7010	1287.7186	-0.0176	0	GSNPNYLALLVK	(No match)
167 - 182	1720.8896	1719.8823	1719.8678	0.0145	1	YVNGDGDVVAVDIKEK	(No match)
192 - 199	1004.4999	1003.4926	1003.4875	0.0051	0	ESWGAIWR	(Ions score 18)
192 - 199	1004.4999	1003.4926	1003.4875	0.0051	0	ESWGAIWR	(No match)
200 - 213	1559.8518	1558.8445	1558.8355	0.0091	1	IDTPDKLTGPFTVR	(Ions score 67)
200 - 213	1559.8518	1558.8445	1558.8355	0.0091	1	IDTPDKLTGPFTVR	(No match)
206 - 213	890.5134	889.5061	889.5021	0.0040	0	LTGPFTVR	(No match)

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	Accession	Mass	Score	Description
1.	gi|28373838	26611	355	Chain A, Crystal Structure Of Phl P 1, A Major Timothy Grass Pollen Allergen
2.	gi|1171008	28838	352	RecName: Full=Pollen allergen Phl p 1; AltName: Full=Allergen Phl p I; AltName: Allergen=Phl p
3.	gi|168314	27685	318	pollen allergen
4.	gi|126385	28819	317	RecName: Full=Pollen allergen Lol p 1; AltName: Full=Allergen Lol p I; AltName: Full=Allergen R
5.	gi|6599300	28742	317	pollen allergen [Lolium perenne]
6.	gi|168316	28807	317	pollen allergen
7.	gi|33149333	26532	232	group 1 allergen Dac g 1.01 precursor [Dactylis glomerata]
8.	gi|33149335	28849	231	group 1 allergen Dac g 1.02 precursor [Dactylis glomerata]
9.	gi|2498576	29448	178	RecName: Full=Major pollen allergen Pha a 1; AltName: Full=Allergen Pha a I; AltName: Allergen=
10.	gi|4090265	28627	147	group I pollen allergen [Poa pratensis]

Results List

1. gi|28373838 **Mass:** 26611 **Score:** 355 **Expect:** 1.9e-030 **Queries matched:** 11

Chain A, Crystal Structure Of Phl P 1, A Major Timothy Grass Pollen Allergen

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1004.5033	1003.4960	1003.4875	0.0085	192	199	0	---	ESWGAIWR
1057.4388	1056.4315	1056.4368	-0.0053	69	77	0	---	GCGSCFEIK
1149.5940	1148.5867	1148.5825	0.0042	127	136	0	---	SAGELELQFR
1149.5940	1148.5867	1148.5825	0.0042	127	136	0	53	SAGELELQFR
1305.6938	1304.6865	1304.6836	0.0029	127	137	1	67	SAGELELQFRR
1305.6938	1304.6865	1304.6836	0.0029	127	137	1	---	SAGELELQFRR
1349.6816	1348.6743	1348.6775	-0.0032	24	36	0	---	STWYGKPTGAGPK
1349.6816	1348.6743	1348.6775	-0.0032	24	36	0	51	STWYGKPTGAGPK
1357.6075	1356.6002	1356.5914	0.0088	66	77	1	---	SGRGCGSCFEIK
1559.8434	1558.8361	1558.8355	0.0007	200	213	1	---	IDTPDKLTGPFTVR
1559.8434	1558.8361	1558.8355	0.0007	200	213	1	84	IDTPDKLTGPFTVR

No match to: 768.5293, 973.5367, 973.5367, 1572.8806, 1574.8756, 3091.3965, 3092.4248

2. gi|1171008 **Mass:** 28838 **Score:** 352 **Expect:** 3.8e-030 **Queries matched:** 11

RecName: Full=Pollen allergen Phl p 1; AltName: Full=Allergen Phl p I; AltName: Allergen=Phl p 1; F

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1004.5033	1003.4960	1003.4875	0.0085	214	221	0	---	ESWGAIWR
1057.4388	1056.4315	1056.4368	-0.0053	91	99	0	---	GCGSCFEIK
1149.5940	1148.5867	1148.5825	0.0042	149	158	0	---	SAGELELQFR
1149.5940	1148.5867	1148.5825	0.0042	149	158	0	53	SAGELELQFR
1305.6938	1304.6865	1304.6836	0.0029	149	159	1	67	SAGELELQFRR

1305.6938	1304.6865	1304.6836	0.0029	149 - 159	1	---	SAGELELQFRR
1349.6816	1348.6743	1348.6775	-0.0032	46 - 58	0	---	STWYGKPTGAGPK
1349.6816	1348.6743	1348.6775	-0.0032	46 - 58	0	51	STWYGKPTGAGPK
1357.6075	1356.6002	1356.5914	0.0088	88 - 99	1	---	SGRGCGSCFEIK
1559.8434	1558.8361	1558.8355	0.0007	222 - 235	1	---	IDTPDKLTGPFTVR
1559.8434	1558.8361	1558.8355	0.0007	222 - 235	1	84	IDTPDKLTGPFTVR

No match to: 768.5293, 973.5367, 973.5367, 1572.8806, 1574.8756, 3091.3965, 3092.4248

3. gi|168314 **Mass:** 27685 **Score:** 318 **Expect:** 9.6e-027 **Queries matched:** 9

pollen allergen

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1057.4388	1056.4315	1056.4368	-0.0053	80 -	88	0	---	GCGSCFEIK
1149.5940	1148.5867	1148.5825	0.0042	138 -	147	0	---	SAGELELQFR
1149.5940	1148.5867	1148.5825	0.0042	138 -	147	0	53	SAGELELQFR
1305.6938	1304.6865	1304.6836	0.0029	138 -	148	1	67	SAGELELQFRR
1305.6938	1304.6865	1304.6836	0.0029	138 -	148	1	---	SAGELELQFRR
1349.6816	1348.6743	1348.6775	-0.0032	35 -	47	0	---	STWYGKPTGAGPK
1349.6816	1348.6743	1348.6775	-0.0032	35 -	47	0	51	STWYGKPTGAGPK
1559.8434	1558.8361	1558.8355	0.0007	211 -	224	1	---	IDTPDKLTGPFTVR
1559.8434	1558.8361	1558.8355	0.0007	211 -	224	1	84	IDTPDKLTGPFTVR

No match to: 768.5293, 973.5367, 973.5367, 1004.5033, 1357.6075, 1572.8806, 1574.8756, 3091.3965, 3092.4248

4. gi|126385 **Mass:** 28819 **Score:** 317 **Expect:** 1.2e-026 **Queries matched:** 9

RecName: Full=Pollen allergen Lol p 1; AltName: Full=Allergen Lol p I; AltName: Full=Allergen R7; A

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1057.4388	1056.4315	1056.4368	-0.0053	91 -	99	0	---	GCGSCFEIK
1149.5940	1148.5867	1148.5825	0.0042	149 -	158	0	---	SAGELELQFR
1149.5940	1148.5867	1148.5825	0.0042	149 -	158	0	53	SAGELELQFR
1305.6938	1304.6865	1304.6836	0.0029	149 -	159	1	67	SAGELELQFRR
1305.6938	1304.6865	1304.6836	0.0029	149 -	159	1	---	SAGELELQFRR
1349.6816	1348.6743	1348.6775	-0.0032	46 -	58	0	---	STWYGKPTGAGPK
1349.6816	1348.6743	1348.6775	-0.0032	46 -	58	0	51	STWYGKPTGAGPK
1559.8434	1558.8361	1558.8355	0.0007	222 -	235	1	---	IDTPDKLTGPFTVR
1559.8434	1558.8361	1558.8355	0.0007	222 -	235	1	84	IDTPDKLTGPFTVR

No match to: 768.5293, 973.5367, 973.5367, 1004.5033, 1357.6075, 1572.8806, 1574.8756, 3091.3965, 3092.4248

5. gi|6599300 **Mass:** 28742 **Score:** 317 **Expect:** 1.2e-026 **Queries matched:** 9

pollen allergen [Lolium perenne]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1057.4388	1056.4315	1056.4368	-0.0053	91 -	99	0	---	GCGSCFEIK
1149.5940	1148.5867	1148.5825	0.0042	149 -	158	0	---	SAGELELQFR

1149.5940	1148.5867	1148.5825	0.0042	149 - 158	0	53	SAGELELQFR
1305.6938	1304.6865	1304.6836	0.0029	149 - 159	1	67	SAGELELQFRR
1305.6938	1304.6865	1304.6836	0.0029	149 - 159	1	---	SAGELELQFRR
1349.6816	1348.6743	1348.6775	-0.0032	46 - 58	0	---	STWYGKPTGAGPK
1349.6816	1348.6743	1348.6775	-0.0032	46 - 58	0	51	STWYGKPTGAGPK
1559.8434	1558.8361	1558.8355	0.0007	222 - 235	1	---	IDTPDKLTGPFTVR
1559.8434	1558.8361	1558.8355	0.0007	222 - 235	1	84	IDTPDKLTGPFTVR

No match to: 768.5293, 973.5367, 973.5367, 1004.5033, 1357.6075, 1572.8806, 1574.8756, 3091.3965, 3092.4248

6. gi|168316 **Mass:** 28807 **Score:** 317 **Expect:** 1.2e-026 **Queries matched:** 9

pollen allergen

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1057.4388	1056.4315	1056.4368	-0.0053	91 -	99	0	---	GCGSCFEIK
1149.5940	1148.5867	1148.5825	0.0042	149 -	158	0	---	SAGELELQFR
1149.5940	1148.5867	1148.5825	0.0042	149 -	158	0	53	SAGELELQFR
1305.6938	1304.6865	1304.6836	0.0029	149 -	159	1	67	SAGELELQFRR
1305.6938	1304.6865	1304.6836	0.0029	149 -	159	1	---	SAGELELQFRR
1349.6816	1348.6743	1348.6775	-0.0032	46 -	58	0	---	STWYGKPTGAGPK
1349.6816	1348.6743	1348.6775	-0.0032	46 -	58	0	51	STWYGKPTGAGPK
1559.8434	1558.8361	1558.8355	0.0007	222 -	235	1	---	IDTPDKLTGPFTVR
1559.8434	1558.8361	1558.8355	0.0007	222 -	235	1	84	IDTPDKLTGPFTVR

No match to: 768.5293, 973.5367, 973.5367, 1004.5033, 1357.6075, 1572.8806, 1574.8756, 3091.3965, 3092.4248

7. gi|33149333 **Mass:** 26532 **Score:** 232 **Expect:** 3.8e-018 **Queries matched:** 8

group 1 allergen Dac g 1.01 precursor [Dactylis glomerata]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1004.5033	1003.4960	1003.4875	0.0085	191 -	198	0	---	ESWGAIWR
1057.4388	1056.4315	1056.4368	-0.0053	68 -	76	0	---	GCGSCFEIK
1149.5940	1148.5867	1148.5825	0.0042	126 -	135	0	---	SAGELELQFR
1149.5940	1148.5867	1148.5825	0.0042	126 -	135	0	53	SAGELELQFR
1305.6938	1304.6865	1304.6836	0.0029	126 -	136	1	67	SAGELELQFRR
1305.6938	1304.6865	1304.6836	0.0029	126 -	136	1	---	SAGELELQFRR
1349.6816	1348.6743	1348.6775	-0.0032	23 -	35	0	---	STWYGKPTGAGPK
1349.6816	1348.6743	1348.6775	-0.0032	23 -	35	0	51	STWYGKPTGAGPK

No match to: 768.5293, 973.5367, 973.5367, 1357.6075, 1559.8434, 1559.8434, 1572.8806, 1574.8756, 3091.3965, 3092.4248

8. gi|33149335 **Mass:** 28849 **Score:** 231 **Expect:** 4.8e-018 **Queries matched:** 8

group 1 allergen Dac g 1.02 precursor [Dactylis glomerata]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1004.5033	1003.4960	1003.4875	0.0085	215 -	222	0	---	ESWGAIWR
1057.4388	1056.4315	1056.4368	-0.0053	92 -	100	0	---	GCGSCFEIK

1149.5940	1148.5867	1148.5825	0.0042	150 - 159	0	---	SAGELELQFR
1149.5940	1148.5867	1148.5825	0.0042	150 - 159	0	53	SAGELELQFR
1305.6938	1304.6865	1304.6836	0.0029	150 - 160	1	67	SAGELELQFRR
1305.6938	1304.6865	1304.6836	0.0029	150 - 160	1	---	SAGELELQFRR
1349.6816	1348.6743	1348.6775	-0.0032	47 - 59	0	---	STWYGKPTGAGPK
1349.6816	1348.6743	1348.6775	-0.0032	47 - 59	0	51	STWYGKPTGAGPK

No match to: 768.5293, 973.5367, 973.5367, 1357.6075, 1559.8434, 1559.8434, 1572.8806, 1574.8756, 3091.3965, 3092.4248

9. gi|2498576 **Mass:** 29448 **Score:** 178 **Expect:** 9.6e-013 **Queries matched:** 6

RecName: Full=Major pollen allergen Pha a 1; AltName: Full=Allergen Pha a I; AltName: Allergen=Pha

Observed	Mr(expt)	Mr(calc)	Delta	Start - End	Miss	Ions	Peptide
1004.5033	1003.4960	1003.4875	0.0085	220 - 227	0	---	ESWGAIWR
1057.4388	1056.4315	1056.4368	-0.0053	97 - 105	0	---	GCGSCFELK
1349.6816	1348.6743	1348.6775	-0.0032	52 - 64	0	---	STWYGKPTGAGPK
1349.6816	1348.6743	1348.6775	-0.0032	52 - 64	0	51	STWYGKPTGAGPK
1559.8434	1558.8361	1558.8355	0.0007	228 - 241	1	---	IDTPDKLTGPFTVR
1559.8434	1558.8361	1558.8355	0.0007	228 - 241	1	84	IDTPDKLTGPFTVR

No match to: 768.5293, 973.5367, 973.5367, 1149.5940, 1149.5940, 1305.6938, 1305.6938, 1357.6075, 1572.8806, 1574.8756, 3091.3965, 3092.4248

10. gi|4090265 **Mass:** 28627 **Score:** 147 **Expect:** 1.2e-009 **Queries matched:** 6

group I pollen allergen [Poa pratensis]

Observed	Mr(expt)	Mr(calc)	Delta	Start - End	Miss	Ions	Peptide
1057.4388	1056.4315	1056.4368	-0.0053	91 - 99	0	---	GCGSCFEIK
1149.5940	1148.5867	1148.6189	-0.0322	149 - 158	1	---	SAGELELKFR
1149.5940	1148.5867	1148.6189	-0.0322	149 - 158	1	53	SAGELELKFR
1349.6816	1348.6743	1348.6775	-0.0032	46 - 58	0	---	STWYGKPTGAGPK
1349.6816	1348.6743	1348.6775	-0.0032	46 - 58	0	51	STWYGKPTGAGPK
1357.6075	1356.6002	1356.5914	0.0088	88 - 99	1	---	SGRGCGSCFEIK

No match to: 768.5293, 973.5367, 973.5367, 1004.5033, 1305.6938, 1305.6938, 1559.8434, 1559.8434, 1572.8806, 1574.8756, 3091.3965, 3092.4248

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 18

Protein View

Match to: **gi|28373838** Score: **355** Expect: **1.9e-030**
Chain A, Crystal Structure Of Phl P 1, A Major Timothy Grass Pollen Allergen

Nominal mass (M_r): **26611**; Calculated pI value: **6.17**
NCBI BLAST search of gi|28373838 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|28373839 from Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **24%**

Matched peptides shown in **Bold Red**

```
     1 AIPKVPPGPN ITATYGDKWL DAKSTWYGKP TGAGPKDNGG ACGYKDVDKP
    51 PFSGMTGCGN TPIFKSGRGC GSCFEIKCTK PEACSGEPVV VHITDDNEEP
   101 IAPYHFDLSG HAFGAMAKKG DEQKLRSAGE LELQFRRVKC KYPEGTKVTF
   151 HVEKGSNPNY LALLVKYVNG DGDVVAVDIK EKGKDKWIEL KESWGAIWRI
   201 DTPDKLTGPF TVRYTTEGGT KTEAEDVIPE GWKADTSYES K
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
24 - 36	1349.6816	1348.6743	1348.6775	-0.0032	0	STWYGKPTGAGPK	(No match)
24 - 36	1349.6816	1348.6743	1348.6775	-0.0032	0	STWYGKPTGAGPK	(Ions score 51)
66 - 77	1357.6075	1356.6002	1356.5914	0.0088	1	SGRGCGSCFEIK	(No match)
69 - 77	1057.4388	1056.4315	1056.4368	-0.0053	0	GCGSCFEIK	(No match)
127 - 136	1149.5940	1148.5867	1148.5825	0.0042	0	SAGELELQFR	(No match)
127 - 136	1149.5940	1148.5867	1148.5825	0.0042	0	SAGELELQFR	(Ions score 53)
127 - 137	1305.6938	1304.6865	1304.6836	0.0029	1	SAGELELQFRR	(Ions score 67)
127 - 137	1305.6938	1304.6865	1304.6836	0.0029	1	SAGELELQFRR	(No match)
192 - 199	1004.5033	1003.4960	1003.4875	0.0085	0	ESWGAIWR	(No match)
200 - 213	1559.8434	1558.8361	1558.8355	0.0007	1	IDTPDKLTGPFTVR	(No match)
200 - 213	1559.8434	1558.8361	1558.8355	0.0007	1	IDTPDKLTGPFTVR	(Ions score 84)

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	Accession	Mass	Score	Description
1.	gi|28373838	26611	238	Chain A, Crystal Structure Of Phl P 1, A Major Timothy Grass Pollen Allergen
2.	gi|1171008	28838	235	RecName: Full=Pollen allergen Phl p 1; AltName: Full=Allergen Phl p I; AltName: Allergen=Phl p
3.	gi|3901094	28584	207	pollen allergen Phl pI [Phleum pratense]
4.	gi|1582250	28542	207	allergen PhI p I
5.	gi|126385	28819	182	RecName: Full=Pollen allergen Lol p 1; AltName: Full=Allergen Lol p I; AltName: Full=Allergen R
6.	gi|168316	28807	182	pollen allergen
7.	gi|6599300	28742	181	pollen allergen [Lolium perenne]
8.	gi|168314	27685	171	pollen allergen
9.	gi|33149333	26532	130	group 1 allergen Dac g 1.01 precursor [Dactylis glomerata]
10.	gi|33149335	28849	127	group 1 allergen Dac g 1.02 precursor [Dactylis glomerata]

Results List

1. gi|28373838 **Mass:** 26611 **Score:** 238 **Expect:** 9.6e-019 **Queries matched:** 13

Chain A, Crystal Structure Of Phl P 1, A Major Timothy Grass Pollen Allergen

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1004.5007	1003.4934	1003.4875	0.0059	192	199	0	---	ESWGAIWR
1057.4449	1056.4376	1056.4368	0.0008	69	77	0	---	GCGSCFEIK
1149.5957	1148.5884	1148.5825	0.0059	127	136	0	30	SAGELELQFR
1149.5957	1148.5884	1148.5825	0.0059	127	136	0	---	SAGELELQFR
1305.6929	1304.6856	1304.6836	0.0020	127	137	1	---	SAGELELQFRR
1305.6929	1304.6856	1304.6836	0.0020	127	137	1	54	SAGELELQFRR
1349.6860	1348.6787	1348.6775	0.0012	24	36	0	---	STWYGKPTGAGPK
1357.6127	1356.6054	1356.5914	0.0140	66	77	1	---	SGRGCGSCFEIK
1418.7854	1417.7781	1417.7677	0.0104	125	136	1	---	LRSAGELELQFR
1559.8521	1558.8448	1558.8355	0.0094	200	213	1	---	IDTPDKLTGPFTVR
1559.8521	1558.8448	1558.8355	0.0094	200	213	1	51	IDTPDKLTGPFTVR
2168.0430	2167.0357	2167.0078	0.0280	46	65	0	---	DVDKPPFSGMTGCGNTPIFK
3090.3972	3089.3899	3089.3680	0.0219	37	65	1	---	DNGGACGYKDVDKPPFSGMTGCGNTPIFK

No match to: 713.4000, 724.4943, 734.4911, 750.5165, 768.5150, 782.4732, 838.5172, 848.5263, 864.5334, 973.5490, 1135.5815, 1275.1226, 1289.1371, 1291.6794, 1291.6794, 1363.6985, 1404.7455, 1448.9166, 1571.8904, 1571.8904, 1574.8932, 1608.8898, 1732.1055, 1805.8870, 2044.1165, 2050.0864, 2231.2319, 2564.1946, 2663.3860, 2790.3096, 2825.3108, 2921.3574, 3092.4331, 3093.4385, 3107.3958, 3332.5796, 3349.6094

2. gi|1171008 **Mass:** 28838 **Score:** 235 **Expect:** 1.9e-018 **Queries matched:** 13

RecName: Full=Pollen allergen Phl p 1; AltName: Full=Allergen Phl p I; AltName: Allergen=Phl p 1; F

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1004.5007	1003.4934	1003.4875	0.0059	214	221	0	---	ESWGAIWR

1057.4449	1056.4376	1056.4368	0.0008	91 - 99	0	---	GCGSCFEIK
1149.5957	1148.5884	1148.5825	0.0059	149 - 158	0	30	SAGELELQFR
1149.5957	1148.5884	1148.5825	0.0059	149 - 158	0	---	SAGELELQFR
1305.6929	1304.6856	1304.6836	0.0020	149 - 159	1	---	SAGELELQFRR
1305.6929	1304.6856	1304.6836	0.0020	149 - 159	1	54	SAGELELQFRR
1349.6860	1348.6787	1348.6775	0.0012	46 - 58	0	---	STWYGKPTGAGPK
1357.6127	1356.6054	1356.5914	0.0140	88 - 99	1	---	SGRGCGSCFEIK
1418.7854	1417.7781	1417.7677	0.0104	147 - 158	1	---	LRSAGELELQFR
1559.8521	1558.8448	1558.8355	0.0094	222 - 235	1	---	IDTPDKLTGPFTVR
1559.8521	1558.8448	1558.8355	0.0094	222 - 235	1	51	IDTPDKLTGPFTVR
2168.0430	2167.0357	2167.0078	0.0280	68 - 87	0	---	DVDKPPFSGMTGCGNTPIFK
3090.3972	3089.3899	3089.3680	0.0219	59 - 87	1	---	DNGGACGYKDVDKPPFSGMTGCGNTPIFK

No match to: 713.4000, 724.4943, 734.4911, 750.5165, 768.5150, 782.4732, 838.5172, 848.5263, 864.5334, 973.5490, 1135.5815, 1275.1226, 1289.1371, 1291.6794, 1291.6794, 1363.6985, 1404.7455, 1448.9166, 1571.8904, 1571.8904, 1574.8932, 1608.8898, 1732.1055, 1805.8870, 2044.1165, 2050.0864, 2231.2319, 2564.1946, 2663.3860, 2790.3096, 2825.3108, 2921.3574, 3092.4331, 3093.4385, 3107.3958, 3332.5796, 3349.6094

3. gi|3901094 **Mass:** 28584 **Score:** 207 **Expect:** 1.2e-015 **Queries matched:** 12

pollen allergen Phl pI [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1004.5007	1003.4934	1003.4875	0.0059	214 - 221	0	---	ESWGAIWR
1057.4449	1056.4376	1056.4368	0.0008	91 - 99	0	---	GCGSCFEIK
1135.5815	1134.5742	1134.5669	0.0074	149 - 158	0	---	SAGEVEIQFR
1291.6794	1290.6721	1290.6680	0.0042	149 - 159	1	---	SAGEVEIQFRR
1291.6794	1290.6721	1290.6680	0.0042	149 - 159	1	48	SAGEVEIQFRR
1357.6127	1356.6054	1356.5914	0.0140	88 - 99	1	---	SGRGCGSCFEIK
1363.6985	1362.6912	1362.6931	-0.0019	46 - 58	0	---	STWYGKPTAAGPK
1404.7455	1403.7382	1403.7296	0.0087	189 - 202	0	---	FVAGDGDVVAVDIK
1571.8904	1570.8831	1570.8718	0.0113	222 - 235	1	---	IDTPEVLKGPFTVR
1571.8904	1570.8831	1570.8718	0.0113	222 - 235	1	60	IDTPEVLKGPFTVR
2168.0430	2167.0357	2167.0078	0.0280	68 - 87	0	---	DVDKPPFSGMTGCGNTPIFK
3090.3972	3089.3899	3089.3680	0.0219	59 - 87	1	---	DNGGACGYKDVDKPPFSGMTGCGNTPIFK

No match to: 713.4000, 724.4943, 734.4911, 750.5165, 768.5150, 782.4732, 838.5172, 848.5263, 864.5334, 973.5490, 1149.5957, 1149.5957, 1275.1226, 1289.1371, 1305.6929, 1305.6929, 1349.6860, 1418.7854, 1448.9166, 1559.8521, 1559.8521, 1574.8932, 1608.8898, 1732.1055, 1805.8870, 2044.1165, 2050.0864, 2231.2319, 2564.1946, 2663.3860, 2790.3096, 2825.3108, 2921.3574, 3092.4331, 3093.4385, 3107.3958, 3332.5796, 3349.6094

4. gi|1582250 **Mass:** 28542 **Score:** 207 **Expect:** 1.2e-015 **Queries matched:** 12

allergen PhI p I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1004.5007	1003.4934	1003.4875	0.0059	213 - 220	0	---	ESWGAIWR
1057.4449	1056.4376	1056.4368	0.0008	91 - 99	0	---	GCGSCFEIK

1135.5815	1134.5742	1134.5669	0.0074	149 - 158	0	---	SAGEVEIQFR
1291.6794	1290.6721	1290.6680	0.0042	149 - 159	1	---	SAGEVEIQFRR
1291.6794	1290.6721	1290.6680	0.0042	149 - 159	1	48	SAGEVEIQFRR
1357.6127	1356.6054	1356.5914	0.0140	88 - 99	1	---	SGRGCGSCFEIK
1363.6985	1362.6912	1362.6931	-0.0019	46 - 58	0	---	STWYGKPTAAGPK
1404.7455	1403.7382	1403.7520	-0.0138	147 - 158	1	---	LRSAGEVEIQFR
1571.8904	1570.8831	1570.8718	0.0113	221 - 234	1	---	IDTPEVLKGPFTVR
1571.8904	1570.8831	1570.8718	0.0113	221 - 234	1	60	IDTPEVLKGPFTVR
2168.0430	2167.0357	2167.0078	0.0280	68 - 87	0	---	DVDKPPFSGMTGCGNTPIFK
3090.3972	3089.3899	3089.3680	0.0219	59 - 87	1	---	DNGGACGYKDVDKPPFSGMTGCGNTPIFK

No match to: 713.4000, 724.4943, 734.4911, 750.5165, 768.5150, 782.4732, 838.5172, 848.5263, 864.5334, 973.5490, 1149.5957, 1149.5957, 1275.1226, 1289.1371, 1305.6929, 1305.6929, 1349.6860, 1418.7854, 1448.9166, 1559.8521, 1559.8521, 1574.8932, 1608.8898, 1732.1055, 1805.8870, 2044.1165, 2050.0864, 2231.2319, 2564.1946, 2663.3860, 2790.3096, 2825.3108, 2921.3574, 3092.4331, 3093.4385, 3107.3958, 3332.5796, 3349.6094

5. gi|126385 **Mass:** 28819 **Score:** 182 **Expect:** 3.8e-013 **Queries matched:** 9

RecName: Full=Pollen allergen Lol p 1; AltName: Full=Allergen Lol p I; AltName: Full=Allergen R7; A

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1057.4449	1056.4376	1056.4368	0.0008	91 -	99	0	---	GCGSCFEIK
1149.5957	1148.5884	1148.5825	0.0059	149 -	158	0	30	SAGELELQFR
1149.5957	1148.5884	1148.5825	0.0059	149 -	158	0	---	SAGELELQFR
1305.6929	1304.6856	1304.6836	0.0020	149 -	159	1	---	SAGELELQFRR
1305.6929	1304.6856	1304.6836	0.0020	149 -	159	1	54	SAGELELQFRR
1349.6860	1348.6787	1348.6775	0.0012	46 -	58	0	---	STWYGKPTGAGPK
1559.8521	1558.8448	1558.8355	0.0094	222 -	235	1	---	IDTPDKLTGPFTVR
1559.8521	1558.8448	1558.8355	0.0094	222 -	235	1	51	IDTPDKLTGPFTVR
2168.0430	2167.0357	2167.0190	0.0168	68 -	87	1	---	NVDKAPFNGMTGCGNTPIFK

No match to: 713.4000, 724.4943, 734.4911, 750.5165, 768.5150, 782.4732, 838.5172, 848.5263, 864.5334, 973.5490, 1004.5007, 1135.5815, 1275.1226, 1289.1371, 1291.6794, 1291.6794, 1357.6127, 1363.6985, 1404.7455, 1418.7854, 1448.9166, 1571.8904, 1571.8904, 1574.8932, 1608.8898, 1732.1055, 1805.8870, 2044.1165, 2050.0864, 2231.2319, 2564.1946, 2663.3860, 2790.3096, 2825.3108, 2921.3574, 3090.3972, 3092.4331, 3093.4385, 3107.3958, 3332.5796, 3349.6094

6. gi|168316 **Mass:** 28807 **Score:** 182 **Expect:** 3.8e-013 **Queries matched:** 9

pollen allergen

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1057.4449	1056.4376	1056.4368	0.0008	91 -	99	0	---	GCGSCFEIK
1149.5957	1148.5884	1148.5825	0.0059	149 -	158	0	30	SAGELELQFR
1149.5957	1148.5884	1148.5825	0.0059	149 -	158	0	---	SAGELELQFR
1305.6929	1304.6856	1304.6836	0.0020	149 -	159	1	---	SAGELELQFRR
1305.6929	1304.6856	1304.6836	0.0020	149 -	159	1	54	SAGELELQFRR
1349.6860	1348.6787	1348.6775	0.0012	46 -	58	0	---	STWYGKPTGAGPK

1559.8521	1558.8448	1558.8355	0.0094	222 - 235	1	---	IDTPDKLTGPFTVR
1559.8521	1558.8448	1558.8355	0.0094	222 - 235	1	51	IDTPDKLTGPFTVR
2168.0430	2167.0357	2167.0190	0.0168	68 - 87	1	---	NVDKAPFNGMTGCGNTPIFK

No match to: 713.4000, 724.4943, 734.4911, 750.5165, 768.5150, 782.4732, 838.5172, 848.5263, 864.5334, 973.5490, 1004.5007, 1135.5815, 1275.1226, 1289.1371, 1291.6794, 1291.6794, 1357.6127, 1363.6985, 1404.7455, 1418.7854, 1448.9166, 1571.8904, 1571.8904, 1574.8932, 1608.8898, 1732.1055, 1805.8870, 2044.1165, 2050.0864, 2231.2319, 2564.1946, 2663.3860, 2790.3096, 2825.3108, 2921.3574, 3090.3972, 3092.4331, 3093.4385, 3107.3958, 3332.5796, 3349.6094

7. gi|6599300 **Mass:** 28742 **Score:** 181 **Expect:** 4.8e-013 **Queries matched:** 9

pollen allergen [Lolium perenne]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1057.4449	1056.4376	1056.4368	0.0008	91 -	99	0	---	GCGSCFEIK
1149.5957	1148.5884	1148.5825	0.0059	149 -	158	0	30	SAGELELQFR
1149.5957	1148.5884	1148.5825	0.0059	149 -	158	0	---	SAGELELQFR
1305.6929	1304.6856	1304.6836	0.0020	149 -	159	1	---	SAGELELQFRR
1305.6929	1304.6856	1304.6836	0.0020	149 -	159	1	54	SAGELELQFRR
1349.6860	1348.6787	1348.6775	0.0012	46 -	58	0	---	STWYGKPTGAGPK
1418.7854	1417.7781	1417.7677	0.0104	147 -	158	1	---	LRSAGELELQFR
1559.8521	1558.8448	1558.8355	0.0094	222 -	235	1	---	IDTPDKLTGPFTVR
1559.8521	1558.8448	1558.8355	0.0094	222 -	235	1	51	IDTPDKLTGPFTVR

No match to: 713.4000, 724.4943, 734.4911, 750.5165, 768.5150, 782.4732, 838.5172, 848.5263, 864.5334, 973.5490, 1004.5007, 1135.5815, 1275.1226, 1289.1371, 1291.6794, 1291.6794, 1357.6127, 1363.6985, 1404.7455, 1448.9166, 1571.8904, 1571.8904, 1574.8932, 1608.8898, 1732.1055, 1805.8870, 2044.1165, 2050.0864, 2168.0430, 2231.2319, 2564.1946, 2663.3860, 2790.3096, 2825.3108, 2921.3574, 3090.3972, 3092.4331, 3093.4385, 3107.3958, 3332.5796, 3349.6094

8. gi|168314 **Mass:** 27685 **Score:** 171 **Expect:** 4.8e-012 **Queries matched:** 8

pollen allergen

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1057.4449	1056.4376	1056.4368	0.0008	80 -	88	0	---	GCGSCFEIK
1149.5957	1148.5884	1148.5825	0.0059	138 -	147	0	30	SAGELELQFR
1149.5957	1148.5884	1148.5825	0.0059	138 -	147	0	---	SAGELELQFR
1305.6929	1304.6856	1304.6836	0.0020	138 -	148	1	---	SAGELELQFRR
1305.6929	1304.6856	1304.6836	0.0020	138 -	148	1	54	SAGELELQFRR
1349.6860	1348.6787	1348.6775	0.0012	35 -	47	0	---	STWYGKPTGAGPK
1559.8521	1558.8448	1558.8355	0.0094	211 -	224	1	---	IDTPDKLTGPFTVR
1559.8521	1558.8448	1558.8355	0.0094	211 -	224	1	51	IDTPDKLTGPFTVR

No match to: 713.4000, 724.4943, 734.4911, 750.5165, 768.5150, 782.4732, 838.5172, 848.5263, 864.5334, 973.5490, 1004.5007, 1135.5815, 1275.1226, 1289.1371, 1291.6794, 1291.6794, 1357.6127, 1363.6985, 1404.7455, 1418.7854, 1448.9166, 1571.8904, 1571.8904, 1574.8932, 1608.8898, 1732.1055, 1805.8870, 2044.1165, 2050.0864, 2168.0430, 2231.2319, 2564.1946, 2663.3860, 2790.3096, 2825.3108, 2921.3574, 3090.3972, 3092.4331, 3093.4385, 3107.3958, 3332.5796, 3349.6094

9. gi|33149333 **Mass:** 26532 **Score:** 130 **Expect:** 6.1e-008 **Queries matched:** 8

group 1 allergen Dac g 1.01 precursor [Dactylis glomerata]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1004.5007	1003.4934	1003.4875	0.0059	191	198	0	---	ESWGAIWR
1057.4449	1056.4376	1056.4368	0.0008	68	76	0	---	GCGSCFEIK
1149.5957	1148.5884	1148.5825	0.0059	126	135	0	30	SAGELELQFR
1149.5957	1148.5884	1148.5825	0.0059	126	135	0	---	SAGELELQFR
1305.6929	1304.6856	1304.6836	0.0020	126	136	1	---	SAGELELQFRR
1305.6929	1304.6856	1304.6836	0.0020	126	136	1	54	SAGELELQFRR
1349.6860	1348.6787	1348.6775	0.0012	23	35	0	---	STWYGKPTGAGPK
1418.7854	1417.7781	1417.7677	0.0104	124	135	1	---	LRSAGELELQFR

No match to: 713.4000, 724.4943, 734.4911, 750.5165, 768.5150, 782.4732, 838.5172, 848.5263, 864.5334, 973.5490, 1135.5815, 1275.1226, 1289.1371, 1291.6794, 1291.6794, 1357.6127, 1363.6985, 1404.7455, 1448.9166, 1559.8521, 1559.8521, 1571.8904, 1571.8904, 1574.8932, 1608.8898, 1732.1055, 1805.8870, 2044.1165, 2050.0864, 2168.0430, 2231.2319, 2564.1946, 2663.3860, 2790.3096, 2825.3108, 2921.3574, 3090.3972, 3092.4331, 3093.4385, 3107.3958, 3332.5796, 3349.6094

10. gi|33149335 **Mass:** 28849 **Score:** 127 **Expect:** 1.2e-007 **Queries matched:** 8

group 1 allergen Dac g 1.02 precursor [Dactylis glomerata]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1004.5007	1003.4934	1003.4875	0.0059	215	222	0	---	ESWGAIWR
1057.4449	1056.4376	1056.4368	0.0008	92	100	0	---	GCGSCFEIK
1149.5957	1148.5884	1148.5825	0.0059	150	159	0	30	SAGELELQFR
1149.5957	1148.5884	1148.5825	0.0059	150	159	0	---	SAGELELQFR
1305.6929	1304.6856	1304.6836	0.0020	150	160	1	---	SAGELELQFRR
1305.6929	1304.6856	1304.6836	0.0020	150	160	1	54	SAGELELQFRR
1349.6860	1348.6787	1348.6775	0.0012	47	59	0	---	STWYGKPTGAGPK
1418.7854	1417.7781	1417.7677	0.0104	148	159	1	---	LRSAGELELQFR

No match to: 713.4000, 724.4943, 734.4911, 750.5165, 768.5150, 782.4732, 838.5172, 848.5263, 864.5334, 973.5490, 1135.5815, 1275.1226, 1289.1371, 1291.6794, 1291.6794, 1357.6127, 1363.6985, 1404.7455, 1448.9166, 1559.8521, 1559.8521, 1571.8904, 1571.8904, 1574.8932, 1608.8898, 1732.1055, 1805.8870, 2044.1165, 2050.0864, 2168.0430, 2231.2319, 2564.1946, 2663.3860, 2790.3096, 2825.3108, 2921.3574, 3090.3972, 3092.4331, 3093.4385, 3107.3958, 3332.5796, 3349.6094

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 50

Protein View

Match to: **gi|28373838** Score: **238** Expect: **9.6e-019**
Chain A, Crystal Structure Of Phl P 1, A Major Timothy Grass Pollen Allergen

Nominal mass (M_r): **26611**; Calculated pI value: **6.17**
NCBI BLAST search of gi|28373838 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|28373839 from Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **36%**

Matched peptides shown in **Bold Red**

```
  1 AIPKVPPGPN ITATYGDKWL DAKSTWYGKP TGAGPKDNGG ACGYKDVDKP
 51 PFSGMTGCGN TPIFKSGRGC GSCFEIKCTK PEACSGEPVV VHITDDNEEP
101 IAPYHFDLSG HAFGAMAKKG DEQKLRSAGE LELQFRRVKC KYPEGTKVTF
151 HVEKGSNPNY LALLVKYVNG DGDVVAVDIK EKGKDKWIEL KESWGAIWRI
201 DTPDKLTGPF TVRYTTEGGT KTEAEDVIPE GWKADTSYES K
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
24 - 36	1349.6860	1348.6787	1348.6775	0.0012	0	STWYGKPTGAGPK (No match)
37 - 65	3090.3972	3089.3899	3089.3680	0.0219	1	DNGGACGYKDVDKPPFSGMTGCGNTPIFK (No match)
46 - 65	2168.0430	2167.0357	2167.0078	0.0280	0	DVDKPPFSGMTGCGNTPIFK (No match)
66 - 77	1357.6127	1356.6054	1356.5914	0.0140	1	SGRGCGSCFEIK (No match)
69 - 77	1057.4449	1056.4376	1056.4368	0.0008	0	GCGSCFEIK (No match)
125 - 136	1418.7854	1417.7781	1417.7677	0.0104	1	LRSAGELELQFR (No match)
127 - 136	1149.5957	1148.5884	1148.5825	0.0059	0	SAGELELQFR (Ions score 30)
127 - 136	1149.5957	1148.5884	1148.5825	0.0059	0	SAGELELQFR (No match)
127 - 137	1305.6929	1304.6856	1304.6836	0.0020	1	SAGELELQFRR (No match)
127 - 137	1305.6929	1304.6856	1304.6836	0.0020	1	SAGELELQFRR (Ions score 54)
192 - 199	1004.5007	1003.4934	1003.4875	0.0059	0	ESWGAIWR (No match)
200 - 213	1559.8521	1558.8448	1558.8355	0.0094	1	IDTPDKLTGPFTVR (No match)
200 - 213	1559.8521	1558.8448	1558.8355	0.0094	1	IDTPDKLTGPFTVR (Ions score 51)

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	Accession	Mass	Score	Description
1.	gi|28373838	26611	348	Chain A, Crystal Structure Of Phl P 1, A Major Timothy Grass Pollen Allergen
2.	gi|1171008	28838	345	RecName: Full=Pollen allergen Phl p 1; AltName: Full=Allergen Phl p I; AltName: Allergen=Phl p
3.	gi|6599300	28742	277	pollen allergen [Lolium perenne]
4.	gi|168314	27685	264	pollen allergen
5.	gi|126385	28819	263	RecName: Full=Pollen allergen Lol p 1; AltName: Full=Allergen Lol p I; AltName: Full=Allergen R
6.	gi|168316	28807	263	pollen allergen
7.	gi|33149333	26532	228	group 1 allergen Dac g 1.01 precursor [Dactylis glomerata]
8.	gi|33149335	28849	225	group 1 allergen Dac g 1.02 precursor [Dactylis glomerata]
9.	gi|2498576	29448	156	RecName: Full=Major pollen allergen Pha a 1; AltName: Full=Allergen Pha a I; AltName: Allergen=
10.	gi|4090265	28627	100	group I pollen allergen [Poa pratensis]

Results List

1. gi|28373838 **Mass:** 26611 **Score:** 348 **Expect:** 9.6e-030 **Queries matched:** 12

Chain A, Crystal Structure Of Phl P 1, A Major Timothy Grass Pollen Allergen

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1004.5177	1003.5104	1003.4875	0.0229	192	199	0	34	ESWGAIWR
1004.5177	1003.5104	1003.4875	0.0229	192	199	0	---	ESWGAIWR
1057.4650	1056.4577	1056.4368	0.0209	69	77	0	---	GCGSCFEIK
1149.6084	1148.6011	1148.5825	0.0186	127	136	0	---	SAGELELQFR
1149.6084	1148.6011	1148.5825	0.0186	127	136	0	60	SAGELELQFR
1305.7100	1304.7027	1304.6836	0.0191	127	137	1	66	SAGELELQFRR
1305.7100	1304.7027	1304.6836	0.0191	127	137	1	---	SAGELELQFRR
1349.6989	1348.6916	1348.6775	0.0141	24	36	0	---	STWYGKPTGAGPK
1357.6211	1356.6138	1356.5914	0.0224	66	77	1	---	SGRGCGSCFEIK
1418.7948	1417.7875	1417.7677	0.0198	125	136	1	---	LRSAGELELQFR
1559.8622	1558.8549	1558.8355	0.0195	200	213	1	---	IDTPDKLTGPFTVR
1559.8622	1558.8549	1558.8355	0.0195	200	213	1	84	IDTPDKLTGPFTVR

No match to: 973.5599, 1036.5134, 1289.1530, 1327.7008, 1572.8920, 1573.8928, 1574.8878, 1581.8369, 2102.1392, 2102.1392, 3091.4067, 3092.4343

2. gi|1171008 **Mass:** 28838 **Score:** 345 **Expect:** 1.9e-029 **Queries matched:** 12

RecName: Full=Pollen allergen Phl p 1; AltName: Full=Allergen Phl p I; AltName: Allergen=Phl p 1; F

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1004.5177	1003.5104	1003.4875	0.0229	214	221	0	34	ESWGAIWR
1004.5177	1003.5104	1003.4875	0.0229	214	221	0	---	ESWGAIWR
1057.4650	1056.4577	1056.4368	0.0209	91	99	0	---	GCGSCFEIK
1149.6084	1148.6011	1148.5825	0.0186	149	158	0	---	SAGELELQFR

1149.6084	1148.6011	1148.5825	0.0186	149 - 158	0	60	SAGELELQFR
1305.7100	1304.7027	1304.6836	0.0191	149 - 159	1	66	SAGELELQFRR
1305.7100	1304.7027	1304.6836	0.0191	149 - 159	1	---	SAGELELQFRR
1349.6989	1348.6916	1348.6775	0.0141	46 - 58	0	---	STWYGKPTGAGPK
1357.6211	1356.6138	1356.5914	0.0224	88 - 99	1	---	SGRGCGSCFEIK
1418.7948	1417.7875	1417.7677	0.0198	147 - 158	1	---	LRSAGELELQFR
1559.8622	1558.8549	1558.8355	0.0195	222 - 235	1	---	IDTPDKLTGPFTVR
1559.8622	1558.8549	1558.8355	0.0195	222 - 235	1	84	IDTPDKLTGPFTVR

No match to: 973.5599, 1036.5134, 1289.1530, 1327.7008, 1572.8920, 1573.8928, 1574.8878, 1581.8369, 2102.1392, 2102.1392, 3091.4067, 3092.4343

3. gi|6599300 **Mass:** 28742 **Score:** 277 **Expect:** 1.2e-022 **Queries matched:** 9

pollen allergen [Lolium perenne]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1057.4650	1056.4577	1056.4368	0.0209	91 -	99	0	---	GCGSCFEIK
1149.6084	1148.6011	1148.5825	0.0186	149 -	158	0	---	SAGELELQFR
1149.6084	1148.6011	1148.5825	0.0186	149 -	158	0	60	SAGELELQFR
1305.7100	1304.7027	1304.6836	0.0191	149 -	159	1	66	SAGELELQFRR
1305.7100	1304.7027	1304.6836	0.0191	149 -	159	1	---	SAGELELQFRR
1349.6989	1348.6916	1348.6775	0.0141	46 -	58	0	---	STWYGKPTGAGPK
1418.7948	1417.7875	1417.7677	0.0198	147 -	158	1	---	LRSAGELELQFR
1559.8622	1558.8549	1558.8355	0.0195	222 -	235	1	---	IDTPDKLTGPFTVR
1559.8622	1558.8549	1558.8355	0.0195	222 -	235	1	84	IDTPDKLTGPFTVR

No match to: 973.5599, 1004.5177, 1004.5177, 1036.5134, 1289.1530, 1327.7008, 1357.6211, 1572.8920, 1573.8928, 1574.8878, 1581.8369, 2102.1392, 2102.1392, 3091.4067, 3092.4343

4. gi|168314 **Mass:** 27685 **Score:** 264 **Expect:** 2.4e-021 **Queries matched:** 8

pollen allergen

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1057.4650	1056.4577	1056.4368	0.0209	80 -	88	0	---	GCGSCFEIK
1149.6084	1148.6011	1148.5825	0.0186	138 -	147	0	---	SAGELELQFR
1149.6084	1148.6011	1148.5825	0.0186	138 -	147	0	60	SAGELELQFR
1305.7100	1304.7027	1304.6836	0.0191	138 -	148	1	66	SAGELELQFRR
1305.7100	1304.7027	1304.6836	0.0191	138 -	148	1	---	SAGELELQFRR
1349.6989	1348.6916	1348.6775	0.0141	35 -	47	0	---	STWYGKPTGAGPK
1559.8622	1558.8549	1558.8355	0.0195	211 -	224	1	---	IDTPDKLTGPFTVR
1559.8622	1558.8549	1558.8355	0.0195	211 -	224	1	84	IDTPDKLTGPFTVR

No match to: 973.5599, 1004.5177, 1004.5177, 1036.5134, 1289.1530, 1327.7008, 1357.6211, 1418.7948, 1572.8920, 1573.8928, 1574.8878, 1581.8369, 2102.1392, 2102.1392, 3091.4067, 3092.4343

5. gi|126385 **Mass:** 28819 **Score:** 263 **Expect:** 3e-021 **Queries matched:** 8

RecName: Full=Pollen allergen Lol p 1; AltName: Full=Allergen Lol p I; AltName: Full=Allergen R7; A

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1057.4650	1056.4577	1056.4368	0.0209	91 -	99	0	---	GCGSCFEIK
1149.6084	1148.6011	1148.5825	0.0186	149 -	158	0	---	SAGELELQFR
1149.6084	1148.6011	1148.5825	0.0186	149 -	158	0	60	SAGELELQFR
1305.7100	1304.7027	1304.6836	0.0191	149 -	159	1	66	SAGELELQFRR
1305.7100	1304.7027	1304.6836	0.0191	149 -	159	1	---	SAGELELQFRR
1349.6989	1348.6916	1348.6775	0.0141	46 -	58	0	---	STWYGKPTGAGPK
1559.8622	1558.8549	1558.8355	0.0195	222 -	235	1	---	IDTPDKLTGPFTVR
1559.8622	1558.8549	1558.8355	0.0195	222 -	235	1	84	IDTPDKLTGPFTVR

No match to: 973.5599, 1004.5177, 1004.5177, 1036.5134, 1289.1530, 1327.7008, 1357.6211, 1418.7948, 1572.8920, 1573.8928, 1574.8878, 1581.8369, 2102.1392, 2102.1392, 3091.4067, 3092.4343

6. gi|168316 **Mass:** 28807 **Score:** 263 **Expect:** 3e-021 **Queries matched:** 8

pollen allergen

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1057.4650	1056.4577	1056.4368	0.0209	91 -	99	0	---	GCGSCFEIK
1149.6084	1148.6011	1148.5825	0.0186	149 -	158	0	---	SAGELELQFR
1149.6084	1148.6011	1148.5825	0.0186	149 -	158	0	60	SAGELELQFR
1305.7100	1304.7027	1304.6836	0.0191	149 -	159	1	66	SAGELELQFRR
1305.7100	1304.7027	1304.6836	0.0191	149 -	159	1	---	SAGELELQFRR
1349.6989	1348.6916	1348.6775	0.0141	46 -	58	0	---	STWYGKPTGAGPK
1559.8622	1558.8549	1558.8355	0.0195	222 -	235	1	---	IDTPDKLTGPFTVR
1559.8622	1558.8549	1558.8355	0.0195	222 -	235	1	84	IDTPDKLTGPFTVR

No match to: 973.5599, 1004.5177, 1004.5177, 1036.5134, 1289.1530, 1327.7008, 1357.6211, 1418.7948, 1572.8920, 1573.8928, 1574.8878, 1581.8369, 2102.1392, 2102.1392, 3091.4067, 3092.4343

7. gi|33149333 **Mass:** 26532 **Score:** 228 **Expect:** 9.6e-018 **Queries matched:** 9

group 1 allergen Dac g 1.01 precursor [Dactylis glomerata]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1004.5177	1003.5104	1003.4875	0.0229	191 -	198	0	34	ESWGAIWR
1004.5177	1003.5104	1003.4875	0.0229	191 -	198	0	---	ESWGAIWR
1057.4650	1056.4577	1056.4368	0.0209	68 -	76	0	---	GCGSCFEIK
1149.6084	1148.6011	1148.5825	0.0186	126 -	135	0	---	SAGELELQFR
1149.6084	1148.6011	1148.5825	0.0186	126 -	135	0	60	SAGELELQFR
1305.7100	1304.7027	1304.6836	0.0191	126 -	136	1	66	SAGELELQFRR
1305.7100	1304.7027	1304.6836	0.0191	126 -	136	1	---	SAGELELQFRR
1349.6989	1348.6916	1348.6775	0.0141	23 -	35	0	---	STWYGKPTGAGPK
1418.7948	1417.7875	1417.7677	0.0198	124 -	135	1	---	LRSAGELELQFR

No match to: 973.5599, 1036.5134, 1289.1530, 1327.7008, 1357.6211, 1559.8622, 1559.8622, 1572.8920, 1573.8928, 1574.8878, 1581.8369, 2102.1392, 2102.1392, 3091.4067, 3092.4343

8. gi|33149335 **Mass:** 28849 **Score:** 225 **Expect:** 1.9e-017 **Queries matched:** 9

group 1 allergen Dac g 1.02 precursor [Dactylis glomerata]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1004.5177	1003.5104	1003.4875	0.0229	215	222	0	34	ESWGAIWR
1004.5177	1003.5104	1003.4875	0.0229	215	222	0	---	ESWGAIWR
1057.4650	1056.4577	1056.4368	0.0209	92	100	0	---	GCGSCFEIK
1149.6084	1148.6011	1148.5825	0.0186	150	159	0	---	SAGELELQFR
1149.6084	1148.6011	1148.5825	0.0186	150	159	0	60	SAGELELQFR
1305.7100	1304.7027	1304.6836	0.0191	150	160	1	66	SAGELELQFRR
1305.7100	1304.7027	1304.6836	0.0191	150	160	1	---	SAGELELQFRR
1349.6989	1348.6916	1348.6775	0.0141	47	59	0	---	STWYGKPTGAGPK
1418.7948	1417.7875	1417.7677	0.0198	148	159	1	---	LRSAGELELQFR

No match to: 973.5599, 1036.5134, 1289.1530, 1327.7008, 1357.6211, 1559.8622, 1559.8622, 1572.8920, 1573.8928, 1574.8878, 1581.8369, 2102.1392, 2102.1392, 3091.4067, 3092.4343

9. gi|2498576 **Mass:** 29448 **Score:** 156 **Expect:** 1.5e-010 **Queries matched:** 6

RecName: Full=Major pollen allergen Pha a 1; AltName: Full=Allergen Pha a I; AltName: Allergen=Pha

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1004.5177	1003.5104	1003.4875	0.0229	220	227	0	34	ESWGAIWR
1004.5177	1003.5104	1003.4875	0.0229	220	227	0	---	ESWGAIWR
1057.4650	1056.4577	1056.4368	0.0209	97	105	0	---	GCGSCFELK
1349.6989	1348.6916	1348.6775	0.0141	52	64	0	---	STWYGKPTGAGPK
1559.8622	1558.8549	1558.8355	0.0195	228	241	1	---	IDTPDKLTGPFTVR
1559.8622	1558.8549	1558.8355	0.0195	228	241	1	84	IDTPDKLTGPFTVR

No match to: 973.5599, 1036.5134, 1149.6084, 1149.6084, 1289.1530, 1305.7100, 1305.7100, 1327.7008, 1357.6211, 1418.7948, 1572.8920, 1573.8928, 1574.8878, 1581.8369, 2102.1392, 2102.1392, 3091.4067, 3092.4343

10. gi|4090265 **Mass:** 28627 **Score:** 100 **Expect:** 6.5e-005 **Queries matched:** 5

group I pollen allergen [Poa pratensis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1057.4650	1056.4577	1056.4368	0.0209	91	99	0	---	GCGSCFEIK
1149.6084	1148.6011	1148.6189	-0.0178	149	158	1	---	SAGELELKFR
1149.6084	1148.6011	1148.6189	-0.0178	149	158	1	63	SAGELELKFR
1349.6989	1348.6916	1348.6775	0.0141	46	58	0	---	STWYGKPTGAGPK
1357.6211	1356.6138	1356.5914	0.0224	88	99	1	---	SGRGCGSCFEIK

No match to: 973.5599, 1004.5177, 1004.5177, 1036.5134, 1289.1530, 1305.7100, 1305.7100, 1327.7008, 1418.7948, 1559.8622, 1559.8622, 1572.8920, 1573.8928, 1574.8878, 1581.8369, 2102.1392, 2102.1392, 3091.4067, 3092.4343

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 24

Protein View

Match to: **gi|28373838** Score: **348** Expect: **9.6e-030**
Chain A, Crystal Structure Of Phl P 1, A Major Timothy Grass Pollen Allergen

Nominal mass (M_r): **26611**; Calculated pI value: **6.17**
NCBI BLAST search of gi|28373838 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|28373839 from Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **24%**

Matched peptides shown in **Bold Red**

```
  1 AIPKVPPGPN ITATYGDKWL DAKSTWYGKP TGAGPKDNGG ACGYKDVDKP
 51 PFSGMTGCGN TPIFKSGRGC GSCFEIKCTK PEACSGEPVV VHITDDNEEP
101 IAPYHFDLSG HAFGAMAKKG DEQKLRSAGE LELQFRRVKC KYPEGTKVTF
151 HVEKGSNPNY LALLVKYVNG DGDVVAVDIK EKGKDKWIEL KESWGAIWRI
201 DTPDKLTGPF TVRYTTEGGT KTEAEDVIPE GWKADTSYES K
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
24 - 36	1349.6989	1348.6916	1348.6775	0.0141	0	STWYGKPTGAGPK	(No match)
66 - 77	1357.6211	1356.6138	1356.5914	0.0224	1	SGRGCGSCFEIK	(No match)
69 - 77	1057.4650	1056.4577	1056.4368	0.0209	0	GCGSCFEIK	(No match)
125 - 136	1418.7948	1417.7875	1417.7677	0.0198	1	LRSAGELELQFR	(No match)
127 - 136	1149.6084	1148.6011	1148.5825	0.0186	0	SAGELELQFR	(No match)
127 - 136	1149.6084	1148.6011	1148.5825	0.0186	0	SAGELELQFR	(Ions score 60)
127 - 137	1305.7100	1304.7027	1304.6836	0.0191	1	SAGELELQFRR	(Ions score 66)
127 - 137	1305.7100	1304.7027	1304.6836	0.0191	1	SAGELELQFRR	(No match)
192 - 199	1004.5177	1003.5104	1003.4875	0.0229	0	ESWGAIWR	(Ions score 34)
192 - 199	1004.5177	1003.5104	1003.4875	0.0229	0	ESWGAIWR	(No match)
200 - 213	1559.8622	1558.8549	1558.8355	0.0195	1	IDTPDKLTGPFTVR	(No match)
200 - 213	1559.8622	1558.8549	1558.8355	0.0195	1	IDTPDKLTGPFTVR	(Ions score 84)

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	Accession	Mass	Score	Description
1.	gi|28373838	26611	299	Chain A, Crystal Structure Of Phl P 1, A Major Timothy Grass Pollen Allergen
2.	gi|1171008	28838	295	RecName: Full=Pollen allergen Phl p 1; AltName: Full=Allergen Phl p I; AltName: Allergen=Phl p
3.	gi|33149335	28849	237	group 1 allergen Dac g 1.02 precursor [Dactylis glomerata]
4.	gi|33149333	26532	224	group 1 allergen Dac g 1.01 precursor [Dactylis glomerata]
5.	gi|168314	27685	181	pollen allergen
6.	gi|6599300	28742	179	pollen allergen [Lolium perenne]
7.	gi|126385	28819	166	RecName: Full=Pollen allergen Lol p 1; AltName: Full=Allergen Lol p I; AltName: Full=Allergen R
8.	gi|168316	28807	166	pollen allergen
9.	gi|3860384	28728	139	major group I allergen Hol l 1 [Holcus lanatus]
10.	gi|4090265	28627	121	group I pollen allergen [Poa pratensis]

Results List

1. gi|28373838 **Mass:** 26611 **Score:** 299 **Expect:** 7.6e-025 **Queries matched:** 14

Chain A, Crystal Structure Of Phl P 1, A Major Timothy Grass Pollen Allergen

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1004.5238	1003.5165	1003.4875	0.0290	192	199	0	28	ESWGAIWR
1004.5238	1003.5165	1003.4875	0.0290	192	199	0	---	ESWGAIWR
1057.4805	1056.4732	1056.4368	0.0364	69	77	0	---	GCGSCFEIK
1149.6229	1148.6156	1148.5825	0.0331	127	136	0	---	SAGELELQFR
1149.6229	1148.6156	1148.5825	0.0331	127	136	0	56	SAGELELQFR
1288.7295	1287.7222	1287.7186	0.0036	155	166	0	---	GSNPNYLALLVK
1305.7271	1304.7198	1304.6836	0.0362	127	137	1	61	SAGELELQFRR
1305.7271	1304.7198	1304.6836	0.0362	127	137	1	---	SAGELELQFRR
1349.7162	1348.7089	1348.6775	0.0314	24	36	0	---	STWYGKPTGAGPK
1357.6415	1356.6342	1356.5914	0.0428	66	77	1	---	SGRGCGSCFEIK
1418.8086	1417.8013	1417.7677	0.0336	125	136	1	---	LRSAGELELQFR
1559.8856	1558.8783	1558.8355	0.0429	200	213	1	---	IDTPDKLTGPFTVR
2129.2266	2128.2193	2128.1680	0.0514	148	166	1	---	VTFHVEKGSNPNYLALLVK
3090.4280	3089.4207	3089.3680	0.0527	37	65	1	---	DNGGACGYKDVDKPPFSGMTGCGNTPIFK

No match to: 917.5872, 973.5709, 973.5709, 1036.5186, 1289.1671, 1471.7822, 1541.8860, 1572.9119, 1572.9119, 2102.1643, 2559.4067, 2808.3599, 3092.4648

2. gi|1171008 **Mass:** 28838 **Score:** 295 **Expect:** 1.9e-024 **Queries matched:** 14

RecName: Full=Pollen allergen Phl p 1; AltName: Full=Allergen Phl p I; AltName: Allergen=Phl p 1; F

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1004.5238	1003.5165	1003.4875	0.0290	214	221	0	28	ESWGAIWR
1004.5238	1003.5165	1003.4875	0.0290	214	221	0	---	ESWGAIWR

1057.4805	1056.4732	1056.4368	0.0364	91 - 99	0	---	GCGSCFEIK
1149.6229	1148.6156	1148.5825	0.0331	149 - 158	0	---	SAGELELQFR
1149.6229	1148.6156	1148.5825	0.0331	149 - 158	0	56	SAGELELQFR
1288.7295	1287.7222	1287.7186	0.0036	177 - 188	0	---	GSNPNYLALLVK
1305.7271	1304.7198	1304.6836	0.0362	149 - 159	1	61	SAGELELQFRR
1305.7271	1304.7198	1304.6836	0.0362	149 - 159	1	---	SAGELELQFRR
1349.7162	1348.7089	1348.6775	0.0314	46 - 58	0	---	STWYGKPTGAGPK
1357.6415	1356.6342	1356.5914	0.0428	88 - 99	1	---	SGRGCGSCFEIK
1418.8086	1417.8013	1417.7677	0.0336	147 - 158	1	---	LRSAGELELQFR
1559.8856	1558.8783	1558.8355	0.0429	222 - 235	1	---	IDTPDKLTGPFTVR
2129.2266	2128.2193	2128.1680	0.0514	170 - 188	1	---	VTFHVEKGSNPNYLALLVK
3090.4280	3089.4207	3089.3680	0.0527	59 - 87	1	---	DNGGACGYKDVDKPPFSGMTGCGNTPIFK

No match to: 917.5872, 973.5709, 973.5709, 1036.5186, 1289.1671, 1471.7822, 1541.8860, 1572.9119, 1572.9119, 2102.1643, 2559.4067, 2808.3599, 3092.4648

3. gi|33149335 **Mass:** 28849 **Score:** 237 **Expect:** 1.2e-018 **Queries matched:** 11

group 1 allergen Dac g 1.02 precursor [Dactylis glomerata]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1004.5238	1003.5165	1003.4875	0.0290	215 - 222		0	28	ESWGAIWR
1004.5238	1003.5165	1003.4875	0.0290	215 - 222		0	---	ESWGAIWR
1057.4805	1056.4732	1056.4368	0.0364	92 - 100		0	---	GCGSCFEIK
1149.6229	1148.6156	1148.5825	0.0331	150 - 159		0	---	SAGELELQFR
1149.6229	1148.6156	1148.5825	0.0331	150 - 159		0	56	SAGELELQFR
1288.7295	1287.7222	1287.7186	0.0036	178 - 189		0	---	GSNPNYLALLVK
1305.7271	1304.7198	1304.6836	0.0362	150 - 160		1	61	SAGELELQFRR
1305.7271	1304.7198	1304.6836	0.0362	150 - 160		1	---	SAGELELQFRR
1349.7162	1348.7089	1348.6775	0.0314	47 - 59		0	---	STWYGKPTGAGPK
1418.8086	1417.8013	1417.7677	0.0336	148 - 159		1	---	LRSAGELELQFR
2129.2266	2128.2193	2128.1680	0.0514	171 - 189		1	---	VTFHVEKGSNPNYLALLVK

No match to: 917.5872, 973.5709, 973.5709, 1036.5186, 1289.1671, 1357.6415, 1471.7822, 1541.8860, 1559.8856, 1572.9119, 1572.9119, 2102.1643, 2559.4067, 2808.3599, 3090.4280, 3092.4648

4. gi|33149333 **Mass:** 26532 **Score:** 224 **Expect:** 2.4e-017 **Queries matched:** 10

group 1 allergen Dac g 1.01 precursor [Dactylis glomerata]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1004.5238	1003.5165	1003.4875	0.0290	191 - 198		0	28	ESWGAIWR
1004.5238	1003.5165	1003.4875	0.0290	191 - 198		0	---	ESWGAIWR
1057.4805	1056.4732	1056.4368	0.0364	68 - 76		0	---	GCGSCFEIK
1149.6229	1148.6156	1148.5825	0.0331	126 - 135		0	---	SAGELELQFR
1149.6229	1148.6156	1148.5825	0.0331	126 - 135		0	56	SAGELELQFR
1288.7295	1287.7222	1287.7186	0.0036	154 - 165		0	---	GSNPNYLALLVK

1305.7271	1304.7198	1304.6836	0.0362	126 - 136	1	61	SAGELELQFRR
1305.7271	1304.7198	1304.6836	0.0362	126 - 136	1	---	SAGELELQFRR
1349.7162	1348.7089	1348.6775	0.0314	23 - 35	0	---	STWYGKPTGAGPK
1418.8086	1417.8013	1417.7677	0.0336	124 - 135	1	---	LRSAGELELQFR

No match to: 917.5872, 973.5709, 973.5709, 1036.5186, 1289.1671, 1357.6415, 1471.7822, 1541.8860, 1559.8856, 1572.9119, 1572.9119, 2102.1643, 2129.2266, 2559.4067, 2808.3599, 3090.4280, 3092.4648

5. gi|168314 **Mass:** 27685 **Score:** 181 **Expect:** 4.8e-013 **Queries matched:** 8

pollen allergen

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1057.4805	1056.4732	1056.4368	0.0364	80 -	88	0	---	GCGSCFEIK
1149.6229	1148.6156	1148.5825	0.0331	138 -	147	0	---	SAGELELQFR
1149.6229	1148.6156	1148.5825	0.0331	138 -	147	0	56	SAGELELQFR
1288.7295	1287.7222	1287.7186	0.0036	166 -	177	0	---	GSNPNYLAILVK
1305.7271	1304.7198	1304.6836	0.0362	138 -	148	1	61	SAGELELQFRR
1305.7271	1304.7198	1304.6836	0.0362	138 -	148	1	---	SAGELELQFRR
1349.7162	1348.7089	1348.6775	0.0314	35 -	47	0	---	STWYGKPTGAGPK
1559.8856	1558.8783	1558.8355	0.0429	211 -	224	1	---	IDTPDKLTGPFTVR

No match to: 917.5872, 973.5709, 973.5709, 1004.5238, 1004.5238, 1036.5186, 1289.1671, 1357.6415, 1418.8086, 1471.7822, 1541.8860, 1572.9119, 1572.9119, 2102.1643, 2129.2266, 2559.4067, 2808.3599, 3090.4280, 3092.4648

6. gi|6599300 **Mass:** 28742 **Score:** 179 **Expect:** 7.6e-013 **Queries matched:** 8

pollen allergen [Lolium perenne]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1057.4805	1056.4732	1056.4368	0.0364	91 -	99	0	---	GCGSCFEIK
1149.6229	1148.6156	1148.5825	0.0331	149 -	158	0	---	SAGELELQFR
1149.6229	1148.6156	1148.5825	0.0331	149 -	158	0	56	SAGELELQFR
1305.7271	1304.7198	1304.6836	0.0362	149 -	159	1	61	SAGELELQFRR
1305.7271	1304.7198	1304.6836	0.0362	149 -	159	1	---	SAGELELQFRR
1349.7162	1348.7089	1348.6775	0.0314	46 -	58	0	---	STWYGKPTGAGPK
1418.8086	1417.8013	1417.7677	0.0336	147 -	158	1	---	LRSAGELELQFR
1559.8856	1558.8783	1558.8355	0.0429	222 -	235	1	---	IDTPDKLTGPFTVR

No match to: 917.5872, 973.5709, 973.5709, 1004.5238, 1004.5238, 1036.5186, 1288.7295, 1289.1671, 1357.6415, 1471.7822, 1541.8860, 1572.9119, 1572.9119, 2102.1643, 2129.2266, 2559.4067, 2808.3599, 3090.4280, 3092.4648

7. gi|126385 **Mass:** 28819 **Score:** 166 **Expect:** 1.5e-011 **Queries matched:** 7

RecName: Full=Pollen allergen Lol p 1; AltName: Full=Allergen Lol p I; AltName: Full=Allergen R7; A

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1057.4805	1056.4732	1056.4368	0.0364	91 -	99	0	---	GCGSCFEIK
1149.6229	1148.6156	1148.5825	0.0331	149 -	158	0	---	SAGELELQFR
1149.6229	1148.6156	1148.5825	0.0331	149 -	158	0	56	SAGELELQFR
1305.7271	1304.7198	1304.6836	0.0362	149 -	159	1	61	SAGELELQFRR

1305.7271	1304.7198	1304.6836	0.0362	149 - 159	1	---	SAGELELQFRR
1349.7162	1348.7089	1348.6775	0.0314	46 - 58	0	---	STWYGKPTGAGPK
1559.8856	1558.8783	1558.8355	0.0429	222 - 235	1	---	IDTPDKLTGPFTVR

No match to: 917.5872, 973.5709, 973.5709, 1004.5238, 1004.5238, 1036.5186, 1288.7295, 1289.1671, 1357.6415, 1418.8086, 1471.7822, 1541.8860, 1572.9119, 1572.9119, 2102.1643, 2129.2266, 2559.4067, 2808.3599, 3090.4280, 3092.4648

8. gi|168316 **Mass:** 28807 **Score:** 166 **Expect:** 1.5e-011 **Queries matched:** 7

pollen allergen

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1057.4805	1056.4732	1056.4368	0.0364	91 -	99	0	---	GCGSCFEIK
1149.6229	1148.6156	1148.5825	0.0331	149 -	158	0	---	SAGELELQFR
1149.6229	1148.6156	1148.5825	0.0331	149 -	158	0	56	SAGELELQFR
1305.7271	1304.7198	1304.6836	0.0362	149 -	159	1	61	SAGELELQFRR
1305.7271	1304.7198	1304.6836	0.0362	149 -	159	1	---	SAGELELQFRR
1349.7162	1348.7089	1348.6775	0.0314	46 -	58	0	---	STWYGKPTGAGPK
1559.8856	1558.8783	1558.8355	0.0429	222 -	235	1	---	IDTPDKLTGPFTVR

No match to: 917.5872, 973.5709, 973.5709, 1004.5238, 1004.5238, 1036.5186, 1288.7295, 1289.1671, 1357.6415, 1418.8086, 1471.7822, 1541.8860, 1572.9119, 1572.9119, 2102.1643, 2129.2266, 2559.4067, 2808.3599, 3090.4280, 3092.4648

9. gi|3860384 **Mass:** 28728 **Score:** 139 **Expect:** 7.6e-009 **Queries matched:** 8

major group I allergen Hol l 1 [Holcus lanatus]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1057.4805	1056.4732	1056.4368	0.0364	91 -	99	0	---	GCGSCFEIK
1149.6229	1148.6156	1148.6189	-0.0033	149 -	158	1	---	SAGELELKFR
1149.6229	1148.6156	1148.6189	-0.0033	149 -	158	1	58	SAGELELKFR
1288.7295	1287.7222	1287.7186	0.0036	177 -	188	0	---	GSNPNYLALLVK
1349.7162	1348.7089	1348.6775	0.0314	46 -	58	0	---	STWYGKPTGAGPK
1357.6415	1356.6342	1356.5914	0.0428	88 -	99	1	---	SGRGCGSCFEIK
2129.2266	2128.2193	2128.1680	0.0514	170 -	188	1	---	VTFHVEKGSNPNYLALLVK
3090.4280	3089.4207	3089.3680	0.0527	59 -	87	1	---	DNGGACGYKDVDKPPFSGMTGCGNTPIFK

No match to: 917.5872, 973.5709, 973.5709, 1004.5238, 1004.5238, 1036.5186, 1289.1671, 1305.7271, 1305.7271, 1418.8086, 1471.7822, 1541.8860, 1559.8856, 1572.9119, 1572.9119, 2102.1643, 2559.4067, 2808.3599, 3092.4648

10. gi|4090265 **Mass:** 28627 **Score:** 121 **Expect:** 4.8e-007 **Queries matched:** 7

group I pollen allergen [Poa pratensis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1057.4805	1056.4732	1056.4368	0.0364	91 -	99	0	---	GCGSCFEIK
1149.6229	1148.6156	1148.6189	-0.0033	149 -	158	1	---	SAGELELKFR
1149.6229	1148.6156	1148.6189	-0.0033	149 -	158	1	58	SAGELELKFR
1288.7295	1287.7222	1287.7186	0.0036	177 -	188	0	---	GSNPNYLALLVK

1349.7162	1348.7089	1348.6775	0.0314	46 - 58	0	---	STWYGKPTGAGPK
1357.6415	1356.6342	1356.5914	0.0428	88 - 99	1	---	SGRGCGSCFEIK
2129.2266	2128.2193	2128.1680	0.0514	170 - 188	1	---	VTFHVEKGSNPNYLALLVK

No match to: 917.5872, 973.5709, 973.5709, 1004.5238, 1004.5238, 1036.5186, 1289.1671, 1305.7271, 1305.7271, 1418.8086, 1471.7822, 1541.8860, 1559.8856, 1572.9119, 1572.9119, 2102.1643, 2559.4067, 2808.3599, 3090.4280, 3092.4648

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 27

Protein View

Match to: **gi|28373838** Score: **299** Expect: **7.6e-025**
Chain A, Crystal Structure Of Phl P 1, A Major Timothy Grass Pollen Allergen

Nominal mass (M_r): **26611**; Calculated pI value: **6.17**
NCBI BLAST search of gi|28373838 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|28373839 from Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **44%**

Matched peptides shown in **Bold Red**

```
   1 AIPKVPPGPN ITATYGDKWL DAKSTWYGKP TGAGPKDNGG ACGYKDVDKP
  51 PFSGMTGCGN TPIFKSGRGC GSCFEIKCTK PEACSGEPVV VHITDDNEEP
 101 IAPYHFDLSG HAFGAMAKKG DEQKLRSAGE LELQFRRVKC KYPEGTKVTF
 151 HVEKGSNPNY LALLVKYVNG DGDVVAVDIK EKGKDKWIEL KESWGAIWRI
 201 DTPDKLTGPF TVRYTTEGGT KTEAEDVIPE GWKADTSYES K
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
24 - 36	1349.7162	1348.7089	1348.6775	0.0314	0	STWYGKPTGAGPK (No match)
37 - 65	3090.4280	3089.4207	3089.3680	0.0527	1	DNGGACGYKDVDKPPFSGMTGCGNTPIFK (No match)
66 - 77	1357.6415	1356.6342	1356.5914	0.0428	1	SGRGCGSCFEIK (No match)
69 - 77	1057.4805	1056.4732	1056.4368	0.0364	0	GCGSCFEIK (No match)
125 - 136	1418.8086	1417.8013	1417.7677	0.0336	1	LRSAGELELQFR (No match)
127 - 136	1149.6229	1148.6156	1148.5825	0.0331	0	SAGELELQFR (No match)
127 - 136	1149.6229	1148.6156	1148.5825	0.0331	0	SAGELELQFR (Ions score 56)
127 - 137	1305.7271	1304.7198	1304.6836	0.0362	1	SAGELELQFRR (Ions score 61)
127 - 137	1305.7271	1304.7198	1304.6836	0.0362	1	SAGELELQFRR (No match)
148 - 166	2129.2266	2128.2193	2128.1680	0.0514	1	VTFHVEKGSNPNYLALLVK (No match)
155 - 166	1288.7295	1287.7222	1287.7186	0.0036	0	GSNPNYLALLVK (No match)
192 - 199	1004.5238	1003.5165	1003.4875	0.0290	0	ESWGAIWR (Ions score 28)
192 - 199	1004.5238	1003.5165	1003.4875	0.0290	0	ESWGAIWR (No match)
200 - 213	1559.8856	1558.8783	1558.8355	0.0429	1	IDTPDKLTGPFTVR (No match)

Spot 76

Index

	Accession	Mass	Score	Description
1.	gi|1582250	28542	263	allergen PhI p I
2.	gi|3901094	28584	263	pollen allergen Phl pI [Phleum pratense]
3.	gi|125528954	37616	62	hypothetical protein OsI_05029 [Oryza sativa Indica Group]
4.	gi|20161829	43970	58	hypothetical protein [Oryza sativa Japonica Group]
5.	gi|57899087	14450	58	hypothetical protein [Oryza sativa Japonica Group]
6.	gi|94502681	12732	56	hypothetical protein ZeamMp106 [Zea mays subsp. mays]
7.	gi|56788719	14999	52	serine:glyoxylate aminotransferase [Chlamydomonas reinhardtii]
8.	gi|222863585	10823	51	predicted protein [Populus trichocarpa]
9.	gi|118489113	44020	48	unknown [Populus trichocarpa x Populus deltoides]
10.	gi|159486062	47260	48	hypothetical protein CHLREDRAFT_167909 [Chlamydomonas reinhardtii]

Results List

1. gi|1582250 **Mass:** 28542 **Score:** 263 **Expect:** 3e-021 **Queries matched:** 9

allergen PhI p I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1057.4497	1056.4424	1056.4368	0.0056	91	99	0	---	GCGSCFEIK
1135.5822	1134.5749	1134.5669	0.0081	149	158	0	---	SAGEVEIQFR
1135.5822	1134.5749	1134.5669	0.0081	149	158	0	48	SAGEVEIQFR
1291.6794	1290.6721	1290.6680	0.0042	149	159	1	37	SAGEVEIQFRR
1291.6794	1290.6721	1290.6680	0.0042	149	159	1	---	SAGEVEIQFRR
1357.6222	1356.6149	1356.5914	0.0235	88	99	1	---	SGRGCGSCFEIK
1363.6964	1362.6891	1362.6931	-0.0040	46	58	0	---	STWYGKPTAAGPK
1571.8884	1570.8811	1570.8718	0.0093	221	234	1	---	IDTPEVLKGPFTVR
1571.8884	1570.8811	1570.8718	0.0093	221	234	1	83	IDTPEVLKGPFTVR

No match to: 713.4075, 768.5239, 973.5482

2. gi|3901094 **Mass:** 28584 **Score:** 263 **Expect:** 3e-021 **Queries matched:** 9

pollen allergen Phl pI [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1057.4497	1056.4424	1056.4368	0.0056	91	99	0	---	GCGSCFEIK
1135.5822	1134.5749	1134.5669	0.0081	149	158	0	---	SAGEVEIQFR
1135.5822	1134.5749	1134.5669	0.0081	149	158	0	48	SAGEVEIQFR
1291.6794	1290.6721	1290.6680	0.0042	149	159	1	37	SAGEVEIQFRR
1291.6794	1290.6721	1290.6680	0.0042	149	159	1	---	SAGEVEIQFRR
1357.6222	1356.6149	1356.5914	0.0235	88	99	1	---	SGRGCGSCFEIK
1363.6964	1362.6891	1362.6931	-0.0040	46	58	0	---	STWYGKPTAAGPK

1571.8884	1570.8811	1570.8718	0.0093	222 - 235	1	---	IDTPEVLKGPFTVR
1571.8884	1570.8811	1570.8718	0.0093	222 - 235	1	83	IDTPEVLKGPFTVR

No match to: 713.4075, 768.5239, 973.5482

3. gi|125528954 **Mass:** 37616 **Score:** 62 **Expect:** 0.4 **Queries matched:** 8

hypothetical protein OsI_05029 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
973.5482	972.5409	972.5538	-0.0129	110 - 117	1	---	SRVVMLPR + Oxidation (M)
1057.4497	1056.4424	1056.4698	-0.0274	102 - 109	0	---	CFLFEADR
1135.5822	1134.5749	1134.5855	-0.0106	7 - 15	0	---	FLNLIMDNR
1135.5822	1134.5749	1134.5855	-0.0106	7 - 15	0	---	FLNLIMDNR
1291.6794	1290.6721	1290.6866	-0.0145	6 - 15	1	0	RFLNLIMDNR
1291.6794	1290.6721	1290.6866	-0.0145	6 - 15	1	---	RFLNLIMDNR
1571.8884	1570.8811	1570.7885	0.0926	295 - 308	1	---	QCRDPQLVNLGSGK
1571.8884	1570.8811	1570.7885	0.0926	295 - 308	1	---	QCRDPQLVNLGSGK

No match to: 713.4075, 768.5239, 1357.6222, 1363.6964

4. gi|20161829 **Mass:** 43970 **Score:** 58 **Expect:** 0.87 **Queries matched:** 8

hypothetical protein [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
973.5482	972.5409	972.5538	-0.0129	110 - 117	1	---	SRVVMLPR + Oxidation (M)
1057.4497	1056.4424	1056.4698	-0.0274	102 - 109	0	---	CFLFEADR
1135.5822	1134.5749	1134.5855	-0.0106	7 - 15	0	---	FLNLIMDNR
1135.5822	1134.5749	1134.5855	-0.0106	7 - 15	0	---	FLNLIMDNR
1291.6794	1290.6721	1290.6866	-0.0145	6 - 15	1	0	RFLNLIMDNR
1291.6794	1290.6721	1290.6866	-0.0145	6 - 15	1	---	RFLNLIMDNR
1571.8884	1570.8811	1570.7885	0.0926	295 - 308	1	---	QCRDPQLVNLGSGK
1571.8884	1570.8811	1570.7885	0.0926	295 - 308	1	---	QCRDPQLVNLGSGK

No match to: 713.4075, 768.5239, 1357.6222, 1363.6964

5. gi|57899087 **Mass:** 14450 **Score:** 58 **Expect:** 0.87 **Queries matched:** 4

hypothetical protein [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1135.5822	1134.5749	1134.5273	0.0476	66 - 77	0	---	GGGATAMAALCR
1135.5822	1134.5749	1134.5273	0.0476	38 - 49	0	---	GGGATAMAALCR
1291.6794	1290.6721	1290.6284	0.0437	37 - 49	1	2	RGGGATAMAALCR
1291.6794	1290.6721	1290.6284	0.0437	66 - 78	1	---	GGGATAMAALCRR

No match to: 713.4075, 768.5239, 973.5482, 1057.4497, 1357.6222, 1363.6964, 1571.8884, 1571.8884

6. gi|94502681 **Mass:** 12732 **Score:** 56 **Expect:** 1.6 **Queries matched:** 5

hypothetical protein ZeamMp106 [Zea mays subsp. mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide

1135.5822	1134.5749	1134.6107	-0.0357	3 - 11	0	---	LLPFLTEMR + Oxidation (M)
1135.5822	1134.5749	1134.6107	-0.0357	3 - 11	0	---	LLPFLTEMR + Oxidation (M)
1291.6794	1290.6721	1290.7118	-0.0397	2 - 11	1	0	RLLPFLTEMR + Oxidation (M)
1291.6794	1290.6721	1290.7118	-0.0397	3 - 12	1	---	LLPFLTEMRR + Oxidation (M)
1357.6222	1356.6149	1356.6350	-0.0201	49 - 58	1	---	TTTYFDYYRK

No match to: 713.4075, 768.5239, 973.5482, 1057.4497, 1363.6964, 1571.8884, 1571.8884

7. gi|56788719 **Mass:** 14999 **Score:** 52 **Expect:** 3.5 **Queries matched:** 4

serine:glyoxylate aminotransferase [Chlamydomonas reinhardtii]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
973.5482	972.5409	972.5028	0.0381	61 -	69	0	---	QAVDGWGLK
1135.5822	1134.5749	1134.4975	0.0775	41 -	51	0	---	EEGGMEAVAAR + Oxidation (M)
1135.5822	1134.5749	1134.4975	0.0775	41 -	51	0	14	EEGGMEAVAAR + Oxidation (M)
1357.6222	1356.6149	1356.6529	-0.0380	122 -	133	0	---	IGHLGNMNELML + Oxidation (M)

No match to: 713.4075, 768.5239, 1057.4497, 1291.6794, 1291.6794, 1363.6964, 1571.8884, 1571.8884

8. gi|222863585 **Mass:** 10823 **Score:** 51 **Expect:** 4.7 **Queries matched:** 4

predicted protein [Populus trichocarpa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1135.5822	1134.5749	1134.5920	-0.0171	85 -	96	0	---	AISATGYTVPGV
1135.5822	1134.5749	1134.5920	-0.0171	85 -	96	0	8	AISATGYTVPGV
1291.6794	1290.6721	1290.6931	-0.0210	84 -	96	1	13	RAISATGYTVPGV
1291.6794	1290.6721	1290.6931	-0.0210	84 -	96	1	---	RAISATGYTVPGV

No match to: 713.4075, 768.5239, 973.5482, 1057.4497, 1357.6222, 1363.6964, 1571.8884, 1571.8884

9. gi|118489113 **Mass:** 44020 **Score:** 48 **Expect:** 8.9 **Queries matched:** 7

unknown [Populus trichocarpa x Populus deltoides]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1135.5822	1134.5749	1134.5669	0.0080	298 -	306	0	---	FNQLSIEER
1135.5822	1134.5749	1134.5669	0.0080	298 -	306	0	---	FNQLSIEER
1291.6794	1290.6721	1290.6680	0.0041	297 -	306	1	---	RFNQLSIEER
1291.6794	1290.6721	1290.6680	0.0041	297 -	306	1	---	RFNQLSIEER
1363.6964	1362.6891	1362.7064	-0.0173	1 -	13	0	---	MATASLIESSPLK + Oxidation (M)
1571.8884	1570.8811	1570.9228	-0.0417	225 -	239	1	---	TSVLKLQVGLLGMGR
1571.8884	1570.8811	1570.9228	-0.0417	225 -	239	1	---	TSVLKLQVGLLGMGR

No match to: 713.4075, 768.5239, 973.5482, 1057.4497, 1357.6222

10. gi|159486062 **Mass:** 47260 **Score:** 48 **Expect:** 9.2 **Queries matched:** 4

hypothetical protein CHLREDRAFT_167909 [Chlamydomonas reinhardtii]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
713.4075	712.4002	712.3867	0.0135	143 -	149	0	---	EGPVVGR
973.5482	972.5409	972.5352	0.0057	228 -	235	1	---	DELLARTR

1135.5822 1134.5749 1134.5127 0.0622 294 - 302 0 --- ESWCEVVAR
1135.5822 1134.5749 1134.5127 0.0622 294 - 302 0 21 ESWCEVVAR
No match to: 768.5239, 1057.4497, 1291.6794, 1291.6794, 1357.6222, 1363.6964, 1571.8884, 1571.8884

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 12

Protein View

Match to: **gi|3901094** Score: **263** Expect: **3e-021**
pollen allergen Phl pI [Phleum pratense]

Nominal mass (M_r): **28584**; Calculated pI value: **7.53**
NCBI BLAST search of gi|3901094 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

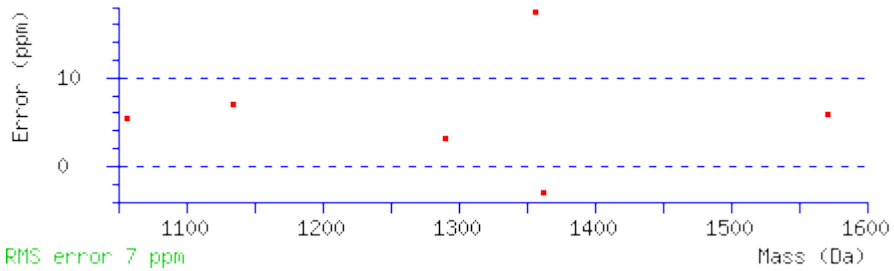
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **19%**

Matched peptides shown in **Bold Red**

```
   1 MASSSSVLLV VALFAVFLGS AHGIPKVPPG PNITATYGDK WLDAKSTWYG
  51 KPTAAGPKDN GGACGYKDVD KPPFSGMTGC GNTPIFKSGR GCGSCFEIKC
 101 TKPEACSGEP VVVHITDDNE EPIAAYHFDL SGIAFGSMAK KGDEQKLRSA
 151 GEVEIQFRRV KCKYPEGTKV TFHVEKGSNP NYLALLVKFV AGDGDVVAVD
 201 IKEKGKDKWI ALKESWGAIW RIDTPEVLKG PFTVRYTTEG GTKGEAKDVI
 251 PEGWKADTAY ESK
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
46 - 58	1363.6964	1362.6891	1362.6931	-0.0040	0	STWYGKPTAAGPK	(No match)
88 - 99	1357.6222	1356.6149	1356.5914	0.0235	1	SGRGCGSCFEIK	(No match)
91 - 99	1057.4497	1056.4424	1056.4368	0.0056	0	GCGSCFEIK	(No match)
149 - 158	1135.5822	1134.5749	1134.5669	0.0081	0	SAGEVEIQFR	(No match)
149 - 158	1135.5822	1134.5749	1134.5669	0.0081	0	SAGEVEIQFR	(Ions score 48)
149 - 159	1291.6794	1290.6721	1290.6680	0.0042	1	SAGEVEIQFRR	(Ions score 37)
149 - 159	1291.6794	1290.6721	1290.6680	0.0042	1	SAGEVEIQFRR	(No match)
222 - 235	1571.8884	1570.8811	1570.8718	0.0093	1	IDTPEVLKGPFTVR	(No match)
222 - 235	1571.8884	1570.8811	1570.8718	0.0093	1	IDTPEVLKGPFTVR	(Ions score 83)



Spot 77

Index

	Accession	Mass	Score	Description
1.	gi|3901094	28584	400	pollen allergen Phl pI [Phleum pratense]
2.	gi|1582250	28542	382	allergen PhI p I
3.	gi|157356134	100482	57	unnamed protein product [Vitis vinifera]
4.	gi|157355157	106395	55	unnamed protein product [Vitis vinifera]
5.	gi|157339397	89856	54	unnamed protein product [Vitis vinifera]
6.	gi|217426790	78420	54	AT5G09930-like protein [Arabidopsis arenosa]
7.	gi|166244740	6022	53	ribosomal protein L2 [Cinnamomum camphora]
8.	gi|171921101	94199	52	unknown protein [Brassica oleracea]
9.	gi|38344145	32478	51	OSJNBa0041A02.12 [Oryza sativa (japonica cultivar-group)]
10.	gi|116310927	32436	51	B0403H10-OSIGBa0105A11.17 [Oryza sativa (indica cultivar-group)]

Results List

1. gi|3901094 **Mass:** 28584 **Score:** 400 **Expect:** 6.1e-035 **Queries matched:** 14

pollen allergen Phl pI [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1004.4914	1003.4841	1003.4875	-0.0034	214	-	221	0	---	ESWGAIWR
1057.4252	1056.4179	1056.4368	-0.0189	91	-	99	0	---	GCGSCFEIK
1135.5668	1134.5595	1134.5669	-0.0073	149	-	158	0	51	SAGEVEIQFR
1135.5668	1134.5595	1134.5669	-0.0073	149	-	158	0	---	SAGEVEIQFR
1291.6631	1290.6558	1290.6680	-0.0121	149	-	159	1	65	SAGEVEIQFRR
1291.6631	1290.6558	1290.6680	-0.0121	149	-	159	1	---	SAGEVEIQFRR
1357.5970	1356.5897	1356.5914	-0.0017	88	-	99	1	---	SGRGCGSCFEIK
1363.6848	1362.6775	1362.6931	-0.0156	46	-	58	0	---	STWYGKPTAAGPK
1363.6848	1362.6775	1362.6931	-0.0156	46	-	58	0	68	STWYGKPTAAGPK
1404.7360	1403.7287	1403.7296	-0.0008	189	-	202	0	---	FVAGDGDVVAVDIK
1571.8635	1570.8562	1570.8718	-0.0156	222	-	235	1	83	IDTPEVLKGPFTVR
1571.8635	1570.8562	1570.8718	-0.0156	222	-	235	1	---	IDTPEVLKGPFTVR
1661.8452	1660.8379	1660.8671	-0.0292	189	-	204	1	---	FVAGDGDVVAVDIKEK
2168.0305	2167.0232	2167.0078	0.0155	68	-	87	0	---	DVDKPPFSGMTGCGNTPIFK

No match to: 768.5269, 845.0930, 973.5339, 973.5339, 1313.6460, 1560.8386, 1570.8405, 1587.8560, 1593.8500, 1761.8862, 2044.0939, 3015.4583, 3091.3755

2. gi|1582250 **Mass:** 28542 **Score:** 382 **Expect:** 3.8e-033 **Queries matched:** 13

allergen PhI p I

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1004.4914	1003.4841	1003.4875	-0.0034	213	-	220	0	---	ESWGAIWR
1057.4252	1056.4179	1056.4368	-0.0189	91	-	99	0	---	GCGSCFEIK

1135.5668	1134.5595	1134.5669	-0.0073	149 - 158	0	51	SAGEVEIQFR
1135.5668	1134.5595	1134.5669	-0.0073	149 - 158	0	---	SAGEVEIQFR
1291.6631	1290.6558	1290.6680	-0.0121	149 - 159	1	65	SAGEVEIQFRR
1291.6631	1290.6558	1290.6680	-0.0121	149 - 159	1	---	SAGEVEIQFRR
1357.5970	1356.5897	1356.5914	-0.0017	88 - 99	1	---	SGRGCGSCFEIK
1363.6848	1362.6775	1362.6931	-0.0156	46 - 58	0	---	STWYGKPTAAGPK
1363.6848	1362.6775	1362.6931	-0.0156	46 - 58	0	68	STWYGKPTAAGPK
1404.7360	1403.7287	1403.7520	-0.0233	147 - 158	1	---	LRSAGEVEIQFR
1571.8635	1570.8562	1570.8718	-0.0156	221 - 234	1	83	IDTPEVLKGPFTVR
1571.8635	1570.8562	1570.8718	-0.0156	221 - 234	1	---	IDTPEVLKGPFTVR
2168.0305	2167.0232	2167.0078	0.0155	68 - 87	0	---	DVDKPPFSGMTGCGNTPIFK

No match to: 768.5269, 845.0930, 973.5339, 973.5339, 1313.6460, 1560.8386, 1570.8405, 1587.8560, 1593.8500, 1661.8452, 1761.8862, 2044.0939, 3015.4583, 3091.3755

3. gi|157356134 **Mass:** 100482 **Score:** 57 **Expect:** 1.2 **Queries matched:** 6

unnamed protein product [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
973.5339	972.5266	972.5352	-0.0086	612 - 619	1	30	DSNIKQLR
973.5339	972.5266	972.5352	-0.0086	612 - 619	1	---	DSNIKQLR
1313.6460	1312.6387	1312.5903	0.0484	824 - 834	1	---	GCCSNLEKFAK
1570.8405	1569.8332	1569.7609	0.0723	832 - 844	1	---	FAKNLEGFCSLER
1587.8560	1586.8487	1586.7657	0.0830	819 - 831	1	---	HLTLRGCCSNLEK
3015.4583	3014.4510	3014.4286	0.0224	767 - 792	1	---	LKSLGILSLNDCSNLDTFPEIMEDMK + 2 Oxidation (M)

No match to: 768.5269, 845.0930, 1004.4914, 1057.4252, 1135.5668, 1135.5668, 1291.6631, 1291.6631, 1357.5970, 1363.6848, 1363.6848, 1404.7360, 1560.8386, 1571.8635, 1571.8635, 1593.8500, 1661.8452, 1761.8862, 2044.0939, 2168.0305, 3091.3755

4. gi|157355157 **Mass:** 106395 **Score:** 55 **Expect:** 1.8 **Queries matched:** 11

unnamed protein product [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
973.5339	972.5266	972.5491	-0.0225	499 - 506	0	---	LLQETIEK
973.5339	972.5266	972.5352	-0.0086	761 - 768	1	---	LDLERTAR
1004.4914	1003.4841	1003.4934	-0.0093	651 - 659	1	---	AATAEEKER
1135.5668	1134.5595	1134.5152	0.0443	383 - 392	0	---	SNEAETESLR
1135.5668	1134.5595	1134.5152	0.0443	383 - 392	0	---	SNEAETESLR
1313.6460	1312.6387	1312.6259	0.0129	212 - 223	0	---	VADLHESTGEQK
1363.6848	1362.6775	1362.6891	-0.0116	700 - 711	1	---	AAENRQEYLAAK
1363.6848	1362.6775	1362.6891	-0.0116	700 - 711	1	---	AAENRQEYLAAK
1587.8560	1586.8487	1586.7648	0.0840	527 - 541	1	---	EAEALAEARANSEAR
1661.8452	1660.8379	1660.8640	-0.0261	339 - 353	1	---	LEMKMLETALQGAAR
1761.8862	1760.8789	1760.8614	0.0175	359 - 373	1	---	ADEIAKLMNENEQLK + Oxidation (M)

No match to: 768.5269, 845.0930, 1057.4252, 1291.6631, 1291.6631, 1357.5970, 1404.7360, 1560.8386, 1570.8405,

1571.8635, 1571.8635, 1593.8500, 2044.0939, 2168.0305, 3015.4583, 3091.3755

5. gi|157339397 **Mass:** 89856 **Score:** 54 **Expect:** 2.2 **Queries matched:** 10

unnamed protein product [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
973.5339	972.5266	972.5100	0.0166	17 -	24	1	---	VLNRNSDR
973.5339	972.5266	972.5100	0.0166	17 -	24	1	---	VLNRNSDR
1313.6460	1312.6387	1312.6671	-0.0284	417 -	426	1	---	FWSNLKLMMK + Oxidation (M)
1363.6848	1362.6775	1362.7077	-0.0302	128 -	139	1	---	VADFGLAKLCNR
1363.6848	1362.6775	1362.7077	-0.0302	128 -	139	1	---	VADFGLAKLCNR
1570.8405	1569.8332	1569.8660	-0.0328	234 -	247	1	---	MLTLSRSVAHNVVK + Oxidation (M)
1593.8500	1592.8427	1592.7616	0.0811	564 -	578	0	---	QAGEQFMAEVGTIGR
1761.8862	1760.8789	1760.7827	0.0962	189 -	203	1	---	NAKVGSNDSMDWFFK + Oxidation (M)
2168.0305	2167.0232	2166.9963	0.0269	21 -	39	1	---	NSDRQTEEQFMAEVGTIGR
3015.4583	3014.4510	3014.3465	0.1045	587 -	611	0	---	LYGFCHDQFMSALVYEYLENGSLDK + Oxidation (M)

No match to: 768.5269, 845.0930, 1004.4914, 1057.4252, 1135.5668, 1135.5668, 1291.6631, 1291.6631, 1357.5970, 1404.7360, 1560.8386, 1571.8635, 1571.8635, 1587.8560, 1661.8452, 2044.0939, 3091.3755

6. gi|217426790 **Mass:** 78420 **Score:** 54 **Expect:** 2.4 **Queries matched:** 10

AT5G09930-like protein [Arabidopsis arenosa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1004.4914	1003.4841	1003.5338	-0.0497	101 -	108	1	---	DVTWEVKK
1291.6631	1290.6558	1290.6502	0.0056	398 -	408	1	---	IRFPECGLSGR
1291.6631	1290.6558	1290.6502	0.0056	398 -	408	1	---	IRFPECGLSGR
1363.6848	1362.6775	1362.6487	0.0288	72 -	85	0	---	QSNNGASSISSGVR
1363.6848	1362.6775	1362.6487	0.0288	72 -	85	0	6	QSNNGASSISSGVR
1571.8635	1570.8562	1570.7701	0.0862	149 -	162	0	---	VAFLSQEFEVSMGK
1571.8635	1570.8562	1570.7701	0.0862	149 -	162	0	---	VAFLSQEFEVSMGK
1587.8560	1586.8487	1586.8304	0.0184	492 -	505	0	---	TVIETVVEAAVDWR
1761.8862	1760.8789	1760.9892	-0.1103	450 -	464	1	---	STLLKLIMGLEKPMR + 2 Oxidation (M)
2044.0939	2043.0866	2043.0636	0.0230	378 -	393	1	---	LEKLQEEEQIEKPFQR

No match to: 768.5269, 845.0930, 973.5339, 973.5339, 1057.4252, 1135.5668, 1135.5668, 1313.6460, 1357.5970, 1404.7360, 1560.8386, 1570.8405, 1593.8500, 1661.8452, 2168.0305, 3015.4583, 3091.3755

7. gi|166244740 **Mass:** 6022 **Score:** 53 **Expect:** 3.4 **Queries matched:** 3

ribosomal protein L2 [Cinnamomum camphora]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1571.8635	1570.8562	1570.8619	-0.0057	22 -	35	1	8	KKPTTPWGYPALGR
1571.8635	1570.8562	1570.8619	-0.0057	23 -	36	1	---	KPTTPWGYPALGRK
2168.0305	2167.0232	2167.0704	-0.0472	1 -	21	1	---	VVMNPVDHPHGGGEGRAPIGR + Oxidation (M)

No match to: 768.5269, 845.0930, 973.5339, 973.5339, 1004.4914, 1057.4252, 1135.5668, 1135.5668, 1291.6631, 1291.6631, 1313.6460, 1357.5970, 1363.6848, 1363.6848, 1404.7360, 1560.8386, 1570.8405, 1587.8560, 1593.8500,

1661.8452, 1761.8862, 2044.0939, 3015.4583, 3091.3755

8. gi|171921101 **Mass:** 94199 **Score:** 52 **Expect:** 3.7 **Queries matched:** 10

unknown protein [Brassica oleracea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1135.5668	1134.5595	1134.5993	-0.0397	75 -	84	1	6	LTRVSTESSR
1135.5668	1134.5595	1134.5993	-0.0397	75 -	84	1	---	LTRVSTESSR
1291.6631	1290.6558	1290.6680	-0.0122	281 -	291	1	---	LNSDPFSRSLR
1291.6631	1290.6558	1290.6680	-0.0122	281 -	291	1	---	LNSDPFSRSLR
1363.6848	1362.6775	1362.7216	-0.0441	705 -	716	0	---	VVFDAVNEMLVK
1363.6848	1362.6775	1362.7216	-0.0441	705 -	716	0	---	VVFDAVNEMLVK
1404.7360	1403.7287	1403.7078	0.0209	533 -	545	0	---	TVVSNLMQNASPK + Oxidation (M)
1560.8386	1559.8313	1559.9286	-0.0973	648 -	661	0	---	YISEILLASGLLLR
1570.8405	1569.8332	1569.7431	0.0901	20 -	32	0	---	IGCMNGIFQIFDR
3015.4583	3014.4510	3014.3893	0.0617	580 -	605	1	---	TNEEDQWNPAYSFSKTTTTLSPEVNR

No match to: 768.5269, 845.0930, 973.5339, 973.5339, 1004.4914, 1057.4252, 1313.6460, 1357.5970, 1571.8635, 1571.8635, 1587.8560, 1593.8500, 1661.8452, 1761.8862, 2044.0939, 2168.0305, 3091.3755

9. gi|38344145 **Mass:** 32478 **Score:** 51 **Expect:** 4.7 **Queries matched:** 7

OSJNBa0041A02.12 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
973.5339	972.5266	972.5100	0.0166	40 -	49	1	15	ESAAAAAARR
973.5339	972.5266	972.5100	0.0166	40 -	49	1	---	ESAAAAAARR
1004.4914	1003.4841	1003.4206	0.0635	89 -	97	0	---	ETSDPENGR
1571.8635	1570.8562	1570.7488	0.1075	16 -	28	1	---	DERVPQWGAQETR
1571.8635	1570.8562	1570.7488	0.1075	16 -	28	1	---	DERVPQWGAQETR
1661.8452	1660.8379	1660.7272	0.1107	203 -	214	1	---	MDIQWHEMMERR
1761.8862	1760.8789	1760.8614	0.0175	115 -	130	0	---	TMQQQLLESESGPSVK

No match to: 768.5269, 845.0930, 1057.4252, 1135.5668, 1135.5668, 1291.6631, 1291.6631, 1313.6460, 1357.5970, 1363.6848, 1363.6848, 1404.7360, 1560.8386, 1570.8405, 1587.8560, 1593.8500, 2044.0939, 2168.0305, 3015.4583, 3091.3755

10. gi|116310927 **Mass:** 32436 **Score:** 51 **Expect:** 4.7 **Queries matched:** 7

B0403H10-OSIGBa0105A11.17 [Oryza sativa (indica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
973.5339	972.5266	972.5100	0.0166	40 -	49	1	15	ESAAAAAARR
973.5339	972.5266	972.5100	0.0166	40 -	49	1	---	ESAAAAAARR
1004.4914	1003.4841	1003.4206	0.0635	89 -	97	0	---	ETSDPENGR
1571.8635	1570.8562	1570.7488	0.1075	16 -	28	1	---	DERVPQWGAQETR
1571.8635	1570.8562	1570.7488	0.1075	16 -	28	1	---	DERVPQWGAQETR
1661.8452	1660.8379	1660.7272	0.1107	203 -	214	1	---	MDIQWHEMMERR
1761.8862	1760.8789	1760.8614	0.0175	115 -	130	0	---	TMQQQLLESESGPSVK

No match to: 768.5269, 845.0930, 1057.4252, 1135.5668, 1135.5668, 1291.6631, 1291.6631, 1313.6460, 1357.5970, 1363.6848, 1363.6848, 1404.7360, 1560.8386, 1570.8405, 1587.8560, 1593.8500, 2044.0939, 2168.0305, 3015.4583, 3091.3755

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 27

Protein View

Match to: **gi|3901094** Score: **400** Expect: **6.1e-035**
pollen allergen Phl pI [Phleum pratense]

Nominal mass (M_r): **28584;** Calculated pI value: **7.53**
NCBI BLAST search of gi|3901094 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **35%**

Matched peptides shown in **Bold Red**

```
    1 MASSSSVLLV VALFAVFLGS AHGIPKVPPG PNITATYGDK WLDAKSTWYG
   51 KPTAAGPKDN GGACGYKDVD KPPFSGMTGC GNTPIFKSGR GCGSCFEIKC
  101 TKPEACSGEP VVVHITDDNE EPIAAYHFDL SGIAFGSMAK KGDEQKLRSA
  151 GEVEIQFRRV KCKYPEGTKV TFHVEKGSNP NYLALLVKFV AGDGDVVAVD
  201 IKEKGKDKWI ALKESWGAIW RIDTPEVLKG PFTVRYTTEG GTKGEAKDVI
  251 PEGWKADTAY ESK
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
46 - 58	1363.6848	1362.6775	1362.6931	-0.0156	0	STWYGKPTAAGPK	(No match)
46 - 58	1363.6848	1362.6775	1362.6931	-0.0156	0	STWYGKPTAAGPK	(Ions score 68)
68 - 87	2168.0305	2167.0232	2167.0078	0.0155	0	DVDKPPFSGMTGCGNTPIFK	(No match)
88 - 99	1357.5970	1356.5897	1356.5914	-0.0017	1	SGRGCGSCFEIK	(No match)
91 - 99	1057.4252	1056.4179	1056.4368	-0.0189	0	GCGSCFEIK	(No match)
149 - 158	1135.5668	1134.5595	1134.5669	-0.0073	0	SAGEVEIQFR	(Ions score 51)
149 - 158	1135.5668	1134.5595	1134.5669	-0.0073	0	SAGEVEIQFR	(No match)
149 - 159	1291.6631	1290.6558	1290.6680	-0.0121	1	SAGEVEIQFRR	(Ions score 65)
149 - 159	1291.6631	1290.6558	1290.6680	-0.0121	1	SAGEVEIQFRR	(No match)
189 - 202	1404.7360	1403.7287	1403.7296	-0.0008	0	FVAGDGDVVAVDIK	(No match)
189 - 204	1661.8452	1660.8379	1660.8671	-0.0292	1	FVAGDGDVVAVDIKEK	(No match)
214 - 221	1004.4914	1003.4841	1003.4875	-0.0034	0	ESWGAIWR	(No match)
222 - 235	1571.8635	1570.8562	1570.8718	-0.0156	1	IDTPEVLKGPFTVR	(Ions score 83)
222 - 235	1571.8635	1570.8562	1570.8718	-0.0156	1	IDTPEVLKGPFTVR	(No match)

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	Accession	Mass	Score	Description
1.	gi|1582250	28542	276	allergen PhI p I
2.	gi|3901094	28584	276	pollen allergen Phl pI [Phleum pratense]
3.	gi|226496679	11983	65	hypothetical protein LOC100278578 [Zea mays]
4.	gi|57899087	14450	60	hypothetical protein [Oryza sativa Japonica Group]
5.	gi|56784475	15383	56	Epstein-Barr virus EBNA-1-like protein [Oryza sativa Japonica Group]
6.	gi|38345098	16756	53	OSJNBa0050F15.9 [Oryza sativa (japonica cultivar-group)]
7.	gi|255562162	14873	53	conserved hypothetical protein [Ricinus communis]
8.	gi|118489113	44020	52	unknown [Populus trichocarpa x Populus deltoides]
9.	gi|224091223	46663	52	predicted protein [Populus trichocarpa]
10.	gi|224124614	10161	51	predicted protein [Populus trichocarpa]

Results List

1. gi|1582250 **Mass:** 28542 **Score:** 276 **Expect:** 1.5e-022 **Queries matched:** 8

allergen PhI p I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1057.4595	1056.4522	1056.4368	0.0154	91	99	0	---	GCGSCFEIK
1135.6018	1134.5945	1134.5669	0.0277	149	158	0	58	SAGEVEIQFR
1135.6018	1134.5945	1134.5669	0.0277	149	158	0	---	SAGEVEIQFR
1291.7092	1290.7019	1290.6680	0.0340	149	159	1	56	SAGEVEIQFRR
1291.7092	1290.7019	1290.6680	0.0340	149	159	1	---	SAGEVEIQFRR
1363.7222	1362.7149	1362.6931	0.0218	46	58	0	---	STWYGKPTAAGPK
1571.9209	1570.9136	1570.8718	0.0418	221	234	1	---	IDTPEVLKGPFTVR
1571.9209	1570.9136	1570.8718	0.0418	221	234	1	84	IDTPEVLKGPFTVR

No match to: 768.5499, 973.5607, 973.5607

2. gi|3901094 **Mass:** 28584 **Score:** 276 **Expect:** 1.5e-022 **Queries matched:** 8

pollen allergen Phl pI [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1057.4595	1056.4522	1056.4368	0.0154	91	99	0	---	GCGSCFEIK
1135.6018	1134.5945	1134.5669	0.0277	149	158	0	58	SAGEVEIQFR
1135.6018	1134.5945	1134.5669	0.0277	149	158	0	---	SAGEVEIQFR
1291.7092	1290.7019	1290.6680	0.0340	149	159	1	56	SAGEVEIQFRR
1291.7092	1290.7019	1290.6680	0.0340	149	159	1	---	SAGEVEIQFRR
1363.7222	1362.7149	1362.6931	0.0218	46	58	0	---	STWYGKPTAAGPK
1571.9209	1570.9136	1570.8718	0.0418	222	235	1	---	IDTPEVLKGPFTVR
1571.9209	1570.9136	1570.8718	0.0418	222	235	1	84	IDTPEVLKGPFTVR

No match to: 768.5499, 973.5607, 973.5607

3. gi|226496679 **Mass:** 11983 **Score:** 65 **Expect:** 0.19 **Queries matched:** 4

hypothetical protein LOC100278578 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1135.6018	1134.5945	1134.6032	-0.0087	49	-	59	0	---	GVASLYGAELR
1135.6018	1134.5945	1134.6032	-0.0087	49	-	59	0	---	GVASLYGAELR
1291.7092	1290.7019	1290.7043	-0.0024	49	-	60	1	35	GVASLYGAELRR
1291.7092	1290.7019	1290.7043	-0.0024	49	-	60	1	---	GVASLYGAELRR

No match to: 768.5499, 973.5607, 973.5607, 1057.4595, 1363.7222, 1571.9209, 1571.9209

4. gi|57899087 **Mass:** 14450 **Score:** 60 **Expect:** 0.55 **Queries matched:** 4

hypothetical protein [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1135.6018	1134.5945	1134.5273	0.0672	38	-	49	0	---	GGGATAMAALCR
1135.6018	1134.5945	1134.5273	0.0672	66	-	77	0	---	GGGATAMAALCR
1291.7092	1290.7019	1290.6284	0.0735	37	-	49	1	---	RGGGATAMAALCR
1291.7092	1290.7019	1290.6284	0.0735	66	-	78	1	---	GGGATAMAALCRR

No match to: 768.5499, 973.5607, 973.5607, 1057.4595, 1363.7222, 1571.9209, 1571.9209

5. gi|56784475 **Mass:** 15383 **Score:** 56 **Expect:** 1.5 **Queries matched:** 6

Epstein-Barr virus EBNA-1-like protein [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
973.5607	972.5534	972.5100	0.0434	21	-	30	1	---	GLTADGGARR
973.5607	972.5534	972.5100	0.0434	20	-	29	1	4	RGLTADGGAR
1135.6018	1134.5945	1134.5339	0.0606	107	-	116	0	---	MEQSSAVEVR
1135.6018	1134.5945	1134.5339	0.0606	107	-	116	0	---	MEQSSAVEVR
1291.7092	1290.7019	1290.6350	0.0669	107	-	117	1	---	MEQSSAVEVRR
1291.7092	1290.7019	1290.6350	0.0669	107	-	117	1	---	MEQSSAVEVRR

No match to: 768.5499, 1057.4595, 1363.7222, 1571.9209, 1571.9209

6. gi|38345098 **Mass:** 16756 **Score:** 53 **Expect:** 3 **Queries matched:** 6

OSJNBa0050F15.9 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
973.5607	972.5534	972.6007	-0.0473	2	-	10	0	---	VGLILPFSK
973.5607	972.5534	972.6007	-0.0473	2	-	10	0	---	VGLILPFSK
1135.6018	1134.5945	1134.6509	-0.0564	110	-	119	1	---	LRLPTGPPER
1135.6018	1134.5945	1134.6509	-0.0564	110	-	119	1	---	LRLPTGPPER
1571.9209	1570.9136	1570.8215	0.0921	77	-	90	1	---	QGVAGQYIDSHLRK
1571.9209	1570.9136	1570.8215	0.0921	77	-	90	1	6	QGVAGQYIDSHLRK

No match to: 768.5499, 1057.4595, 1291.7092, 1291.7092, 1363.7222

7. gi|255562162 **Mass:** 14873 **Score:** 53 **Expect:** 3.4 **Queries matched:** 7

conserved hypothetical protein [Ricinus communis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
768.5499	767.5426	767.5017	0.0409	14 -	20	1	---	IARAPIK
973.5607	972.5534	972.4988	0.0546	95 -	102	1	---	LGRIDEDR
973.5607	972.5534	972.4988	0.0546	95 -	102	1	---	LGRIDEDR
1135.6018	1134.5945	1134.5669	0.0276	109 -	117	0	---	DLVNENLYR
1135.6018	1134.5945	1134.5669	0.0276	109 -	117	0	---	DLVNENLYR
1291.7092	1290.7019	1290.6680	0.0339	109 -	118	1	---	DLVNENLYRR
1291.7092	1290.7019	1290.6680	0.0339	109 -	118	1	---	DLVNENLYRR

No match to: 1057.4595, 1363.7222, 1571.9209, 1571.9209

8. gi|118489113 **Mass:** 44020 **Score:** 52 **Expect:** 3.6 **Queries matched:** 7

unknown [Populus trichocarpa x Populus deltoides]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1135.6018	1134.5945	1134.5669	0.0276	298 -	306	0	1	FNQLSIEER
1135.6018	1134.5945	1134.5669	0.0276	298 -	306	0	---	FNQLSIEER
1291.7092	1290.7019	1290.6680	0.0339	297 -	306	1	1	RFNQLSIEER
1291.7092	1290.7019	1290.6680	0.0339	297 -	306	1	---	RFNQLSIEER
1363.7222	1362.7149	1362.7064	0.0085	1 -	13	0	---	MATASLIESSPLK + Oxidation (M)
1571.9209	1570.9136	1570.9228	-0.0092	225 -	239	1	---	TSVLKLQVGLLGMGR
1571.9209	1570.9136	1570.9228	-0.0092	225 -	239	1	---	TSVLKLQVGLLGMGR

No match to: 768.5499, 973.5607, 973.5607, 1057.4595

9. gi|224091223 **Mass:** 46663 **Score:** 52 **Expect:** 4 **Queries matched:** 7

predicted protein [Populus trichocarpa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
973.5607	972.5534	972.5127	0.0407	400 -	409	0	---	LVDVAAASVE
973.5607	972.5534	972.5127	0.0407	400 -	409	0	2	LVDVAAASVE
1135.6018	1134.5945	1134.5669	0.0276	108 -	117	0	---	IVDAVFSNDR
1135.6018	1134.5945	1134.5669	0.0276	108 -	117	0	---	IVDAVFSNDR
1291.7092	1290.7019	1290.6680	0.0339	108 -	118	1	---	IVDAVFSNDRR
1291.7092	1290.7019	1290.6680	0.0339	108 -	118	1	---	IVDAVFSNDRR
1363.7222	1362.7149	1362.7506	-0.0357	267 -	279	1	---	NYVSKIGDVGLAK

No match to: 768.5499, 1057.4595, 1571.9209, 1571.9209

10. gi|224124614 **Mass:** 10161 **Score:** 51 **Expect:** 5.2 **Queries matched:** 6

predicted protein [Populus trichocarpa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
973.5607	972.5534	972.5967	-0.0433	1 -	10	1	---	GGLGKTTLVK
973.5607	972.5534	972.5967	-0.0433	1 -	10	1	---	GGLGKTTLVK

1135.6018	1134.5945	1134.5961	-0.0015	80 - 88	0	---	YVIVLDDIW
1135.6018	1134.5945	1134.5961	-0.0015	80 - 88	0	---	YVIVLDDIW
1291.7092	1290.7019	1290.6972	0.0047	79 - 88	1	---	RYVIVLDDIW
1291.7092	1290.7019	1290.6972	0.0047	79 - 88	1	---	RYVIVLDDIW

No match to: 768.5499, 1057.4595, 1363.7222, 1571.9209, 1571.9209

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 11

Protein View

Match to: **gi|3901094** Score: **276** Expect: **1.5e-022**
pollen allergen Phl pI [Phleum pratense]

Nominal mass (M_r): **28584**; Calculated pI value: **7.53**
NCBI BLAST search of gi|3901094 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

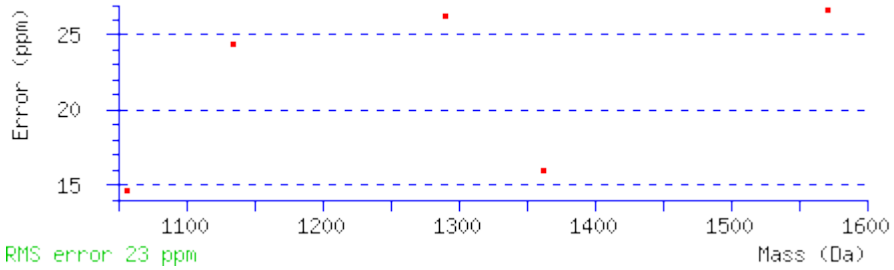
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **17%**

Matched peptides shown in **Bold Red**

```
   1 MASSSSVLLV VALFAVFLGS AHGIPKVPPG PNITATYGDK WLDAKSTWYG
  51 KPTAAGPKDN GGACGYKDVD KPPFSGMTGC GNTPIFKSGR GCGSCFEIKC
 101 TKPEACSGEP VVVHITDDNE EPIAAYHFDL SGIAFGSMAK KGDEQKLRSA
 151 GEVEIQFRRV KCKYPEGTKV TFHVEKGSNP NYLALLVKFV AGDGDVVAVD
 201 IKEKGKDKWI ALKESWGAIW RIDTPEVLKG PFTVRYTTEG GTKGEAKDVI
 251 PEGWKADTAY ESK
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
46 - 58	1363.7222	1362.7149	1362.6931	0.0218	0	**STWYGKPTAAGPK**	(No match)
91 - 99	1057.4595	1056.4522	1056.4368	0.0154	0	**GCGSCFEIK**	(No match)
149 - 158	1135.6018	1134.5945	1134.5669	0.0277	0	**SAGEVEIQFR**	(Ions score 58)
149 - 158	1135.6018	1134.5945	1134.5669	0.0277	0	**SAGEVEIQFR**	(No match)
149 - 159	1291.7092	1290.7019	1290.6680	0.0340	1	**SAGEVEIQFRR**	(Ions score 56)
149 - 159	1291.7092	1290.7019	1290.6680	0.0340	1	**SAGEVEIQFRR**	(No match)
222 - 235	1571.9209	1570.9136	1570.8718	0.0418	1	**IDTPEVLKGPFTVR**	(No match)
222 - 235	1571.9209	1570.9136	1570.8718	0.0418	1	**IDTPEVLKGPFTVR**	(Ions score 84)



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	Accession	Mass	Score	Description
1.	gi|3901094	28584	300	pollen allergen Phl pI [Phleum pratense]
2.	gi|1582250	28542	284	allergen PhI p I
3.	gi|57899087	14450	56	hypothetical protein [Oryza sativa Japonica Group]
4.	gi|223544849	30222	50	hypothetical protein RCOM_1487630 [Ricinus communis]
5.	gi|108705735	13020	49	hypothetical protein LOC_Os03g01560 [Oryza sativa (japonica cultivar-group)]

Results List

1. gi|3901094 **Mass:** 28584 **Score:** 300 **Expect:** 6e-025 **Queries matched:** 14

pollen allergen Phl pI [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1004.4966	1003.4893	1003.4875	0.0018	214	221	0	---	ESWGAIWR
1057.4363	1056.4290	1056.4368	-0.0078	91	99	0	---	GCGSCFEIK
1135.5729	1134.5656	1134.5669	-0.0012	149	158	0	---	SAGEVEIQFR
1135.5729	1134.5656	1134.5669	-0.0012	149	158	0	57	SAGEVEIQFR
1288.7108	1287.7035	1287.7186	-0.0151	177	188	0	---	GSNPNYLALLVK
1291.6696	1290.6623	1290.6680	-0.0056	149	159	1	51	SAGEVEIQFRR
1291.6696	1290.6623	1290.6680	-0.0056	149	159	1	---	SAGEVEIQFRR
1357.5947	1356.5874	1356.5914	-0.0040	88	99	1	---	SGRGCGSCFEIK
1357.5947	1356.5874	1356.5914	-0.0040	88	99	1	---	SGRGCGSCFEIK
1363.6908	1362.6835	1362.6931	-0.0096	46	58	0	---	STWYGKPTAAGPK
1404.7397	1403.7324	1403.7296	0.0029	189	202	0	---	FVAGDGDVVAVDIK
1571.8734	1570.8661	1570.8718	-0.0057	222	235	1	86	IDTPEVLKGPFTVR
1571.8734	1570.8661	1570.8718	-0.0057	222	235	1	---	IDTPEVLKGPFTVR
1661.8700	1660.8627	1660.8671	-0.0044	189	204	1	---	FVAGDGDVVAVDIKEK

No match to: 713.4094, 724.4968, 734.4932, 750.5140, 768.5231, 838.5264, 864.5500, 886.9850, 973.5438, 1233.6614, 1275.1046, 1279.7638, 1334.8768, 1345.5873, 1448.9070, 1518.8370, 1560.8547, 1618.0477, 1792.8677, 1826.9592, 2050.0659, 2166.0669, 2246.1929, 2287.0544, 2565.1943, 3015.4890, 3015.4890, 3031.4861, 3091.4011

2. gi|1582250 **Mass:** 28542 **Score:** 284 **Expect:** 2.4e-023 **Queries matched:** 13

allergen PhI p I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1004.4966	1003.4893	1003.4875	0.0018	213	220	0	---	ESWGAIWR
1057.4363	1056.4290	1056.4368	-0.0078	91	99	0	---	GCGSCFEIK
1135.5729	1134.5656	1134.5669	-0.0012	149	158	0	---	SAGEVEIQFR
1135.5729	1134.5656	1134.5669	-0.0012	149	158	0	57	SAGEVEIQFR
1288.7108	1287.7035	1287.7186	-0.0151	177	188	0	---	GSNPNYLALLVK

1291.6696	1290.6623	1290.6680	-0.0056	149 - 159	1	51	SAGEVEIQFRR
1291.6696	1290.6623	1290.6680	-0.0056	149 - 159	1	---	SAGEVEIQFRR
1357.5947	1356.5874	1356.5914	-0.0040	88 - 99	1	---	SGRGCGSCFEIK
1357.5947	1356.5874	1356.5914	-0.0040	88 - 99	1	---	SGRGCGSCFEIK
1363.6908	1362.6835	1362.6931	-0.0096	46 - 58	0	---	STWYGKPTAAGPK
1404.7397	1403.7324	1403.7520	-0.0196	147 - 158	1	---	LRSAGEVEIQFR
1571.8734	1570.8661	1570.8718	-0.0057	221 - 234	1	86	IDTPEVLKGPFTVR
1571.8734	1570.8661	1570.8718	-0.0057	221 - 234	1	---	IDTPEVLKGPFTVR

No match to: 713.4094, 724.4968, 734.4932, 750.5140, 768.5231, 838.5264, 864.5500, 886.9850, 973.5438, 1233.6614, 1275.1046, 1279.7638, 1334.8768, 1345.5873, 1448.9070, 1518.8370, 1560.8547, 1618.0477, 1661.8700, 1792.8677, 1826.9592, 2050.0659, 2166.0669, 2246.1929, 2287.0544, 2565.1943, 3015.4890, 3015.4890, 3031.4861, 3091.4011

3. gi|57899087 **Mass:** 14450 **Score:** 56 **Expect:** 1.6 **Queries matched:** 4

hypothetical protein [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1135.5729	1134.5656	1134.5273	0.0383	66 -	77	0	---	GGGATAMAALCR
1135.5729	1134.5656	1134.5273	0.0383	38 -	49	0	11	GGGATAMAALCR
1291.6696	1290.6623	1290.6284	0.0339	38 -	50	1	12	GGGATAMAALCRR
1291.6696	1290.6623	1290.6284	0.0339	66 -	78	1	---	GGGATAMAALCRR

No match to: 713.4094, 724.4968, 734.4932, 750.5140, 768.5231, 838.5264, 864.5500, 886.9850, 973.5438, 1004.4966, 1057.4363, 1233.6614, 1275.1046, 1279.7638, 1288.7108, 1334.8768, 1345.5873, 1357.5947, 1357.5947, 1363.6908, 1404.7397, 1448.9070, 1518.8370, 1560.8547, 1571.8734, 1571.8734, 1618.0477, 1661.8700, 1792.8677, 1826.9592, 2050.0659, 2166.0669, 2246.1929, 2287.0544, 2565.1943, 3015.4890, 3015.4890, 3031.4861, 3091.4011

4. gi|223544849 **Mass:** 30222 **Score:** 50 **Expect:** 6.5 **Queries matched:** 5

hypothetical protein RCOM_1487630 [Ricinus communis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1291.6696	1290.6623	1290.6237	0.0386	206 -	217	0	24	VSGAEVTENMVR
1291.6696	1290.6623	1290.6237	0.0386	206 -	217	0	---	VSGAEVTENMVR
1571.8734	1570.8661	1570.8063	0.0599	144 -	157	1	---	KADLVDNIVSNNNR
1571.8734	1570.8661	1570.8063	0.0599	145 -	158	1	---	ADLVDNIVSNNNRK
1792.8677	1791.8604	1791.8533	0.0072	201 -	217	1	---	SGNSRVSGAEVTENMVR

No match to: 713.4094, 724.4968, 734.4932, 750.5140, 768.5231, 838.5264, 864.5500, 886.9850, 973.5438, 1004.4966, 1057.4363, 1135.5729, 1135.5729, 1233.6614, 1275.1046, 1279.7638, 1288.7108, 1334.8768, 1345.5873, 1357.5947, 1357.5947, 1363.6908, 1404.7397, 1448.9070, 1518.8370, 1560.8547, 1618.0477, 1661.8700, 1826.9592, 2050.0659, 2166.0669, 2246.1929, 2287.0544, 2565.1943, 3015.4890, 3015.4890, 3031.4861, 3091.4011

5. gi|108705735 **Mass:** 13020 **Score:** 49 **Expect:** 7.8 **Queries matched:** 6

hypothetical protein LOC_Os03g01560 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1135.5729	1134.5656	1134.6032	-0.0376	3 -	15	0	---	TGGGFGGAALSIK
1135.5729	1134.5656	1134.6032	-0.0376	3 -	15	0	5	TGGGFGGAALSIK
1291.6696	1290.6623	1290.7043	-0.0420	2 -	15	1	---	RTGGGFGGAALSIK

1291.6696	1290.6623	1290.7043	-0.0420	2 - 15	1	---	RTGGGFGGAALSIK
1518.8370	1517.8297	1517.7851	0.0446	91 - 103	1	---	TGPYPLPTRHSHR
2166.0669	2165.0596	2165.0952	-0.0356	81 - 99	1	---	QALHGVWGCRTGPYPLPTR

No match to: 713.4094, 724.4968, 734.4932, 750.5140, 768.5231, 838.5264, 864.5500, 886.9850, 973.5438, 1004.4966, 1057.4363, 1233.6614, 1275.1046, 1279.7638, 1288.7108, 1334.8768, 1345.5873, 1357.5947, 1357.5947, 1363.6908, 1404.7397, 1448.9070, 1560.8547, 1571.8734, 1571.8734, 1618.0477, 1661.8700, 1792.8677, 1826.9592, 2050.0659, 2246.1929, 2287.0544, 2565.1943, 3015.4890, 3015.4890, 3031.4861, 3091.4011

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 43

P

rotein View

Match to: **gi|3901094** Score: **300** Expect: **6e-025**
pollen allergen Phl pI [Phleum pratense]

Nominal mass (M_r): **28584**; Calculated pI value: **7.53**
NCBI BLAST search of gi|3901094 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **32%**

Matched peptides shown in **Bold Red**

```
    1 MASSSSVLLV VALFAVFLGS AHGIPKVPPG PNITATYGDK WLDAKSTWYG
   51 KPTAAGPKDN GGACGYKDVD KPPFSGMTGC GNTPIFKSGR GCGSCFEIKC
  101 TKPEACSGEP VVVHITDDNE EPIAAYHFDL SGIAFGSMAK KGDEQKLRSA
  151 GEVEIQFRRV KCKYPEGTKV TFHVEKGSNP NYLALLVKFV AGDGDVVAVD
  201 IKEKGKDKWI ALKESWGAIW RIDTPEVLKG PFTVRYTTEG GTKGEAKDVI
  251 PEGWKADTAY ESK
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
46 - 58	1363.6908	1362.6835	1362.6931	-0.0096	0	STWYGKPTAAGPK	(No match)
88 - 99	1357.5947	1356.5874	1356.5914	-0.0040	1	SGRGCGSCFEIK	(No match)
88 - 99	1357.5947	1356.5874	1356.5914	-0.0040	1	SGRGCGSCFEIK	(No match)
91 - 99	1057.4363	1056.4290	1056.4368	-0.0078	0	GCGSCFEIK	(No match)
149 - 158	1135.5729	1134.5656	1134.5669	-0.0012	0	SAGEVEIQFR	(No match)
149 - 158	1135.5729	1134.5656	1134.5669	-0.0012	0	SAGEVEIQFR	(Ions score 57)
149 - 159	1291.6696	1290.6623	1290.6680	-0.0056	1	SAGEVEIQFRR	(Ions score 51)
149 - 159	1291.6696	1290.6623	1290.6680	-0.0056	1	SAGEVEIQFRR	(No match)
177 - 188	1288.7108	1287.7035	1287.7186	-0.0151	0	GSNPNYLALLVK	(No match)
189 - 202	1404.7397	1403.7324	1403.7296	0.0029	0	FVAGDGDVVAVDIK	(No match)
189 - 204	1661.8700	1660.8627	1660.8671	-0.0044	1	FVAGDGDVVAVDIKEK	(No match)
214 - 221	1004.4966	1003.4893	1003.4875	0.0018	0	ESWGAIWR	(No match)
222 - 235	1571.8734	1570.8661	1570.8718	-0.0057	1	IDTPEVLKGPFTVR	(Ions score 86)
222 - 235	1571.8734	1570.8661	1570.8718	-0.0057	1	IDTPEVLKGPFTVR	(No match)

Spot 80

Index

	Accession	Mass	Score	Description
1.	gi|3901094	28584	385	pollen allergen Phl pI [Phleum pratense]
2.	gi|1582250	28542	370	allergen PhI p I
3.	gi|28373838	26611	58	Chain A, Crystal Structure Of Phl P 1, A Major Timothy Grass Pollen Allergen
4.	gi|1171008	28838	56	RecName: Full=Pollen allergen Phl p 1; AltName: Full=Allergen Phl p I; AltName: Allergen=Phl
5.	gi|125536787	101113	54	hypothetical protein OsI_38484 [Oryza sativa Indica Group]
6.	gi|42601003	11254	54	beta-expansin 1 [Triticum aestivum]
7.	gi|115453645	52978	52	Os03g0430400 [Oryza sativa (japonica cultivar-group)]
8.	gi|147784954	64903	50	hypothetical protein [Vitis vinifera]
9.	gi|222625176	110501	49	hypothetical protein OsJ_11363 [Oryza sativa Japonica Group]
10.	gi|108705735	13020	49	hypothetical protein LOC_Os03g01560 [Oryza sativa (japonica cultivar-group)]

Results List

1. gi|3901094 **Mass:** 28584 **Score:** 385 **Expect:** 1.9e-033 **Queries matched:** 20

pollen allergen Phl pI [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1004.4955	1003.4882	1003.4875	0.0007	214	221	0	---	ESWGAIWR
1057.4424	1056.4351	1056.4368	-0.0017	91	99	0	---	GCGSCFEIK
1135.5764	1134.5691	1134.5669	0.0023	149	158	0	---	SAGEVEIQFR
1135.5764	1134.5691	1134.5669	0.0023	149	158	0	73	SAGEVEIQFR
1288.7236	1287.7163	1287.7186	-0.0023	177	188	0	---	GSNPNYLALLVK
1291.6775	1290.6702	1290.6680	0.0023	149	159	1	---	SAGEVEIQFRR
1291.6775	1290.6702	1290.6680	0.0023	149	159	1	67	SAGEVEIQFRR
1357.6047	1356.5974	1356.5914	0.0060	88	99	1	---	SGRGCGSCFEIK
1363.7029	1362.6956	1362.6931	0.0025	46	58	0	---	STWYGKPTAAGPK
1404.7593	1403.7520	1403.7520	-0.0000	147	158	1	---	LRSAGEVEIQFR
1571.8845	1570.8772	1570.8718	0.0054	222	235	1	84	IDTPEVLKGPFTVR
1571.8845	1570.8772	1570.8718	0.0054	222	235	1	---	IDTPEVLKGPFTVR
1615.8837	1614.8764	1614.8670	0.0094	209	221	1	---	WIALKESWGAIWR
1661.8792	1660.8719	1660.8671	0.0048	189	204	1	---	FVAGDGDVVAVDIKEK
1808.8849	1807.8776	1807.8628	0.0148	248	263	1	---	DVIPEGWKADTAYESK
2129.1853	2128.1780	2128.1680	0.0101	170	188	1	---	VTFHVEKGSNPNYLALLVK
2168.0444	2167.0371	2167.0078	0.0294	68	87	0	---	DVDKPPFSGMTGCGNTPIFK
2184.0315	2183.0242	2183.0027	0.0216	68	87	0	---	DVDKPPFSGMTGCGNTPIFK + Oxidation (M)
3090.4109	3089.4036	3089.3680	0.0356	59	87	1	---	DNGGACGYKDVDKPPFSGMTGCGNTPIFK
3106.4290	3105.4217	3105.3629	0.0588	59	87	1	---	DNGGACGYKDVDKPPFSGMTGCGNTPIFK + Oxidation (M)

No match to: 713.4070, 734.4840, 736.4979, 750.5205, 768.5208, 782.4771, 973.5434, 973.5434, 1016.4991,

1032.4938, 1233.6632, 1250.7023, 1273.6692, 1275.1025, 1334.8889, 1375.6990, 1379.7025, 1395.7023, 1434.7445, 1448.9146, 1471.7473, 1518.8418, 1528.9095, 1541.8488, 1560.8643, 1618.0677, 1732.1136, 1792.8837, 1805.8929, 1822.9192, 1859.0009, 1920.0510, 1975.1290, 2044.1151, 2050.0935, 2166.0881, 2172.1736, 2246.2246, 2287.0603, 2300.1536, 2427.2058, 2888.3799, 3015.4905, 3015.4905, 3031.4749

2. gi|1582250 **Mass:** 28542 **Score:** 370 **Expect:** 6e-032 **Queries matched:** 19

allergen PhI p I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1004.4955	1003.4882	1003.4875	0.0007	213	220	0	---	ESWGAIWR
1057.4424	1056.4351	1056.4368	-0.0017	91	99	0	---	GCGSCFEIK
1135.5764	1134.5691	1134.5669	0.0023	149	158	0	---	SAGEVEIQFR
1135.5764	1134.5691	1134.5669	0.0023	149	158	0	73	SAGEVEIQFR
1288.7236	1287.7163	1287.7186	-0.0023	177	188	0	---	GSNPNYLALLVK
1291.6775	1290.6702	1290.6680	0.0023	149	159	1	---	SAGEVEIQFRR
1291.6775	1290.6702	1290.6680	0.0023	149	159	1	67	SAGEVEIQFRR
1357.6047	1356.5974	1356.5914	0.0060	88	99	1	---	SGRGCGSCFEIK
1363.7029	1362.6956	1362.6931	0.0025	46	58	0	---	STWYGKPTAAGPK
1404.7593	1403.7520	1403.7520	-0.0000	147	158	1	---	LRSAGEVEIQFR
1571.8845	1570.8772	1570.8718	0.0054	221	234	1	84	IDTPEVLKGPFTVR
1571.8845	1570.8772	1570.8718	0.0054	221	234	1	---	IDTPEVLKGPFTVR
1615.8837	1614.8764	1614.8670	0.0094	208	220	1	---	WIALKESWGAIWR
1808.8849	1807.8776	1807.8628	0.0148	247	262	1	---	DVIPEGWKADTAYESK
2129.1853	2128.1780	2128.1680	0.0101	170	188	1	---	VTFHVEKGSNPNYLALLVK
2168.0444	2167.0371	2167.0078	0.0294	68	87	0	---	DVDKPPFSGMTGCGNTPIFK
2184.0315	2183.0242	2183.0027	0.0216	68	87	0	---	DVDKPPFSGMTGCGNTPIFK + Oxidation (M)
3090.4109	3089.4036	3089.3680	0.0356	59	87	1	---	DNGGACGYKDVDKPPFSGMTGCGNTPIFK
3106.4290	3105.4217	3105.3629	0.0588	59	87	1	---	DNGGACGYKDVDKPPFSGMTGCGNTPIFK + Oxidation (M)

No match to: 713.4070, 734.4840, 736.4979, 750.5205, 768.5208, 782.4771, 973.5434, 973.5434, 1016.4991, 1032.4938, 1233.6632, 1250.7023, 1273.6692, 1275.1025, 1334.8889, 1375.6990, 1379.7025, 1395.7023, 1434.7445, 1448.9146, 1471.7473, 1518.8418, 1528.9095, 1541.8488, 1560.8643, 1618.0677, 1661.8792, 1732.1136, 1792.8837, 1805.8929, 1822.9192, 1859.0009, 1920.0510, 1975.1290, 2044.1151, 2050.0935, 2166.0881, 2172.1736, 2246.2246, 2287.0603, 2300.1536, 2427.2058, 2888.3799, 3015.4905, 3015.4905, 3031.4749

3. gi|28373838 **Mass:** 26611 **Score:** 58 **Expect:** 0.94 **Queries matched:** 9

Chain A, Crystal Structure Of Phl P 1, A Major Timothy Grass Pollen Allergen

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1004.4955	1003.4882	1003.4875	0.0007	192	199	0	---	ESWGAIWR
1057.4424	1056.4351	1056.4368	-0.0017	69	77	0	---	GCGSCFEIK
1288.7236	1287.7163	1287.7186	-0.0023	155	166	0	---	GSNPNYLALLVK
1357.6047	1356.5974	1356.5914	0.0060	66	77	1	---	SGRGCGSCFEIK
2129.1853	2128.1780	2128.1680	0.0101	148	166	1	---	VTFHVEKGSNPNYLALLVK
2168.0444	2167.0371	2167.0078	0.0294	46	65	0	---	DVDKPPFSGMTGCGNTPIFK

2184.0315	2183.0242	2183.0027	0.0216	46 - 65	0	---	DVDKPPFSGMTGCGNTPIFK + Oxidation (M)
3090.4109	3089.4036	3089.3680	0.0356	37 - 65	1	---	DNGGACGYKDVDKPPFSGMTGCGNTPIFK
3106.4290	3105.4217	3105.3629	0.0588	37 - 65	1	---	DNGGACGYKDVDKPPFSGMTGCGNTPIFK + Oxidation (M)

No match to: 713.4070, 734.4840, 736.4979, 750.5205, 768.5208, 782.4771, 973.5434, 973.5434, 1016.4991, 1032.4938, 1135.5764, 1135.5764, 1233.6632, 1250.7023, 1273.6692, 1275.1025, 1291.6775, 1291.6775, 1334.8889, 1363.7029, 1375.6990, 1379.7025, 1395.7023, 1404.7593, 1434.7445, 1448.9146, 1471.7473, 1518.8418, 1528.9095, 1541.8488, 1560.8643, 1571.8845, 1571.8845, 1615.8837, 1618.0677, 1661.8792, 1732.1136, 1792.8837, 1805.8929, 1808.8849, 1822.9192, 1859.0009, 1920.0510, 1975.1290, 2044.1151, 2050.0935, 2166.0881, 2172.1736, 2246.2246, 2287.0603, 2300.1536, 2427.2058, 2888.3799, 3015.4905, 3015.4905, 3031.4749

4. gi|1171008 **Mass:** 28838 **Score:** 56 **Expect:** 1.7 **Queries matched:** 9

RecName: Full=Pollen allergen Phl p 1; AltName: Full=Allergen Phl p I; AltName: Allergen=Phl p 1; F

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1004.4955	1003.4882	1003.4875	0.0007	214 - 221		0	---	ESWGAIWR
1057.4424	1056.4351	1056.4368	-0.0017	91 - 99		0	---	GCGSCFEIK
1288.7236	1287.7163	1287.7186	-0.0023	177 - 188		0	---	GSNPNYLALLVK
1357.6047	1356.5974	1356.5914	0.0060	88 - 99		1	---	SGRGCGSCFEIK
2129.1853	2128.1780	2128.1680	0.0101	170 - 188		1	---	VTFHVEKGSNPNYLALLVK
2168.0444	2167.0371	2167.0078	0.0294	68 - 87		0	---	DVDKPPFSGMTGCGNTPIFK
2184.0315	2183.0242	2183.0027	0.0216	68 - 87		0	---	DVDKPPFSGMTGCGNTPIFK + Oxidation (M)
3090.4109	3089.4036	3089.3680	0.0356	59 - 87		1	---	DNGGACGYKDVDKPPFSGMTGCGNTPIFK
3106.4290	3105.4217	3105.3629	0.0588	59 - 87		1	---	DNGGACGYKDVDKPPFSGMTGCGNTPIFK + Oxidation (M)

No match to: 713.4070, 734.4840, 736.4979, 750.5205, 768.5208, 782.4771, 973.5434, 973.5434, 1016.4991, 1032.4938, 1135.5764, 1135.5764, 1233.6632, 1250.7023, 1273.6692, 1275.1025, 1291.6775, 1291.6775, 1334.8889, 1363.7029, 1375.6990, 1379.7025, 1395.7023, 1404.7593, 1434.7445, 1448.9146, 1471.7473, 1518.8418, 1528.9095, 1541.8488, 1560.8643, 1571.8845, 1571.8845, 1615.8837, 1618.0677, 1661.8792, 1732.1136, 1792.8837, 1805.8929, 1808.8849, 1822.9192, 1859.0009, 1920.0510, 1975.1290, 2044.1151, 2050.0935, 2166.0881, 2172.1736, 2246.2246, 2287.0603, 2300.1536, 2427.2058, 2888.3799, 3015.4905, 3015.4905, 3031.4749

5. gi|125536787 **Mass:** 101113 **Score:** 54 **Expect:** 2.3 **Queries matched:** 16

hypothetical protein OsI_38484 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1135.5764	1134.5691	1134.5855	-0.0164	502 - 511		0	---	CLVLHPGPDK
1135.5764	1134.5691	1134.5855	-0.0164	502 - 511		0	---	CLVLHPGPDK
1250.7023	1249.6950	1249.6666	0.0284	804 - 814		0	---	ISSLTNLEAFR
1273.6692	1272.6619	1272.6422	0.0198	471 - 481		1	---	ELAISEGRENR
1291.6775	1290.6702	1290.6866	-0.0164	502 - 512		1	---	CLVLHPGPDKR
1291.6775	1290.6702	1290.6972	-0.0270	241 - 250		0	---	YLIVLDDVWR
1363.7029	1362.6956	1362.7242	-0.0285	404 - 415		1	---	EESEISISKLTK
1518.8418	1517.8345	1517.7886	0.0459	392 - 403		1	---	MKLCFLYLGAFR
1661.8792	1660.8719	1660.9222	-0.0502	771 - 784		1	---	TLGSLTCLWELKLK
1808.8849	1807.8776	1807.8952	-0.0175	432 - 446		1	---	KEDTATDYLNELIQR
1859.0009	1857.9936	1858.0247	-0.0310	584 - 598		1	---	SIQSSLIHLRYLCLR

2166.0881	2165.0808	2165.1302	-0.0494	594 - 611	1	---	YLCLRNTQLVAFPLNESK
2246.2246	2245.2173	2245.2616	-0.0442	130 - 150	1	---	LLQPTEHREVIVIVGMGGIGK
3015.4905	3014.4832	3014.4915	-0.0082	653 - 678	0	---	CLTNLQTFCGVLVSNDQIAMEFLTLK
3015.4905	3014.4832	3014.4915	-0.0082	653 - 678	0	---	CLTNLQTFCGVLVSNDQIAMEFLTLK
3031.4749	3030.4676	3030.4864	-0.0187	653 - 678	0	---	CLTNLQTFCGVLVSNDQIAMEFLTLK + Oxidation (M)

No match to: 713.4070, 734.4840, 736.4979, 750.5205, 768.5208, 782.4771, 973.5434, 973.5434, 1004.4955, 1016.4991, 1032.4938, 1057.4424, 1233.6632, 1275.1025, 1288.7236, 1334.8889, 1357.6047, 1375.6990, 1379.7025, 1395.7023, 1404.7593, 1434.7445, 1448.9146, 1471.7473, 1528.9095, 1541.8488, 1560.8643, 1571.8845, 1571.8845, 1615.8837, 1618.0677, 1732.1136, 1792.8837, 1805.8929, 1822.9192, 1920.0510, 1975.1290, 2044.1151, 2050.0935, 2129.1853, 2168.0444, 2172.1736, 2184.0315, 2287.0603, 2300.1536, 2427.2058, 2888.3799, 3090.4109, 3106.4290

6. gi|42601003 **Mass:** 11254 **Score:** 54 **Expect:** 2.5 **Queries matched:** 4

beta-expansin 1 [Triticum aestivum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1571.8845	1570.8772	1570.8619	0.0153	58 -	71	1	26	WDGAKPLKGPFSIR
1571.8845	1570.8772	1570.8619	0.0153	58 -	71	1	---	WDGAKPLKGPFSIR
2129.1853	2128.1780	2128.1680	0.0101	6 -	24	1	---	ITFHVEKGSNPNYLAVLVK
2168.0444	2167.0371	2167.0585	-0.0214	84 -	102	1	---	DVIPANWKADTVYTSNVQF

No match to: 713.4070, 734.4840, 736.4979, 750.5205, 768.5208, 782.4771, 973.5434, 973.5434, 1004.4955, 1016.4991, 1032.4938, 1057.4424, 1135.5764, 1135.5764, 1233.6632, 1250.7023, 1273.6692, 1275.1025, 1288.7236, 1291.6775, 1291.6775, 1334.8889, 1357.6047, 1363.7029, 1375.6990, 1379.7025, 1395.7023, 1404.7593, 1434.7445, 1448.9146, 1471.7473, 1518.8418, 1528.9095, 1541.8488, 1560.8643, 1615.8837, 1618.0677, 1661.8792, 1732.1136, 1792.8837, 1805.8929, 1808.8849, 1822.9192, 1859.0009, 1920.0510, 1975.1290, 2044.1151, 2050.0935, 2166.0881, 2172.1736, 2184.0315, 2246.2246, 2287.0603, 2300.1536, 2427.2058, 2888.3799, 3015.4905, 3015.4905, 3031.4749, 3090.4109, 3106.4290

7. gi|115453645 **Mass:** 52978 **Score:** 52 **Expect:** 3.7 **Queries matched:** 7

Os03g0430400 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1004.4955	1003.4882	1003.5021	-0.0139	288 -	295	0	---	HIHCNPVK
1135.5764	1134.5691	1134.5821	-0.0130	259 -	268	0	---	TGGALWDIFR
1135.5764	1134.5691	1134.5821	-0.0130	259 -	268	0	17	TGGALWDIFR
1291.6775	1290.6702	1290.6832	-0.0130	259 -	269	1	---	TGGALWDIFRR
1291.6775	1290.6702	1290.6832	-0.0130	259 -	269	1	22	TGGALWDIFRR
1395.7023	1394.6950	1394.6677	0.0273	270 -	280	1	---	EDSEKLQDYLR
2427.2058	2426.1985	2426.2382	-0.0397	42 -	62	1	---	LPRHGAEFITALPFPEYTDPR

No match to: 713.4070, 734.4840, 736.4979, 750.5205, 768.5208, 782.4771, 973.5434, 973.5434, 1016.4991, 1032.4938, 1057.4424, 1233.6632, 1250.7023, 1273.6692, 1275.1025, 1288.7236, 1334.8889, 1357.6047, 1363.7029, 1375.6990, 1379.7025, 1404.7593, 1434.7445, 1448.9146, 1471.7473, 1518.8418, 1528.9095, 1541.8488, 1560.8643, 1571.8845, 1571.8845, 1615.8837, 1618.0677, 1661.8792, 1732.1136, 1792.8837, 1805.8929, 1808.8849, 1822.9192, 1859.0009, 1920.0510, 1975.1290, 2044.1151, 2050.0935, 2129.1853, 2166.0881, 2168.0444, 2172.1736, 2184.0315, 2246.2246, 2287.0603, 2300.1536, 2888.3799, 3015.4905, 3015.4905, 3031.4749, 3090.4109, 3106.4290

8. gi|147784954 **Mass:** 64903 **Score:** 50 **Expect:** 6.8 **Queries matched:** 3

hypothetical protein [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1233.6632	1232.6559	1232.6183	0.0376	301 -	311	1	---	MTKSDGKPVDR
1291.6775	1290.6702	1290.6680	0.0022	80 -	90	1	---	ADGTVERYKPR
1291.6775	1290.6702	1290.6680	0.0022	80 -	90	1	45	ADGTVERYKPR

No match to: 713.4070, 734.4840, 736.4979, 750.5205, 768.5208, 782.4771, 973.5434, 973.5434, 1004.4955, 1016.4991, 1032.4938, 1057.4424, 1135.5764, 1135.5764, 1250.7023, 1273.6692, 1275.1025, 1288.7236, 1334.8889, 1357.6047, 1363.7029, 1375.6990, 1379.7025, 1395.7023, 1404.7593, 1434.7445, 1448.9146, 1471.7473, 1518.8418, 1528.9095, 1541.8488, 1560.8643, 1571.8845, 1571.8845, 1615.8837, 1618.0677, 1661.8792, 1732.1136, 1792.8837, 1805.8929, 1808.8849, 1822.9192, 1859.0009, 1920.0510, 1975.1290, 2044.1151, 2050.0935, 2129.1853, 2166.0881, 2168.0444, 2172.1736, 2184.0315, 2246.2246, 2287.0603, 2300.1536, 2427.2058, 2888.3799, 3015.4905, 3015.4905, 3031.4749, 3090.4109, 3106.4290

9. gi|222625176 **Mass:** 110501 **Score:** 49 **Expect:** 8 **Queries matched:** 7

hypothetical protein OsJ_11363 [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1004.4955	1003.4882	1003.5021	-0.0139	783 -	790	0	---	HIHCNPVK
1135.5764	1134.5691	1134.5821	-0.0130	754 -	763	0	---	TGGALWDIFR
1135.5764	1134.5691	1134.5821	-0.0130	754 -	763	0	17	TGGALWDIFR
1291.6775	1290.6702	1290.6832	-0.0130	754 -	764	1	---	TGGALWDIFRR
1291.6775	1290.6702	1290.6832	-0.0130	754 -	764	1	22	TGGALWDIFRR
1395.7023	1394.6950	1394.6677	0.0273	765 -	775	1	---	EDSEKLQDYLR
2427.2058	2426.1985	2426.2382	-0.0397	537 -	557	1	---	LPRHGAEFITALPFPEYTDPR

No match to: 713.4070, 734.4840, 736.4979, 750.5205, 768.5208, 782.4771, 973.5434, 973.5434, 1016.4991, 1032.4938, 1057.4424, 1233.6632, 1250.7023, 1273.6692, 1275.1025, 1288.7236, 1334.8889, 1357.6047, 1363.7029, 1375.6990, 1379.7025, 1404.7593, 1434.7445, 1448.9146, 1471.7473, 1518.8418, 1528.9095, 1541.8488, 1560.8643, 1571.8845, 1571.8845, 1615.8837, 1618.0677, 1661.8792, 1732.1136, 1792.8837, 1805.8929, 1808.8849, 1822.9192, 1859.0009, 1920.0510, 1975.1290, 2044.1151, 2050.0935, 2129.1853, 2166.0881, 2168.0444, 2172.1736, 2184.0315, 2246.2246, 2287.0603, 2300.1536, 2888.3799, 3015.4905, 3015.4905, 3031.4749, 3090.4109, 3106.4290

10. gi|108705735 **Mass:** 13020 **Score:** 49 **Expect:** 8.2 **Queries matched:** 6

hypothetical protein LOC_Os03g01560 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1135.5764	1134.5691	1134.6032	-0.0341	3 -	15	0	---	TGGGFGGAALSIK
1135.5764	1134.5691	1134.6032	-0.0341	3 -	15	0	6	TGGGFGGAALSIK
1291.6775	1290.6702	1290.7043	-0.0341	2 -	15	1	---	RTGGGFGGAALSIK
1291.6775	1290.6702	1290.7043	-0.0341	2 -	15	1	6	RTGGGFGGAALSIK
1518.8418	1517.8345	1517.7851	0.0494	91 -	103	1	---	TGPYPLPTRHSHR
2166.0881	2165.0808	2165.0952	-0.0144	81 -	99	1	---	QALHGVWGCRTGPYPLPTR

No match to: 713.4070, 734.4840, 736.4979, 750.5205, 768.5208, 782.4771, 973.5434, 973.5434, 1004.4955, 1016.4991, 1032.4938, 1057.4424, 1233.6632, 1250.7023, 1273.6692, 1275.1025, 1288.7236, 1334.8889, 1357.6047, 1363.7029, 1375.6990, 1379.7025, 1395.7023, 1404.7593, 1434.7445, 1448.9146, 1471.7473, 1528.9095, 1541.8488, 1560.8643, 1571.8845, 1571.8845, 1615.8837, 1618.0677, 1661.8792, 1732.1136, 1792.8837, 1805.8929, 1808.8849, 1822.9192, 1859.0009, 1920.0510, 1975.1290, 2044.1151, 2050.0935, 2129.1853, 2168.0444, 2172.1736, 2184.0315,

2246.2246, 2287.0603, 2300.1536, 2427.2058, 2888.3799, 3015.4905, 3015.4905, 3031.4749, 3090.4109, 3106.4290

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 65

Protein View

Match to: **gi|3901094** Score: **385** Expect: **1.9e-033**
pollen allergen Phl pI [Phleum pratense]

Nominal mass (M_r): **28584**; Calculated pI value: **7.53**
NCBI BLAST search of gi|3901094 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **55%**

Matched peptides shown in **Bold Red**

```
     1 MASSSSVLLV VALFAVFLGS AHGIPKVPPG PNITATYGDK WLDAKSTWYG
    51 KPTAAGPKDN GGACGYKDVD KPPFSGMTGC GNTPIFKSGR GCGSCFEIKC
   101 TKPEACSGEP VVVHITDDNE EPIAAYHFDL SGIAFGSMAK KGDEQKLRSA
   151 GEVEIQFRRV KCKYPEGTKV TFHVEKGSNP NYLALLVKFV AGDGDVVAVD
   201 IKEKGKDKWI ALKESWGAIW RIDTPEVLKG PFTVRYTTEG GTKGEAKDVI
   251 PEGWKADTAY ESK
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
46 - 58	1363.7029	1362.6956	1362.6931	0.0025	0	**STWYGKPTAAGPK** (No match)
59 - 87	3090.4109	3089.4036	3089.3680	0.0356	1	**DNGGACGYKDVDKPPFSGMTGCGNTPIFK** (No match)
59 - 87	3106.4290	3105.4217	3105.3629	0.0588	1	**DNGGACGYKDVDKPPFSGMTGCGNTPIFK** Oxidation (M) (No match)
68 - 87	2168.0444	2167.0371	2167.0078	0.0294	0	**DVDKPPFSGMTGCGNTPIFK** (No match)
68 - 87	2184.0315	2183.0242	2183.0027	0.0216	0	**DVDKPPFSGMTGCGNTPIFK** Oxidation (M) (No match)
88 - 99	1357.6047	1356.5974	1356.5914	0.0060	1	**SGRGCGSCFEIK** (No match)
91 - 99	1057.4424	1056.4351	1056.4368	-0.0017	0	**GCGSCFEIK** (No match)
147 - 158	1404.7593	1403.7520	1403.7520	-0.0000	1	**LRSAGEVEIQFR** (No match)
149 - 158	1135.5764	1134.5691	1134.5669	0.0023	0	**SAGEVEIQFR** (No match)
149 - 158	1135.5764	1134.5691	1134.5669	0.0023	0	**SAGEVEIQFR** (Ions score 73)
149 - 159	1291.6775	1290.6702	1290.6680	0.0023	1	**SAGEVEIQFRR** (No match)
149 - 159	1291.6775	1290.6702	1290.6680	0.0023	1	**SAGEVEIQFRR** (Ions score 67)
170 - 188	2129.1853	2128.1780	2128.1680	0.0101	1	**VTFHVEKGSNPNYLALLVK** (No match)
177 - 188	1288.7236	1287.7163	1287.7186	-0.0023	0	**GSNPNYLALLVK** (No match)
189 - 204	1661.8792	1660.8719	1660.8671	0.0048	1	**FVAGDGDVVAVDIKEK** (No match)
209 - 221	1615.8837	1614.8764	1614.8670	0.0094	1	**WIALKESWGAIWR** (No match)
214 - 221	1004.4955	1003.4882	1003.4875	0.0007	0	**ESWGAIWR** (No match)
222 - 235	1571.8845	1570.8772	1570.8718	0.0054	1	**IDTPEVLKGPFTVR** (Ions score 84)
222 - 235	1571.8845	1570.8772	1570.8718	0.0054	1	**IDTPEVLKGPFTVR** (No match)
248 - 263	1808.8849	1807.8776	1807.8628	0.0148	1	**DVIPEGWKADTAYESK** (No match)

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	Accession	Mass	Score	Description
1.	gi|1582250	28542	340	allergen PhI p I
2.	gi|3901094	28584	340	pollen allergen Phl pI [Phleum pratense]
3.	gi|57899087	14450	61	hypothetical protein [Oryza sativa Japonica Group]
4.	gi|56788719	14999	60	serine:glyoxylate aminotransferase [Chlamydomonas reinhardtii]
5.	gi|6002081	22787	60	ribosomal protein S4 [Setcreasea purpurea]
6.	gi|6002087	22821	60	ribosomal protein S4 [Tradescantia virginiana]
7.	gi|24430042	166224	57	Hypothetical protein [Arabidopsis thaliana]
8.	gi|157359972	25751	55	unnamed protein product [Vitis vinifera]
9.	gi|157345966	69857	55	unnamed protein product [Vitis vinifera]
10.	gi|50252996	28947	54	UDP-glycosyltransferase-like [Oryza sativa Japonica Group]

Results List

1. gi|1582250 **Mass:** 28542 **Score:** 340 **Expect:** 6e-029 **Queries matched:** 12

allergen PhI p I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1004.4983	1003.4910	1003.4875	0.0035	213	220	0	---	ESWGAIWR
1057.4427	1056.4354	1056.4368	-0.0014	91	99	0	---	GCGSCFEIK
1135.5817	1134.5744	1134.5669	0.0076	149	158	0	72	SAGEVEIQFR
1135.5817	1134.5744	1134.5669	0.0076	149	158	0	---	SAGEVEIQFR
1291.6809	1290.6736	1290.6680	0.0057	149	159	1	---	SAGEVEIQFRR
1291.6809	1290.6736	1290.6680	0.0057	149	159	1	66	SAGEVEIQFRR
1357.6116	1356.6043	1356.5914	0.0129	88	99	1	19	SGRGCGSCFEIK
1357.6116	1356.6043	1356.5914	0.0129	88	99	1	---	SGRGCGSCFEIK
1363.7034	1362.6961	1362.6931	0.0030	46	58	0	---	STWYGKPTAAGPK
1404.7681	1403.7608	1403.7520	0.0088	147	158	1	---	LRSAGEVEIQFR
1571.8876	1570.8803	1570.8718	0.0085	221	234	1	---	IDTPEVLKGPFTVR
1571.8876	1570.8803	1570.8718	0.0085	221	234	1	86	IDTPEVLKGPFTVR

No match to: 713.4088, 768.5215, 973.5449, 973.5449, 1233.6727, 1250.6991, 1266.6095, 1275.1119, 1560.8618, 1792.8712, 2044.1055, 2246.2288, 3015.4739, 3031.4729

2. gi|3901094 **Mass:** 28584 **Score:** 340 **Expect:** 6e-029 **Queries matched:** 12

pollen allergen Phl pI [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1004.4983	1003.4910	1003.4875	0.0035	214	221	0	---	ESWGAIWR
1057.4427	1056.4354	1056.4368	-0.0014	91	99	0	---	GCGSCFEIK
1135.5817	1134.5744	1134.5669	0.0076	149	158	0	72	SAGEVEIQFR
1135.5817	1134.5744	1134.5669	0.0076	149	158	0	---	SAGEVEIQFR

1291.6809	1290.6736	1290.6680	0.0057	149 - 159	1	---	SAGEVEIQFRR
1291.6809	1290.6736	1290.6680	0.0057	149 - 159	1	66	SAGEVEIQFRR
1357.6116	1356.6043	1356.5914	0.0129	88 - 99	1	19	SGRGCGSCFEIK
1357.6116	1356.6043	1356.5914	0.0129	88 - 99	1	---	SGRGCGSCFEIK
1363.7034	1362.6961	1362.6931	0.0030	46 - 58	0	---	STWYGKPTAAGPK
1404.7681	1403.7608	1403.7520	0.0088	147 - 158	1	---	LRSAGEVEIQFR
1571.8876	1570.8803	1570.8718	0.0085	222 - 235	1	---	IDTPEVLKGPFTVR
1571.8876	1570.8803	1570.8718	0.0085	222 - 235	1	86	IDTPEVLKGPFTVR

No match to: 713.4088, 768.5215, 973.5449, 973.5449, 1233.6727, 1250.6991, 1266.6095, 1275.1119, 1560.8618, 1792.8712, 2044.1055, 2246.2288, 3015.4739, 3031.4729

3. gi|57899087 **Mass:** 14450 **Score:** 61 **Expect:** 0.46 **Queries matched:** 4

hypothetical protein [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1135.5817	1134.5744	1134.5273	0.0471	38 -	49	0	9	GGGATAMAALCR
1135.5817	1134.5744	1134.5273	0.0471	66 -	77	0	---	GGGATAMAALCR
1291.6809	1290.6736	1290.6284	0.0452	66 -	78	1	---	GGGATAMAALCRR
1291.6809	1290.6736	1290.6284	0.0452	37 -	49	1	11	RGGGATAMAALCR

No match to: 713.4088, 768.5215, 973.5449, 973.5449, 1004.4983, 1057.4427, 1233.6727, 1250.6991, 1266.6095, 1275.1119, 1357.6116, 1357.6116, 1363.7034, 1404.7681, 1560.8618, 1571.8876, 1571.8876, 1792.8712, 2044.1055, 2246.2288, 3015.4739, 3031.4729

4. gi|56788719 **Mass:** 14999 **Score:** 60 **Expect:** 0.65 **Queries matched:** 6

serine:glyoxylate aminotransferase [Chlamydomonas reinhardtii]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
973.5449	972.5376	972.5028	0.0348	61 -	69	0	14	QAVDGWGLK
973.5449	972.5376	972.5028	0.0348	61 -	69	0	---	QAVDGWGLK
1135.5817	1134.5744	1134.4975	0.0770	41 -	51	0	18	EEGGMEAVAAR + Oxidation (M)
1135.5817	1134.5744	1134.4975	0.0770	41 -	51	0	---	EEGGMEAVAAR + Oxidation (M)
1357.6116	1356.6043	1356.6529	-0.0486	122 -	133	0	---	IGHLGNMNELML + Oxidation (M)
1357.6116	1356.6043	1356.6529	-0.0486	122 -	133	0	---	IGHLGNMNELML + Oxidation (M)

No match to: 713.4088, 768.5215, 1004.4983, 1057.4427, 1233.6727, 1250.6991, 1266.6095, 1275.1119, 1291.6809, 1291.6809, 1363.7034, 1404.7681, 1560.8618, 1571.8876, 1571.8876, 1792.8712, 2044.1055, 2246.2288, 3015.4739, 3031.4729

5. gi|6002081 **Mass:** 22787 **Score:** 60 **Expect:** 0.66 **Queries matched:** 6

ribosomal protein S4 [Setcreasea purpurea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
973.5449	972.5376	972.5352	0.0024	30 -	37	1	23	SDLKNQLR
973.5449	972.5376	972.5352	0.0024	30 -	37	1	---	SDLKNQLR
1291.6809	1290.6736	1290.6832	-0.0096	54 -	63	1	---	LRFHYGLTER
1291.6809	1290.6736	1290.6832	-0.0096	54 -	63	1	---	LRFHYGLTER

1560.8618	1559.8545	1559.8341	0.0205	77 - 90	0	---	GSTGQVLLQLLEMR + Oxidation (M)
1792.8712	1791.8639	1791.9777	-0.1138	98 - 114	1	---	LGMASTIPGARQLVNHK

No match to: 713.4088, 768.5215, 1004.4983, 1057.4427, 1135.5817, 1135.5817, 1233.6727, 1250.6991, 1266.6095, 1275.1119, 1357.6116, 1357.6116, 1363.7034, 1404.7681, 1571.8876, 1571.8876, 2044.1055, 2246.2288, 3015.4739, 3031.4729

6. gi|6002087 **Mass:** 22821 **Score:** 60 **Expect:** 0.66 **Queries matched:** 6

ribosomal protein S4 [Tradescantia virginiana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
973.5449	972.5376	972.5352	0.0024	30 -	37	1	23	SDLKNQLR
973.5449	972.5376	972.5352	0.0024	30 -	37	1	---	SDLKNQLR
1291.6809	1290.6736	1290.6832	-0.0096	54 -	63	1	---	LRFHYGLTER
1291.6809	1290.6736	1290.6832	-0.0096	54 -	63	1	---	LRFHYGLTER
1560.8618	1559.8545	1559.8341	0.0205	77 -	90	0	---	GSTGQVLLQLLEMR + Oxidation (M)
1792.8712	1791.8639	1791.9777	-0.1138	98 -	114	1	---	LGMASTIPGARQLVNHK

No match to: 713.4088, 768.5215, 1004.4983, 1057.4427, 1135.5817, 1135.5817, 1233.6727, 1250.6991, 1266.6095, 1275.1119, 1357.6116, 1357.6116, 1363.7034, 1404.7681, 1571.8876, 1571.8876, 2044.1055, 2246.2288, 3015.4739, 3031.4729

7. gi|24430042 **Mass:** 166224 **Score:** 57 **Expect:** 1.2 **Queries matched:** 9

Hypothetical protein [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
973.5449	972.5376	972.5101	0.0276	845 -	852	1	12	TQNRDALR
973.5449	972.5376	972.5101	0.0276	845 -	852	1	---	TQNRDALR
1135.5817	1134.5744	1134.5153	0.0592	902 -	912	0	12	SAASVDDIDSR
1135.5817	1134.5744	1134.5451	0.0293	871 -	880	1	---	AVMAEERSAR + Oxidation (M)
1266.6095	1265.6022	1265.6139	-0.0117	316 -	327	0	---	SSDVPFTSVAEK
1291.6809	1290.6736	1290.6350	0.0386	1466 -	1475	1	---	DQILEQSMRR + Oxidation (M)
1291.6809	1290.6736	1290.6350	0.0386	1466 -	1475	1	6	DQILEQSMRR + Oxidation (M)
1404.7681	1403.7608	1403.7078	0.0530	888 -	899	0	---	QEIEALQSMISR
1560.8618	1559.8545	1559.8089	0.0456	887 -	899	1	---	RQEIEALQSMISR

No match to: 713.4088, 768.5215, 1004.4983, 1057.4427, 1233.6727, 1250.6991, 1275.1119, 1357.6116, 1357.6116, 1363.7034, 1571.8876, 1571.8876, 1792.8712, 2044.1055, 2246.2288, 3015.4739, 3031.4729

8. gi|157359972 **Mass:** 25751 **Score:** 55 **Expect:** 1.8 **Queries matched:** 6

unnamed protein product [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
973.5449	972.5376	972.4875	0.0501	78 -	86	0	14	EALEEAGVR
973.5449	972.5376	972.5464	-0.0088	2 -	10	1	---	SSVQARIGR
1004.4983	1003.4910	1003.5410	-0.0500	192 -	200	1	---	ERSILSSGR
1291.6809	1290.6736	1290.6819	-0.0083	161 -	171	1	---	NFLTSLPEDKK
1291.6809	1290.6736	1290.6819	-0.0083	161 -	171	1	---	NFLTSLPEDKK

1792.8712	1791.8639	1791.8423	0.0217	176 - 191	0	---	EELVEFSMMPVPDAAK

No match to: 713.4088, 768.5215, 1057.4427, 1135.5817, 1135.5817, 1233.6727, 1250.6991, 1266.6095, 1275.1119, 1357.6116, 1357.6116, 1363.7034, 1404.7681, 1560.8618, 1571.8876, 1571.8876, 2044.1055, 2246.2288, 3015.4739, 3031.4729

9. gi|157345966 **Mass:** 69857 **Score:** 55 **Expect:** 1.9 **Queries matched:** 8

unnamed protein product [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
973.5449	972.5376	972.5967	-0.0591	267 - 276	1	12		TLLAKATAGK
973.5449	972.5376	972.5967	-0.0591	267 - 276	1	---		TLLAKATAGK
1004.4983	1003.4910	1003.5120	-0.0210	378 - 386	0	---		VECSLVAAR
1057.4427	1056.4354	1056.5022	-0.0668	401 - 409	0	---		LSNMHNTPK + Oxidation (M)
1357.6116	1356.6043	1356.6310	-0.0266	572 - 582	1	---		TSEPTNYDRFK
1357.6116	1356.6043	1356.6310	-0.0266	572 - 582	1	---		TSEPTNYDRFK
1404.7681	1403.7608	1403.8499	-0.0891	252 - 266	1	---		IPKGALLVGPPGTGK
1792.8712	1791.8639	1791.9202	-0.0563	419 - 432	1	---		RNSCFSLLNYHLLR

No match to: 713.4088, 768.5215, 1135.5817, 1135.5817, 1233.6727, 1250.6991, 1266.6095, 1275.1119, 1291.6809, 1291.6809, 1363.7034, 1560.8618, 1571.8876, 1571.8876, 2044.1055, 2246.2288, 3015.4739, 3031.4729

10. gi|50252996 **Mass:** 28947 **Score:** 54 **Expect:** 2.6 **Queries matched:** 5

UDP-glycosyltransferase-like [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1135.5817	1134.5744	1134.5273	0.0471	95 - 106	0	12		MAACSGGGVAVR
1135.5817	1134.5744	1134.5273	0.0471	95 - 106	0	---		MAACSGGGVAVR
1233.6727	1232.6654	1232.7465	-0.0811	241 - 251	1	---		LASRLRPPPAR
1291.6809	1290.6736	1290.6284	0.0452	94 - 106	1	---		RMAACSGGGVAVR
1291.6809	1290.6736	1290.6284	0.0452	94 - 106	1	20		RMAACSGGGVAVR

No match to: 713.4088, 768.5215, 973.5449, 973.5449, 1004.4983, 1057.4427, 1250.6991, 1266.6095, 1275.1119, 1357.6116, 1357.6116, 1363.7034, 1404.7681, 1560.8618, 1571.8876, 1571.8876, 1792.8712, 2044.1055, 2246.2288, 3015.4739, 3031.4729

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 26

Protein View

Match to: **gi|3901094** Score: **340** Expect: **9.6e-018**
pollen allergen Phl pI [Phleum pratense]

Nominal mass (M_r): **28584**; Calculated pI value: **7.53**
NCBI BLAST search of gi|3901094 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **22%**

Matched peptides shown in **Bold Red**

```
    1 MASSSSVLLV VALFAVFLGS AHGIPKVPPG PNITATYGDK WLDAKSTWYG
   51 KPTAAGPKDN GGACGYKDVD KPPFSGMTGC GNTPIFKSGR GCGSCFEIKC
  101 TKPEACSGEP VVVHITDDNE EPIAAYHFDL SGIAFGSMAK KGDEQKLRSA
  151 GEVEIQFRRV KCKYPEGTKV TFHVEKGSNP NYLALLVKFS GDGDVVAVDI
  201 KEKGKDKWIA LKESWGAIWR IDTPEVLKGP FTVRYTTEGG TKARAKDVIP
  251 EGWKADTAYE SK
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
46 - 58	1363.7034	1362.6961	1362.6931	0.0030	0	STWYGKPTAAGPK	(No match)
88 - 99	1357.6116	1356.6043	1356.5914	0.0129	1	SGRGCGSCFEIK	(Ions score 19)
88 - 99	1357.6116	1356.6043	1356.5914	0.0129	1	SGRGCGSCFEIK	(No match)
91 - 99	1057.4427	1056.4354	1056.4368	-0.0014	0	GCGSCFEIK	(No match)
147 - 158	1404.7681	1403.7608	1403.7520	0.0088	1	LRSAGEVEIQFR	(No match)
149 - 158	1135.5817	1134.5744	1134.5669	0.0076	0	SAGEVEIQFR	(Ions score 72)
149 - 158	1135.5817	1134.5744	1134.5669	0.0076	0	SAGEVEIQFR	(No match)
149 - 159	1291.6809	1290.6736	1290.6680	0.0057	1	SAGEVEIQFRR	(No match)
149 - 159	1291.6809	1290.6736	1290.6680	0.0057	1	SAGEVEIQFRR	(Ions score 66)
213 - 220	1004.4983	1003.4910	1003.4875	0.0035	0	ESWGAIWR	(No match)
221 - 234	1571.8876	1570.8803	1570.8718	0.0085	1	IDTPEVLKGPFTVR	(No match)
221 - 234	1571.8876	1570.8803	1570.8718	0.0085	1	IDTPEVLKGPFTVR	(Ions score 86)

Spot 82

Index

	Accession	Mass	Score	Description
1.	gi|3901094	28584	382	pollen allergen Phl pI [Phleum pratense]
2.	gi|1582250	28542	364	allergen PhI p I
3.	gi|168030852	134911	56	predicted protein [Physcomitrella patens subsp. patens]
4.	gi|218193377	169934	54	hypothetical protein OsI_12743 [Oryza sativa Indica Group]
5.	gi|125536787	101113	52	hypothetical protein OsI_38484 [Oryza sativa Indica Group]
6.	gi|79322231	12069	50	unknown protein [Arabidopsis thaliana]
7.	gi|224094817	24153	49	predicted protein [Populus trichocarpa]
8.	gi|125525852	71934	48	hypothetical protein OsI_01850 [Oryza sativa Indica Group]
9.	gi|149286884	25577	48	superoxide dismutase [Ginkgo biloba]
10.	gi|57899087	14450	48	hypothetical protein [Oryza sativa Japonica Group]

Results List

1. gi|3901094 **Mass:** 28584 **Score:** 382 **Expect:** 3.8e-033 **Queries matched:** 13

pollen allergen Phl pI [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1004.4970	1003.4897	1003.4875	0.0022	214	221	0	---	ESWGAIWR
1057.4351	1056.4278	1056.4368	-0.0090	91	99	0	---	GCGSCFEIK
1135.5752	1134.5679	1134.5669	0.0011	149	158	0	---	SAGEVEIQFR
1135.5752	1134.5679	1134.5669	0.0011	149	158	0	54	SAGEVEIQFR
1291.6743	1290.6670	1290.6680	-0.0009	149	159	1	61	SAGEVEIQFRR
1291.6743	1290.6670	1290.6680	-0.0009	149	159	1	---	SAGEVEIQFRR
1357.6019	1356.5946	1356.5914	0.0032	88	99	1	---	SGRGCGSCFEIK
1363.6918	1362.6845	1362.6931	-0.0086	46	58	0	70	STWYGKPTAAGPK
1363.6918	1362.6845	1362.6931	-0.0086	46	58	0	---	STWYGKPTAAGPK
1404.7568	1403.7495	1403.7520	-0.0025	147	158	1	---	LRSAGEVEIQFR
1571.8770	1570.8697	1570.8718	-0.0021	222	235	1	84	IDTPEVLKGPFTVR
1571.8770	1570.8697	1570.8718	-0.0021	222	235	1	---	IDTPEVLKGPFTVR
1661.8732	1660.8659	1660.8671	-0.0012	189	204	1	---	FVAGDGDVVAVDIKEK

No match to: 768.5237, 973.5460, 973.5460, 1233.6765, 1560.8558, 1570.8469, 1587.8699, 1792.8699, 2044.1144, 2166.0635, 2808.3186, 3015.4663, 3032.4600, 3091.3806

2. gi|1582250 **Mass:** 28542 **Score:** 364 **Expect:** 2.4e-031 **Queries matched:** 12

allergen PhI p I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1004.4970	1003.4897	1003.4875	0.0022	213	220	0	---	ESWGAIWR
1057.4351	1056.4278	1056.4368	-0.0090	91	99	0	---	GCGSCFEIK
1135.5752	1134.5679	1134.5669	0.0011	149	158	0	---	SAGEVEIQFR

1135.5752	1134.5679	1134.5669	0.0011	149 - 158	0	54	SAGEVEIQFR
1291.6743	1290.6670	1290.6680	-0.0009	149 - 159	1	61	SAGEVEIQFRR
1291.6743	1290.6670	1290.6680	-0.0009	149 - 159	1	---	SAGEVEIQFRR
1357.6019	1356.5946	1356.5914	0.0032	88 - 99	1	---	SGRGCGSCFEIK
1363.6918	1362.6845	1362.6931	-0.0086	46 - 58	0	70	STWYGKPTAAGPK
1363.6918	1362.6845	1362.6931	-0.0086	46 - 58	0	---	STWYGKPTAAGPK
1404.7568	1403.7495	1403.7520	-0.0025	147 - 158	1	---	LRSAGEVEIQFR
1571.8770	1570.8697	1570.8718	-0.0021	221 - 234	1	84	IDTPEVLKGPFTVR
1571.8770	1570.8697	1570.8718	-0.0021	221 - 234	1	---	IDTPEVLKGPFTVR

No match to: 768.5237, 973.5460, 973.5460, 1233.6765, 1560.8558, 1570.8469, 1587.8699, 1661.8732, 1792.8699, 2044.1144, 2166.0635, 2808.3186, 3015.4663, 3032.4600, 3091.3806

3. gi|168030852 **Mass:** 134911 **Score:** 56 **Expect:** 1.6 **Queries matched:** 11

predicted protein [Physcomitrella patens subsp. patens]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1363.6918	1362.6845	1362.7044	-0.0199	137 - 147	0	---	RPDPVFVYQSR
1363.6918	1362.6845	1362.7044	-0.0199	137 - 147	0	---	RPDPVFVYQSR
1404.7568	1403.7495	1403.6867	0.0628	780 - 791	0	---	VAWLEASNMDLR
1560.8558	1559.8485	1559.7878	0.0607	780 - 792	1	---	VAWLEASNMDLRR
1571.8770	1570.8697	1570.8579	0.0118	557 - 569	1	---	SHAIFTITLEQRR
1571.8770	1570.8697	1570.8579	0.0118	557 - 569	1	---	SHAIFTITLEQRR
1587.8699	1586.8626	1586.8086	0.0540	765 - 779	1	---	AGGPSNTEVQMLKQK
1792.8699	1791.8626	1791.8461	0.0165	528 - 543	0	---	SLEEMAAYLEHGSLSR
2044.1144	2043.1071	2042.9706	0.1366	1 - 17	1	---	MDVLWTFQGEKLGGFCR
2166.0635	2165.0562	2165.1884	-0.1322	683 - 700	0	---	FIIDEFVNLTFVKPNLTR
3015.4663	3014.4590	3014.4987	-0.0396	751 - 777	1	---	QQLELMQAELLCARAGGPSNTEVQMLK

No match to: 768.5237, 973.5460, 973.5460, 1004.4970, 1057.4351, 1135.5752, 1135.5752, 1233.6765, 1291.6743, 1291.6743, 1357.6019, 1570.8469, 1661.8732, 2808.3186, 3032.4600, 3091.3806

4. gi|218193377 **Mass:** 169934 **Score:** 54 **Expect:** 2.7 **Queries matched:** 14

hypothetical protein OsI_12743 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
973.5460	972.5387	972.5790	-0.0403	288 - 295	1	---	MRLLALEK
973.5460	972.5387	972.5790	-0.0403	288 - 295	1	---	MRLLALEK
1004.4970	1003.4897	1003.4545	0.0352	23 - 29	1	---	AEMYYRR + Oxidation (M)
1135.5752	1134.5679	1134.6073	-0.0394	648 - 656	0	---	AQTEIFIWK
1135.5752	1134.5679	1134.6073	-0.0394	648 - 656	0	---	AQTEIFIWK
1291.6743	1290.6670	1290.6527	0.0143	1125 - 1136	1	---	SSGDQNTVRTVK
1291.6743	1290.6670	1290.6527	0.0143	1125 - 1136	1	---	SSGDQNTVRTVK
1357.6019	1356.5946	1356.6087	-0.0141	888 - 898	1	---	MMNMKLGDLEK + 3 Oxidation (M)
1560.8558	1559.8485	1559.7977	0.0509	224 - 236	1	---	ANQEMNLELNKLK + Oxidation (M)

1571.8770	1570.8697	1570.7851	0.0846	46 - 59	1	---	ALAERYDHAAGELR
1571.8770	1570.8697	1570.7851	0.0846	46 - 59	1	---	ALAERYDHAAGELR
1587.8699	1586.8626	1586.8376	0.0250	1093 - 1106	1	---	QTLSLANDRLQSNK
2808.3186	2807.3113	2807.3681	-0.0567	840 - 863	1	---	SLQSEIIKLIQENSMLSDELCDSR
3015.4663	3014.4590	3014.3962	0.0628	868 - 892	1	---	VFEDDFSILITGSELYQDIKMMNMK + 3 Oxidation (M)

No match to: 768.5237, 1057.4351, 1233.6765, 1363.6918, 1363.6918, 1404.7568, 1570.8469, 1661.8732, 1792.8699, 2044.1144, 2166.0635, 3032.4600, 3091.3806

5. gi|125536787 **Mass:** 101113 **Score:** 52 **Expect:** 3.7 **Queries matched:** 10

hypothetical protein OsI_38484 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1135.5752	1134.5679	1134.5855	-0.0176	502 - 511	0	---	CLVLHPGPDK
1135.5752	1134.5679	1134.5855	-0.0176	502 - 511	0	---	CLVLHPGPDK
1291.6743	1290.6670	1290.6972	-0.0302	241 - 250	0	---	YLIVLDDVWR
1291.6743	1290.6670	1290.6866	-0.0196	502 - 512	1	---	CLVLHPGPDKR
1363.6918	1362.6845	1362.7242	-0.0396	404 - 415	1	---	EESEISISKLTK
1363.6918	1362.6845	1362.7242	-0.0396	404 - 415	1	---	EESEISISKLTK
1661.8732	1660.8659	1660.9222	-0.0562	771 - 784	1	---	TLGSLTCLWELKLK
2166.0635	2165.0562	2165.1302	-0.0740	594 - 611	1	---	YLCLRNTQLVAFPLNESK
2808.3186	2807.3113	2807.5037	-0.1924	569 - 593	1	---	VIEVEGLMMPTDALRSIQSSLIHLR
3015.4663	3014.4590	3014.4915	-0.0324	653 - 678	0	---	CLTNLQTFCGVLVSNDQIAMEFLTLK

No match to: 768.5237, 973.5460, 973.5460, 1004.4970, 1057.4351, 1233.6765, 1357.6019, 1404.7568, 1560.8558, 1570.8469, 1571.8770, 1571.8770, 1587.8699, 1792.8699, 2044.1144, 3032.4600, 3091.3806

6. gi|79322231 **Mass:** 12069 **Score:** 50 **Expect:** 6.5 **Queries matched:** 4

unknown protein [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1233.6765	1232.6692	1232.6546	0.0146	91 - 101	1	---	RSLAELSCVAK
1571.8770	1570.8697	1570.7781	0.0916	13 - 25	1	---	RVFLLLGGMCMSR + 2 Oxidation (M)
1571.8770	1570.8697	1570.7781	0.0916	14 - 26	1	---	VFLLLGGMCMSRR + 2 Oxidation (M)
3091.3806	3090.3733	3090.4071	-0.0338	58 - 84	1	---	YCFWVVSASRCAASTSFLCSLGISSMK + Oxidation (M)

No match to: 768.5237, 973.5460, 973.5460, 1004.4970, 1057.4351, 1135.5752, 1135.5752, 1291.6743, 1291.6743, 1357.6019, 1363.6918, 1363.6918, 1404.7568, 1560.8558, 1570.8469, 1587.8699, 1661.8732, 1792.8699, 2044.1144, 2166.0635, 2808.3186, 3015.4663, 3032.4600

7. gi|224094817 **Mass:** 24153 **Score:** 49 **Expect:** 7.3 **Queries matched:** 7

predicted protein [Populus trichocarpa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1004.4970	1003.4897	1003.4763	0.0135	168 - 174	1	---	RFFEDYK
1135.5752	1134.5679	1134.4975	0.0704	1 - 11	0	---	MANNDGEVTGK
1135.5752	1134.5679	1134.4975	0.0704	1 - 11	0	---	MANNDGEVTGK
1291.6743	1290.6670	1290.5986	0.0684	1 - 12	1	---	MANNDGEVTGKR

1291.6743	1290.6670	1290.5986	0.0684	1 - 12	1	---	MANNDGEVTGKR
1661.8732	1660.8659	1660.8276	0.0383	121 - 135	1	---	ARAIGLMPMIDQGEK + 2 Oxidation (M)
1792.8699	1791.8626	1791.8382	0.0244	123 - 138	1	---	AIGLMPMIDQGEKDDK + 2 Oxidation (M)

No match to: 768.5237, 973.5460, 973.5460, 1057.4351, 1233.6765, 1357.6019, 1363.6918, 1363.6918, 1404.7568, 1560.8558, 1570.8469, 1571.8770, 1571.8770, 1587.8699, 2044.1144, 2166.0635, 2808.3186, 3015.4663, 3032.4600, 3091.3806

8. gi|125525852 **Mass:** 71934 **Score:** 48 **Expect:** 9.2 **Queries matched:** 9

hypothetical protein OsI_01850 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
973.5460	972.5387	972.5215	0.0173	324 - 331	0	1		QIHGFMIK
973.5460	972.5387	972.5215	0.0173	324 - 331	0	---		QIHGFMIK
1135.5752	1134.5679	1134.4957	0.0722	50 - 57	1	---		CRRPCCAR
1135.5752	1134.5679	1134.4957	0.0722	50 - 57	1	---		CRRPCCAR
1571.8770	1570.8697	1570.9042	-0.0345	398 - 412	1	---		EGLGVNRTTLTAVLK
1571.8770	1570.8697	1570.9042	-0.0345	398 - 412	1	---		EGLGVNRTTLTAVLK
1661.8732	1660.8659	1660.9399	-0.0740	296 - 311	0	---		SSGLVPNVFTLSSILK
2166.0635	2165.0562	2165.0509	0.0053	312 - 331	1	---		ACAGTGAFDLGRQIHGFMIK + Oxidation (M)
3015.4663	3014.4590	3014.4517	0.0073	324 - 350	1	---		QIHGFMIKVNADSDDYIGVGLVDMYAK + Oxidation (M)

No match to: 768.5237, 1004.4970, 1057.4351, 1233.6765, 1291.6743, 1291.6743, 1357.6019, 1363.6918, 1363.6918, 1404.7568, 1560.8558, 1570.8469, 1587.8699, 1792.8699, 2044.1144, 2808.3186, 3032.4600, 3091.3806

9. gi|149286884 **Mass:** 25577 **Score:** 48 **Expect:** 10 **Queries matched:** 7

superoxide dismutase [Ginkgo biloba]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
973.5460	972.5387	972.5756	-0.0369	8 - 16	1	---		WKLSGIAAK
973.5460	972.5387	972.5756	-0.0369	8 - 16	1	---		WKLSGIAAK
1004.4970	1003.4897	1003.5450	-0.0553	198 - 205	0	---		NVRPDYLK
1135.5752	1134.5679	1134.6042	-0.0362	1 - 9	1	---		MALSMLRWK
1135.5752	1134.5679	1134.6042	-0.0362	1 - 9	1	---		MALSMLRWK
1404.7568	1403.7495	1403.6582	0.0914	55 - 65	0	---		HHQTYVTNYNK
1587.8699	1586.8626	1586.9143	-0.0517	77 - 90	1	---		RNVEAIVFLQSAIK

No match to: 768.5237, 1057.4351, 1233.6765, 1291.6743, 1291.6743, 1357.6019, 1363.6918, 1363.6918, 1560.8558, 1570.8469, 1571.8770, 1571.8770, 1661.8732, 1792.8699, 2044.1144, 2166.0635, 2808.3186, 3015.4663, 3032.4600, 3091.3806

10. gi|57899087 **Mass:** 14450 **Score:** 48 **Expect:** 11 **Queries matched:** 4

hypothetical protein [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1135.5752	1134.5679	1134.5273	0.0406	66 - 77	0	---		GGGATAMAALCR
1135.5752	1134.5679	1134.5273	0.0406	38 - 49	0	5		GGGATAMAALCR
1291.6743	1290.6670	1290.6284	0.0386	37 - 49	1	---		RGGGATAMAALCR

1291.6743 1290.6670 1290.6284 0.0386 66 - 78 1 --- GGGATAMAALCRR

No match to: 768.5237, 973.5460, 973.5460, 1004.4970, 1057.4351, 1233.6765, 1357.6019, 1363.6918, 1363.6918, 1404.7568, 1560.8558, 1570.8469, 1571.8770, 1571.8770, 1587.8699, 1661.8732, 1792.8699, 2044.1144, 2166.0635, 2808.3186, 3015.4663, 3032.4600, 3091.3806

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 27

Protein View

Match to: **gi|3901094** Score: **382** Expect: **3.8e-033**
pollen allergen Phl pI [Phleum pratense]

Nominal mass (M_r): **28584**; Calculated pI value: **7.53**
NCBI BLAST search of gi|3901094 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **28%**

Matched peptides shown in **Bold Red**

```
    1 MASSSSVLLV VALFAVFLGS AHGIPKVPPG PNITATYGDK WLDAKSTWYG
   51 KPTAAGPKDN GGACGYKDVD KPPFSGMTGC GNTPIFKSGR GCGSCFEIKC
  101 TKPEACSGEP VVVHITDDNE EPIAAYHFDL SGIAFGSMAK KGDEQKLRSA
  151 GEVEIQFRRV KCKYPEGTKV TFHVEKGSNP NYLALLVKFV AGDGDVVAVD
  201 IKEKGKDKWI ALKESWGAIW RIDTPEVLKG PFTVRYTTEG GTKGEAKDVI
  251 PEGWKADTAY ESK
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
46 - 58	1363.6918	1362.6845	1362.6931	-0.0086	0	**STWYGKPTAAGPK**	(Ions score 70)
46 - 58	1363.6918	1362.6845	1362.6931	-0.0086	0	**STWYGKPTAAGPK**	(No match)
88 - 99	1357.6019	1356.5946	1356.5914	0.0032	1	**SGRGCGSCFEIK**	(No match)
91 - 99	1057.4351	1056.4278	1056.4368	-0.0090	0	**GCGSCFEIK**	(No match)
147 - 158	1404.7568	1403.7495	1403.7520	-0.0025	1	**LRSAGEVEIQFR**	(No match)
149 - 158	1135.5752	1134.5679	1134.5669	0.0011	0	**SAGEVEIQFR**	(No match)
149 - 158	1135.5752	1134.5679	1134.5669	0.0011	0	**SAGEVEIQFR**	(Ions score 54)
149 - 159	1291.6743	1290.6670	1290.6680	-0.0009	1	**SAGEVEIQFRR**	(Ions score 61)
149 - 159	1291.6743	1290.6670	1290.6680	-0.0009	1	**SAGEVEIQFRR**	(No match)
189 - 204	1661.8732	1660.8659	1660.8671	-0.0012	1	**FVAGDGDVVAVDIKEK**	(No match)
214 - 221	1004.4970	1003.4897	1003.4875	0.0022	0	**ESWGAIWR**	(No match)
222 - 235	1571.8770	1570.8697	1570.8718	-0.0021	1	**IDTPEVLKGPFTVR**	(Ions score 84)
222 - 235	1571.8770	1570.8697	1570.8718	-0.0021	1	**IDTPEVLKGPFTVR**	(No match)

Spot 83

Index

	Accession	Mass	Score	Description
1.	gi|1582250	28542	306	allergen PhI p I
2.	gi|3901094	28584	306	pollen allergen Phl pI [Phleum pratense]
3.	gi|115453645	52978	52	Os03g0430400 [Oryza sativa (japonica cultivar-group)]
4.	gi|147743028	50803	52	RecName: Full=Cyclin-A2-1; AltName: Full=G2/mitotic-specific cyclin-A2-1; Short=CycA2;1; AltNa
5.	gi|149392547	7051	52	60S ribosomal protein l15 [Oryza sativa (indica cultivar-group)]
6.	gi|22327058	50017	52	CYCA2;1 (cyclin a2;1); cyclin-dependent protein kinase regulator [Arabidopsis thaliana]
7.	gi|115457882	56978	51	Os04g0354600 [Oryza sativa (japonica cultivar-group)]
8.	gi|222615618	68105	51	hypothetical protein OsJ_33169 [Oryza sativa Japonica Group]
9.	gi|20197623	86232	51	putative myosin heavy chain [Arabidopsis thaliana]
10.	gi|57899087	14450	50	hypothetical protein [Oryza sativa Japonica Group]

Results List

1. gi|1582250 **Mass:** 28542 **Score:** 306 **Expect:** 1.5e-025 **Queries matched:** 11

allergen PhI p I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1004.5204	1003.5131	1003.4875	0.0256	213	220	0	---	ESWGAIWR
1057.4832	1056.4759	1056.4368	0.0391	91	99	0	---	GCGSCFEIK
1135.6041	1134.5968	1134.5669	0.0300	149	158	0	58	SAGEVEIQFR
1135.6041	1134.5968	1134.5669	0.0300	149	158	0	---	SAGEVEIQFR
1291.7079	1290.7006	1290.6680	0.0327	149	159	1	---	SAGEVEIQFRR
1291.7079	1290.7006	1290.6680	0.0327	149	159	1	61	SAGEVEIQFRR
1357.6398	1356.6325	1356.5914	0.0411	88	99	1	---	SGRGCGSCFEIK
1363.7239	1362.7166	1362.6931	0.0235	46	58	0	---	STWYGKPTAAGPK
1404.7889	1403.7816	1403.7520	0.0296	147	158	1	---	LRSAGEVEIQFR
1571.9081	1570.9008	1570.8718	0.0290	221	234	1	86	IDTPEVLKGPFTVR
1571.9081	1570.9008	1570.8718	0.0290	221	234	1	---	IDTPEVLKGPFTVR

No match to: 973.5645, 973.5645, 1560.8958, 1570.8867, 1587.8990, 2044.1371, 2044.1371, 2061.1313, 2076.1248, 2302.2766, 3015.4741, 3091.3997

2. gi|3901094 **Mass:** 28584 **Score:** 306 **Expect:** 1.5e-025 **Queries matched:** 11

pollen allergen Phl pI [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1004.5204	1003.5131	1003.4875	0.0256	214	221	0	---	ESWGAIWR
1057.4832	1056.4759	1056.4368	0.0391	91	99	0	---	GCGSCFEIK
1135.6041	1134.5968	1134.5669	0.0300	149	158	0	58	SAGEVEIQFR
1135.6041	1134.5968	1134.5669	0.0300	149	158	0	---	SAGEVEIQFR
1291.7079	1290.7006	1290.6680	0.0327	149	159	1	---	SAGEVEIQFRR

1291.7079	1290.7006	1290.6680	0.0327	149 - 159	1	61	SAGEVEIQFRR
1357.6398	1356.6325	1356.5914	0.0411	88 - 99	1	---	SGRGCGSCFEIK
1363.7239	1362.7166	1362.6931	0.0235	46 - 58	0	---	STWYGKPTAAGPK
1404.7889	1403.7816	1403.7520	0.0296	147 - 158	1	---	LRSAGEVEIQFR
1571.9081	1570.9008	1570.8718	0.0290	222 - 235	1	86	IDTPEVLKGPFTVR
1571.9081	1570.9008	1570.8718	0.0290	222 - 235	1	---	IDTPEVLKGPFTVR

No match to: 973.5645, 973.5645, 1560.8958, 1570.8867, 1587.8990, 2044.1371, 2044.1371, 2061.1313, 2076.1248, 2302.2766, 3015.4741, 3091.3997

3. gi|115453645 **Mass:** 52978 **Score:** 52 **Expect:** 3.7 **Queries matched:** 6

Os03g0430400 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1004.5204	1003.5131	1003.5021	0.0110	288 - 295		0	---	HIHCNPVK
1135.6041	1134.5968	1134.5821	0.0147	259 - 268		0	11	TGGALWDIFR
1135.6041	1134.5968	1134.5821	0.0147	259 - 268		0	---	TGGALWDIFR
1291.7079	1290.7006	1290.6832	0.0174	259 - 269		1	---	TGGALWDIFRR
1291.7079	1290.7006	1290.6832	0.0174	259 - 269		1	18	TGGALWDIFRR
2061.1313	2060.1240	2060.0003	0.1237	45 - 62		0	---	HGAEFITALPFPEYTDPR

No match to: 973.5645, 973.5645, 1057.4832, 1357.6398, 1363.7239, 1404.7889, 1560.8958, 1570.8867, 1571.9081, 1571.9081, 1587.8990, 2044.1371, 2044.1371, 2076.1248, 2302.2766, 3015.4741, 3091.3997

4. gi|147743028 **Mass:** 50803 **Score:** 52 **Expect:** 3.7 **Queries matched:** 7

RecName: Full=Cyclin-A2-1; AltName: Full=G2/mitotic-specific cyclin-A2-1; Short=CycA2;1; AltName: F

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
973.5645	972.5572	972.5100	0.0472	23 - 30		1	---	DNNVRVTR
973.5645	972.5572	972.5240	0.0333	429 - 437		0	---	VATLTSPER
1004.5204	1003.5131	1003.5662	-0.0530	14 - 22		1	---	EAISTSKIR
1560.8958	1559.8885	1559.8779	0.0107	256 - 269		0	---	LQLLGITCMLIASK
2044.1371	2043.1298	2043.1186	0.0112	292 - 308		1	---	LEVLSMEIKVLNSLHFR + Oxidation (M)
2044.1371	2043.1298	2043.1186	0.0112	292 - 308		1	---	LEVLSMEIKVLNSLHFR + Oxidation (M)
2302.2766	2301.2693	2301.2427	0.0267	76 - 97		1	---	AVLKDVTNTLAESIISTEGNVK

No match to: 1057.4832, 1135.6041, 1135.6041, 1291.7079, 1291.7079, 1357.6398, 1363.7239, 1404.7889, 1570.8867, 1571.9081, 1571.9081, 1587.8990, 2061.1313, 2076.1248, 3015.4741, 3091.3997

5. gi|149392547 **Mass:** 7051 **Score:** 52 **Expect:** 4 **Queries matched:** 3

60S ribosomal protein l15 [Oryza sativa (indica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
973.5645	972.5572	972.5464	0.0108	48 - 55		1	17	RNQTVSLR
973.5645	972.5572	972.5464	0.0108	49 - 56		1	---	NQTVSLRR
1587.8990	1586.8917	1586.8616	0.0302	2 - 13		1	---	INWLCKPVHKHR

No match to: 1004.5204, 1057.4832, 1135.6041, 1135.6041, 1291.7079, 1291.7079, 1357.6398, 1363.7239, 1404.7889, 1560.8958, 1570.8867, 1571.9081, 1571.9081, 2044.1371, 2044.1371, 2061.1313, 2076.1248, 2302.2766, 3015.4741,

3091.3997

6. gi|22327058 **Mass:** 50017 **Score:** 52 **Expect:** 4.2 **Queries matched:** 7

CYCA2;1 (cyclin a2;1); cyclin-dependent protein kinase regulator [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
973.5645	972.5572	972.5100	0.0472	23	30	1	---	DNNVRVTR
973.5645	972.5572	972.5240	0.0333	422	430	0	---	VATLTSPER
1004.5204	1003.5131	1003.5662	-0.0530	14	22	1	---	EAISTSKIR
1560.8958	1559.8885	1559.8779	0.0107	249	262	0	---	LQLLGITCMLIASK
2044.1371	2043.1298	2043.1186	0.0112	285	301	1	---	LEVLSMEIKVLNSLHFR + Oxidation (M)
2044.1371	2043.1298	2043.1186	0.0112	285	301	1	---	LEVLSMEIKVLNSLHFR + Oxidation (M)
2302.2766	2301.2693	2301.2427	0.0267	76	97	1	---	AVLKDVTNTLAESIISTEGNVK

No match to: 1057.4832, 1135.6041, 1135.6041, 1291.7079, 1291.7079, 1357.6398, 1363.7239, 1404.7889, 1570.8867, 1571.9081, 1571.9081, 1587.8990, 2061.1313, 2076.1248, 3015.4741, 3091.3997

7. gi|115457882 **Mass:** 56978 **Score:** 51 **Expect:** 4.5 **Queries matched:** 8

Os04g0354600 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
973.5645	972.5572	972.5868	-0.0296	372	379	1	---	NKRPLAFK
973.5645	972.5572	972.5868	-0.0296	372	379	1	---	NKRPLAFK
1135.6041	1134.5968	1134.5781	0.0187	2	11	1	14	ETGGIAERFR
1135.6041	1134.5968	1134.5781	0.0187	2	11	1	---	ETGGIAERFR
1291.7079	1290.7006	1290.7547	-0.0540	14	26	0	---	TILITGATGFLGK
1291.7079	1290.7006	1290.7547	-0.0540	14	26	0	---	TILITGATGFLGK
1404.7889	1403.7816	1403.7271	0.0545	381	391	0	---	LAYFQAYMILR + Oxidation (M)
1560.8958	1559.8885	1559.8282	0.0603	380	391	1	---	RLAYFQAYMILR + Oxidation (M)

No match to: 1004.5204, 1057.4832, 1357.6398, 1363.7239, 1570.8867, 1571.9081, 1571.9081, 1587.8990, 2044.1371, 2044.1371, 2061.1313, 2076.1248, 2302.2766, 3015.4741, 3091.3997

8. gi|222615618 **Mass:** 68105 **Score:** 51 **Expect:** 4.9 **Queries matched:** 6

hypothetical protein OsJ_33169 [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1357.6398	1356.6325	1356.6819	-0.0494	273	284	0	---	TVVMSVHQPSTR + Oxidation (M)
1560.8958	1559.8885	1559.8895	-0.0010	482	496	1	---	ERASGILALPAAVHR
1570.8867	1569.8794	1569.8045	0.0749	271	284	1	---	GRTVVMSVHQPSTR + Oxidation (M)
2061.1313	2060.1240	2060.0915	0.0325	156	173	1	---	RTGFVAQDDVLHPHLTVR
2076.1248	2075.1175	2074.9891	0.1284	74	96	1	---	GAPPGRISHAGGTGGGGGAQEER
3015.4741	3014.4668	3014.5873	-0.1205	606	633	1	---	GEASPAACVAALVAMFFAYRLLAYLALR

No match to: 973.5645, 973.5645, 1004.5204, 1057.4832, 1135.6041, 1135.6041, 1291.7079, 1291.7079, 1363.7239, 1404.7889, 1571.9081, 1571.9081, 1587.8990, 2044.1371, 2044.1371, 2302.2766, 3091.3997

9. gi|20197623 **Mass:** 86232 **Score:** 51 **Expect:** 5.3 **Queries matched:** 10

putative myosin heavy chain [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
973.5645	972.5572	972.5603	-0.0031	688 -	696	1	---	VQLADAKTK
973.5645	972.5572	972.5603	-0.0031	688 -	696	1	---	VQLADAKTK
1004.5204	1003.5131	1003.5185	-0.0054	653 -	661	0	---	QSELESALK
1291.7079	1290.7006	1290.6125	0.0881	199 -	210	0	---	AAGLQESEVMEK
1291.7079	1290.7006	1290.6125	0.0881	199 -	210	0	---	AAGLQESEVMEK
1357.6398	1356.6325	1356.7248	-0.0923	683 -	694	1	---	DLEQKVQLADAK
1363.7239	1362.7166	1362.6779	0.0387	316 -	326	1	---	LKQEFDQAQEK
2044.1371	2043.1298	2043.0483	0.0815	181 -	198	1	---	NELNVTQGKLESIENDLK
2044.1371	2043.1298	2043.0483	0.0815	181 -	198	1	---	NELNVTQGKLESIENDLK
2061.1313	2060.1240	2060.0273	0.0968	474 -	492	1	---	LSALEAEKEQTANELEASK

No match to: 1057.4832, 1135.6041, 1135.6041, 1404.7889, 1560.8958, 1570.8867, 1571.9081, 1571.9081, 1587.8990, 2076.1248, 2302.2766, 3015.4741, 3091.3997

10. gi|57899087 **Mass:** 14450 **Score:** 50 **Expect:** 5.7 **Queries matched:** 4

hypothetical protein [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1135.6041	1134.5968	1134.5273	0.0695	38 -	49	0	5	GGGATAMAALCR
1135.6041	1134.5968	1134.5273	0.0695	66 -	77	0	---	GGGATAMAALCR
1291.7079	1290.7006	1290.6284	0.0722	66 -	78	1	---	GGGATAMAALCRR
1291.7079	1290.7006	1290.6284	0.0722	37 -	49	1	---	RGGGATAMAALCR

No match to: 973.5645, 973.5645, 1004.5204, 1057.4832, 1357.6398, 1363.7239, 1404.7889, 1560.8958, 1570.8867, 1571.9081, 1571.9081, 1587.8990, 2044.1371, 2044.1371, 2061.1313, 2076.1248, 2302.2766, 3015.4741, 3091.3997

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 23

Protein View

Match to: **gi|3901094** Score: **306** Expect: **1.5e-025**
pollen allergen Phl pI [Phleum pratense]

Nominal mass (M_r): **28584**; Calculated pI value: **7.53**
NCBI BLAST search of gi|3901094 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **22%**

Matched peptides shown in **Bold Red**

```
    1 MASSSSVLLV VALFAVFLGS AHGIPKVPPG PNITATYGDK WLDAKSTWYG
   51 KPTAAGPKDN GGACGYKDVD KPPFSGMTGC GNTPIFKSGR GCGSCFEIKC
  101 TKPEACSGEP VVVHITDDNE EPIAAYHFDL SGIAFGSMAK KGDEQKLRSA
  151 GEVEIQFRRV KCKYPEGTKV TFHVEKGSNP NYLALLVKFV AGDGDVVAVD
  201 IKEKGKDKWI ALKESWGAIW RIDTPEVLKG PFTVRYTTEG GTKGEAKDVI
  251 PEGWKADTAY ESK
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
46 - 58	1363.7239	1362.7166	1362.6931	0.0235	0	STWYGKPTAAGPK	(No match)
88 - 99	1357.6398	1356.6325	1356.5914	0.0411	1	SGRGCGSCFEIK	(No match)
91 - 99	1057.4832	1056.4759	1056.4368	0.0391	0	GCGSCFEIK	(No match)
147 - 158	1404.7889	1403.7816	1403.7520	0.0296	1	LRSAGEVEIQFR	(No match)
149 - 158	1135.6041	1134.5968	1134.5669	0.0300	0	SAGEVEIQFR	(Ions score 58)
149 - 158	1135.6041	1134.5968	1134.5669	0.0300	0	SAGEVEIQFR	(No match)
149 - 159	1291.7079	1290.7006	1290.6680	0.0327	1	SAGEVEIQFRR	(No match)
149 - 159	1291.7079	1290.7006	1290.6680	0.0327	1	SAGEVEIQFRR	(Ions score 61)
214 - 221	1004.5204	1003.5131	1003.4875	0.0256	0	ESWGAIWR	(No match)
222 - 235	1571.9081	1570.9008	1570.8718	0.0290	1	IDTPEVLKGPFTVR	(Ions score 86)
222 - 235	1571.9081	1570.9008	1570.8718	0.0290	1	IDTPEVLKGPFTVR	(No match)

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	Accession	Mass	Score	Description
1.	gi|1582250	28542	202	allergen PhI p I
2.	gi|3901094	28584	202	pollen allergen Phl pI [Phleum pratense]
3.	gi|79322231	12069	55	unknown protein [Arabidopsis thaliana]
4.	gi|115479765	58942	54	Os09g0479100 [Oryza sativa (japonica cultivar-group)]
5.	gi|147778208	11777	47	hypothetical protein [Vitis vinifera]
6.	gi|125528954	37616	47	hypothetical protein OsI_05029 [Oryza sativa Indica Group]
7.	gi|168051439	44337	47	predicted protein [Physcomitrella patens subsp. patens]
8.	gi|25453062	45640	46	RecName: Full=Isovaleryl-CoA dehydrogenase 1, mitochondrial; Short=IVD 1; Flags: Precursor
9.	gi|94502681	12732	46	hypothetical protein ZeamMp106 [Zea mays subsp. mays]
10.	gi|157352107	89480	46	unnamed protein product [Vitis vinifera]

Results List

1. gi|1582250 **Mass:** 28542 **Score:** 202 **Expect:** 3.8e-015 **Queries matched:** 8

allergen PhI p I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1057.4358	1056.4285	1056.4368	-0.0083	91	99	0	---	GCGSCFEIK
1135.5707	1134.5634	1134.5669	-0.0034	149	158	0	---	SAGEVEIQFR
1291.6749	1290.6676	1290.6680	-0.0003	149	159	1	---	SAGEVEIQFRR
1291.6749	1290.6676	1290.6680	-0.0003	149	159	1	38	SAGEVEIQFRR
1357.6007	1356.5934	1356.5914	0.0020	88	99	1	---	SGRGCGSCFEIK
1363.6917	1362.6844	1362.6931	-0.0087	46	58	0	---	STWYGKPTAAGPK
1571.8717	1570.8644	1570.8718	-0.0074	221	234	1	91	IDTPEVLKGPFTVR
1571.8717	1570.8644	1570.8718	-0.0074	221	234	1	---	IDTPEVLKGPFTVR

No match to: 768.5260, 845.0975, 973.5378, 973.5378, 1077.5681, 1077.5681, 1233.6660, 1233.6660, 1255.6412, 1594.8462, 3016.4756

2. gi|3901094 **Mass:** 28584 **Score:** 202 **Expect:** 3.8e-015 **Queries matched:** 8

pollen allergen Phl pI [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1057.4358	1056.4285	1056.4368	-0.0083	91	99	0	---	GCGSCFEIK
1135.5707	1134.5634	1134.5669	-0.0034	149	158	0	---	SAGEVEIQFR
1291.6749	1290.6676	1290.6680	-0.0003	149	159	1	---	SAGEVEIQFRR
1291.6749	1290.6676	1290.6680	-0.0003	149	159	1	38	SAGEVEIQFRR
1357.6007	1356.5934	1356.5914	0.0020	88	99	1	---	SGRGCGSCFEIK
1363.6917	1362.6844	1362.6931	-0.0087	46	58	0	---	STWYGKPTAAGPK
1571.8717	1570.8644	1570.8718	-0.0074	222	235	1	91	IDTPEVLKGPFTVR
1571.8717	1570.8644	1570.8718	-0.0074	222	235	1	---	IDTPEVLKGPFTVR

No match to: 768.5260, 845.0975, 973.5378, 973.5378, 1077.5681, 1077.5681, 1233.6660, 1233.6660, 1255.6412, 1594.8462, 3016.4756

3. gi|79322231 **Mass:** 12069 **Score:** 55 **Expect:** 1.8 **Queries matched:** 6

unknown protein [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1077.5681	1076.5608	1076.5535	0.0073	92	101	0	---	SLAELSCVAK
1077.5681	1076.5608	1076.5535	0.0073	92	101	0	---	SLAELSCVAK
1233.6660	1232.6587	1232.6546	0.0041	91	101	1	---	RSLAELSCVAK
1233.6660	1232.6587	1232.6546	0.0041	91	101	1	1	RSLAELSCVAK
1571.8717	1570.8644	1570.7781	0.0863	13	25	1	---	RVFLLLGGMCMSR + 2 Oxidation (M)
1571.8717	1570.8644	1570.7781	0.0863	14	26	1	---	VFLLLGGMCMSRR + 2 Oxidation (M)

No match to: 768.5260, 845.0975, 973.5378, 973.5378, 1057.4358, 1135.5707, 1255.6412, 1291.6749, 1291.6749, 1357.6007, 1363.6917, 1594.8462, 3016.4756

4. gi|115479765 **Mass:** 58942 **Score:** 54 **Expect:** 2.3 **Queries matched:** 7

Os09g0479100 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
973.5378	972.5305	972.5426	-0.0121	5	13	1	---	KALAMQPSK
973.5378	972.5305	972.5426	-0.0121	6	14	1	---	ALAMQPSKK
1233.6660	1232.6587	1232.6612	-0.0024	341	351	1	---	NSEIESSKLVK
1233.6660	1232.6587	1232.6612	-0.0024	341	351	1	0	NSEIESSKLVK
1255.6412	1254.6339	1254.7044	-0.0705	197	207	1	---	DVRTPQALSLR
1357.6007	1356.5934	1356.6608	-0.0674	53	63	0	---	DPQFAMVHIQR + Oxidation (M)
3016.4756	3015.4683	3015.3741	0.0942	208	233	1	---	CVERSGVVNVGGAMYWLTEDEESVWK + Oxidation (M)

No match to: 768.5260, 845.0975, 1057.4358, 1077.5681, 1077.5681, 1135.5707, 1291.6749, 1291.6749, 1363.6917, 1571.8717, 1571.8717, 1594.8462

5. gi|147778208 **Mass:** 11777 **Score:** 47 **Expect:** 12 **Queries matched:** 4

hypothetical protein [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1077.5681	1076.5608	1076.5502	0.0107	26	36	0	5	LSGSTPSGFPK
1077.5681	1076.5608	1076.5502	0.0107	26	36	0	---	LSGSTPSGFPK
1233.6660	1232.6587	1232.6513	0.0074	26	37	1	---	LSGSTPSGFPKR
1233.6660	1232.6587	1232.6513	0.0074	26	37	1	21	LSGSTPSGFPKR

No match to: 768.5260, 845.0975, 973.5378, 973.5378, 1057.4358, 1135.5707, 1255.6412, 1291.6749, 1291.6749, 1357.6007, 1363.6917, 1571.8717, 1571.8717, 1594.8462, 3016.4756

6. gi|125528954 **Mass:** 37616 **Score:** 47 **Expect:** 14 **Queries matched:** 8

hypothetical protein OsI_05029 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
973.5378	972.5305	972.5538	-0.0233	110	117	1	---	SRVVMLPR + Oxidation (M)

973.5378	972.5305	972.5538	-0.0233	110 - 117	1	---	SRVVMLPR + Oxidation (M)
1057.4358	1056.4285	1056.4698	-0.0413	102 - 109	0	---	CFLFEADR
1135.5707	1134.5634	1134.5855	-0.0221	7 - 15	0	---	FLNLIMDNR
1291.6749	1290.6676	1290.6866	-0.0190	6 - 15	1	---	RFLNLIMDNR
1291.6749	1290.6676	1290.6866	-0.0190	6 - 15	1	---	RFLNLIMDNR
1571.8717	1570.8644	1570.7885	0.0759	295 - 308	1	---	QCRDPQLVNLGSGK
1571.8717	1570.8644	1570.7885	0.0759	295 - 308	1	---	QCRDPQLVNLGSGK

No match to: 768.5260, 845.0975, 1077.5681, 1077.5681, 1233.6660, 1233.6660, 1255.6412, 1357.6007, 1363.6917, 1594.8462, 3016.4756

7. gi|168051439 **Mass:** 44337 **Score:** 47 **Expect:** 14 **Queries matched:** 7

predicted protein [Physcomitrella patens subsp. patens]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
973.5378	972.5305	972.4988	0.0317	226 - 233	1	---	RESPSELR
973.5378	972.5305	972.4988	0.0317	226 - 233	1	---	RESPSELR
1077.5681	1076.5608	1076.5865	-0.0257	216 - 225	0	---	IVDFQAIGSK
1077.5681	1076.5608	1076.5865	-0.0257	216 - 225	0	---	IVDFQAIGSK
1233.6660	1232.6587	1232.6877	-0.0289	216 - 226	1	---	IVDFQAIGSKR
1233.6660	1232.6587	1232.6877	-0.0289	216 - 226	1	7	IVDFQAIGSKR
3016.4756	3015.4683	3015.3450	0.1233	2 - 27	1	---	DLSLTLSHRPSGGNSKWNPEECEDCK

No match to: 768.5260, 845.0975, 1057.4358, 1135.5707, 1255.6412, 1291.6749, 1291.6749, 1357.6007, 1363.6917, 1571.8717, 1571.8717, 1594.8462

8. gi|25453062 **Mass:** 45640 **Score:** 46 **Expect:** 14 **Queries matched:** 6

RecName: Full=Isovaleryl-CoA dehydrogenase 1, mitochondrial; Short=IVD 1; Flags: Precursor

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
973.5378	972.5305	972.4875	0.0430	253 - 261	0	5	ENVLGQEGK
973.5378	972.5305	972.4875	0.0430	253 - 261	0	---	ENVLGQEGK
1077.5681	1076.5608	1076.5614	-0.0006	60 - 68	1	3	IDRTNSFPK
1077.5681	1076.5608	1076.5614	-0.0006	60 - 68	1	---	IDRTNSFPK
1135.5707	1134.5634	1134.5668	-0.0034	175 - 185	0	---	VDGGYVLNGNK
3016.4756	3015.4683	3015.5044	-0.0361	141 - 169	1	---	YLPKLISGDHIGALAMSEPNAGSDVVSMK + Oxidation (M)

No match to: 768.5260, 845.0975, 1057.4358, 1233.6660, 1233.6660, 1255.6412, 1291.6749, 1291.6749, 1357.6007, 1363.6917, 1571.8717, 1571.8717, 1594.8462

9. gi|94502681 **Mass:** 12732 **Score:** 46 **Expect:** 15 **Queries matched:** 4

hypothetical protein ZeamMp106 [Zea mays subsp. mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1135.5707	1134.5634	1134.6107	-0.0472	3 - 11	0	---	LLPFLTEMR + Oxidation (M)
1291.6749	1290.6676	1290.7118	-0.0442	3 - 12	1	---	LLPFLTEMRR + Oxidation (M)
1291.6749	1290.6676	1290.7118	-0.0442	2 - 11	1	---	RLLPFLTEMR + Oxidation (M)
1357.6007	1356.5934	1356.6350	-0.0416	49 - 58	1	---	TTTYFDYYRK

No match to: 768.5260, 845.0975, 973.5378, 973.5378, 1057.4358, 1077.5681, 1077.5681, 1233.6660, 1233.6660, 1255.6412, 1363.6917, 1571.8717, 1571.8717, 1594.8462, 3016.4756

10. gi|157352107 **Mass:** 89480 **Score:** 46 **Expect:** 16 **Queries matched:** 6

unnamed protein product [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1077.5681	1076.5608	1076.5614	-0.0006	230	239	0	3	ASADYAVRPK
1077.5681	1076.5608	1076.5614	-0.0006	230	239	0	---	ASADYAVRPK
1233.6660	1232.6587	1232.6625	-0.0038	230	240	1	---	ASADYAVRPKR
1233.6660	1232.6587	1232.6625	-0.0038	230	240	1	18	ASADYAVRPKR
1255.6412	1254.6339	1254.6430	-0.0091	177	187	0	---	ALYLGCLGNFK
1357.6007	1356.5934	1356.6343	-0.0409	645	655	1	---	FSSETKNELMR + Oxidation (M)

No match to: 768.5260, 845.0975, 973.5378, 973.5378, 1057.4358, 1135.5707, 1291.6749, 1291.6749, 1363.6917, 1571.8717, 1571.8717, 1594.8462, 3016.4756

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 19

Protein View

Match to: **gi|3901094** Score: **202** Expect: **3.8e-015**
pollen allergen Phl pI [Phleum pratense]

Nominal mass (M_r): **28584**; Calculated pI value: **7.53**
NCBI BLAST search of gi|3901094 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

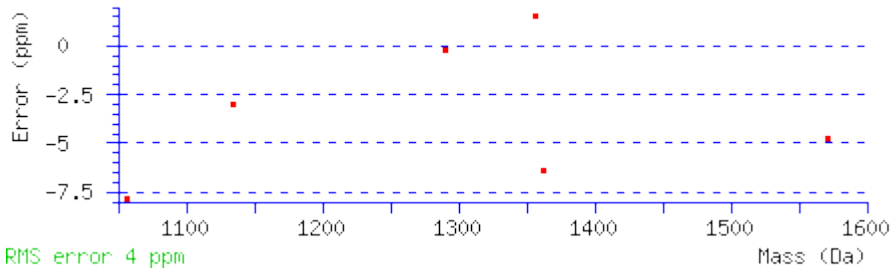
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **19%**

Matched peptides shown in **Bold Red**

```
   1 MASSSSVLLV VALFAVFLGS AHGIPKVPPG PNITATYGDK WLDAKSTWYG
  51 KPTAAGPKDN GGACGYKDVD KPPFSGMTGC GNTPIFKSGR GCGSCFEIKC
 101 TKPEACSGEP VVVHITDDNE EPIAAYHFDL SGIAFGSMAK KGDEQKLRSA
 151 GEVEIQFRRV KCKYPEGTKV TFHVEKGSNP NYLALLVKFV AGDGDVVAVD
 201 IKEKGKDKWI ALKESWGAIW RIDTPEVLKG PFTVRYTTEG GTKGEAKDVI
 251 PEGWKADTAY ESK
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
46 - 58	1363.6917	1362.6844	1362.6931	-0.0087	0	STWYGKPTAAGPK	(No match)
88 - 99	1357.6007	1356.5934	1356.5914	0.0020	1	SGRGCGSCFEIK	(No match)
91 - 99	1057.4358	1056.4285	1056.4368	-0.0083	0	GCGSCFEIK	(No match)
149 - 158	1135.5707	1134.5634	1134.5669	-0.0034	0	SAGEVEIQFR	(No match)
149 - 159	1291.6749	1290.6676	1290.6680	-0.0003	1	SAGEVEIQFRR	(No match)
149 - 159	1291.6749	1290.6676	1290.6680	-0.0003	1	SAGEVEIQFRR	(Ions score 38)
222 - 235	1571.8717	1570.8644	1570.8718	-0.0074	1	IDTPEVLKGPFTVR	(Ions score 91)
222 - 235	1571.8717	1570.8644	1570.8718	-0.0074	1	IDTPEVLKGPFTVR	(No match)



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	Accession	Mass	Score	Description
1.	gi|1582250	28542	149	allergen PhI p I
2.	gi|3901094	28584	149	pollen allergen Phl pI [Phleum pratense]
3.	gi|15227940	69393	62	ATSLY1; protein transporter [Arabidopsis thaliana]
4.	gi|159471149	83042	62	predicted protein [Chlamydomonas reinhardtii]
5.	gi|79322231	12069	61	unknown protein [Arabidopsis thaliana]
6.	gi|49328149	25884	54	hypothetical protein [Oryza sativa Japonica Group]
7.	gi|125534619	10606	54	hypothetical protein OsI_36350 [Oryza sativa Indica Group]
8.	gi|51535431	8145	52	hypothetical protein [Oryza sativa Japonica Group]
9.	gi|168036921	168745	51	predicted protein [Physcomitrella patens subsp. patens]
10.	gi|73658412	16734	49	ATPase beta subunit [Arabidopsis thaliana]

Results List

1. gi|1582250 **Mass:** 28542 **Score:** 149 **Expect:** 7.6e-010 **Queries matched:** 6

allergen PhI p I

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1057.4370	1056.4297	1056.4368	-0.0071	91	-	99	0	---	GCGSCFEIK
1291.6700	1290.6627	1290.6680	-0.0052	149	-	159	1	---	SAGEVEIQFRR
1291.6700	1290.6627	1290.6680	-0.0052	149	-	159	1	13	SAGEVEIQFRR
1363.6869	1362.6796	1362.6931	-0.0135	46	-	58	0	---	STWYGKPTAAGPK
1571.8755	1570.8682	1570.8718	-0.0036	221	-	234	1	89	IDTPEVLKGPFTVR
1571.8755	1570.8682	1570.8718	-0.0036	221	-	234	1	---	IDTPEVLKGPFTVR

No match to: 768.5328, 973.5354, 973.5354, 1077.5703, 1077.5703, 1233.6686, 1233.6686, 2045.1074, 3015.4888

2. gi|3901094 **Mass:** 28584 **Score:** 149 **Expect:** 7.6e-010 **Queries matched:** 6

pollen allergen Phl pI [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1057.4370	1056.4297	1056.4368	-0.0071	91	-	99	0	---	GCGSCFEIK
1291.6700	1290.6627	1290.6680	-0.0052	149	-	159	1	---	SAGEVEIQFRR
1291.6700	1290.6627	1290.6680	-0.0052	149	-	159	1	13	SAGEVEIQFRR
1363.6869	1362.6796	1362.6931	-0.0135	46	-	58	0	---	STWYGKPTAAGPK
1571.8755	1570.8682	1570.8718	-0.0036	222	-	235	1	89	IDTPEVLKGPFTVR
1571.8755	1570.8682	1570.8718	-0.0036	222	-	235	1	---	IDTPEVLKGPFTVR

No match to: 768.5328, 973.5354, 973.5354, 1077.5703, 1077.5703, 1233.6686, 1233.6686, 2045.1074, 3015.4888

3. gi|15227940 **Mass:** 69393 **Score:** 62 **Expect:** 0.37 **Queries matched:** 8

ATSLY1; protein transporter [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide

973.5354	972.5281	972.5538	-0.0257	1 - 8	1	8	MALNLRQK
973.5354	972.5281	972.5538	-0.0257	1 - 8	1	---	MALNLRQK
1077.5703	1076.5630	1076.5899	-0.0269	407 - 416	1	---	TELMAALKGK + Oxidation (M)
1077.5703	1076.5630	1076.5899	-0.0269	407 - 416	1	---	TELMAALKGK + Oxidation (M)
1571.8755	1570.8682	1570.7773	0.0910	611 - 627	1	---	KMGLGGPVASTSLSGGH + Oxidation (M)
1571.8755	1570.8682	1570.7773	0.0910	611 - 627	1	---	KMGLGGPVASTSLSGGH + Oxidation (M)
2045.1074	2044.1001	2044.0081	0.0921	199 - 217	1	---	CPSGGPAEMVASLLDQKLR + Oxidation (M)
3015.4888	3014.4815	3014.4402	0.0413	329 - 357	1	---	KTGGGSGAEFDGTDLIGNIHTEHLMNTVK + Oxidation (M)

No match to: 768.5328, 1057.4370, 1233.6686, 1233.6686, 1291.6700, 1291.6700, 1363.6869

4. gi|159471149 **Mass:** 83042 **Score:** 62 **Expect:** 0.4 **Queries matched:** 6

predicted protein [Chlamydomonas reinhardtii]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
973.5354	972.5281	972.5253	0.0028	406 - 412	1	---	WSQRLQR
973.5354	972.5281	972.5253	0.0028	406 - 412	1	---	WSQRLQR
1077.5703	1076.5630	1076.5614	0.0017	49 - 59	0	---	ASGEFAVGLAR
1077.5703	1076.5630	1076.5614	0.0017	49 - 59	0	26	ASGEFAVGLAR
1233.6686	1232.6613	1232.6625	-0.0012	48 - 59	1	16	RASGEFAVGLAR
1233.6686	1232.6613	1232.6625	-0.0012	48 - 59	1	---	RASGEFAVGLAR

No match to: 768.5328, 1057.4370, 1291.6700, 1291.6700, 1363.6869, 1571.8755, 1571.8755, 2045.1074, 3015.4888

5. gi|79322231 **Mass:** 12069 **Score:** 61 **Expect:** 0.47 **Queries matched:** 6

unknown protein [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1077.5703	1076.5630	1076.5535	0.0095	92 - 101	0	---	SLAELSCVAK
1077.5703	1076.5630	1076.5535	0.0095	92 - 101	0	---	SLAELSCVAK
1233.6686	1232.6613	1232.6546	0.0067	91 - 101	1	1	RSLAELSCVAK
1233.6686	1232.6613	1232.6546	0.0067	91 - 101	1	---	RSLAELSCVAK
1571.8755	1570.8682	1570.7781	0.0901	13 - 25	1	---	RVFLLLGGMCMSR + 2 Oxidation (M)
1571.8755	1570.8682	1570.7781	0.0901	14 - 26	1	---	VFLLLGGMCMSRR + 2 Oxidation (M)

No match to: 768.5328, 973.5354, 973.5354, 1057.4370, 1291.6700, 1291.6700, 1363.6869, 2045.1074, 3015.4888

6. gi|49328149 **Mass:** 25884 **Score:** 54 **Expect:** 2.6 **Queries matched:** 4

hypothetical protein [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1077.5703	1076.5630	1076.5648	-0.0018	204 - 214	0	---	MATATALTAAR
1077.5703	1076.5630	1076.5648	-0.0018	204 - 214	0	---	MATATALTAAR
1233.6686	1232.6613	1232.6659	-0.0046	203 - 214	1	25	RMATATALTAAR
1233.6686	1232.6613	1232.6659	-0.0046	204 - 215	1	---	MATATALTAARR

No match to: 768.5328, 973.5354, 973.5354, 1057.4370, 1291.6700, 1291.6700, 1363.6869, 1571.8755, 1571.8755, 2045.1074, 3015.4888

7. gi|125534619 **Mass:** 10606 **Score:** 54 **Expect:** 2.7 **Queries matched:** 4

hypothetical protein OsI_36350 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1077.5703	1076.5630	1076.4920	0.0710	37 -	47	0	---	TGAADPATAMR + Oxidation (M)
1077.5703	1076.5630	1076.4920	0.0710	37 -	47	0	13	TGAADPATAMR + Oxidation (M)
1233.6686	1232.6613	1232.5931	0.0682	37 -	48	1	18	TGAADPATAMRR + Oxidation (M)
1233.6686	1232.6613	1232.5931	0.0682	37 -	48	1	---	TGAADPATAMRR + Oxidation (M)

No match to: 768.5328, 973.5354, 973.5354, 1057.4370, 1291.6700, 1291.6700, 1363.6869, 1571.8755, 1571.8755, 2045.1074, 3015.4888

8. gi|51535431 **Mass:** 8145 **Score:** 52 **Expect:** 3.7 **Queries matched:** 4

hypothetical protein [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
973.5354	972.5281	972.4810	0.0471	1 -	9	0	---	MGSITGVHR + Oxidation (M)
973.5354	972.5281	972.4810	0.0471	1 -	9	0	---	MGSITGVHR + Oxidation (M)
2045.1074	2044.1001	2044.1251	-0.0249	1 -	19	1	---	MGSITGVHRVGLVSLLFSR + Oxidation (M)
3015.4888	3014.4815	3014.4973	-0.0157	24 -	52	0	---	ASPGYGPATAFLAGRPVFGWHAPTTAQMR

No match to: 768.5328, 1057.4370, 1077.5703, 1077.5703, 1233.6686, 1233.6686, 1291.6700, 1291.6700, 1363.6869, 1571.8755, 1571.8755

9. gi|168036921 **Mass:** 168745 **Score:** 51 **Expect:** 5 **Queries matched:** 7

predicted protein [Physcomitrella patens subsp. patens]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
973.5354	972.5281	972.5464	-0.0183	160 -	169	1	12	SGRISGAAVR
973.5354	972.5281	972.5464	-0.0183	160 -	169	1	---	SGRISGAAVR
1057.4370	1056.4297	1056.4433	-0.0136	402 -	409	0	---	MEQEEYTK
1233.6686	1232.6613	1232.6414	0.0199	458 -	466	1	---	LFQQYRNHK
1233.6686	1232.6613	1232.6625	-0.0012	742 -	752	1	---	EAVIRAQSGFR
2045.1074	2044.1001	2044.1105	-0.0104	2 -	19	1	---	TKLAYLHEPGVLYNLASR
3015.4888	3014.4815	3014.5024	-0.0209	349 -	375	1	---	VNRSIGQDPDSPYLVGVLDIYGFESFK

No match to: 768.5328, 1077.5703, 1077.5703, 1291.6700, 1291.6700, 1363.6869, 1571.8755, 1571.8755

10. gi|73658412 **Mass:** 16734 **Score:** 49 **Expect:** 7 **Queries matched:** 6

ATPase beta subunit [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1077.5703	1076.5630	1076.5535	0.0095	76 -	86	0	---	AVAMSATEGLK
1077.5703	1076.5630	1076.5535	0.0095	76 -	86	0	---	AVAMSATEGLK
1233.6686	1232.6613	1232.6546	0.0067	76 -	87	1	10	AVAMSATEGLKR
1233.6686	1232.6613	1232.6546	0.0067	76 -	87	1	---	AVAMSATEGLKR
1571.8755	1570.8682	1570.8063	0.0619	2 -	15	1	---	RTNPTTSNPEVSIR
1571.8755	1570.8682	1570.8063	0.0619	2 -	15	1	---	RTNPTTSNPEVSIR

No match to: 768.5328, 973.5354, 973.5354, 1057.4370, 1291.6700, 1291.6700, 1363.6869, 2045.1074, 3015.4888

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 15

Protein View

Match to: **gi|3901094** Score: **149** Expect: **7.6e-010**
pollen allergen Phl pI [Phleum pratense]

Nominal mass (M_r): **28584**; Calculated pI value: **7.53**
NCBI BLAST search of gi|3901094 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

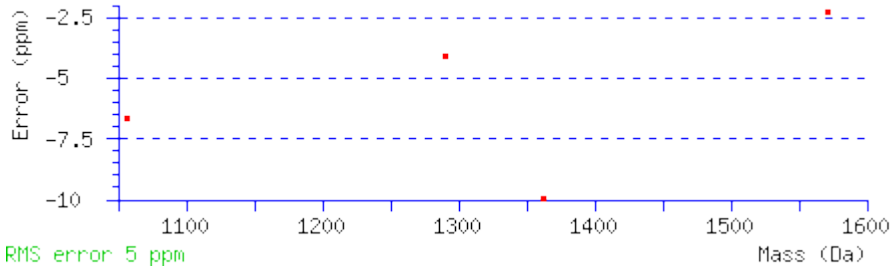
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **17%**

Matched peptides shown in **Bold Red**

```
     1 MASSSSVLLV VALFAVFLGS AHGIPKVPPG PNITATYGDK WLDAKSTWYG
    51 KPTAAGPKDN GGACGYKDVD KPPFSGMTGC GNTPIFKSGR GCGSCFEIKC
   101 TKPEACSGEP VVVHITDDNE EPIAAYHFDL SGIAFGSMAK KGDEQKLRSA
   151 GEVEIQFRRV KCKYPEGTKV TFHVEKGSNP NYLALLVKFV AGDGDVVAVD
   201 IKEKGKDKWI ALKESWGAIW RIDTPEVLKG PFTVRYTTEG GTKGEAKDVI
   251 PEGWKADTAY ESK
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
46 - 58	1363.6869	1362.6796	1362.6931	-0.0135	0	STWYGKPTAAGPK	(No match)
91 - 99	1057.4370	1056.4297	1056.4368	-0.0071	0	GCGSCFEIK	(No match)
149 - 159	1291.6700	1290.6627	1290.6680	-0.0052	1	SAGEVEIQFRR	(No match)
149 - 159	1291.6700	1290.6627	1290.6680	-0.0052	1	SAGEVEIQFRR	(Ions score 13)
222 - 235	1571.8755	1570.8682	1570.8718	-0.0036	1	IDTPEVLKGPFTVR	(Ions score 89)
222 - 235	1571.8755	1570.8682	1570.8718	-0.0036	1	IDTPEVLKGPFTVR	(No match)



No match to: 768.5347, 801.4731, 929.5572, 986.5854, 1187.6769, 1267.6949, 1308.6554, 1312.6703, 1328.6448, 1378.6145, 1378.6145, 1486.6553, 1523.7795, 1534.7015, 1813.0037, 1813.0037, 1825.8046, 1828.9818, 1841.7904, 1857.7968, 1911.9114, 1941.1030, 1957.0912, 2256.0757, 2256.0757, 2357.2041, 2572.3315

3. gi|224081931 **Mass:** 63298 **Score:** 61 **Expect:** 0.52 **Queries matched:** 11

predicted protein [Populus trichocarpa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
875.5130	874.5057	874.4773	0.0285	424	431	1	---	GRVYGAPR
1312.6703	1311.6630	1311.6419	0.0212	22	33	1	---	STSSKSFQTPSR
1329.6777	1328.6704	1328.6217	0.0488	393	403	1	---	MEMISKYGTNR
1345.6866	1344.6793	1344.6166	0.0628	393	403	1	---	MEMISKYGTNR + Oxidation (M)
1470.6659	1469.6586	1469.7150	-0.0564	38	50	0	---	GSTFQQPVYQTSK
1470.6659	1469.6586	1469.6674	-0.0088	244	255	0	---	YSFPEEDESIVR
1486.6553	1485.6480	1485.7207	-0.0726	387	398	1	---	VVENYKMEMISK + Oxidation (M)
1826.8331	1825.8258	1825.8635	-0.0376	359	374	0	---	EPPWDDVFSALHQSAK
1826.8331	1825.8258	1825.8958	-0.0700	35	50	1	---	NNKGSTFQQPVYQTSK
2256.0757	2255.0684	2255.0382	0.0303	244	261	1	---	YSFPEEDESIVRNIWEDK
2256.0757	2255.0684	2255.0382	0.0303	244	261	1	---	YSFPEEDESIVRNIWEDK

No match to: 768.5347, 801.4731, 929.5572, 986.5854, 1187.6769, 1267.6949, 1308.6554, 1328.6448, 1378.6145, 1378.6145, 1523.7795, 1534.7015, 1813.0037, 1813.0037, 1825.8046, 1828.9818, 1841.7904, 1857.7968, 1911.9114, 1941.1030, 1957.0912, 2357.2041, 2572.3315

4. gi|152003254 **Mass:** 55286 **Score:** 59 **Expect:** 0.86 **Queries matched:** 10

(S)-N-methylcoclaurine-3'-hydroxylase [Coptis chinensis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
875.5130	874.5057	874.4759	0.0298	158	165	1	---	SKEGEVVK
1378.6145	1377.6072	1377.6676	-0.0604	412	424	0	---	GNDFELIPFGGGR
1378.6145	1377.6072	1377.6676	-0.0604	412	424	0	---	GNDFELIPFGGGR
1534.7015	1533.6942	1533.7687	-0.0745	412	425	1	---	GNDFELIPFGGGRR
1813.0037	1811.9964	1811.8909	0.1055	360	374	1	---	RALETCTVMNYTIPK + Oxidation (M)
1813.0037	1811.9964	1811.8909	0.1055	360	374	1	---	RALETCTVMNYTIPK + Oxidation (M)
1857.7968	1856.7895	1856.9057	-0.1161	388	402	1	---	DPKTWDDPLNFKPER
2256.0757	2255.0684	2255.1949	-0.1265	330	348	1	1	ESDLPHLPYLQAFVKETLR
2256.0757	2255.0684	2255.1949	-0.1265	330	348	1	---	ESDLPHLPYLQAFVKETLR
2572.3315	2571.3242	2571.2281	0.0961	391	411	1	---	TWDDPLNFKPERFLSSDVDYK

No match to: 768.5347, 801.4731, 929.5572, 986.5854, 1187.6769, 1267.6949, 1308.6554, 1312.6703, 1328.6448, 1329.6777, 1345.6866, 1470.6659, 1470.6659, 1486.6553, 1523.7795, 1825.8046, 1826.8331, 1826.8331, 1828.9818, 1841.7904, 1911.9114, 1941.1030, 1957.0912, 2357.2041

5. gi|222618186 **Mass:** 104658 **Score:** 54 **Expect:** 2.4 **Queries matched:** 11

hypothetical protein OsJ_01275 [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide

801.4731	800.4658	800.4392	0.0267	361 - 367	0	---	DGLLVER
875.5130	874.5057	874.5024	0.0033	732 - 739	0	---	NVIFAVGR
929.5572	928.5499	928.5090	0.0410	880 - 887	1	---	DGRLAELR
986.5854	985.5781	985.5133	0.0648	376 - 383	1	---	WYKHGAPK
1328.6448	1327.6375	1327.6480	-0.0105	110 - 121	1	---	HGRASISSQEEK
1378.6145	1377.6072	1377.5520	0.0553	889 - 901	0	---	GADGCGGGWEWAR
1378.6145	1377.6072	1377.5520	0.0553	889 - 901	0	---	GADGCGGGWEWAR
1534.7015	1533.6942	1533.6531	0.0412	888 - 901	1	---	RGADGCGGGWEWAR
1841.7904	1840.7831	1840.8825	-0.0993	576 - 590	1	---	SIDINFHMRVMHADR
1857.7968	1856.7895	1856.8774	-0.0878	576 - 590	1	---	SIDINFHMRVMHADR + Oxidation (M)
2357.2041	2356.1968	2356.3365	-0.1397	255 - 275	1	---	KLFLSITNGSLVEVTELQPLR

No match to: 768.5347, 1187.6769, 1267.6949, 1308.6554, 1312.6703, 1329.6777, 1345.6866, 1470.6659, 1470.6659, 1486.6553, 1523.7795, 1813.0037, 1813.0037, 1825.8046, 1826.8331, 1826.8331, 1828.9818, 1911.9114, 1941.1030, 1957.0912, 2256.0757, 2256.0757, 2572.3315

6. gi|218187788 **Mass:** 14410 **Score:** 51 **Expect:** 5.2 **Queries matched:** 5

hypothetical protein OsI_00973 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
801.4731	800.4658	800.4140	0.0518	75 -	81	0	---	VNAVNER
929.5572	928.5499	928.5090	0.0410	74 -	81	1	---	KVNAVNER
1267.6949	1266.6876	1266.6945	-0.0069	49 -	58	1	---	HARYQLVQPR
1312.6703	1311.6630	1311.6531	0.0099	5 -	16	1	---	ELDAANTSHAKR
2572.3315	2571.3242	2571.3002	0.0240	104 -	128	1	---	VKTYAGAVDPLPESMPTQAAVTPGR + Oxidation (M)

No match to: 768.5347, 875.5130, 986.5854, 1187.6769, 1308.6554, 1328.6448, 1329.6777, 1345.6866, 1378.6145, 1378.6145, 1470.6659, 1470.6659, 1486.6553, 1523.7795, 1534.7015, 1813.0037, 1813.0037, 1825.8046, 1826.8331, 1826.8331, 1828.9818, 1841.7904, 1857.7968, 1911.9114, 1941.1030, 1957.0912, 2256.0757, 2256.0757, 2357.2041

7. gi|116056879 **Mass:** 49571 **Score:** 48 **Expect:** 8.8 **Queries matched:** 9

unnamed protein product [Ostreococcus tauri]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
875.5130	874.5057	874.4760	0.0298	130 -	137	0	---	SVQELTAK
1312.6703	1311.6630	1311.7510	-0.0879	138 -	149	1	---	NGALVKELEALR
1329.6777	1328.6704	1328.6935	-0.0231	169 -	179	1	---	NVELAEEIEKR
1378.6145	1377.6072	1377.6749	-0.0676	296 -	308	0	---	GVQDAPGNLQSHR
1378.6145	1377.6072	1377.6749	-0.0676	296 -	308	0	5	GVQDAPGNLQSHR
1534.7015	1533.6942	1533.7760	-0.0817	296 -	309	1	---	GVQDAPGNLQSHRR
1813.0037	1811.9964	1811.8835	0.1129	150 -	166	1	---	HELEDGKMAISGLDAAR
1813.0037	1811.9964	1811.8835	0.1129	150 -	166	1	---	HELEDGKMAISGLDAAR
1828.9818	1827.9745	1827.8784	0.0961	150 -	166	1	---	HELEDGKMAISGLDAAR + Oxidation (M)

No match to: 768.5347, 801.4731, 929.5572, 986.5854, 1187.6769, 1267.6949, 1308.6554, 1328.6448, 1345.6866, 1470.6659, 1470.6659, 1486.6553, 1523.7795, 1825.8046, 1826.8331, 1826.8331, 1841.7904, 1857.7968, 1911.9114, 1941.1030, 1957.0912, 2256.0757, 2256.0757, 2357.2041, 2572.3315

8. gi|9971208 **Mass:** 55032 **Score:** 48 **Expect:** 9.2 **Queries matched:** 9

(S)-N-methylcoclaurine-3'-hydroxylase [Coptis japonica]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1378.6145	1377.6072	1377.6676	-0.0604	412 -	424	0	---	GNDFELIPFGGGR
1378.6145	1377.6072	1377.6676	-0.0604	412 -	424	0	---	GNDFELIPFGGGR
1534.7015	1533.6942	1533.7687	-0.0745	412 -	425	1	---	GNDFELIPFGGGRR
1813.0037	1811.9964	1811.8909	0.1055	360 -	374	1	---	RALETCTVMNYTIPK + Oxidation (M)
1813.0037	1811.9964	1811.8909	0.1055	360 -	374	1	---	RALETCTVMNYTIPK + Oxidation (M)
1857.7968	1856.7895	1856.9057	-0.1161	388 -	402	1	---	DPKTWDDPLNFKPER
2256.0757	2255.0684	2255.1949	-0.1265	330 -	348	1	1	ESDLPHLPYLQAFVKETLR
2256.0757	2255.0684	2255.1949	-0.1265	330 -	348	1	---	ESDLPHLPYLQAFVKETLR
2572.3315	2571.3242	2571.2281	0.0961	391 -	411	1	---	TWDDPLNFKPERFLSSDVDYK

No match to: 768.5347, 801.4731, 875.5130, 929.5572, 986.5854, 1187.6769, 1267.6949, 1308.6554, 1312.6703, 1328.6448, 1329.6777, 1345.6866, 1470.6659, 1470.6659, 1486.6553, 1523.7795, 1825.8046, 1826.8331, 1826.8331, 1828.9818, 1841.7904, 1911.9114, 1941.1030, 1957.0912, 2357.2041

9. gi|157359830 **Mass:** 2817 **Score:** 48 **Expect:** 11 **Queries matched:** 3

unnamed protein product [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
986.5854	985.5781	985.5920	-0.0138	2 -	11	0	---	LATGLLVGSR
1328.6448	1327.6375	1327.7149	-0.0774	15 -	25	0	---	WNPVRPVQPVH
1523.7795	1522.7722	1522.8289	-0.0567	1 -	14	1	---	MLATGLLVGSRFSR + Oxidation (M)

No match to: 768.5347, 801.4731, 875.5130, 929.5572, 1187.6769, 1267.6949, 1308.6554, 1312.6703, 1329.6777, 1345.6866, 1378.6145, 1378.6145, 1470.6659, 1470.6659, 1486.6553, 1534.7015, 1813.0037, 1813.0037, 1825.8046, 1826.8331, 1826.8331, 1828.9818, 1841.7904, 1857.7968, 1911.9114, 1941.1030, 1957.0912, 2256.0757, 2256.0757, 2357.2041, 2572.3315

10. gi|224123468 **Mass:** 10262 **Score:** 44 **Expect:** 23 **Queries matched:** 5

predicted protein [Populus trichocarpa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
986.5854	985.5781	985.5556	0.0226	28 -	36	1	---	NNGLAIEKK
1187.6769	1186.6696	1186.6808	-0.0112	58 -	67	1	---	IEIVLEKSEK
1911.9114	1910.9041	1910.8567	0.0474	68 -	85	0	---	FDSLMNAVSSAPEEEAAK + Oxidation (M)
2256.0757	2255.0684	2255.0263	0.0422	65 -	85	1	---	SEKFDSLMNAVSSAPEEEAAK + Oxidation (M)
2256.0757	2255.0684	2255.0263	0.0422	65 -	85	1	---	SEKFDSLMNAVSSAPEEEAAK + Oxidation (M)

No match to: 768.5347, 801.4731, 875.5130, 929.5572, 1267.6949, 1308.6554, 1312.6703, 1328.6448, 1329.6777, 1345.6866, 1378.6145, 1378.6145, 1470.6659, 1470.6659, 1486.6553, 1523.7795, 1534.7015, 1813.0037, 1813.0037, 1825.8046, 1826.8331, 1826.8331, 1828.9818, 1841.7904, 1857.7968, 1941.1030, 1957.0912, 2357.2041, 2572.3315

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 34

Protein View

Match to: **gi|125583637** Score: **87** Expect: **0.0014**
hypothetical protein OsJ_08330 [Oryza sativa Japonica Group]

Nominal mass (M_r): **46268**; Calculated pI value: **6.25**
NCBI BLAST search of gi|125583637 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Oryza sativa Japonica Group

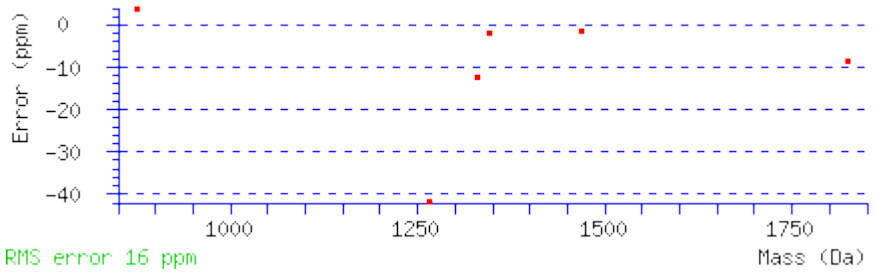
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **11%**

Matched peptides shown in **Bold Red**

```
     1 MRPSFLLLLV VFAGVLAGGA RAGPPLAGEN LPGQLLPGEK PPGQPLPGAA
    51 VAGATVARAI VAGAAVAGAA VARAIVAGAA FGQSLPGQPL PGQPLVGEKP
   101 PGQPLVPGQP LVGEKPPGQP LGGDKLSPDY YAQTCPRAER IVAEVVQSKQ
   151 MANPTTAAGV LRLFFHDCFV SGCDASVLVA ATAFEKSEQS AEINHSLPGD
   201 AFDAVVRAKL ALELECPEVV SCADILALAA RVLITMTGGP RYPISFGRKD
   251 SLTSSPTAPD KEMPQSNFTM DQVIKLFQDK GFTVQEMVAL SGGHTLGFSH
   301 CKEFAQRIYD YQGKPGNVDP TMNPVLSKGL QTACKEYLKD PTIAAFNDVM
   351 TPGKFDNMYF VNLERGLGLL ATDEEMWSDK RTQPFVKLYA SNPTAFFDDF
   401 SRAIDKLSLF GVKTGAAGEI RRRCDTYNHG PMPK
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
59 - 73	1267.6949	1266.6876	1266.7407	-0.0531	0	**AIVAGAAVAGAAVAR** (No match)
126 - 137	1470.6659	1469.6586	1469.6609	-0.0023	0	**LSPDYYAQTCPR** (Ions score 42)
126 - 137	1470.6659	1469.6586	1469.6609	-0.0023	0	**LSPDYYAQTCPR** (No match)
126 - 140	1826.8331	1825.8258	1825.8417	-0.0159	1	**LSPDYYAQTCPRAER** (No match)
126 - 140	1826.8331	1825.8258	1825.8417	-0.0159	1	**LSPDYYAQTCPRAER** (Ions score 10)
150 - 162	1329.6777	1328.6704	1328.6870	-0.0166	0	**QMANPTTAAGVLR** (No match)
150 - 162	1345.6866	1344.6793	1344.6819	-0.0026	0	**QMANPTTAAGVLR** Oxidation (M) (No match)
381 - 387	875.5130	874.5057	874.5024	0.0033	1	**RTQPFVK** (No match)



Spot 86

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	Accession	Mass	Score	Description
1.	gi|130076566	54409	83	ribosomal protein S3 [Daphniphyllum sp. Qiu 94162]
2.	gi|133907949	40705	72	ribosomal protein S3 [Tetrastigma rumicispermum]
3.	gi|255603581	20852	70	conserved hypothetical protein [Ricinus communis]
4.	gi|130076576	58648	64	ribosomal protein S3 [Itea virginica]
5.	gi|130076598	57760	64	ribosomal protein S3 [Tetracarpaea tasmanica]
6.	gi|224365643	65035	62	ribosomal protein S3 [Vitis vinifera]
7.	gi|116792016	37144	57	unknown [Picea sitchensis]
8.	gi|224020972	64246	57	ribosomal protein S3 [Carica papaya]
9.	gi|147856448	92880	56	hypothetical protein [Vitis vinifera]
10.	gi|225444613	92898	56	PREDICTED: hypothetical protein [Vitis vinifera]

Results List

1. gi|130076566 **Mass:** 54409 **Score:** 83 **Expect:** 0.0034 **Queries matched:** 9

ribosomal protein S3 [Daphniphyllum sp. Qiu 94162]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1177.6451	1176.6378	1176.6443	-0.0065	4	12	0	---	TFIHFFLPR
1177.6451	1176.6378	1176.6443	-0.0065	4	12	0	---	TFIHFFLPR
1268.6604	1267.6531	1267.6520	0.0011	147	157	1	---	SDDPTSHLLKR
1333.7263	1332.7190	1332.7455	-0.0264	3	12	1	12	RTFIHFFLPR
1333.7263	1332.7190	1332.7145	0.0045	330	340	0	---	GIEMMIEIILR + Oxidation (M)
1587.8885	1586.8812	1586.8636	0.0176	330	342	1	---	GIEMMIEIILRNR
1587.8885	1586.8812	1586.7940	0.0873	219	232	1	---	SRIAFFVESSTSEK
1603.8807	1602.8734	1602.8585	0.0149	330	342	1	---	GIEMMIEIILRNR + Oxidation (M)
1603.8807	1602.8734	1602.8585	0.0149	330	342	1	---	GIEMMIEIILRNR + Oxidation (M)

No match to: 1506.8647, 1929.0585

2. gi|133907949 **Mass:** 40705 **Score:** 72 **Expect:** 0.042 **Queries matched:** 8

ribosomal protein S3 [Tetrastigma rumicispermum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1177.6451	1176.6378	1176.6443	-0.0065	5	13	0	---	TFIHFFLPR
1177.6451	1176.6378	1176.6443	-0.0065	5	13	0	---	TFIHFFLPR
1333.7263	1332.7190	1332.7455	-0.0264	4	13	1	12	RTFIHFFLPR
1333.7263	1332.7190	1332.7145	0.0045	336	346	0	---	GIEMMIEIILR + Oxidation (M)
1587.8885	1586.8812	1586.8636	0.0176	336	348	1	---	GIEMMIEIILRNR
1587.8885	1586.8812	1586.7940	0.0873	225	238	1	---	SRIAFFVESSTSEK
1603.8807	1602.8734	1602.8585	0.0149	336	348	1	---	GIEMMIEIILRNR + Oxidation (M)

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	Accession	Mass	Score	Description
1.	gi|29500897	28269	721	phl p5a allergen precursor [Phleum pratense]
2.	gi|13430402	27795	553	group V allergen Phl p 5 precursor [Phleum pratense]
3.	gi|398830	31083	544	Phlp5 [Phleum pratense]
4.	gi|1092249	28713	512	major allergen Phl p Va
5.	gi|2851456	28513	511	RecName: Full=Pollen allergen Phl p 5a; AltName: Full=Allergen Phl p Va; AltName: Allergen=Phl
6.	gi|422005	26530	482	PHLP5A protein - common timothy (fragment)
7.	gi|3135501	27586	417	major allergen Phl p 5 [Phleum pratense]
8.	gi|3135499	27658	417	major allergen Phl p 5 [Phleum pratense]
9.	gi|3135503	27692	400	major allergen Phl p 5 [Phleum pratense]
10.	gi|3309039	31010	372	group V allergen Phl p 5.0103 precursor [Phleum pratense]

Results List

1. gi|29500897 **Mass:** 28269 **Score:** 721 **Expect:** 4.8e-067 **Queries matched:** 19

phl p5a allergen precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1058.6141	1057.6068	1057.6171	-0.0103	209	218	0	---	FIPALEAAVK
1065.5106	1064.5033	1064.5172	-0.0138	243	252	0	---	AITAMSEAQK + Oxidation (M)
1071.5646	1070.5573	1070.5648	-0.0074	233	241	0	---	YTVFETALK
1105.5419	1104.5346	1104.5451	-0.0104	76	86	0	96	AFAEGLSGEPK
1105.5419	1104.5346	1104.5451	-0.0104	76	86	0	---	AFAEGLSGEPK
1199.6609	1198.6536	1198.6597	-0.0061	233	242	1	---	YTVFETALKK
1213.6147	1212.6074	1212.6138	-0.0064	64	75	0	---	TFVATFGAASNK
1289.6852	1288.6779	1288.6874	-0.0095	31	41	1	---	ATTEEQKLIEK
1295.7638	1294.7565	1294.7496	0.0070	153	164	0	---	VIPAGELQVIEK
1471.7454	1470.7381	1470.7354	0.0027	121	133	0	---	YDAYVATLSEALR
1471.7454	1470.7381	1470.7354	0.0027	121	133	0	109	YDAYVATLSEALR
1541.8490	1540.8417	1540.8361	0.0056	48	63	1	128	AALAAAAGVPPADKYR
1541.8490	1540.8417	1540.8361	0.0056	48	63	1	---	AALAAAAGVPPADKYR
1927.0920	1926.0847	1926.0825	0.0022	153	170	1	---	VIPAGELQVIEKVDAAFK
1975.1290	1974.1217	1974.1149	0.0069	134	152	0	---	IIAGTLEVHAVKPAAEEVK
2300.1614	2299.1541	2299.1483	0.0058	64	86	1	---	TFVATFGAASNKAFAEGLSGEPK
2427.2056	2426.1983	2426.1964	0.0019	111	133	1	---	TAEGATPEAKYDAYVATLSEALR
2427.2056	2426.1983	2426.1964	0.0019	111	133	1	170	TAEGATPEAKYDAYVATLSEALR
2737.4329	2736.4256	2736.3870	0.0386	171	197	1	---	VAATAANAAPANDKFTVFEAAFNNAIK

No match to: 713.4029, 768.5154, 1135.5865, 1291.6776, 1571.8823, 1726.9725, 1920.0474, 2172.1956, 2172.1956, 2444.2896, 2656.5139, 3442.8713

2. gi|13430402 **Mass:** 27795 **Score:** 553 **Expect:** 3e-050 **Queries matched:** 16

group V allergen Phl p 5 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1058.6141	1057.6068	1057.6171	-0.0103	200	209	0	---	FIPALEAAVK
1065.5106	1064.5033	1064.5172	-0.0138	234	243	0	---	AITAMSEAQK + Oxidation (M)
1071.5646	1070.5573	1070.5648	-0.0074	224	232	0	---	YTVFETALK
1105.5419	1104.5346	1104.5451	-0.0104	67	77	0	96	AFAEGLSGEPK
1105.5419	1104.5346	1104.5451	-0.0104	67	77	0	---	AFAEGLSGEPK
1199.6609	1198.6536	1198.6597	-0.0061	224	233	1	---	YTVFETALKK
1213.6147	1212.6074	1212.6138	-0.0064	55	66	0	---	TFVATFGAASNK
1295.7638	1294.7565	1294.7496	0.0070	144	155	0	---	VIPAGELQVIEK
1471.7454	1470.7381	1470.7354	0.0027	112	124	0	---	YDAYVATLSEALR
1471.7454	1470.7381	1470.7354	0.0027	112	124	0	109	YDAYVATLSEALR
1927.0920	1926.0847	1926.0825	0.0022	144	161	1	---	VIPAGELQVIEKVDAAFK
1975.1290	1974.1217	1974.1149	0.0069	125	143	0	---	IIAGTLEVHAVKPAAEEVK
2300.1614	2299.1541	2299.1483	0.0058	55	77	1	---	TFVATFGAASNKAFAEGLSGEPK
2427.2056	2426.1983	2426.1964	0.0019	102	124	1	---	TAEGATPEAKYDAYVATLSEALR
2427.2056	2426.1983	2426.1964	0.0019	102	124	1	170	TAEGATPEAKYDAYVATLSEALR
2737.4329	2736.4256	2736.3870	0.0386	162	188	1	---	VAATAANAAPANDKFTVFEAAFNNAIK

No match to: 713.4029, 768.5154, 1135.5865, 1289.6852, 1291.6776, 1541.8490, 1541.8490, 1571.8823, 1726.9725, 1920.0474, 2172.1956, 2172.1956, 2444.2896, 2656.5139, 3442.8713

3. gi|398830 **Mass:** 31083 **Score:** 544 **Expect:** 2.4e-049 **Queries matched:** 16

Phlp5 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1058.6141	1057.6068	1057.6171	-0.0103	237	246	0	---	FIPALEAAVK
1065.5106	1064.5033	1064.5172	-0.0138	271	280	0	---	AITAMSEAQK + Oxidation (M)
1071.5646	1070.5573	1070.5648	-0.0074	261	269	0	---	YTVFETALK
1105.5419	1104.5346	1104.5451	-0.0104	104	114	0	96	AFAEGLSGEPK
1105.5419	1104.5346	1104.5451	-0.0104	104	114	0	---	AFAEGLSGEPK
1199.6609	1198.6536	1198.6597	-0.0061	261	270	1	---	YTVFETALKK
1213.6147	1212.6074	1212.6138	-0.0064	92	103	0	---	TFVATFGAASNK
1289.6852	1288.6779	1288.6874	-0.0095	59	69	1	---	ATTEEQKLIEK
1295.7638	1294.7565	1294.7496	0.0070	181	192	0	---	VIPAGELQVIEK
1471.7454	1470.7381	1470.7354	0.0027	149	161	0	---	YDAYVATLSEALR
1471.7454	1470.7381	1470.7354	0.0027	149	161	0	109	YDAYVATLSEALR
1927.0920	1926.0847	1926.0825	0.0022	181	198	1	---	VIPAGELQVIEKVDAAFK
1975.1290	1974.1217	1974.1149	0.0069	162	180	0	---	IIAGTLEVHAVKPAAEEVK
2300.1614	2299.1541	2299.1483	0.0058	92	114	1	---	TFVATFGAASNKAFAEGLSGEPK
2427.2056	2426.1983	2426.1964	0.0019	139	161	1	---	TAEGATPEAKYDAYVATLSEALR

2427.2056	2426.1983	2426.1964	0.0019	139 - 161	1	170	TAEGATPEAKYDAYVATLSEALR

No match to: 713.4029, 768.5154, 1135.5865, 1291.6776, 1541.8490, 1541.8490, 1571.8823, 1726.9725, 1920.0474, 2172.1956, 2172.1956, 2444.2896, 2656.5139, 2737.4329, 3442.8713

4. gi|1092249 **Mass:** 28713 **Score:** 512 **Expect:** 3.8e-046 **Queries matched:** 14

major allergen Phl p Va

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1058.6141	1057.6068	1057.6171	-0.0103	211 - 220		0	---	FIPALEAAVK
1065.5106	1064.5033	1064.5172	-0.0138	245 - 254		0	---	AITAMSEAQK + Oxidation (M)
1071.5646	1070.5573	1070.5648	-0.0074	235 - 243		0	---	YTVFETALK
1105.5419	1104.5346	1104.5451	-0.0104	78 - 88		0	96	AFAEGLSGEPK
1105.5419	1104.5346	1104.5451	-0.0104	78 - 88		0	---	AFAEGLSGEPK
1199.6609	1198.6536	1198.6597	-0.0061	235 - 244		1	---	YTVFETALKK
1289.6852	1288.6779	1288.6874	-0.0095	34 - 44		1	---	ATTEEQKLIEK
1295.7638	1294.7565	1294.7496	0.0070	155 - 166		0	---	VIPAGELQVIEK
1471.7454	1470.7381	1470.7354	0.0027	123 - 135		0	---	YDAYVATLSEALR
1471.7454	1470.7381	1470.7354	0.0027	123 - 135		0	109	YDAYVATLSEALR
1927.0920	1926.0847	1926.0825	0.0022	155 - 172		1	---	VIPAGELQVIEKVDAAFK
1975.1290	1974.1217	1974.1149	0.0069	136 - 154		0	---	IIAGTLEVHAVKPAAEEVK
2427.2056	2426.1983	2426.1964	0.0019	113 - 135		1	---	TAEGATPEAKYDAYVATLSEALR
2427.2056	2426.1983	2426.1964	0.0019	113 - 135		1	170	TAEGATPEAKYDAYVATLSEALR

No match to: 713.4029, 768.5154, 1135.5865, 1213.6147, 1291.6776, 1541.8490, 1541.8490, 1571.8823, 1726.9725, 1920.0474, 2172.1956, 2172.1956, 2300.1614, 2444.2896, 2656.5139, 2737.4329, 3442.8713

5. gi|2851456 **Mass:** 28513 **Score:** 511 **Expect:** 4.8e-046 **Queries matched:** 14

RecName: Full=Pollen allergen Phl p 5a; AltName: Full=Allergen Phl p Va; AltName: Allergen=Phl p 5a

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1058.6141	1057.6068	1057.6171	-0.0103	211 - 220		0	---	FIPALEAAVK
1065.5106	1064.5033	1064.5172	-0.0138	245 - 254		0	---	AITAMSEAQK + Oxidation (M)
1071.5646	1070.5573	1070.5648	-0.0074	235 - 243		0	---	YTVFETALK
1105.5419	1104.5346	1104.5451	-0.0104	78 - 88		0	96	AFAEGLSGEPK
1105.5419	1104.5346	1104.5451	-0.0104	78 - 88		0	---	AFAEGLSGEPK
1199.6609	1198.6536	1198.6597	-0.0061	235 - 244		1	---	YTVFETALKK
1289.6852	1288.6779	1288.6874	-0.0095	34 - 44		1	---	ATTEEQKLIEK
1295.7638	1294.7565	1294.7496	0.0070	155 - 166		0	---	VIPAGELQVIEK
1471.7454	1470.7381	1470.7354	0.0027	123 - 135		0	---	YDAYVATLSEALR
1471.7454	1470.7381	1470.7354	0.0027	123 - 135		0	109	YDAYVATLSEALR
1927.0920	1926.0847	1926.0825	0.0022	155 - 172		1	---	VIPAGELQVIEKVDAAFK
1975.1290	1974.1217	1974.1149	0.0069	136 - 154		0	---	IIAGTLEVHAVKPAAEEVK
2427.2056	2426.1983	2426.1964	0.0019	113 - 135		1	---	TAEGATPEAKYDAYVATLSEALR
2427.2056	2426.1983	2426.1964	0.0019	113 - 135		1	170	TAEGATPEAKYDAYVATLSEALR

No match to: 713.4029, 768.5154, 1135.5865, 1213.6147, 1291.6776, 1541.8490, 1541.8490, 1571.8823, 1726.9725,

1920.0474, 2172.1956, 2172.1956, 2300.1614, 2444.2896, 2656.5139, 2737.4329, 3442.8713

6. gi|422005 **Mass:** 26530 **Score:** 482 **Expect:** 3.8e-043 **Queries matched:** 12

PHLP5A protein - common timothy (fragment)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1058.6141	1057.6068	1057.6171	-0.0103	183	192	0	---	FIPALEAAVK
1065.5106	1064.5033	1064.5172	-0.0138	217	226	0	---	AITAMSEAQK + Oxidation (M)
1071.5646	1070.5573	1070.5648	-0.0074	207	215	0	---	YTVFETALK
1105.5419	1104.5346	1104.5451	-0.0104	50	60	0	96	AFAEGLSGEPK
1105.5419	1104.5346	1104.5451	-0.0104	50	60	0	---	AFAEGLSGEPK
1199.6609	1198.6536	1198.6597	-0.0061	207	216	1	---	YTVFETALKK
1289.6852	1288.6779	1288.6874	-0.0095	7	17	1	---	ATTEEQKLIEK
1471.7454	1470.7381	1470.7354	0.0027	95	107	0	---	YDAYVATLSEALR
1471.7454	1470.7381	1470.7354	0.0027	95	107	0	109	YDAYVATLSEALR
1975.1290	1974.1217	1974.1149	0.0069	108	126	0	---	IIAGTLEVHAVKPAAEEVK
2427.2056	2426.1983	2426.1964	0.0019	85	107	1	---	TAEGATPEAKYDAYVATLSEALR
2427.2056	2426.1983	2426.1964	0.0019	85	107	1	170	TAEGATPEAKYDAYVATLSEALR

No match to: 713.4029, 768.5154, 1135.5865, 1213.6147, 1291.6776, 1295.7638, 1541.8490, 1541.8490, 1571.8823, 1726.9725, 1920.0474, 1927.0920, 2172.1956, 2172.1956, 2300.1614, 2444.2896, 2656.5139, 2737.4329, 3442.8713

7. gi|3135501 **Mass:** 27586 **Score:** 417 **Expect:** 1.2e-036 **Queries matched:** 13

major allergen Phl p 5 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1058.6141	1057.6068	1057.6171	-0.0103	201	210	0	---	FIPALEAAVK
1065.5106	1064.5033	1064.5172	-0.0138	235	244	0	---	AITAMSEAQK + Oxidation (M)
1071.5646	1070.5573	1070.5648	-0.0074	225	233	0	---	YTVFETALK
1199.6609	1198.6536	1198.6597	-0.0061	225	234	1	---	YTVFETALKK
1213.6147	1212.6074	1212.6138	-0.0064	56	67	0	---	TFVATFGAASNK
1289.6852	1288.6779	1288.6874	-0.0095	23	33	1	---	ATTEEQKLIEK
1295.7638	1294.7565	1294.7496	0.0070	145	156	0	---	VIPAGELQVIEK
1471.7454	1470.7381	1470.7354	0.0027	113	125	0	---	YDAYVATLSEALR
1471.7454	1470.7381	1470.7354	0.0027	113	125	0	109	YDAYVATLSEALR
1975.1290	1974.1217	1974.1149	0.0069	126	144	0	---	IIAGTLEVHAVKPAAEEVK
2427.2056	2426.1983	2426.1964	0.0019	103	125	1	---	TAEGATPEAKYDAYVATLSEALR
2427.2056	2426.1983	2426.1964	0.0019	103	125	1	170	TAEGATPEAKYDAYVATLSEALR
2737.4329	2736.4256	2736.3870	0.0386	163	189	1	---	VAATAANAAPANDKFTVFEAAFNNAIK

No match to: 713.4029, 768.5154, 1105.5419, 1105.5419, 1135.5865, 1291.6776, 1541.8490, 1541.8490, 1571.8823, 1726.9725, 1920.0474, 1927.0920, 2172.1956, 2172.1956, 2300.1614, 2444.2896, 2656.5139, 3442.8713

8. gi|3135499 **Mass:** 27658 **Score:** 417 **Expect:** 1.2e-036 **Queries matched:** 13

major allergen Phl p 5 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide

1058.6141	1057.6068	1057.6171	-0.0103	201 - 210	0	---	FIPALEAAVK
1065.5106	1064.5033	1064.5172	-0.0138	235 - 244	0	---	AITAMSEAQK + Oxidation (M)
1071.5646	1070.5573	1070.5648	-0.0074	225 - 233	0	---	YTVFETALK
1199.6609	1198.6536	1198.6597	-0.0061	225 - 234	1	---	YTVFETALKK
1213.6147	1212.6074	1212.6138	-0.0064	56 - 67	0	---	TFVATFGAASNK
1289.6852	1288.6779	1288.6874	-0.0095	23 - 33	1	---	ATTEEQKLIEK
1295.7638	1294.7565	1294.7496	0.0070	145 - 156	0	---	VIPAGELQVIEK
1471.7454	1470.7381	1470.7354	0.0027	113 - 125	0	---	YDAYVATLSEALR
1471.7454	1470.7381	1470.7354	0.0027	113 - 125	0	109	YDAYVATLSEALR
1975.1290	1974.1217	1974.1149	0.0069	126 - 144	0	---	IIAGTLEVHAVKPAAEEVK
2427.2056	2426.1983	2426.1964	0.0019	103 - 125	1	---	TAEGATPEAKYDAYVATLSEALR
2427.2056	2426.1983	2426.1964	0.0019	103 - 125	1	170	TAEGATPEAKYDAYVATLSEALR
2737.4329	2736.4256	2736.3870	0.0386	163 - 189	1	---	VAATAANAAPANDKFTVFEAAFNNAIK

No match to: 713.4029, 768.5154, 1105.5419, 1105.5419, 1135.5865, 1291.6776, 1541.8490, 1541.8490, 1571.8823, 1726.9725, 1920.0474, 1927.0920, 2172.1956, 2172.1956, 2300.1614, 2444.2896, 2656.5139, 3442.8713

9. gi|3135503 **Mass:** 27692 **Score:** 400 **Expect:** 6e-035 **Queries matched:** 12

major allergen Phl p 5 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1058.6141	1057.6068	1057.6171	-0.0103	201 - 210	0	---	FIPALEAAVK
1071.5646	1070.5573	1070.5648	-0.0074	225 - 233	0	---	YTVFETALK
1199.6609	1198.6536	1198.6597	-0.0061	225 - 234	1	---	YTVFETALKK
1213.6147	1212.6074	1212.6138	-0.0064	56 - 67	0	---	TFVATFGAASNK
1289.6852	1288.6779	1288.6874	-0.0095	23 - 33	1	---	ATTEEQKLIEK
1295.7638	1294.7565	1294.7496	0.0070	145 - 156	0	---	VIPAGELQVIEK
1471.7454	1470.7381	1470.7354	0.0027	113 - 125	0	---	YDAYVATLSEALR
1471.7454	1470.7381	1470.7354	0.0027	113 - 125	0	109	YDAYVATLSEALR
1975.1290	1974.1217	1974.1149	0.0069	126 - 144	0	---	IIAGTLEVHAVKPAAEEVK
2427.2056	2426.1983	2426.1964	0.0019	103 - 125	1	---	TAEGATPEAKYDAYVATLSEALR
2427.2056	2426.1983	2426.1964	0.0019	103 - 125	1	170	TAEGATPEAKYDAYVATLSEALR
2737.4329	2736.4256	2736.3870	0.0386	163 - 189	1	---	VAATAANAAPANDKFTVFEAAFNNAIK

No match to: 713.4029, 768.5154, 1065.5106, 1105.5419, 1105.5419, 1135.5865, 1291.6776, 1541.8490, 1541.8490, 1571.8823, 1726.9725, 1920.0474, 1927.0920, 2172.1956, 2172.1956, 2300.1614, 2444.2896, 2656.5139, 3442.8713

10. gi|3309039 **Mass:** 31010 **Score:** 372 **Expect:** 3.8e-032 **Queries matched:** 14

group V allergen Phl p 5.0103 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1058.6141	1057.6068	1057.6171	-0.0103	237 - 246	0	---	FIPALEAAVK
1065.5106	1064.5033	1064.5172	-0.0138	271 - 280	0	---	AITAMSEAQK + Oxidation (M)
1071.5646	1070.5573	1070.5648	-0.0074	261 - 269	0	---	YTVFETALK
1105.5419	1104.5346	1104.5451	-0.0104	104 - 114	0	96	AFAEGLSGEPK

1105.5419	1104.5346	1104.5451	-0.0104	104 - 114	0	---	AFAEGLSGEPK
1199.6609	1198.6536	1198.6597	-0.0061	261 - 270	1	---	YTVFETALKK
1213.6147	1212.6074	1212.6138	-0.0064	92 - 103	0	---	TFVATFGAASNK
1289.6852	1288.6779	1288.6874	-0.0095	59 - 69	1	---	ATTEEQKLIEK
1295.7638	1294.7565	1294.7496	0.0070	181 - 192	0	---	VIPAGELQVIEK
1541.8490	1540.8417	1540.8361	0.0056	76 - 91	1	128	AALAAAAGVPPADKYR
1541.8490	1540.8417	1540.8361	0.0056	76 - 91	1	---	AALAAAAGVPPADKYR
1927.0920	1926.0847	1926.0825	0.0022	181 - 198	1	---	VIPAGELQVIEKVDAAFK
1975.1290	1974.1217	1974.1149	0.0069	162 - 180	0	---	IIAGTLEVHAVKPAAEEVK
2300.1614	2299.1541	2299.1483	0.0058	92 - 114	1	---	TFVATFGAASNKAFAEGLSGEPK

No match to: 713.4029, 768.5154, 1135.5865, 1291.6776, 1471.7454, 1471.7454, 1571.8823, 1726.9725, 1920.0474, 2172.1956, 2172.1956, 2427.2056, 2427.2056, 2444.2896, 2656.5139, 2737.4329, 3442.8713

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 31

Protein View

Match to: **gi|29500897** Score: **721** Expect: **4.8e-067**
phl p5a allergen precursor [Phleum pratense]

Nominal mass (M_r): **28269**; Calculated pI value: **7.94**
NCBI BLAST search of gi|29500897 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **58%**

Matched peptides shown in **Bold Red**

```
   1 ADLGYGPATP AAPAAGYTPA APAGAEPAGK ATTEEQKLIE KINAGFKAAL
  51 AAAAGVPPAD KYRTFVATFG AASNKAFAEG LSGEPKGAAE SSSKAALTSK
 101 LDAAYKLAYK TAEGATPEAK YDAYVATLSE ALRIIAGTLE VHAVKPAAEE
 151 VKVIPAGELQ VIEKVDAAFK VAATAANAAP ANDKFTVFEA AFNNAIKAST
 201 GGAYESYKFI PALEAAVKQA YAATVATAPE VKYTVFETAL KKAITAMSEA
 251 QKAAKPAAAA TATATSAVGA ATGAATAATG GYKV
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
31 - 41	1289.6852	1288.6779	1288.6874	-0.0095	1	ATTEEQKLIEK (No match)
48 - 63	1541.8490	1540.8417	1540.8361	0.0056	1	AALAAAAGVPPADKYR (Ions score 128)
48 - 63	1541.8490	1540.8417	1540.8361	0.0056	1	AALAAAAGVPPADKYR (No match)
64 - 75	1213.6147	1212.6074	1212.6138	-0.0064	0	TFVATFGAASNK (No match)
64 - 86	2300.1614	2299.1541	2299.1483	0.0058	1	TFVATFGAASNKAFAEGLSGEPK (No match)
76 - 86	1105.5419	1104.5346	1104.5451	-0.0104	0	AFAEGLSGEPK (Ions score 96)
76 - 86	1105.5419	1104.5346	1104.5451	-0.0104	0	AFAEGLSGEPK (No match)
111 - 133	2427.2056	2426.1983	2426.1964	0.0019	1	TAEGATPEAKYDAYVATLSEALR (No match)
111 - 133	2427.2056	2426.1983	2426.1964	0.0019	1	TAEGATPEAKYDAYVATLSEALR (Ions score 170)
121 - 133	1471.7454	1470.7381	1470.7354	0.0027	0	YDAYVATLSEALR (No match)
121 - 133	1471.7454	1470.7381	1470.7354	0.0027	0	YDAYVATLSEALR (Ions score 109)
134 - 152	1975.1290	1974.1217	1974.1149	0.0069	0	IIAGTLEVHAVKPAAEEVK (No match)
153 - 164	1295.7638	1294.7565	1294.7496	0.0070	0	VIPAGELQVIEK (No match)
153 - 170	1927.0920	1926.0847	1926.0825	0.0022	1	VIPAGELQVIEKVDAAFK (No match)
171 - 197	2737.4329	2736.4256	2736.3870	0.0386	1	VAATAANAAPANDKFTVFEAAFNNAIK (No match)
209 - 218	1058.6141	1057.6068	1057.6171	-0.0103	0	FIPALEAAVK (No match)
233 - 241	1071.5646	1070.5573	1070.5648	-0.0074	0	YTVFETALK (No match)
233 - 242	1199.6609	1198.6536	1198.6597	-0.0061	1	YTVFETALKK (No match)
243 - 252	1065.5106	1064.5033	1064.5172	-0.0138	0	AITAMSEAQK Oxidation (M) (No match)

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	Accession	Mass	Score	Description
1.	gi|29500897	28269	809	phl p5a allergen precursor [Phleum pratense]
2.	gi|398830	31083	667	Phlp5 [Phleum pratense]
3.	gi|13430402	27795	644	group V allergen Phl p 5 precursor [Phleum pratense]
4.	gi|3309039	31010	462	group V allergen Phl p 5.0103 precursor [Phleum pratense]
5.	gi|1092249	28713	439	major allergen Phl p Va

Results List

1. gi|29500897 **Mass:** 28269 **Score:** 809 **Expect:** 7.6e-076 **Queries matched:** 22

phl p5a allergen precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1058.6224	1057.6151	1057.6171	-0.0020	209	218	0	---	FIPALEAAVK
1065.5217	1064.5144	1064.5172	-0.0027	243	252	0	---	AITAMSEAQK + Oxidation (M)
1071.5658	1070.5585	1070.5648	-0.0062	233	241	0	---	YTVFETALK
1105.5505	1104.5432	1104.5451	-0.0018	76	86	0	---	AFAEGLSGEPK
1199.6663	1198.6590	1198.6597	-0.0007	233	242	1	---	YTVFETALKK
1213.6216	1212.6143	1212.6138	0.0005	64	75	0	---	TFVATFGAASNK
1251.6912	1250.6839	1250.6870	-0.0031	95	106	1	---	AALTSKLDAAYK
1289.6952	1288.6879	1288.6874	0.0005	31	41	1	---	ATTEEQKLIEK
1295.7474	1294.7401	1294.7496	-0.0094	153	164	0	---	VIPAGELQVIEK
1419.7549	1418.7476	1418.7405	0.0071	219	232	0	---	QAYAATVATAPEVK
1471.7468	1470.7395	1470.7354	0.0041	121	133	0	---	YDAYVATLSEALR
1471.7468	1470.7395	1470.7354	0.0041	121	133	0	109	YDAYVATLSEALR
1541.8501	1540.8428	1540.8361	0.0067	48	63	1	113	AALAAAAGVPPADKYR
1541.8501	1540.8428	1540.8361	0.0067	48	63	1	---	AALAAAAGVPPADKYR
1822.8927	1821.8854	1821.8744	0.0111	76	94	1	---	AFAEGLSGEPKGAAESSSK
1927.1006	1926.0933	1926.0825	0.0108	153	170	1	---	VIPAGELQVIEKVDAAFK
1975.1299	1974.1226	1974.1149	0.0078	134	152	0	---	IIAGTLEVHAVKPAAEEVK
2300.1716	2299.1643	2299.1483	0.0160	64	86	1	---	TFVATFGAASNKAFAEGLSGEPK
2300.1716	2299.1643	2299.1483	0.0160	64	86	1	182	TFVATFGAASNKAFAEGLSGEPK
2427.2117	2426.2044	2426.1964	0.0080	111	133	1	173	TAEGATPEAKYDAYVATLSEALR
2427.2117	2426.2044	2426.1964	0.0080	111	133	1	---	TAEGATPEAKYDAYVATLSEALR
2737.4248	2736.4175	2736.3870	0.0305	171	197	1	---	VAATAANAAPANDKFTVFEAAFNNAIK

No match to: 713.4125, 724.5040, 768.5264, 973.5480, 1004.4981, 1149.5956, 1195.6110, 1291.6786, 1305.6938, 1571.8850, 1572.8779, 1726.9786, 1920.0525, 2172.1975, 2172.1975, 2444.3027, 2655.5164, 2706.4626, 2902.4739, 3017.4983, 3252.8818, 3350.6189, 3442.8757, 3809.8357, 3823.9841, 3884.2361

2. gi|398830 **Mass:** 31083 **Score:** 667 **Expect:** 1.2e-061 **Queries matched:** 20

Phlp5 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1058.6224	1057.6151	1057.6171	-0.0020	237	246	0	---	FIPALEAAVK
1065.5217	1064.5144	1064.5172	-0.0027	271	280	0	---	AITAMSEAQK + Oxidation (M)
1071.5658	1070.5585	1070.5648	-0.0062	261	269	0	---	YTVFETALK
1105.5505	1104.5432	1104.5451	-0.0018	104	114	0	---	AFAEGLSGEPK
1199.6663	1198.6590	1198.6597	-0.0007	261	270	1	---	YTVFETALKK
1213.6216	1212.6143	1212.6138	0.0005	92	103	0	---	TFVATFGAASNK
1251.6912	1250.6839	1250.6870	-0.0031	123	134	1	---	AALTSKLDAAYK
1289.6952	1288.6879	1288.6874	0.0005	59	69	1	---	ATTEEQKLIEK
1295.7474	1294.7401	1294.7496	-0.0094	181	192	0	---	VIPAGELQVIEK
1419.7549	1418.7476	1418.7405	0.0071	247	260	0	---	QAYAATVATAPEVK
1471.7468	1470.7395	1470.7354	0.0041	149	161	0	---	YDAYVATLSEALR
1471.7468	1470.7395	1470.7354	0.0041	149	161	0	109	YDAYVATLSEALR
1572.8779	1571.8706	1571.8419	0.0287	76	91	1	---	AALAAAAGVQPADKYR
1822.8927	1821.8854	1821.8744	0.0111	104	122	1	---	AFAEGLSGEPKGAAESSSK
1927.1006	1926.0933	1926.0825	0.0108	181	198	1	---	VIPAGELQVIEKVDAAFK
1975.1299	1974.1226	1974.1149	0.0078	162	180	0	---	IIAGTLEVHAVKPAAEEVK
2300.1716	2299.1643	2299.1483	0.0160	92	114	1	---	TFVATFGAASNKAFAEGLSGEPK
2300.1716	2299.1643	2299.1483	0.0160	92	114	1	182	TFVATFGAASNKAFAEGLSGEPK
2427.2117	2426.2044	2426.1964	0.0080	139	161	1	173	TAEGATPEAKYDAYVATLSEALR
2427.2117	2426.2044	2426.1964	0.0080	139	161	1	---	TAEGATPEAKYDAYVATLSEALR

No match to: 713.4125, 724.5040, 768.5264, 973.5480, 1004.4981, 1149.5956, 1195.6110, 1291.6786, 1305.6938, 1541.8501, 1541.8501, 1571.8850, 1726.9786, 1920.0525, 2172.1975, 2172.1975, 2444.3027, 2655.5164, 2706.4626, 2737.4248, 2902.4739, 3017.4983, 3252.8818, 3350.6189, 3442.8757, 3809.8357, 3823.9841, 3884.2361

3. gi|13430402 **Mass:** 27795 **Score:** 644 **Expect:** 2.4e-059 **Queries matched:** 18

group V allergen Phl p 5 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1058.6224	1057.6151	1057.6171	-0.0020	200	209	0	---	FIPALEAAVK
1065.5217	1064.5144	1064.5172	-0.0027	234	243	0	---	AITAMSEAQK + Oxidation (M)
1071.5658	1070.5585	1070.5648	-0.0062	224	232	0	---	YTVFETALK
1105.5505	1104.5432	1104.5451	-0.0018	67	77	0	---	AFAEGLSGEPK
1199.6663	1198.6590	1198.6597	-0.0007	224	233	1	---	YTVFETALKK
1213.6216	1212.6143	1212.6138	0.0005	55	66	0	---	TFVATFGAASNK
1251.6912	1250.6839	1250.6870	-0.0031	86	97	1	---	AALTSKLDAAYK
1295.7474	1294.7401	1294.7496	-0.0094	144	155	0	---	VIPAGELQVIEK
1419.7549	1418.7476	1418.7405	0.0071	210	223	0	---	QAYAATVATAPEVK
1471.7468	1470.7395	1470.7354	0.0041	112	124	0	---	YDAYVATLSEALR
1471.7468	1470.7395	1470.7354	0.0041	112	124	0	109	YDAYVATLSEALR

1927.1006	1926.0933	1926.0825	0.0108	144 - 161	1	---	VIPAGELQVIEKVDAAFK
1975.1299	1974.1226	1974.1149	0.0078	125 - 143	0	---	IIAGTLEVHAVKPAAEEVK
2300.1716	2299.1643	2299.1483	0.0160	55 - 77	1	---	TFVATFGAASNKAFAEGLSGEPK
2300.1716	2299.1643	2299.1483	0.0160	55 - 77	1	182	TFVATFGAASNKAFAEGLSGEPK
2427.2117	2426.2044	2426.1964	0.0080	102 - 124	1	173	TAEGATPEAKYDAYVATLSEALR
2427.2117	2426.2044	2426.1964	0.0080	102 - 124	1	---	TAEGATPEAKYDAYVATLSEALR
2737.4248	2736.4175	2736.3870	0.0305	162 - 188	1	---	VAATAANAAPANDKFTVFEAAFNNAIK

No match to: 713.4125, 724.5040, 768.5264, 973.5480, 1004.4981, 1149.5956, 1195.6110, 1289.6952, 1291.6786, 1305.6938, 1541.8501, 1541.8501, 1571.8850, 1572.8779, 1726.9786, 1822.8927, 1920.0525, 2172.1975, 2172.1975, 2444.3027, 2655.5164, 2706.4626, 2902.4739, 3017.4983, 3252.8818, 3350.6189, 3442.8757, 3809.8357, 3823.9841, 3884.2361

4. gi|3309039 **Mass:** 31010 **Score:** 462 **Expect:** 3.8e-041 **Queries matched:** 17

group V allergen Phl p 5.0103 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1058.6224	1057.6151	1057.6171	-0.0020	237 - 246	0	---	FIPALEAAVK
1065.5217	1064.5144	1064.5172	-0.0027	271 - 280	0	---	AITAMSEAQK + Oxidation (M)
1071.5658	1070.5585	1070.5648	-0.0062	261 - 269	0	---	YTVFETALK
1105.5505	1104.5432	1104.5451	-0.0018	104 - 114	0	---	AFAEGLSGEPK
1199.6663	1198.6590	1198.6597	-0.0007	261 - 270	1	---	YTVFETALKK
1213.6216	1212.6143	1212.6138	0.0005	92 - 103	0	---	TFVATFGAASNK
1251.6912	1250.6839	1250.6870	-0.0031	123 - 134	1	---	AALTSKLDAAYK
1289.6952	1288.6879	1288.6874	0.0005	59 - 69	1	---	ATTEEQKLIEK
1295.7474	1294.7401	1294.7496	-0.0094	181 - 192	0	---	VIPAGELQVIEK
1419.7549	1418.7476	1418.7405	0.0071	247 - 260	0	---	QAYAATVATAPEVK
1541.8501	1540.8428	1540.8361	0.0067	76 - 91	1	113	AALAAAAGVPPADKYR
1541.8501	1540.8428	1540.8361	0.0067	76 - 91	1	---	AALAAAAGVPPADKYR
1822.8927	1821.8854	1821.8744	0.0111	104 - 122	1	---	AFAEGLSGEPKGAAESSSK
1927.1006	1926.0933	1926.0825	0.0108	181 - 198	1	---	VIPAGELQVIEKVDAAFK
1975.1299	1974.1226	1974.1149	0.0078	162 - 180	0	---	IIAGTLEVHAVKPAAEEVK
2300.1716	2299.1643	2299.1483	0.0160	92 - 114	1	---	TFVATFGAASNKAFAEGLSGEPK
2300.1716	2299.1643	2299.1483	0.0160	92 - 114	1	182	TFVATFGAASNKAFAEGLSGEPK

No match to: 713.4125, 724.5040, 768.5264, 973.5480, 1004.4981, 1149.5956, 1195.6110, 1291.6786, 1305.6938, 1471.7468, 1471.7468, 1571.8850, 1572.8779, 1726.9786, 1920.0525, 2172.1975, 2172.1975, 2427.2117, 2427.2117, 2444.3027, 2655.5164, 2706.4626, 2737.4248, 2902.4739, 3017.4983, 3252.8818, 3350.6189, 3442.8757, 3809.8357, 3823.9841, 3884.2361

5. gi|1092249 **Mass:** 28713 **Score:** 439 **Expect:** 7.6e-039 **Queries matched:** 16

major allergen Phl p Va

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1058.6224	1057.6151	1057.6171	-0.0020	211 - 220	0	---	FIPALEAAVK
1065.5217	1064.5144	1064.5172	-0.0027	245 - 254	0	---	AITAMSEAQK + Oxidation (M)

1071.5658	1070.5585	1070.5648	-0.0062	235 - 243	0	---	YTVFETALK
1105.5505	1104.5432	1104.5451	-0.0018	78 - 88	0	---	AFAEGLSGEPK
1199.6663	1198.6590	1198.6597	-0.0007	235 - 244	1	---	YTVFETALKK
1251.6912	1250.6839	1250.6870	-0.0031	97 - 108	1	---	AALTSKLDAAYK
1289.6952	1288.6879	1288.6874	0.0005	34 - 44	1	---	ATTEEQKLIEK
1295.7474	1294.7401	1294.7496	-0.0094	155 - 166	0	---	VIPAGELQVIEK
1419.7549	1418.7476	1418.7405	0.0071	221 - 234	0	---	QAYAATVATAPEVK
1471.7468	1470.7395	1470.7354	0.0041	123 - 135	0	---	YDAYVATLSEALR
1471.7468	1470.7395	1470.7354	0.0041	123 - 135	0	109	YDAYVATLSEALR
1822.8927	1821.8854	1821.8744	0.0111	78 - 96	1	---	AFAEGLSGEPKGAAESSSK
1927.1006	1926.0933	1926.0825	0.0108	155 - 172	1	---	VIPAGELQVIEKVDAAFK
1975.1299	1974.1226	1974.1149	0.0078	136 - 154	0	---	IIAGTLEVHAVKPAAEEVK
2427.2117	2426.2044	2426.1964	0.0080	113 - 135	1	173	TAEGATPEAKYDAYVATLSEALR
2427.2117	2426.2044	2426.1964	0.0080	113 - 135	1	---	TAEGATPEAKYDAYVATLSEALR

No match to: 713.4125, 724.5040, 768.5264, 973.5480, 1004.4981, 1149.5956, 1195.6110, 1213.6216, 1291.6786, 1305.6938, 1541.8501, 1541.8501, 1571.8850, 1572.8779, 1726.9786, 1920.0525, 2172.1975, 2172.1975, 2300.1716, 2300.1716, 2444.3027, 2655.5164, 2706.4626, 2737.4248, 2902.4739, 3017.4983, 3252.8818, 3350.6189, 3442.8757, 3809.8357, 3823.9841, 3884.2361

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 48

Protein View

Match to: **gi|29500897** Score: **809** Expect: **7.6e-076**
phl p5a allergen precursor [Phleum pratense]

Nominal mass (M_r): **28269**; Calculated pI value: **7.94**
NCBI BLAST search of gi|29500897 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **70%**

Matched peptides shown in **Bold Red**

```
   1 ADLGYGPATP AAPAAGYTPA APAGAEPAGK ATTEEQKLIE KINAGFKAAL
  51 AAAAGVPPAD KYRTFVATFG AASNKAFAEG LSGEPKGAAE SSSKAALTSK
 101 LDAAYKLAYK TAEGATPEAK YDAYVATLSE ALRIIAGTLE VHAVKPAAEE
 151 VKVIPAGELQ VIEKVDAAFK VAATAANAAP ANDKFTVFEA AFNNAIKAST
 201 GGAYESYKFI PALEAAVKQA YAATVATAPE VKYTVFETAL KKAITAMSEA
 251 QKAAKPAAAA TATATSAVGA ATGAATAATG GYKV
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
31 - 41	1289.6952	1288.6879	1288.6874	0.0005	1	**ATTEEQKLIEK** (No match)
48 - 63	1541.8501	1540.8428	1540.8361	0.0067	1	**AALAAAAGVPPADKYR** (Ions score 113)
48 - 63	1541.8501	1540.8428	1540.8361	0.0067	1	**AALAAAAGVPPADKYR** (No match)
64 - 75	1213.6216	1212.6143	1212.6138	0.0005	0	**TFVATFGAASNK** (No match)
64 - 86	2300.1716	2299.1643	2299.1483	0.0160	1	**TFVATFGAASNKAFAEGLSGEPK** (No match)
64 - 86	2300.1716	2299.1643	2299.1483	0.0160	1	**TFVATFGAASNKAFAEGLSGEPK** (Ions score 182)
76 - 86	1105.5505	1104.5432	1104.5451	-0.0018	0	**AFAEGLSGEPK** (No match)
76 - 94	1822.8927	1821.8854	1821.8744	0.0111	1	**AFAEGLSGEPKGAAESSSK** (No match)
95 - 106	1251.6912	1250.6839	1250.6870	-0.0031	1	**AALTSKLDAAYK** (No match)
111 - 133	2427.2117	2426.2044	2426.1964	0.0080	1	**TAEGATPEAKYDAYVATLSEALR** (Ions score 173)
111 - 133	2427.2117	2426.2044	2426.1964	0.0080	1	**TAEGATPEAKYDAYVATLSEALR** (No match)
121 - 133	1471.7468	1470.7395	1470.7354	0.0041	0	**YDAYVATLSEALR** (No match)
121 - 133	1471.7468	1470.7395	1470.7354	0.0041	0	**YDAYVATLSEALR** (Ions score 109)
134 - 152	1975.1299	1974.1226	1974.1149	0.0078	0	**IIAGTLEVHAVKPAAEEVK** (No match)
153 - 164	1295.7474	1294.7401	1294.7496	-0.0094	0	**VIPAGELQVIEK** (No match)
153 - 170	1927.1006	1926.0933	1926.0825	0.0108	1	**VIPAGELQVIEKVDAAFK** (No match)
171 - 197	2737.4248	2736.4175	2736.3870	0.0305	1	**VAATAANAAPANDKFTVFEAAFNNAIK** (No match)
209 - 218	1058.6224	1057.6151	1057.6171	-0.0020	0	**FIPALEAAVK** (No match)
219 - 232	1419.7549	1418.7476	1418.7405	0.0071	0	**QAYAATVATAPEVK** (No match)
233 - 241	1071.5658	1070.5585	1070.5648	-0.0062	0	**YTVFETALK** (No match)
233 - 242	1199.6663	1198.6590	1198.6597	-0.0007	1	**YTVFETALKK** (No match)
243 - 252	1065.5217	1064.5144	1064.5172	-0.0027	0	**AITAMSEAQK** Oxidation (M) (No match)

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	Accession	Mass	Score	Description
1.	gi|29500897	28269	284	phl p5a allergen precursor [Phleum pratense]
2.	gi|3309039	31010	238	group V allergen Phl p 5.0103 precursor [Phleum pratense]
3.	gi|13430402	27795	205	group V allergen Phl p 5 precursor [Phleum pratense]
4.	gi|398830	31083	204	Phlp5 [Phleum pratense]
5.	gi|422005	26530	105	PHLP5A protein - common timothy (fragment)
6.	gi|113561	32641	105	RecName: Full=Pollen allergen KBG 41; AltName: Full=Pollen allergen Poa p 9; AltName: Full=Alle
7.	gi|1092249	28713	104	major allergen Phl p Va
8.	gi|2851456	28513	104	RecName: Full=Pollen allergen Phl p 5a; AltName: Full=Allergen Phl p Va; AltName: Allergen=Phl
9.	gi|113560	37798	103	RecName: Full=Pollen allergen KBG 31; AltName: Full=Pollen allergen Poa p 9; AltName: Full=Alle
10.	gi|1684720	27685	93	major allergen Phl p 5 [Phleum pratense]

Results List

1. gi|29500897 **Mass:** 28269 **Score:** 284 **Expect:** 2.4e-023 **Queries matched:** 9

phl p5a allergen precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1105.5435	1104.5362	1104.5451	-0.0088	76	86	0	---	AFAEGLSGEPK
1199.6622	1198.6549	1198.6597	-0.0048	233	242	1	47	YTVFETALKK
1199.6622	1198.6549	1198.6597	-0.0048	233	242	1	---	YTVFETALKK
1471.7388	1470.7315	1470.7354	-0.0039	121	133	0	29	YDAYVATLSEALR
1471.7388	1470.7315	1470.7354	-0.0039	121	133	0	---	YDAYVATLSEALR
1541.8369	1540.8296	1540.8361	-0.0065	48	63	1	---	AALAAAAGVPPADKYR
1541.8369	1540.8296	1540.8361	-0.0065	48	63	1	62	AALAAAAGVPPADKYR
2300.1538	2299.1465	2299.1483	-0.0018	64	86	1	---	TFVATFGAASNKAFAEGLSGEPK
2300.1538	2299.1465	2299.1483	-0.0018	64	86	1	84	TFVATFGAASNKAFAEGLSGEPK

No match to: 713.4063, 768.5220, 864.4973, 1726.9666, 1920.0356, 1976.1205, 2172.1836, 2172.1836, 2429.2002, 2721.4209

2. gi|3309039 **Mass:** 31010 **Score:** 238 **Expect:** 9.6e-019 **Queries matched:** 7

group V allergen Phl p 5.0103 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1105.5435	1104.5362	1104.5451	-0.0088	104	114	0	---	AFAEGLSGEPK
1199.6622	1198.6549	1198.6597	-0.0048	261	270	1	47	YTVFETALKK
1199.6622	1198.6549	1198.6597	-0.0048	261	270	1	---	YTVFETALKK
1541.8369	1540.8296	1540.8361	-0.0065	76	91	1	---	AALAAAAGVPPADKYR
1541.8369	1540.8296	1540.8361	-0.0065	76	91	1	62	AALAAAAGVPPADKYR
2300.1538	2299.1465	2299.1483	-0.0018	92	114	1	---	TFVATFGAASNKAFAEGLSGEPK
2300.1538	2299.1465	2299.1483	-0.0018	92	114	1	84	TFVATFGAASNKAFAEGLSGEPK

No match to: 713.4063, 768.5220, 864.4973, 1471.7388, 1471.7388, 1726.9666, 1920.0356, 1976.1205, 2172.1836, 2172.1836, 2429.2002, 2721.4209

3. gi|13430402 **Mass:** 27795 **Score:** 205 **Expect:** 1.9e-015 **Queries matched:** 7

group V allergen Phl p 5 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1105.5435	1104.5362	1104.5451	-0.0088	67	77	0	---	AFAEGLSGEPK
1199.6622	1198.6549	1198.6597	-0.0048	224	233	1	47	YTVFETALKK
1199.6622	1198.6549	1198.6597	-0.0048	224	233	1	---	YTVFETALKK
1471.7388	1470.7315	1470.7354	-0.0039	112	124	0	29	YDAYVATLSEALR
1471.7388	1470.7315	1470.7354	-0.0039	112	124	0	---	YDAYVATLSEALR
2300.1538	2299.1465	2299.1483	-0.0018	55	77	1	---	TFVATFGAASNKAFAEGLSGEPK
2300.1538	2299.1465	2299.1483	-0.0018	55	77	1	84	TFVATFGAASNKAFAEGLSGEPK

No match to: 713.4063, 768.5220, 864.4973, 1541.8369, 1541.8369, 1726.9666, 1920.0356, 1976.1205, 2172.1836, 2172.1836, 2429.2002, 2721.4209

4. gi|398830 **Mass:** 31083 **Score:** 204 **Expect:** 2.4e-015 **Queries matched:** 7

Phlp5 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1105.5435	1104.5362	1104.5451	-0.0088	104	114	0	---	AFAEGLSGEPK
1199.6622	1198.6549	1198.6597	-0.0048	261	270	1	47	YTVFETALKK
1199.6622	1198.6549	1198.6597	-0.0048	261	270	1	---	YTVFETALKK
1471.7388	1470.7315	1470.7354	-0.0039	149	161	0	29	YDAYVATLSEALR
1471.7388	1470.7315	1470.7354	-0.0039	149	161	0	---	YDAYVATLSEALR
2300.1538	2299.1465	2299.1483	-0.0018	92	114	1	---	TFVATFGAASNKAFAEGLSGEPK
2300.1538	2299.1465	2299.1483	-0.0018	92	114	1	84	TFVATFGAASNKAFAEGLSGEPK

No match to: 713.4063, 768.5220, 864.4973, 1541.8369, 1541.8369, 1726.9666, 1920.0356, 1976.1205, 2172.1836, 2172.1836, 2429.2002, 2721.4209

5. gi|422005 **Mass:** 26530 **Score:** 105 **Expect:** 1.9e-005 **Queries matched:** 5

PHLP5A protein - common timothy (fragment)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1105.5435	1104.5362	1104.5451	-0.0088	50	60	0	---	AFAEGLSGEPK
1199.6622	1198.6549	1198.6597	-0.0048	207	216	1	47	YTVFETALKK
1199.6622	1198.6549	1198.6597	-0.0048	207	216	1	---	YTVFETALKK
1471.7388	1470.7315	1470.7354	-0.0039	95	107	0	29	YDAYVATLSEALR
1471.7388	1470.7315	1470.7354	-0.0039	95	107	0	---	YDAYVATLSEALR

No match to: 713.4063, 768.5220, 864.4973, 1541.8369, 1541.8369, 1726.9666, 1920.0356, 1976.1205, 2172.1836, 2172.1836, 2300.1538, 2300.1538, 2429.2002, 2721.4209

6. gi|113561 **Mass:** 32641 **Score:** 105 **Expect:** 1.9e-005 **Queries matched:** 6

RecName: Full=Pollen allergen KBG 41; AltName: Full=Pollen allergen Poa p 9; AltName: Full=Allergen

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1199.6622	1198.6549	1198.6597	-0.0048	263 -	272	1	47	YTVFETALKK
1199.6622	1198.6549	1198.6597	-0.0048	263 -	272	1	---	YTVFETALKK
1471.7388	1470.7315	1470.7354	-0.0039	151 -	163	0	29	YDAYVATLSEALR
1471.7388	1470.7315	1470.7354	-0.0039	151 -	163	0	---	YDAYVATLSEALR
2172.1836	2171.1763	2171.1262	0.0502	228 -	248	1	---	ASTGGAYQSYKFIPALEAAVK
2172.1836	2171.1763	2171.1262	0.0502	228 -	248	1	---	ASTGGAYQSYKFIPALEAAVK

No match to: 713.4063, 768.5220, 864.4973, 1105.5435, 1541.8369, 1541.8369, 1726.9666, 1920.0356, 1976.1205, 2300.1538, 2300.1538, 2429.2002, 2721.4209

7. gi|1092249 **Mass:** 28713 **Score:** 104 **Expect:** 2.4e-005 **Queries matched:** 5

major allergen Phl p Va

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1105.5435	1104.5362	1104.5451	-0.0088	78 -	88	0	---	AFAEGLSGEPK
1199.6622	1198.6549	1198.6597	-0.0048	235 -	244	1	47	YTVFETALKK
1199.6622	1198.6549	1198.6597	-0.0048	235 -	244	1	---	YTVFETALKK
1471.7388	1470.7315	1470.7354	-0.0039	123 -	135	0	29	YDAYVATLSEALR
1471.7388	1470.7315	1470.7354	-0.0039	123 -	135	0	---	YDAYVATLSEALR

No match to: 713.4063, 768.5220, 864.4973, 1541.8369, 1541.8369, 1726.9666, 1920.0356, 1976.1205, 2172.1836, 2172.1836, 2300.1538, 2300.1538, 2429.2002, 2721.4209

8. gi|2851456 **Mass:** 28513 **Score:** 104 **Expect:** 2.4e-005 **Queries matched:** 5

RecName: Full=Pollen allergen Phl p 5a; AltName: Full=Allergen Phl p Va; AltName: Allergen=Phl p 5a

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1105.5435	1104.5362	1104.5451	-0.0088	78 -	88	0	---	AFAEGLSGEPK
1199.6622	1198.6549	1198.6597	-0.0048	235 -	244	1	47	YTVFETALKK
1199.6622	1198.6549	1198.6597	-0.0048	235 -	244	1	---	YTVFETALKK
1471.7388	1470.7315	1470.7354	-0.0039	123 -	135	0	29	YDAYVATLSEALR
1471.7388	1470.7315	1470.7354	-0.0039	123 -	135	0	---	YDAYVATLSEALR

No match to: 713.4063, 768.5220, 864.4973, 1541.8369, 1541.8369, 1726.9666, 1920.0356, 1976.1205, 2172.1836, 2172.1836, 2300.1538, 2300.1538, 2429.2002, 2721.4209

9. gi|113560 **Mass:** 37798 **Score:** 103 **Expect:** 3e-005 **Queries matched:** 6

RecName: Full=Pollen allergen KBG 31; AltName: Full=Pollen allergen Poa p 9; AltName: Full=Allergen

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1199.6622	1198.6549	1198.6597	-0.0048	322 -	331	1	47	YTVFETALKK
1199.6622	1198.6549	1198.6597	-0.0048	322 -	331	1	---	YTVFETALKK
1471.7388	1470.7315	1470.7354	-0.0039	210 -	222	0	29	YDAYVATLSEALR
1471.7388	1470.7315	1470.7354	-0.0039	210 -	222	0	---	YDAYVATLSEALR
2172.1836	2171.1763	2171.1262	0.0502	287 -	307	1	---	ASTGGAYQSYKFIPALEAAVK
2172.1836	2171.1763	2171.1262	0.0502	287 -	307	1	---	ASTGGAYQSYKFIPALEAAVK

No match to: 713.4063, 768.5220, 864.4973, 1105.5435, 1541.8369, 1541.8369, 1726.9666, 1920.0356, 1976.1205,

2300.1538, 2300.1538, 2429.2002, 2721.4209

10. gi|1684720 **Mass:** 27685 **Score:** 93 **Expect:** 0.00031 **Queries matched:** 4
major allergen Phl p 5 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1199.6622	1198.6549	1198.6597	-0.0048	225 -	234	1	47	YTVFETALKK
1199.6622	1198.6549	1198.6597	-0.0048	225 -	234	1	---	YTVFETALKK
1471.7388	1470.7315	1470.7354	-0.0039	113 -	125	0	29	YDAYVATLSEALR
1471.7388	1470.7315	1470.7354	-0.0039	113 -	125	0	---	YDAYVATLSEALR

No match to: 713.4063, 768.5220, 864.4973, 1105.5435, 1541.8369, 1541.8369, 1726.9666, 1920.0356, 1976.1205, 2172.1836, 2172.1836, 2300.1538, 2300.1538, 2429.2002, 2721.4209

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 19

Protein View

Match to: **gi|29500897** Score: **284** Expect: **2.4e-023**
phl p5a allergen precursor [Phleum pratense]

Nominal mass (M_r): **28269**; Calculated pI value: **7.94**
NCBI BLAST search of gi|29500897 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

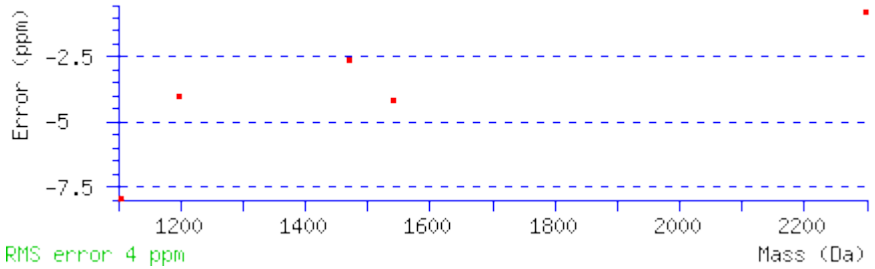
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **21%**

Matched peptides shown in **Bold Red**

```
   1 ADLGYGPATP AAPAAGYTPA APAGAEPAGK ATTEEQKLIE KINAGFKAAL
  51 AAAAGVPPAD KYRTFVATFG AASNKAFAEG LSGEPKGAAE SSSKAALTSK
 101 LDAAYKLAYK TAEGATPEAK YDAYVATLSE ALRIIAGTLE VHAVKPAAEE
 151 VKVIPAGELQ VIEKVDAAFK VAATAANAAP ANDKFTVFEA AFNNAIKAST
 201 GGAYESYKFI PALEAAVKQA YAATVATAPE VKYTVFETAL KKAITAMSEA
 251 QKAAKPAAAA TATATSAVGA ATGAATAATG GYKV
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
48 - 63	1541.8369	1540.8296	1540.8361	-0.0065	1	**AALAAAAGVPPADKYR**	(No match)
48 - 63	1541.8369	1540.8296	1540.8361	-0.0065	1	**AALAAAAGVPPADKYR**	(Ions score 62)
64 - 86	2300.1538	2299.1465	2299.1483	-0.0018	1	**TFVATFGAASNKAFAEGLSGEPK**	(No match)
64 - 86	2300.1538	2299.1465	2299.1483	-0.0018	1	**TFVATFGAASNKAFAEGLSGEPK**	(Ions score 84)
76 - 86	1105.5435	1104.5362	1104.5451	-0.0088	0	**AFAEGLSGEPK**	(No match)
121 - 133	1471.7388	1470.7315	1470.7354	-0.0039	0	**YDAYVATLSEALR**	(Ions score 29)
121 - 133	1471.7388	1470.7315	1470.7354	-0.0039	0	**YDAYVATLSEALR**	(No match)
233 - 242	1199.6622	1198.6549	1198.6597	-0.0048	1	**YTVFETALKK**	(Ions score 47)
233 - 242	1199.6622	1198.6549	1198.6597	-0.0048	1	**YTVFETALKK**	(No match)



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	Accession	Mass	Score	Description
1.	gi|29500897	28269	88	phl p5a allergen precursor [Phleum pratense]
2.	gi|3309039	31010	74	group V allergen Phl p 5.0103 precursor [Phleum pratense]
3.	gi|3135497	27595	65	major allergen Phl p 5 [Phleum pratense]
4.	gi|422005	26530	50	PHLP5A protein - common timothy (fragment)
5.	gi|13430402	27795	49	group V allergen Phl p 5 precursor [Phleum pratense]
6.	gi|3135503	27692	49	major allergen Phl p 5 [Phleum pratense]
7.	gi|3135501	27586	49	major allergen Phl p 5 [Phleum pratense]
8.	gi|3135499	27658	49	major allergen Phl p 5 [Phleum pratense]
9.	gi|1684720	27685	49	major allergen Phl p 5 [Phleum pratense]
10.	gi|1092249	28713	49	major allergen Phl p Va

Results List

1. gi|29500897 **Mass:** 28269 **Score:** 88 **Expect:** 0.00087 **Queries matched:** 6

phl p5a allergen precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1199.6577	1198.6504	1198.6597	-0.0093	233	242	1	---	YTVFETALKK
1471.7479	1470.7406	1470.7354	0.0052	121	133	0	---	YDAYVATLSEALR
1541.8420	1540.8347	1540.8361	-0.0014	48	63	1	---	AALAAAAGVPPADKYR
1541.8420	1540.8347	1540.8361	-0.0014	48	63	1	25	AALAAAAGVPPADKYR
1975.1201	1974.1128	1974.1149	-0.0020	134	152	0	19	IIAGTLEVHAVKPAAEEVK
1975.1201	1974.1128	1974.1149	-0.0020	134	152	0	---	IIAGTLEVHAVKPAAEEVK

No match to: 713.4103, 750.5139, 768.5247, 939.4847, 1021.5499, 1021.5499, 1334.8708, 1336.6455, 1448.9093, 1622.8771, 2123.0999, 2301.1658, 2428.2026

2. gi|3309039 **Mass:** 31010 **Score:** 74 **Expect:** 0.026 **Queries matched:** 5

group V allergen Phl p 5.0103 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1199.6577	1198.6504	1198.6597	-0.0093	261	270	1	---	YTVFETALKK
1541.8420	1540.8347	1540.8361	-0.0014	76	91	1	---	AALAAAAGVPPADKYR
1541.8420	1540.8347	1540.8361	-0.0014	76	91	1	25	AALAAAAGVPPADKYR
1975.1201	1974.1128	1974.1149	-0.0020	162	180	0	19	IIAGTLEVHAVKPAAEEVK
1975.1201	1974.1128	1974.1149	-0.0020	162	180	0	---	IIAGTLEVHAVKPAAEEVK

No match to: 713.4103, 750.5139, 768.5247, 939.4847, 1021.5499, 1021.5499, 1334.8708, 1336.6455, 1448.9093, 1471.7479, 1622.8771, 2123.0999, 2301.1658, 2428.2026

3. gi|3135497 **Mass:** 27595 **Score:** 65 **Expect:** 0.2 **Queries matched:** 5

major allergen Phl p 5 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1199.6577	1198.6504	1198.6597	-0.0093	225	234	1	---	YTVFETALKK
1471.7479	1470.7406	1470.7506	-0.0100	177	189	0	---	FTVFEAAFNNAIK
1975.1201	1974.1128	1974.1149	-0.0020	126	144	0	19	IIAGTLEVHAVKPAAEEVK
1975.1201	1974.1128	1974.1149	-0.0020	126	144	0	---	IIAGTLEVHAVKPAAEEVK
2428.2026	2427.1953	2427.1441	0.0513	103	125	0	---	TAEGATPEAEYDAYVATLSEALR

No match to: 713.4103, 750.5139, 768.5247, 939.4847, 1021.5499, 1021.5499, 1334.8708, 1336.6455, 1448.9093, 1541.8420, 1541.8420, 1622.8771, 2123.0999, 2301.1658

4. gi|422005 **Mass:** 26530 **Score:** 50 **Expect:** 6.2 **Queries matched:** 4

PHLP5A protein - common timothy (fragment)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1199.6577	1198.6504	1198.6597	-0.0093	207	216	1	---	YTVFETALKK
1471.7479	1470.7406	1470.7354	0.0052	95	107	0	---	YDAYVATLSEALR
1975.1201	1974.1128	1974.1149	-0.0020	108	126	0	19	IIAGTLEVHAVKPAAEEVK
1975.1201	1974.1128	1974.1149	-0.0020	108	126	0	---	IIAGTLEVHAVKPAAEEVK

No match to: 713.4103, 750.5139, 768.5247, 939.4847, 1021.5499, 1021.5499, 1334.8708, 1336.6455, 1448.9093, 1541.8420, 1541.8420, 1622.8771, 2123.0999, 2301.1658, 2428.2026

5. gi|13430402 **Mass:** 27795 **Score:** 49 **Expect:** 7.4 **Queries matched:** 4

group V allergen Phl p 5 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1199.6577	1198.6504	1198.6597	-0.0093	224	233	1	---	YTVFETALKK
1471.7479	1470.7406	1470.7354	0.0052	112	124	0	---	YDAYVATLSEALR
1975.1201	1974.1128	1974.1149	-0.0020	125	143	0	19	IIAGTLEVHAVKPAAEEVK
1975.1201	1974.1128	1974.1149	-0.0020	125	143	0	---	IIAGTLEVHAVKPAAEEVK

No match to: 713.4103, 750.5139, 768.5247, 939.4847, 1021.5499, 1021.5499, 1334.8708, 1336.6455, 1448.9093, 1541.8420, 1541.8420, 1622.8771, 2123.0999, 2301.1658, 2428.2026

6. gi|3135503 **Mass:** 27692 **Score:** 49 **Expect:** 7.4 **Queries matched:** 4

major allergen Phl p 5 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1199.6577	1198.6504	1198.6597	-0.0093	225	234	1	---	YTVFETALKK
1471.7479	1470.7406	1470.7354	0.0052	113	125	0	---	YDAYVATLSEALR
1975.1201	1974.1128	1974.1149	-0.0020	126	144	0	19	IIAGTLEVHAVKPAAEEVK
1975.1201	1974.1128	1974.1149	-0.0020	126	144	0	---	IIAGTLEVHAVKPAAEEVK

No match to: 713.4103, 750.5139, 768.5247, 939.4847, 1021.5499, 1021.5499, 1334.8708, 1336.6455, 1448.9093, 1541.8420, 1541.8420, 1622.8771, 2123.0999, 2301.1658, 2428.2026

7. gi|3135501 **Mass:** 27586 **Score:** 49 **Expect:** 7.4 **Queries matched:** 4

major allergen Phl p 5 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide

1199.6577	1198.6504	1198.6597	-0.0093	225 - 234	1	---	YTVFETALKK
1471.7479	1470.7406	1470.7354	0.0052	113 - 125	0	---	YDAYVATLSEALR
1975.1201	1974.1128	1974.1149	-0.0020	126 - 144	0	19	IIAGTLEVHAVKPAAEEVK
1975.1201	1974.1128	1974.1149	-0.0020	126 - 144	0	---	IIAGTLEVHAVKPAAEEVK

No match to: 713.4103, 750.5139, 768.5247, 939.4847, 1021.5499, 1021.5499, 1334.8708, 1336.6455, 1448.9093, 1541.8420, 1541.8420, 1622.8771, 2123.0999, 2301.1658, 2428.2026

8. gi|3135499 **Mass:** 27658 **Score:** 49 **Expect:** 7.4 **Queries matched:** 4

major allergen Phl p 5 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1199.6577	1198.6504	1198.6597	-0.0093	225 - 234	1	---	YTVFETALKK
1471.7479	1470.7406	1470.7354	0.0052	113 - 125	0	---	YDAYVATLSEALR
1975.1201	1974.1128	1974.1149	-0.0020	126 - 144	0	19	IIAGTLEVHAVKPAAEEVK
1975.1201	1974.1128	1974.1149	-0.0020	126 - 144	0	---	IIAGTLEVHAVKPAAEEVK

No match to: 713.4103, 750.5139, 768.5247, 939.4847, 1021.5499, 1021.5499, 1334.8708, 1336.6455, 1448.9093, 1541.8420, 1541.8420, 1622.8771, 2123.0999, 2301.1658, 2428.2026

9. gi|1684720 **Mass:** 27685 **Score:** 49 **Expect:** 7.4 **Queries matched:** 4

major allergen Phl p 5 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1199.6577	1198.6504	1198.6597	-0.0093	225 - 234	1	---	YTVFETALKK
1471.7479	1470.7406	1470.7354	0.0052	113 - 125	0	---	YDAYVATLSEALR
1975.1201	1974.1128	1974.1149	-0.0020	126 - 144	0	19	IIAGTLEVHAVKPAAEEVK
1975.1201	1974.1128	1974.1149	-0.0020	126 - 144	0	---	IIAGTLEVHAVKPAAEEVK

No match to: 713.4103, 750.5139, 768.5247, 939.4847, 1021.5499, 1021.5499, 1334.8708, 1336.6455, 1448.9093, 1541.8420, 1541.8420, 1622.8771, 2123.0999, 2301.1658, 2428.2026

10. gi|1092249 **Mass:** 28713 **Score:** 49 **Expect:** 8.2 **Queries matched:** 4

major allergen Phl p Va

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1199.6577	1198.6504	1198.6597	-0.0093	235 - 244	1	---	YTVFETALKK
1471.7479	1470.7406	1470.7354	0.0052	123 - 135	0	---	YDAYVATLSEALR
1975.1201	1974.1128	1974.1149	-0.0020	136 - 154	0	19	IIAGTLEVHAVKPAAEEVK
1975.1201	1974.1128	1974.1149	-0.0020	136 - 154	0	---	IIAGTLEVHAVKPAAEEVK

No match to: 713.4103, 750.5139, 768.5247, 939.4847, 1021.5499, 1021.5499, 1334.8708, 1336.6455, 1448.9093, 1541.8420, 1541.8420, 1622.8771, 2123.0999, 2301.1658, 2428.2026

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 19

Protein View

Match to: **gi|29500897** Score: **88** Expect: **0.00087**
phl p5a allergen precursor [Phleum pratense]

Nominal mass (M_r): **28269**; Calculated pI value: **7.94**
NCBI BLAST search of gi|29500897 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

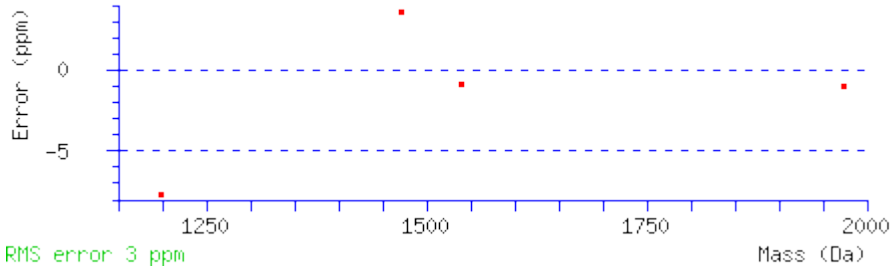
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **20%**

Matched peptides shown in **Bold Red**

```
     1 ADLGYGPATP AAPAAGYTPA APAGAEPAGK ATTEEQKLIE KINAGFKAAL
    51 AAAAGVPPAD KYRTFVATFG AASNKAFAEG LSGEPKGAAE SSSKAALTSK
   101 LDAAYKLAYK TAEGATPEAK YDAYVATLSE ALRIIAGTLE VHAVKPAAEE
   151 VKVIPAGELQ VIEKVDAAFK VAATAANAAP ANDKFTVFEA AFNNAIKAST
   201 GGAYESYKFI PALEAAVKQA YAATVATAPE VKYTVFETAL KKAITAMSEA
   251 QKAAKPAAAA TATATSAVGA ATGAATAATG GYKV
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
48 - 63	1541.8420	1540.8347	1540.8361	-0.0014	1	AALAAAAGVPPADKYR	(No match)
48 - 63	1541.8420	1540.8347	1540.8361	-0.0014	1	AALAAAAGVPPADKYR	(Ions score 25)
121 - 133	1471.7479	1470.7406	1470.7354	0.0052	0	YDAYVATLSEALR	(No match)
134 - 152	1975.1201	1974.1128	1974.1149	-0.0020	0	IIAGTLEVHAVKPAAEEVK	(Ions score 19)
134 - 152	1975.1201	1974.1128	1974.1149	-0.0020	0	IIAGTLEVHAVKPAAEEVK	(No match)
233 - 242	1199.6577	1198.6504	1198.6597	-0.0093	1	YTVFETALKK	(No match)



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	Accession	Mass	Score	Description
1.	gi|115441785	24874	90	Os01g0913600 [Oryza sativa (japonica cultivar-group)]
2.	gi|226529012	24186	66	rho GDP-dissociation inhibitor 1 [Zea mays]
3.	gi|219362545	24709	66	hypothetical protein LOC100217248 [Zea mays]
4.	gi|195629600	24723	66	rho GDP-dissociation inhibitor 1 [Zea mays]
5.	gi|78708686	10911	52	hypothetical protein LOC_Os10g29590 [Oryza sativa (japonica cultivar-group)]
6.	gi|145349015	25964	38	predicted protein [Ostreococcus lucimarinus CCE9901]
7.	gi|3513728	7589	38	F8M12.18 gene product [Arabidopsis thaliana]
8.	gi|116830195	7646	38	unknown [Arabidopsis thaliana]
9.	gi|404688	60603	37	cytochrome P450 [Catharanthus roseus]
10.	gi|255578009	64145	37	ATP binding protein, putative [Ricinus communis]

Results List

1. gi|115441785 **Mass:** 24874 **Score:** 90 **Expect:** 0.00065 **Queries matched:** 4

Os01g0913600 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1030.5740	1029.5667	1029.5566	0.0101	146	154	1	---	TGVRVENQK
1030.5740	1029.5667	1029.5566	0.0101	146	154	1	8	TGVRVENQK
2627.3215	2626.3142	2626.3125	0.0017	62	84	1	---	WKEQLLGQVDTEQLGETAEPEVK
2627.3215	2626.3142	2626.3125	0.0017	62	84	1	52	WKEQLLGQVDTEQLGETAEPEVK

No match to: 713.3876, 724.4669, 768.5028, 825.0901

2. gi|226529012 **Mass:** 24186 **Score:** 66 **Expect:** 0.17 **Queries matched:** 2

rho GDP-dissociation inhibitor 1 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
2627.3215	2626.3142	2626.3125	0.0017	56	78	1	---	WKEQLLGQVDTEQLGETAEPEVK
2627.3215	2626.3142	2626.3125	0.0017	56	78	1	52	WKEQLLGQVDTEQLGETAEPEVK

No match to: 713.3876, 724.4669, 768.5028, 825.0901, 1030.5740, 1030.5740

3. gi|219362545 **Mass:** 24709 **Score:** 66 **Expect:** 0.17 **Queries matched:** 2

hypothetical protein LOC100217248 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
2627.3215	2626.3142	2626.3125	0.0017	60	82	1	---	WKEQLLGQVDTEQLGETAEPEVK
2627.3215	2626.3142	2626.3125	0.0017	60	82	1	52	WKEQLLGQVDTEQLGETAEPEVK

No match to: 713.3876, 724.4669, 768.5028, 825.0901, 1030.5740, 1030.5740

4. gi|195629600 **Mass:** 24723 **Score:** 66 **Expect:** 0.17 **Queries matched:** 2

rho GDP-dissociation inhibitor 1 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
2627.3215	2626.3142	2626.3125	0.0017	60 -	82	1	---	WKEQLLGQVDTEQLGETAEPEVK
2627.3215	2626.3142	2626.3125	0.0017	60 -	82	1	52	WKEQLLGQVDTEQLGETAEPEVK

No match to: 713.3876, 724.4669, 768.5028, 825.0901, 1030.5740, 1030.5740

5. gi|78708686 **Mass:** 10911 **Score:** 52 **Expect:** 3.9 **Queries matched:** 4

hypothetical protein LOC_Os10g29590 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1030.5740	1029.5667	1029.5679	-0.0011	76 -	85	1	---	TVGGSRQGIR
1030.5740	1029.5667	1029.5494	0.0173	33 -	41	1	---	GKFYSTLSK
2627.3215	2626.3142	2626.1555	0.1587	1 -	21	0	---	MDCHVHWMDGNQNIYLFGVYK
2627.3215	2626.3142	2626.1555	0.1587	1 -	21	0	---	MDCHVHWMDGNQNIYLFGVYK

No match to: 713.3876, 724.4669, 768.5028, 825.0901

6. gi|145349015 **Mass:** 25964 **Score:** 38 **Expect:** 94 **Queries matched:** 3

predicted protein [Ostreococcus lucimarinus CCE9901]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
713.3876	712.3803	712.3755	0.0048	114 -	120	0	---	APATEPK
1030.5740	1029.5667	1029.5494	0.0173	182 -	191	0	---	VGELFPGPSK
1030.5740	1029.5667	1029.5494	0.0173	182 -	191	0	13	VGELFPGPSK

No match to: 724.4669, 768.5028, 825.0901, 2627.3215, 2627.3215

7. gi|3513728 **Mass:** 7589 **Score:** 38 **Expect:** 96 **Queries matched:** 3

F8M12.18 gene product [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
713.3876	712.3803	712.3867	-0.0064	2 -	9	0	---	AGPAQAAK
2627.3215	2626.3142	2626.3132	0.0010	49 -	74	1	---	KPEASAGDVAKVMSGVGGTPENTRPR + Oxidation (M)
2627.3215	2626.3142	2626.3132	0.0010	49 -	74	1	---	KPEASAGDVAKVMSGVGGTPENTRPR + Oxidation (M)

No match to: 724.4669, 768.5028, 825.0901, 1030.5740, 1030.5740

8. gi|116830195 **Mass:** 7646 **Score:** 38 **Expect:** 96 **Queries matched:** 3

unknown [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
713.3876	712.3803	712.3867	-0.0064	2 -	9	0	---	AGPAQAAK
2627.3215	2626.3142	2626.3132	0.0010	49 -	74	1	---	KPEASAGDVAKVMSGVGGTPENTRPR + Oxidation (M)
2627.3215	2626.3142	2626.3132	0.0010	49 -	74	1	---	KPEASAGDVAKVMSGVGGTPENTRPR + Oxidation (M)

No match to: 724.4669, 768.5028, 825.0901, 1030.5740, 1030.5740

9. gi|404688 **Mass:** 60603 **Score:** 37 **Expect:** 1.2e+002 **Queries matched:** 5

cytochrome P450 [Catharanthus roseus]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
713.3876	712.3803	712.3769	0.0035	153 -	157	1	---	WSKHR

1030.5740	1029.5667	1029.6004	-0.0337	482 - 490	0	---	LGLAMILQR + Oxidation (M)
1030.5740	1029.5667	1029.6004	-0.0337	482 - 490	0	---	LGLAMILQR + Oxidation (M)
2627.3215	2626.3142	2626.2121	0.1021	432 - 455	1	---	SIWGEDATEFNPMRFADGVANATK
2627.3215	2626.3142	2626.2121	0.1021	432 - 455	1	---	SIWGEDATEFNPMRFADGVANATK

No match to: 724.4669, 768.5028, 825.0901

10. gi|255578009 **Mass:** 64145 **Score:** 37 **Expect:** 1.2e+002 **Queries matched:** 4

ATP binding protein, putative [Ricinus communis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1030.5740	1029.5667	1029.5502	0.0166	541 - 548		1	---	RQNRPTMK
1030.5740	1029.5667	1029.5502	0.0166	541 - 548		1	---	RQNRPTMK
2627.3215	2626.3142	2626.4589	-0.1447	210 - 234		1	---	TSLIGALAVGAMFLGITTMVVVYRK + Oxidation (M)
2627.3215	2626.3142	2626.4589	-0.1447	209 - 233		1	---	KTSLIGALAVGAMFLGITTMVVVYR + Oxidation (M)

No match to: 713.3876, 724.4669, 768.5028, 825.0901

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 8

Protein View

Match to: **gi|115441785** Score: **90** Expect: **0.00065**
Os01g0913600 [Oryza sativa (japonica cultivar-group)]

Nominal mass (M_r): **24874**; Calculated pI value: **4.52**
NCBI BLAST search of gi|115441785 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Oryza sativa Japonica Group
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|20161386 from Oryza sativa Japonica Group
gi|113534703 from Oryza sativa Japonica Group
gi|215701236 from Oryza sativa Japonica Group
gi|218189591 from Oryza sativa Indica Group
gi|222619744 from Oryza sativa Japonica Group

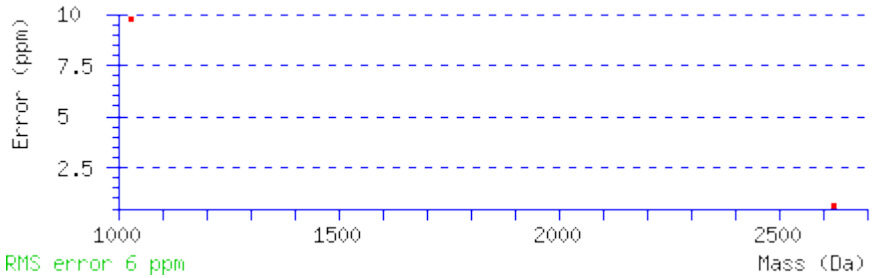
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **14%**

Matched peptides shown in **Bold Red**

```
    1 MDSKDKEKEH EQTASGRNPD VNDVEEEEED EEGNKRAVVL GPQVPLKEQL
   51 ELDKDDESLR RWKEQLLGQV DTEQLGETAE PEVKVLNLTI LSPDRPDLVL
  101 PIPFVPDEKG YAFALKDGST YSFRFSFIVS NNIVSGLKYT NTVWKTGVRV
  151 ENQKVMLGTF SPQLEPYTYE GEEETTPAGM FARGSYSAKL KFVDDDGKCY
  201 LEMSYYFEIR KEWPTIQ
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
62 - 84	2627.3215	2626.3142	2626.3125	0.0017	1	WKEQLLGQVDTEQLGETAEPEVK	(No match)
62 - 84	2627.3215	2626.3142	2626.3125	0.0017	1	WKEQLLGQVDTEQLGETAEPEVK	(Ions score 52)
146 - 154	1030.5740	1029.5667	1029.5566	0.0101	1	TGVRVENQK	(No match)
146 - 154	1030.5740	1029.5667	1029.5566	0.0101	1	TGVRVENQK	(Ions score 8)



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	Accession	Mass	Score	Description
1.	gi|115441785	24874	180	Os01g0913600 [Oryza sativa (japonica cultivar-group)]
2.	gi|219362545	24709	140	hypothetical protein LOC100217248 [Zea mays]
3.	gi|195629600	24723	140	rho GDP-dissociation inhibitor 1 [Zea mays]
4.	gi|195634635	24186	131	rho GDP-dissociation inhibitor 1 [Zea mays]
5.	gi|145344336	19699	37	predicted protein [Ostreococcus lucimarinus CCE9901]

Results List

1. gi|115441785 **Mass:** 24874 **Score:** 180 **Expect:** 6e-013 **Queries matched:** 7

Os01g0913600 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1030.5653	1029.5580	1029.5566	0.0014	146	154	1	18	TGVRVENQK
1030.5653	1029.5580	1029.5566	0.0014	146	154	1	---	TGVRVENQK
1524.8396	1523.8323	1523.8347	-0.0024	125	138	0	---	FSFIVSNNIVSGLK
1682.8185	1681.8112	1681.8099	0.0013	110	124	1	---	GYAFALKDGSTYSFR
2313.1392	2312.1319	2312.1383	-0.0063	64	84	0	---	EQLLGQVDTEQLGETAEPEVK
2627.3289	2626.3216	2626.3125	0.0091	62	84	1	---	WKEQLLGQVDTEQLGETAEPEVK
2627.3289	2626.3216	2626.3125	0.0091	62	84	1	114	WKEQLLGQVDTEQLGETAEPEVK

No match to: 700.4003, 713.4099, 724.4949, 734.4924, 736.4937, 750.5174, 768.5239, 782.4756, 838.5328, 848.5203, 864.5367, 886.9846, 1007.6791, 1133.7106, 1279.7673, 1334.8822, 1434.8868, 1448.9143, 1562.9321, 1618.0618, 1732.0984, 1901.2494, 1923.0050, 1940.9639, 2015.2787, 2240.1194, 2428.0266, 2643.3257, 2643.3257, 2761.5308, 2761.5308, 2824.3157, 2861.5676, 2861.5676, 3264.5872, 3763.6646

2. gi|219362545 **Mass:** 24709 **Score:** 140 **Expect:** 6e-009 **Queries matched:** 4

hypothetical protein LOC100217248 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1524.8396	1523.8323	1523.8347	-0.0024	123	136	0	---	FSFIVSNNIVSGLK
2313.1392	2312.1319	2312.1383	-0.0063	62	82	0	---	EQLLGQVDTEQLGETAEPEVK
2627.3289	2626.3216	2626.3125	0.0091	60	82	1	---	WKEQLLGQVDTEQLGETAEPEVK
2627.3289	2626.3216	2626.3125	0.0091	60	82	1	114	WKEQLLGQVDTEQLGETAEPEVK

No match to: 700.4003, 713.4099, 724.4949, 734.4924, 736.4937, 750.5174, 768.5239, 782.4756, 838.5328, 848.5203, 864.5367, 886.9846, 1007.6791, 1030.5653, 1030.5653, 1133.7106, 1279.7673, 1334.8822, 1434.8868, 1448.9143, 1562.9321, 1618.0618, 1682.8185, 1732.0984, 1901.2494, 1923.0050, 1940.9639, 2015.2787, 2240.1194, 2428.0266, 2643.3257, 2643.3257, 2761.5308, 2761.5308, 2824.3157, 2861.5676, 2861.5676, 3264.5872, 3763.6646

3. gi|195629600 **Mass:** 24723 **Score:** 140 **Expect:** 6e-009 **Queries matched:** 4

rho GDP-dissociation inhibitor 1 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide

1524.8396	1523.8323	1523.8347	-0.0024	123 - 136	0	---	FSFIVSNNIVSGLK
2313.1392	2312.1319	2312.1383	-0.0063	62 - 82	0	---	EQLLGQVDTEQLGETAEPEVK
2627.3289	2626.3216	2626.3125	0.0091	60 - 82	1	---	WKEQLLGQVDTEQLGETAEPEVK
2627.3289	2626.3216	2626.3125	0.0091	60 - 82	1	114	WKEQLLGQVDTEQLGETAEPEVK

No match to: 700.4003, 713.4099, 724.4949, 734.4924, 736.4937, 750.5174, 768.5239, 782.4756, 838.5328, 848.5203, 864.5367, 886.9846, 1007.6791, 1030.5653, 1030.5653, 1133.7106, 1279.7673, 1334.8822, 1434.8868, 1448.9143, 1562.9321, 1618.0618, 1682.8185, 1732.0984, 1901.2494, 1923.0050, 1940.9639, 2015.2787, 2240.1194, 2428.0266, 2643.3257, 2643.3257, 2761.5308, 2761.5308, 2824.3157, 2861.5676, 2861.5676, 3264.5872, 3763.6646

4. gi|195634635 **Mass:** 24186 **Score:** 131 **Expect:** 4.8e-008 **Queries matched:** 3

rho GDP-dissociation inhibitor 1 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
2313.1392	2312.1319	2312.1383	-0.0063	58 -	78	0	---	EQLLGQVDTEQLGETAEPEVK
2627.3289	2626.3216	2626.3125	0.0091	56 -	78	1	---	WKEQLLGQVDTEQLGETAEPEVK
2627.3289	2626.3216	2626.3125	0.0091	56 -	78	1	114	WKEQLLGQVDTEQLGETAEPEVK

No match to: 700.4003, 713.4099, 724.4949, 734.4924, 736.4937, 750.5174, 768.5239, 782.4756, 838.5328, 848.5203, 864.5367, 886.9846, 1007.6791, 1030.5653, 1030.5653, 1133.7106, 1279.7673, 1334.8822, 1434.8868, 1448.9143, 1524.8396, 1562.9321, 1618.0618, 1682.8185, 1732.0984, 1901.2494, 1923.0050, 1940.9639, 2015.2787, 2240.1194, 2428.0266, 2643.3257, 2643.3257, 2761.5308, 2761.5308, 2824.3157, 2861.5676, 2861.5676, 3264.5872, 3763.6646

5. gi|145344336 **Mass:** 19699 **Score:** 37 **Expect:** 1.3e+002 **Queries matched:** 5

predicted protein [Ostreococcus lucimarinus CCE9901]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
700.4003	699.3930	699.3816	0.0114	132 -	137	0	---	HAIFGR
1524.8396	1523.8323	1523.8241	0.0082	138 -	152	1	---	VESGMHAVRAIGAVK
1682.8185	1681.8112	1681.8470	-0.0358	132 -	146	1	---	HAIFGRVESGMHAVR + Oxidation (M)
2761.5308	2760.5235	2760.4347	0.0889	16 -	40	1	---	GAPVVTLHTTHGDVTVELYYKHAPR
2761.5308	2760.5235	2760.4347	0.0889	16 -	40	1	---	GAPVVTLHTTHGDVTVELYYKHAPR

No match to: 713.4099, 724.4949, 734.4924, 736.4937, 750.5174, 768.5239, 782.4756, 838.5328, 848.5203, 864.5367, 886.9846, 1007.6791, 1030.5653, 1030.5653, 1133.7106, 1279.7673, 1334.8822, 1434.8868, 1448.9143, 1562.9321, 1618.0618, 1732.0984, 1901.2494, 1923.0050, 1940.9639, 2015.2787, 2240.1194, 2313.1392, 2428.0266, 2627.3289, 2627.3289, 2643.3257, 2643.3257, 2824.3157, 2861.5676, 2861.5676, 3264.5872, 3763.6646

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 43

Protein View

Match to: **gi|115441785** Score: **180** Expect: **6e-013**
Os01g0913600 [Oryza sativa (japonica cultivar-group)]

Nominal mass (M_r): **24874**; Calculated pI value: **4.52**
NCBI BLAST search of gi|115441785 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Oryza sativa Japonica Group
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|20161386 from Oryza sativa Japonica Group
gi|113534703 from Oryza sativa Japonica Group
gi|215701236 from Oryza sativa Japonica Group
gi|218189591 from Oryza sativa Indica Group
gi|222619744 from Oryza sativa Japonica Group

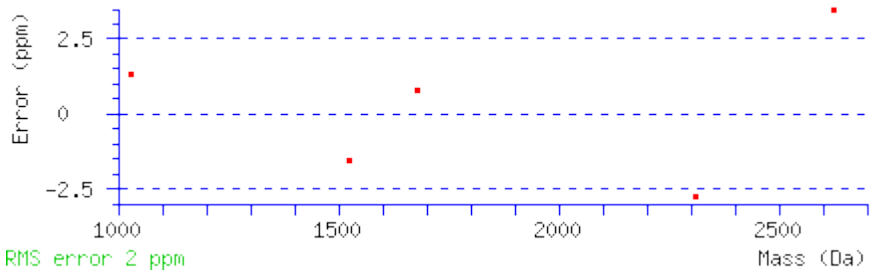
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **28%**

Matched peptides shown in **Bold Red**

```
     1 MDSKDKEKEH EQTASGRNPD VNDVEEEEED EEGNKRAVVL GPQVPLKEQL
    51 ELDKDDESLR RWKEQLLGQV DTEQLGETAE PEVKVLNLTI LSPDRPDLVL
   101 PIPFVPDEKG YAFALKDGST YSFRFSFIVS NNIVSGLKYT NTVWKTGVRV
   151 ENQKVMLGTF SPQLEPYTYE GEEETTPAGM FARGSYSAKL KFVDDDGKCY
   201 LEMSYYFEIR KEWPTIQ
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
62 - 84	2627.3289	2626.3216	2626.3125	0.0091	1	WKEQLLGQVDTEQLGETAEPEVK	(No match)
62 - 84	2627.3289	2626.3216	2626.3125	0.0091	1	WKEQLLGQVDTEQLGETAEPEVK	(Ions score 114)
64 - 84	2313.1392	2312.1319	2312.1383	-0.0063	0	EQLLGQVDTEQLGETAEPEVK	(No match)
110 - 124	1682.8185	1681.8112	1681.8099	0.0013	1	GYAFALKDGSTYSFR	(No match)
125 - 138	1524.8396	1523.8323	1523.8347	-0.0024	0	FSFIVSNNIVSGLK	(No match)
146 - 154	1030.5653	1029.5580	1029.5566	0.0014	1	TGVRVENQK	(Ions score 18)
146 - 154	1030.5653	1029.5580	1029.5566	0.0014	1	TGVRVENQK	(No match)



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	Accession	Mass	Score	Description
1.	gi|83271058	29533	243	14-3-3E [Hordeum vulgare subsp. vulgare]
2.	gi|9798603	29491	227	TaWIN1 [Triticum aestivum]
3.	gi|226501092	29620	188	hypothetical protein LOC100273134 [Zea mays]
4.	gi|226499592	29594	188	LOC100282460 [Zea mays]
5.	gi|194701240	29411	188	unknown [Zea mays]
6.	gi|110278805	29358	170	RecName: Full=14-3-3-like protein GF14-D; AltName: Full=G-box factor 14-3-3 homolog D
7.	gi|115485847	29697	169	Os11g0546900 [Oryza sativa (japonica cultivar-group)]
8.	gi|149391465	25000	153	14-3-3-like protein [Oryza sativa (indica cultivar-group)]
9.	gi|255545912	28647	129	14-3-3 protein, putative [Ricinus communis]
10.	gi|115476520	28979	129	Os08g0430500 [Oryza sativa (japonica cultivar-group)]

Results List

1. gi|83271058 **Mass:** 29533 **Score:** 243 **Expect:** 3e-019 **Queries matched:** 12

14-3-3E [Hordeum vulgare subsp. vulgare]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
770.4382	769.4309	769.4010	0.0299	141	146	0	---	YLAEFK
1270.6539	1269.6466	1269.6353	0.0114	141	151	1	---	YLAEFKSGAER
1388.7455	1387.7382	1387.7306	0.0076	72	83	1	---	IISSIEQKEEGR
1398.7268	1397.7195	1397.6727	0.0468	136	146	1	---	GDYHRYLAEFK
1517.8978	1516.8905	1516.8725	0.0181	53	66	1	---	NLLSVAYKNVIGAR
1558.7546	1557.7473	1557.7270	0.0204	37	52	0	---	ATGGAGPGEELSVEER
1558.7546	1557.7473	1557.7270	0.0204	37	52	0	55	ATGGAGPGEELSVEER
1772.9852	1771.9779	1771.9580	0.0199	164	180	0	---	AAQDIALADLAPTHPIR
1772.9852	1771.9779	1771.9580	0.0199	164	180	0	94	AAQDIALADLAPTHPIR
2160.0020	2158.9947	2158.9663	0.0285	17	33	1	---	LAEQAERYEEMVEFMER
2175.9924	2174.9851	2174.9612	0.0240	17	33	1	---	LAEQAERYEEMVEFMER + Oxidation (M)
2191.9890	2190.9817	2190.9561	0.0257	17	33	1	---	LAEQAERYEEMVEFMER + 2 Oxidation (M)

No match to: 768.5375, 1213.6306, 1214.1436, 1279.7734, 1334.8979, 1448.8717, 1694.8259, 1694.8259, 1710.8218, 1710.8218, 1754.9828, 2425.2744, 2425.2744, 2448.2715, 2808.3516

2. gi|9798603 **Mass:** 29491 **Score:** 227 **Expect:** 1.2e-017 **Queries matched:** 11

TaWIN1 [Triticum aestivum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
770.4382	769.4309	769.4010	0.0299	141	146	0	---	YLAEFK
1388.7455	1387.7382	1387.7306	0.0076	72	83	1	---	IISSIEQKEEGR
1398.7268	1397.7195	1397.6727	0.0468	136	146	1	---	GDYHRYLAEFK
1517.8978	1516.8905	1516.8725	0.0181	53	66	1	---	NLLSVAYKNVIGAR

1558.7546	1557.7473	1557.7270	0.0204	37 - 52	0	---	ATGGAGPGEELSVEER
1558.7546	1557.7473	1557.7270	0.0204	37 - 52	0	55	ATGGAGPGEELSVEER
1772.9852	1771.9779	1771.9580	0.0199	164 - 180	0	---	AAQDIALADLAPTHPIR
1772.9852	1771.9779	1771.9580	0.0199	164 - 180	0	94	AAQDIALADLAPTHPIR
2160.0020	2158.9947	2158.9663	0.0285	17 - 33	1	---	LAEQAERYEEMVEFMER
2175.9924	2174.9851	2174.9612	0.0240	17 - 33	1	---	LAEQAERYEEMVEFMER + Oxidation (M)
2191.9890	2190.9817	2190.9561	0.0257	17 - 33	1	---	LAEQAERYEEMVEFMER + 2 Oxidation (M)

No match to: 768.5375, 1213.6306, 1214.1436, 1270.6539, 1279.7734, 1334.8979, 1448.8717, 1694.8259, 1694.8259, 1710.8218, 1710.8218, 1754.9828, 2425.2744, 2425.2744, 2448.2715, 2808.3516

3. gi|226501092 **Mass:** 29620 **Score:** 188 **Expect:** 9.6e-014 **Queries matched:** 12

hypothetical protein LOC100273134 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start - End	Miss	Ions	Peptide
770.4382	769.4309	769.4010	0.0299	141 - 146	0	---	YLAEFK
1270.6539	1269.6466	1269.6353	0.0114	141 - 151	1	---	YLAEFKSGAER
1388.7455	1387.7382	1387.7306	0.0076	72 - 83	1	---	IISSIEQKEEGR
1398.7268	1397.7195	1397.6727	0.0468	136 - 146	1	---	GDYHRYLAEFK
1517.8978	1516.8905	1516.8725	0.0181	53 - 66	1	---	NLLSVAYKNVIGAR
1710.8218	1709.8145	1709.7930	0.0215	2 - 16	1	---	SPSEPTREESVYMAK
1710.8218	1709.8145	1709.7930	0.0215	2 - 16	1	---	SPSEPTREESVYMAK
1772.9852	1771.9779	1771.9580	0.0199	164 - 180	0	---	AAQDIALADLAPTHPIR
1772.9852	1771.9779	1771.9580	0.0199	164 - 180	0	94	AAQDIALADLAPTHPIR
2160.0020	2158.9947	2158.9663	0.0285	17 - 33	1	---	LAEQAERYEEMVEFMER
2175.9924	2174.9851	2174.9612	0.0240	17 - 33	1	---	LAEQAERYEEMVEFMER + Oxidation (M)
2191.9890	2190.9817	2190.9561	0.0257	17 - 33	1	---	LAEQAERYEEMVEFMER + 2 Oxidation (M)

No match to: 768.5375, 1213.6306, 1214.1436, 1279.7734, 1334.8979, 1448.8717, 1558.7546, 1558.7546, 1694.8259, 1694.8259, 1754.9828, 2425.2744, 2425.2744, 2448.2715, 2808.3516

4. gi|226499592 **Mass:** 29594 **Score:** 188 **Expect:** 9.6e-014 **Queries matched:** 12

LOC100282460 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start - End	Miss	Ions	Peptide
770.4382	769.4309	769.4010	0.0299	141 - 146	0	---	YLAEFK
1270.6539	1269.6466	1269.6353	0.0114	141 - 151	1	---	YLAEFKSGAER
1388.7455	1387.7382	1387.7306	0.0076	72 - 83	1	---	IISSIEQKEEGR
1398.7268	1397.7195	1397.6727	0.0468	136 - 146	1	---	GDYHRYLAEFK
1517.8978	1516.8905	1516.8725	0.0181	53 - 66	1	---	NLLSVAYKNVIGAR
1710.8218	1709.8145	1709.7930	0.0215	2 - 16	1	---	SPSEPTREESVYMAK
1710.8218	1709.8145	1709.7930	0.0215	2 - 16	1	---	SPSEPTREESVYMAK
1772.9852	1771.9779	1771.9580	0.0199	164 - 180	0	---	AAQDIALADLAPTHPIR
1772.9852	1771.9779	1771.9580	0.0199	164 - 180	0	94	AAQDIALADLAPTHPIR
2160.0020	2158.9947	2158.9663	0.0285	17 - 33	1	---	LAEQAERYEEMVEFMER

2175.9924	2174.9851	2174.9612	0.0240	17 - 33	1	---	LAEQAERYEEMVEFMER + Oxidation (M)
2191.9890	2190.9817	2190.9561	0.0257	17 - 33	1	---	LAEQAERYEEMVEFMER + 2 Oxidation (M)

No match to: 768.5375, 1213.6306, 1214.1436, 1279.7734, 1334.8979, 1448.8717, 1558.7546, 1558.7546, 1694.8259, 1694.8259, 1754.9828, 2425.2744, 2425.2744, 2448.2715, 2808.3516

5. gi|194701240 **Mass:** 29411 **Score:** 188 **Expect:** 9.6e-014 **Queries matched:** 12

unknown [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
770.4382	769.4309	769.4010	0.0299	141 - 146		0	---	YLAEFK
1270.6539	1269.6466	1269.6353	0.0114	141 - 151		1	---	YLAEFKSGAER
1388.7455	1387.7382	1387.7306	0.0076	72 - 83		1	---	IISSIEQKEEGR
1398.7268	1397.7195	1397.6727	0.0468	136 - 146		1	---	GDYHRYLAEFK
1517.8978	1516.8905	1516.8725	0.0181	53 - 66		1	---	NLLSVAYKNVIGAR
1710.8218	1709.8145	1709.7930	0.0215	2 - 16		1	---	SPSEPTREESVYMAK
1710.8218	1709.8145	1709.7930	0.0215	2 - 16		1	---	SPSEPTREESVYMAK
1772.9852	1771.9779	1771.9580	0.0199	164 - 180		0	---	AAQDIALADLAPTHPIR
1772.9852	1771.9779	1771.9580	0.0199	164 - 180		0	94	AAQDIALADLAPTHPIR
2160.0020	2158.9947	2158.9663	0.0285	17 - 33		1	---	LAEQAERYEEMVEFMER
2175.9924	2174.9851	2174.9612	0.0240	17 - 33		1	---	LAEQAERYEEMVEFMER + Oxidation (M)
2191.9890	2190.9817	2190.9561	0.0257	17 - 33		1	---	LAEQAERYEEMVEFMER + 2 Oxidation (M)

No match to: 768.5375, 1213.6306, 1214.1436, 1279.7734, 1334.8979, 1448.8717, 1558.7546, 1558.7546, 1694.8259, 1694.8259, 1754.9828, 2425.2744, 2425.2744, 2448.2715, 2808.3516

6. gi|110278805 **Mass:** 29358 **Score:** 170 **Expect:** 6.1e-012 **Queries matched:** 9

RecName: Full=14-3-3-like protein GF14-D; AltName: Full=G-box factor 14-3-3 homolog D

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
770.4382	769.4309	769.4010	0.0299	141 - 146		0	---	YLAEFK
1213.6306	1212.6233	1212.5444	0.0789	153 - 163		0	---	QAAESTMNAYK
1388.7455	1387.7382	1387.7306	0.0076	72 - 83		1	---	IISSIEQKEEGR
1398.7268	1397.7195	1397.6727	0.0468	136 - 146		1	---	GDYHRYLAEFK
1517.8978	1516.8905	1516.8725	0.0181	53 - 66		1	---	NLLSVAYKNVIGAR
1772.9852	1771.9779	1771.9580	0.0199	164 - 180		0	---	AAQDIALADLAPTHPIR
1772.9852	1771.9779	1771.9580	0.0199	164 - 180		0	94	AAQDIALADLAPTHPIR
2175.9924	2174.9851	2174.9612	0.0239	17 - 33		1	---	LAEQAERYEEMVEYMER
2191.9890	2190.9817	2190.9561	0.0256	17 - 33		1	---	LAEQAERYEEMVEYMER + Oxidation (M)

No match to: 768.5375, 1214.1436, 1270.6539, 1279.7734, 1334.8979, 1448.8717, 1558.7546, 1558.7546, 1694.8259, 1694.8259, 1710.8218, 1710.8218, 1754.9828, 2160.0020, 2425.2744, 2425.2744, 2448.2715, 2808.3516

7. gi|115485847 **Mass:** 29697 **Score:** 169 **Expect:** 7.6e-012 **Queries matched:** 9

Os11g0546900 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
770.4382	769.4309	769.4010	0.0299	142 - 147		0	---	YLAEFK

1213.6306	1212.6233	1212.5444	0.0789	154 - 164	0	---	QAAESTMNAYK
1388.7455	1387.7382	1387.7306	0.0076	73 - 84	1	---	IISSIEQKEEGR
1398.7268	1397.7195	1397.6727	0.0468	137 - 147	1	---	GDYHRYLAEFK
1517.8978	1516.8905	1516.8725	0.0181	54 - 67	1	---	NLLSVAYKNVIGAR
1772.9852	1771.9779	1771.9580	0.0199	165 - 181	0	---	AAQDIALADLAPTHPIR
1772.9852	1771.9779	1771.9580	0.0199	165 - 181	0	94	AAQDIALADLAPTHPIR
2175.9924	2174.9851	2174.9612	0.0239	18 - 34	1	---	LAEQAERYEEMVEYMER
2191.9890	2190.9817	2190.9561	0.0256	18 - 34	1	---	LAEQAERYEEMVEYMER + Oxidation (M)

No match to: 768.5375, 1214.1436, 1270.6539, 1279.7734, 1334.8979, 1448.8717, 1558.7546, 1558.7546, 1694.8259, 1694.8259, 1710.8218, 1710.8218, 1754.9828, 2160.0020, 2425.2744, 2425.2744, 2448.2715, 2808.3516

8. gi|149391465 **Mass:** 25000 **Score:** 153 **Expect:** 3e-010 **Queries matched:** 7

14-3-3-like protein [Oryza sativa (indica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
770.4382	769.4309	769.4010	0.0299	104 - 109		0	---	YLAEFK
1213.6306	1212.6233	1212.5444	0.0789	116 - 126		0	---	QAAESTMNAYK
1388.7455	1387.7382	1387.7306	0.0076	35 - 46		1	---	IISSIEQKEEGR
1398.7268	1397.7195	1397.6727	0.0468	99 - 109		1	---	GDYHRYLAEFK
1517.8978	1516.8905	1516.8725	0.0181	16 - 29		1	---	NLLSVAYKNVIGAR
1772.9852	1771.9779	1771.9580	0.0199	127 - 143		0	---	AAQDIALADLAPTHPIR
1772.9852	1771.9779	1771.9580	0.0199	127 - 143		0	94	AAQDIALADLAPTHPIR

No match to: 768.5375, 1214.1436, 1270.6539, 1279.7734, 1334.8979, 1448.8717, 1558.7546, 1558.7546, 1694.8259, 1694.8259, 1710.8218, 1710.8218, 1754.9828, 2160.0020, 2175.9924, 2191.9890, 2425.2744, 2425.2744, 2448.2715, 2808.3516

9. gi|255545912 **Mass:** 28647 **Score:** 129 **Expect:** 7.6e-008 **Queries matched:** 5

14-3-3 protein, putative [Ricinus communis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
770.4382	769.4309	769.4010	0.0299	143 - 148		0	---	YLAEFK
1213.6306	1212.6233	1212.5696	0.0537	155 - 165		0	---	TAAEDTMLAYK
1398.7268	1397.7195	1397.6727	0.0468	138 - 148		1	---	GDYHRYLAEFK
1772.9852	1771.9779	1771.9580	0.0199	166 - 182		0	---	AAQDIALADLAPTHPIR
1772.9852	1771.9779	1771.9580	0.0199	166 - 182		0	94	AAQDIALADLAPTHPIR

No match to: 768.5375, 1214.1436, 1270.6539, 1279.7734, 1334.8979, 1388.7455, 1448.8717, 1517.8978, 1558.7546, 1558.7546, 1694.8259, 1694.8259, 1710.8218, 1710.8218, 1754.9828, 2160.0020, 2175.9924, 2191.9890, 2425.2744, 2425.2744, 2448.2715, 2808.3516

10. gi|115476520 **Mass:** 28979 **Score:** 129 **Expect:** 7.6e-008 **Queries matched:** 5

Os08g0430500 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
770.4382	769.4309	769.4010	0.0299	132 - 137		0	---	YLAEFK
1398.7268	1397.7195	1397.6727	0.0468	127 - 137		1	---	GDYHRYLAEFK

1517.8978	1516.8905	1516.8725	0.0181	44 - 57	1	---	NLLSVAYKNVIGAR
1772.9852	1771.9779	1771.9580	0.0199	155 - 171	0	---	AAQDIALADLAPTHPIR
1772.9852	1771.9779	1771.9580	0.0199	155 - 171	0	94	AAQDIALADLAPTHPIR

No match to: 768.5375, 1213.6306, 1214.1436, 1270.6539, 1279.7734, 1334.8979, 1388.7455, 1448.8717, 1558.7546, 1558.7546, 1694.8259, 1694.8259, 1710.8218, 1710.8218, 1754.9828, 2160.0020, 2175.9924, 2191.9890, 2425.2744, 2425.2744, 2448.2715, 2808.3516

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 27

Protein View

Match to: **gi|83271058** Score: **243** Expect: **3e-019**
14-3-3E [Hordeum vulgare subsp. vulgare]

Nominal mass (M_r): **29533**; Calculated pI value: **4.76**
NCBI BLAST search of gi|83271058 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Hordeum vulgare subsp. vulgare

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **34%**

Matched peptides shown in **Bold Red**

```
   1 MSPAEPTRDE SVYMAKLAEQ AERYEEMVEF MERVAKATGG AGPGEELSVE
  51 ERNLLSVAYK NVIGARRASW RIISSIEQKE EGRGNEAHAA TIRSYRTKIE
 101 AELAKICDGI LALLDSHLVP SAGAAESKVF YLKMKGDYHR YLAEFKSGAE
 151 RKEAAESTMN AYKAAQDIAL ADLAPTHPIR LGLALNFSVF YYEILNSPDR
 201 ACNLAKQAFD EAISELDSLG EESYKDSTLI MQLLRDNLTL WTSDTNEDDV
 251 DEIKEAPAPK ESGDGQ
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
17 - 33	2160.0020	2158.9947	2158.9663	0.0285	1	**LAEQAERYEEMVEFMER** (No match)
17 - 33	2175.9924	2174.9851	2174.9612	0.0240	1	**LAEQAERYEEMVEFMER** Oxidation (M) (No match)
17 - 33	2191.9890	2190.9817	2190.9561	0.0257	1	**LAEQAERYEEMVEFMER** 2 Oxidation (M) (No match)
37 - 52	1558.7546	1557.7473	1557.7270	0.0204	0	**ATGGAGPGEELSVEER** (No match)
37 - 52	1558.7546	1557.7473	1557.7270	0.0204	0	**ATGGAGPGEELSVEER** (Ions score 55)
53 - 66	1517.8978	1516.8905	1516.8725	0.0181	1	**NLLSVAYKNVIGAR** (No match)
72 - 83	1388.7455	1387.7382	1387.7306	0.0076	1	**IISSIEQKEEGR** (No match)
136 - 146	1398.7268	1397.7195	1397.6727	0.0468	1	**GDYHRYLAEFK** (No match)
141 - 146	770.4382	769.4309	769.4010	0.0299	0	**YLAEFK** (No match)
141 - 151	1270.6539	1269.6466	1269.6353	0.0114	1	**YLAEFKSGAER** (No match)
164 - 180	1772.9852	1771.9779	1771.9580	0.0199	0	**AAQDIALADLAPTHPIR** (No match)
164 - 180	1772.9852	1771.9779	1771.9580	0.0199	0	**AAQDIALADLAPTHPIR** (Ions score 94)

Spot 94

Index

	Accession	Mass	Score	Description
1.	gi|22607	29361	278	14-3-3 protein homologue [Hordeum vulgare subsp. vulgare]
2.	gi|40781605	29388	278	14-3-3 protein [Triticum aestivum]
3.	gi|112684	29448	277	RecName: Full=14-3-3-like protein A; Short=14-3-3A
4.	gi|303859	29226	248	brain specific protein [Oryza sativa]
5.	gi|115454901	29274	248	Os03g0710800 [Oryza sativa (japonica cultivar-group)]
6.	gi|8515888	29754	151	14-3-3 protein [Populus x canescens]
7.	gi|224127634	29664	151	predicted protein [Populus trichocarpa]
8.	gi|225468983	28877	138	PREDICTED: hypothetical protein [Vitis vinifera]
9.	gi|8099063	29421	108	14-3-3 protein [Populus x canescens]
10.	gi|90657613	30545	105	hypothetical protein [Cleome spinosa]

Results List

1. gi|22607 **Mass:** 29361 **Score:** 278 **Expect:** 9.6e-023 **Queries matched:** 12

14-3-3 protein homologue [Hordeum vulgare subsp. vulgare]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
770.4330	769.4257	769.4010	0.0247	137	142	0	---	YLAEFK
1254.6697	1253.6624	1253.6403	0.0221	137	147	1	---	YLAEFKAGAER
1318.6641	1317.6568	1317.6412	0.0157	37	48	0	---	TADVGELTVEER
1418.7664	1417.7591	1417.7412	0.0179	68	79	1	---	IISSIEQKEESR
1499.7688	1498.7615	1498.7415	0.0200	80	92	1	29	GNEAYVASIKEYR
1499.7688	1498.7615	1498.7415	0.0200	80	92	1	---	GNEAYVASIKEYR
1517.9020	1516.8947	1516.8725	0.0223	49	62	1	---	NLLSVAYKNVIGAR
1517.9020	1516.8947	1516.8725	0.0223	49	62	1	58	NLLSVAYKNVIGAR
1818.9951	1817.9878	1817.9635	0.0243	160	176	0	97	SAQDIALADLPTTHPIR
1818.9951	1817.9878	1817.9635	0.0243	160	176	0	---	SAQDIALADLPTTHPIR
2131.9919	2130.9846	2130.9601	0.0245	17	33	1	---	LAEQAERYEEMVEFMEK
2163.9839	2162.9766	2162.9499	0.0267	17	33	1	---	LAEQAERYEEMVEFMEK + 2 Oxidation (M)

No match to: 764.4402, 768.5429, 799.4712, 1382.7509, 1710.9929, 1741.8220, 1741.8220, 1757.8259, 1757.8259, 1822.9207, 1867.1001, 2000.9924, 2148.9824, 2452.2988, 2900.5300

2. gi|40781605 **Mass:** 29388 **Score:** 278 **Expect:** 9.6e-023 **Queries matched:** 12

14-3-3 protein [Triticum aestivum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
770.4330	769.4257	769.4010	0.0247	137	142	0	---	YLAEFK
1254.6697	1253.6624	1253.6403	0.0221	137	147	1	---	YLAEFKAGAER
1318.6641	1317.6568	1317.6412	0.0157	37	48	0	---	TADVGELTVEER
1418.7664	1417.7591	1417.7412	0.0179	68	79	1	---	IISSIEQKEESR

1499.7688	1498.7615	1498.7415	0.0200	80 - 92	1	29	GNEAYVASIKEYR
1499.7688	1498.7615	1498.7415	0.0200	80 - 92	1	---	GNEAYVASIKEYR
1517.9020	1516.8947	1516.8725	0.0223	49 - 62	1	---	NLLSVAYKNVIGAR
1517.9020	1516.8947	1516.8725	0.0223	49 - 62	1	58	NLLSVAYKNVIGAR
1818.9951	1817.9878	1817.9635	0.0243	160 - 176	0	97	SAQDIALADLPTTHPIR
1818.9951	1817.9878	1817.9635	0.0243	160 - 176	0	---	SAQDIALADLPTTHPIR
2131.9919	2130.9846	2130.9601	0.0245	17 - 33	1	---	LAEQAERYEEMVEFMEK
2163.9839	2162.9766	2162.9499	0.0267	17 - 33	1	---	LAEQAERYEEMVEFMEK + 2 Oxidation (M)

No match to: 764.4402, 768.5429, 799.4712, 1382.7509, 1710.9929, 1741.8220, 1741.8220, 1757.8259, 1757.8259, 1822.9207, 1867.1001, 2000.9924, 2148.9824, 2452.2988, 2900.5300

3. gi|112684 **Mass:** 29448 **Score:** 277 **Expect:** 1.2e-022 **Queries matched:** 12

RecName: Full=14-3-3-like protein A; Short=14-3-3A

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
770.4330	769.4257	769.4010	0.0247	137 - 142		0	---	YLAEFK
1254.6697	1253.6624	1253.6403	0.0221	137 - 147		1	---	YLAEFKAGAER
1318.6641	1317.6568	1317.6412	0.0157	37 - 48		0	---	TADVGELTVEER
1418.7664	1417.7591	1417.7412	0.0179	68 - 79		1	---	IISSIEQKEESR
1499.7688	1498.7615	1498.7415	0.0200	80 - 92		1	29	GNEAYVASIKEYR
1499.7688	1498.7615	1498.7415	0.0200	80 - 92		1	---	GNEAYVASIKEYR
1517.9020	1516.8947	1516.8725	0.0223	49 - 62		1	---	NLLSVAYKNVIGAR
1517.9020	1516.8947	1516.8725	0.0223	49 - 62		1	58	NLLSVAYKNVIGAR
1818.9951	1817.9878	1817.9635	0.0243	160 - 176		0	97	SAQDIALADLPTTHPIR
1818.9951	1817.9878	1817.9635	0.0243	160 - 176		0	---	SAQDIALADLPTTHPIR
2131.9919	2130.9846	2130.9601	0.0245	17 - 33		1	---	LAEQAERYEEMVEFMEK
2163.9839	2162.9766	2162.9499	0.0267	17 - 33		1	---	LAEQAERYEEMVEFMEK + 2 Oxidation (M)

No match to: 764.4402, 768.5429, 799.4712, 1382.7509, 1710.9929, 1741.8220, 1741.8220, 1757.8259, 1757.8259, 1822.9207, 1867.1001, 2000.9924, 2148.9824, 2452.2988, 2900.5300

4. gi|303859 **Mass:** 29226 **Score:** 248 **Expect:** 9.6e-020 **Queries matched:** 10

brain specific protein [Oryza sativa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
770.4330	769.4257	769.4010	0.0247	137 - 142		0	---	YLAEFK
1418.7664	1417.7591	1417.7412	0.0179	68 - 79		1	---	IISSIEQKEESR
1499.7688	1498.7615	1498.7415	0.0200	80 - 92		1	29	GNEAYVASIKEYR
1499.7688	1498.7615	1498.7415	0.0200	80 - 92		1	---	GNEAYVASIKEYR
1517.9020	1516.8947	1516.8725	0.0223	49 - 62		1	---	NLLSVAYKNVIGAR
1517.9020	1516.8947	1516.8725	0.0223	49 - 62		1	58	NLLSVAYKNVIGAR
1818.9951	1817.9878	1817.9635	0.0243	160 - 176		0	97	SAQDIALADLPTTHPIR
1818.9951	1817.9878	1817.9635	0.0243	160 - 176		0	---	SAQDIALADLPTTHPIR
2131.9919	2130.9846	2130.9601	0.0245	17 - 33		1	---	LAEQAERYEEMVEFMEK

2163.9839	2162.9766	2162.9499	0.0267	17 - 33	1	---	LAEQAERYEEMVEFMEK + 2 Oxidation (M)

No match to: 764.4402, 768.5429, 799.4712, 1254.6697, 1318.6641, 1382.7509, 1710.9929, 1741.8220, 1741.8220, 1757.8259, 1757.8259, 1822.9207, 1867.1001, 2000.9924, 2148.9824, 2452.2988, 2900.5300

5. gi|115454901 **Mass:** 29274 **Score:** 248 **Expect:** 9.6e-020 **Queries matched:** 10

Os03g0710800 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
770.4330	769.4257	769.4010	0.0247	137 -	142	0	---	YLAEFK
1418.7664	1417.7591	1417.7412	0.0179	68 -	79	1	---	IISSIEQKEESR
1499.7688	1498.7615	1498.7415	0.0200	80 -	92	1	29	GNEAYVASIKEYR
1499.7688	1498.7615	1498.7415	0.0200	80 -	92	1	---	GNEAYVASIKEYR
1517.9020	1516.8947	1516.8725	0.0223	49 -	62	1	---	NLLSVAYKNVIGAR
1517.9020	1516.8947	1516.8725	0.0223	49 -	62	1	58	NLLSVAYKNVIGAR
1818.9951	1817.9878	1817.9635	0.0243	160 -	176	0	97	SAQDIALADLPTTHPIR
1818.9951	1817.9878	1817.9635	0.0243	160 -	176	0	---	SAQDIALADLPTTHPIR
2131.9919	2130.9846	2130.9601	0.0245	17 -	33	1	---	LAEQAERYEEMVEFMEK
2163.9839	2162.9766	2162.9499	0.0267	17 -	33	1	---	LAEQAERYEEMVEFMEK + 2 Oxidation (M)

No match to: 764.4402, 768.5429, 799.4712, 1254.6697, 1318.6641, 1382.7509, 1710.9929, 1741.8220, 1741.8220, 1757.8259, 1757.8259, 1822.9207, 1867.1001, 2000.9924, 2148.9824, 2452.2988, 2900.5300

6. gi|8515888 **Mass:** 29754 **Score:** 151 **Expect:** 4.8e-010 **Queries matched:** 8

14-3-3 protein [Populus x canescens]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
770.4330	769.4257	769.4010	0.0247	137 -	142	0	---	YLAEFK
1418.7664	1417.7591	1417.7412	0.0179	68 -	79	1	---	IISSIEQKEESR
1517.9020	1516.8947	1516.8725	0.0223	49 -	62	1	---	NLLSVAYKNVIGAR
1517.9020	1516.8947	1516.8725	0.0223	49 -	62	1	58	NLLSVAYKNVIGAR
1818.9951	1817.9878	1817.9635	0.0243	160 -	176	0	46	SAQDIALSELAPTHPIR
1818.9951	1817.9878	1817.9635	0.0243	160 -	176	0	---	SAQDIALSELAPTHPIR
2131.9919	2130.9846	2130.9601	0.0245	17 -	33	1	---	LAEQAERYEEMVEFMEK
2163.9839	2162.9766	2162.9499	0.0267	17 -	33	1	---	LAEQAERYEEMVEFMEK + 2 Oxidation (M)

No match to: 764.4402, 768.5429, 799.4712, 1254.6697, 1318.6641, 1382.7509, 1499.7688, 1499.7688, 1710.9929, 1741.8220, 1741.8220, 1757.8259, 1757.8259, 1822.9207, 1867.1001, 2000.9924, 2148.9824, 2452.2988, 2900.5300

7. gi|224127634 **Mass:** 29664 **Score:** 151 **Expect:** 4.8e-010 **Queries matched:** 8

predicted protein [Populus trichocarpa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
770.4330	769.4257	769.4010	0.0247	137 -	142	0	---	YLAEFK
1418.7664	1417.7591	1417.7412	0.0179	68 -	79	1	---	IISSIEQKEESR
1517.9020	1516.8947	1516.8725	0.0223	49 -	62	1	---	NLLSVAYKNVIGAR
1517.9020	1516.8947	1516.8725	0.0223	49 -	62	1	58	NLLSVAYKNVIGAR
1818.9951	1817.9878	1817.9635	0.0243	160 -	176	0	46	SAQDIALSELAPTHPIR

1818.9951	1817.9878	1817.9635	0.0243	160 - 176	0	---	SAQDIALSELAPTHPIR
2131.9919	2130.9846	2130.9601	0.0245	17 - 33	1	---	LAEQAERYEEMVEFMEK
2163.9839	2162.9766	2162.9499	0.0267	17 - 33	1	---	LAEQAERYEEMVEFMEK + 2 Oxidation (M)

No match to: 764.4402, 768.5429, 799.4712, 1254.6697, 1318.6641, 1382.7509, 1499.7688, 1499.7688, 1710.9929, 1741.8220, 1741.8220, 1757.8259, 1757.8259, 1822.9207, 1867.1001, 2000.9924, 2148.9824, 2452.2988, 2900.5300

8. gi|225468983 **Mass:** 28877 **Score:** 138 **Expect:** 9.6e-009 **Queries matched:** 6

PREDICTED: hypothetical protein [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
770.4330	769.4257	769.4010	0.0247	134 -	139	0	---	YLAEFK
1418.7664	1417.7591	1417.7412	0.0179	65 -	76	1	---	IISSIEQKEESR
1517.9020	1516.8947	1516.8725	0.0223	46 -	59	1	---	NLLSVAYKNVIGAR
1517.9020	1516.8947	1516.8725	0.0223	46 -	59	1	58	NLLSVAYKNVIGAR
1818.9951	1817.9878	1817.9635	0.0243	157 -	173	0	47	SAQDIATVELAPTHPIR
1818.9951	1817.9878	1817.9635	0.0243	157 -	173	0	---	SAQDIATVELAPTHPIR

No match to: 764.4402, 768.5429, 799.4712, 1254.6697, 1318.6641, 1382.7509, 1499.7688, 1499.7688, 1710.9929, 1741.8220, 1741.8220, 1757.8259, 1757.8259, 1822.9207, 1867.1001, 2000.9924, 2131.9919, 2148.9824, 2163.9839, 2452.2988, 2900.5300

9. gi|8099063 **Mass:** 29421 **Score:** 108 **Expect:** 9.6e-006 **Queries matched:** 9

14-3-3 protein [Populus x canescens]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
770.4330	769.4257	769.4010	0.0247	137 -	142	0	---	YLAEFK
1418.7664	1417.7591	1417.7412	0.0179	68 -	79	1	---	IISSIEQKEESR
1517.9020	1516.8947	1516.8725	0.0223	49 -	62	1	---	NLLSVAYKNVIGAR
1517.9020	1516.8947	1516.8725	0.0223	49 -	62	1	58	NLLSVAYKNVIGAR
1741.8220	1740.8147	1740.8174	-0.0027	1 -	16	1	---	MAATPSAREESVYMAK
1741.8220	1740.8147	1740.8174	-0.0027	1 -	16	1	---	MAATPSAREESVYMAK
1757.8259	1756.8186	1756.8123	0.0063	1 -	16	1	---	MAATPSAREESVYMAK + Oxidation (M)
1757.8259	1756.8186	1756.8123	0.0063	1 -	16	1	1	MAATPSAREESVYMAK + Oxidation (M)
2163.9839	2162.9766	2162.9499	0.0267	17 -	33	1	---	LAEQAERYEEMVEYMEK + Oxidation (M)

No match to: 764.4402, 768.5429, 799.4712, 1254.6697, 1318.6641, 1382.7509, 1499.7688, 1499.7688, 1710.9929, 1818.9951, 1818.9951, 1822.9207, 1867.1001, 2000.9924, 2131.9919, 2148.9824, 2452.2988, 2900.5300

10. gi|90657613 **Mass:** 30545 **Score:** 105 **Expect:** 1.9e-005 **Queries matched:** 7

hypothetical protein [Cleome spinosa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
770.4330	769.4257	769.4010	0.0247	137 -	142	0	---	YLAEFK
1418.7664	1417.7591	1417.7412	0.0179	68 -	79	1	---	IISSIEQKEESR
1517.9020	1516.8947	1516.8725	0.0223	49 -	62	1	---	NLLSVAYKNVIGAR
1517.9020	1516.8947	1516.8725	0.0223	49 -	62	1	58	NLLSVAYKNVIGAR
2131.9919	2130.9846	2130.9601	0.0245	17 -	33	1	---	LAEQAERYEEMVEFMEK

2148.9824 2147.9751 2147.9858 -0.0107 232 - 250 0 --- DNLTLWTSDINDEAGDEIK
2163.9839 2162.9766 2162.9499 0.0267 17 - 33 1 --- LAEQAERYEEMVEFMEK + 2 Oxidation (M)

No match to: 764.4402, 768.5429, 799.4712, 1254.6697, 1318.6641, 1382.7509, 1499.7688, 1499.7688, 1710.9929, 1741.8220, 1741.8220, 1757.8259, 1757.8259, 1818.9951, 1818.9951, 1822.9207, 1867.1001, 2000.9924, 2452.2988, 2900.5300

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 27

Protein View

Match to: **gi|40781605** Score: **278** Expect: **9.6e-023**
14-3-3 protein [Triticum aestivum]

Nominal mass (M_r): **29388**; Calculated pI value: **4.83**
NCBI BLAST search of gi|40781605 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Triticum aestivum

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **36%**

Matched peptides shown in **Bold Red**

```
   1 MSTAEATREE NVYMAKLAEQ AERYEEMVEF MEKVAKTADV GELTVEERNL
  51 LSVAYKNVIG ARRASWRIIS SIEQKEESRG NEAYVASIKE YRTRIETELN
 101 KICDGILKLL DSHLVPSATA AESKVFYLKM KGDYHRYLAE FKAGAERKEA
 151 AENTLVAYKS AQDIALADLP TTHPIRLGLA LNFSVFYYEI LNSPDRACNL
 201 AKQAFDEAIA ELDSLGEESY KDSTLIMQLL RDNLTLWTSD NAEEGGDEIK
 251 EAASKPEGEG H
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
17 - 33	2131.9919	2130.9846	2130.9601	0.0245	1	**LAEQAERYEEMVEFMEK** (No match)
17 - 33	2163.9839	2162.9766	2162.9499	0.0267	1	**LAEQAERYEEMVEFMEK** 2 Oxidation (M) (No match)
37 - 48	1318.6641	1317.6568	1317.6412	0.0157	0	**TADVGELTVEER** (No match)
49 - 62	1517.9020	1516.8947	1516.8725	0.0223	1	**NLLSVAYKNVIGAR** (No match)
49 - 62	1517.9020	1516.8947	1516.8725	0.0223	1	**NLLSVAYKNVIGAR** (Ions score 58)
68 - 79	1418.7664	1417.7591	1417.7412	0.0179	1	**IISSIEQKEESR** (No match)
80 - 92	1499.7688	1498.7615	1498.7415	0.0200	1	**GNEAYVASIKEYR** (Ions score 29)
80 - 92	1499.7688	1498.7615	1498.7415	0.0200	1	**GNEAYVASIKEYR** (No match)
137 - 142	770.4330	769.4257	769.4010	0.0247	0	**YLAEFK** (No match)
137 - 147	1254.6697	1253.6624	1253.6403	0.0221	1	**YLAEFKAGAER** (No match)
160 - 176	1818.9951	1817.9878	1817.9635	0.0243	0	**SAQDIALADLPTTHPIR** (Ions score 97)
160 - 176	1818.9951	1817.9878	1817.9635	0.0243	0	**SAQDIALADLPTTHPIR** (No match)

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	Accession	Mass	Score	Description
1.	gi|3309043	26252	80	group V allergen Phl p 5.0204 [Phleum pratense]
2.	gi|481397	28182	80	allergen Phl p Vb - common timothy
3.	gi|1684718	27903	80	major allergen Phl p 5 [Phleum pratense]
4.	gi|2851457	28042	79	RecName: Full=Pollen allergen Phl p 5b; AltName: Full=Allergen Phl p Vb; AltName: Allergen=Phl
5.	gi|3309047	28384	79	group V allergen Phl p 5.0207 precursor [Phleum pratense]
6.	gi|3309045	28869	79	group V allergen Phl p 5.0206 precursor [Phleum pratense]
7.	gi|3309041	29351	78	group V allergen Phl p 5.0203 precursor [Phleum pratense]
8.	gi|28948464	10653	67	Chain A, Crystal Structure Of The Functional Domain Of The Major Grass Pollen Allergen Phl P 5b
9.	gi|2266623	24693	63	group V grass pollen allergen [Holcus lanatus]
10.	gi|14423120	26342	63	group 5 isoallergen 1 [Dactylis glomerata]

Results List

1. gi|3309043 **Mass:** 26252 **Score:** 80 **Expect:** 0.0061 **Queries matched:** 3

group V allergen Phl p 5.0204 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1112.6005	1111.5932	1111.5913	0.0019	210	219	0	---	YAVFEAALTK
1112.6005	1111.5932	1111.5913	0.0019	210	219	0	50	YAVFEAALTK
1455.7651	1454.7578	1454.7405	0.0173	96	108	0	---	FDSFVASLTEALR

No match to: 768.5368, 2352.2546

2. gi|481397 **Mass:** 28182 **Score:** 80 **Expect:** 0.0068 **Queries matched:** 3

allergen Phl p Vb - common timothy

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1112.6005	1111.5932	1111.5913	0.0019	225	234	0	---	YAVFEAALTK
1112.6005	1111.5932	1111.5913	0.0019	225	234	0	50	YAVFEAALTK
1455.7651	1454.7578	1454.7405	0.0173	111	123	0	---	FDSFVASLTEALR

No match to: 768.5368, 2352.2546

3. gi|1684718 **Mass:** 27903 **Score:** 80 **Expect:** 0.0068 **Queries matched:** 3

major allergen Phl p 5 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1112.6005	1111.5932	1111.5913	0.0019	226	235	0	---	YAVFEAALTK
1112.6005	1111.5932	1111.5913	0.0019	226	235	0	50	YAVFEAALTK
1455.7651	1454.7578	1454.7405	0.0173	112	124	0	---	FDSFVASLTEALR

No match to: 768.5368, 2352.2546

4. gi|2851457 **Mass:** 28042 **Score:** 79 **Expect:** 0.007 **Queries matched:** 3

RecName: Full=Pollen allergen Phl p 5b; AltName: Full=Allergen Phl p Vb; AltName: Allergen=Phl p 5b

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1112.6005	1111.5932	1111.5913	0.0019	229 -	238	0	---	YAVFEAALTK
1112.6005	1111.5932	1111.5913	0.0019	229 -	238	0	50	YAVFEAALTK
1455.7651	1454.7578	1454.7405	0.0173	115 -	127	0	---	FDSFVASLTEALR

No match to: 768.5368, 2352.2546

5. gi|3309047 **Mass:** 28384 **Score:** 79 **Expect:** 0.0071 **Queries matched:** 3

group V allergen Phl p 5.0207 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1112.6005	1111.5932	1111.5913	0.0019	232 -	241	0	---	YAVFEAALTK
1112.6005	1111.5932	1111.5913	0.0019	232 -	241	0	50	YAVFEAALTK
1455.7651	1454.7578	1454.7405	0.0173	121 -	133	0	---	FDSFVASLTEALR

No match to: 768.5368, 2352.2546

6. gi|3309045 **Mass:** 28869 **Score:** 79 **Expect:** 0.0073 **Queries matched:** 3

group V allergen Phl p 5.0206 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1112.6005	1111.5932	1111.5913	0.0019	235 -	244	0	---	YAVFEAALTK
1112.6005	1111.5932	1111.5913	0.0019	235 -	244	0	50	YAVFEAALTK
1455.7651	1454.7578	1454.7405	0.0173	121 -	133	0	---	FDSFVASLTEALR

No match to: 768.5368, 2352.2546

7. gi|3309041 **Mass:** 29351 **Score:** 78 **Expect:** 0.0094 **Queries matched:** 3

group V allergen Phl p 5.0203 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1112.6005	1111.5932	1111.5913	0.0019	240 -	249	0	---	YAVFEAALTK
1112.6005	1111.5932	1111.5913	0.0019	240 -	249	0	50	YAVFEAALTK
1455.7651	1454.7578	1454.7405	0.0173	126 -	138	0	---	FDSFVASLTEALR

No match to: 768.5368, 2352.2546

8. gi|28948464 **Mass:** 10653 **Score:** 67 **Expect:** 0.14 **Queries matched:** 2

Chain A, Crystal Structure Of The Functional Domain Of The Major Grass Pollen Allergen Phl P 5b

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1112.6005	1111.5932	1111.5913	0.0019	80 -	89	0	---	YAVFEAALTK
1112.6005	1111.5932	1111.5913	0.0019	80 -	89	0	50	YAVFEAALTK

No match to: 768.5368, 1455.7651, 2352.2546

9. gi|2266623 **Mass:** 24693 **Score:** 63 **Expect:** 0.3 **Queries matched:** 2

group V grass pollen allergen [Holcus lanatus]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1112.6005	1111.5932	1111.5913	0.0019	193 -	202	0	---	YAVFEAALTK

1112.6005	1111.5932	1111.5913	0.0019	193 - 202	0	50	YAVFEAALTK

No match to: 768.5368, 1455.7651, 2352.2546

10. gi|14423120 **Mass:** 26342 **Score:** 63 **Expect:** 0.33 **Queries matched:** 2

group 5 isoallergen 1 [Dactylis glomerata]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1112.6005	1111.5932	1111.5913	0.0019	214 - 223	0	---		YAVFEAALTK
1112.6005	1111.5932	1111.5913	0.0019	214 - 223	0	50		YAVFEAALTK

No match to: 768.5368, 1455.7651, 2352.2546

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 5

Protein View

Match to: **gi|3309043** Score: **80** Expect: **0.0061**
group V allergen Phl p 5.0204 [Phleum pratense]

Nominal mass (M_r): **26252**; Calculated pI value: **5.61**
NCBI BLAST search of gi|3309043 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

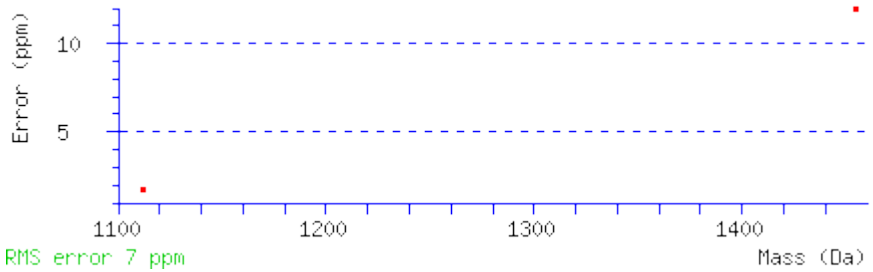
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **8%**

Matched peptides shown in **Bold Red**

```
   1 ADAGYAPATP AAAGAEAGKA TTEEQKLIED INVGFKAAVA AAASVPAADK
  51 FKTFEAAFTS SSKAATAKAP GLVPKLDAAY SVAYKAAVGA TPEAKFDSFV
 101 ASLTEALRVI AGALEVHAVK PVTEEPGMAK IPAGELQIID KIDAAFKVAA
 151 TAAATAPADD KFTVFEAAFN KAIKESTGGA YDTYKCIPSL EAAVKQAYAA
 201 TVAAAPQVKY AVFEAALTKA ITAMSEVQKV SQPATGAATV AAGAATTAAG
 251 AASGAATVAA GGYKV
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
96 - 108	1455.7651	1454.7578	1454.7405	0.0173	0	FDSFVASLTEALR	(No match)
210 - 219	1112.6005	1111.5932	1111.5913	0.0019	0	YAVFEAALTK	(No match)
210 - 219	1112.6005	1111.5932	1111.5913	0.0019	0	YAVFEAALTK	(Ions score 50)



Peptide View

MS/MS Fragmentation of **YAVFEAALTK**
Found in **gi|3309043**, group V allergen Phl p 5.0204 [Phleum pratense]

Match to Query 3: 1111.593224 from(1112.600500,1+)
MaldiWellID: 84606, SpectrumID: 219535,

Click mouse within plot area to zoom in by factor of two about that point
Or, to Da

MONOISOTOPIC mass of neutral peptide Mr(calc): 1111.5913
Fixed modifications: Carbamidomethyl (C)
Ions Score: 50 **Expect:** 0.0075
Matches (Bold Red): 38/115 fragment ions using 56 most intense peaks

#	Immon.	a	a^0	b	b^0	Seq.	y	y*	y^0	#
1	**136.0757**	**136.0757**		164.0706		Y				10
2	44.0495	**207.1128**		**235.1077**		A	949.5353	932.5087	931.5247	9
3	**72.0808**	306.1812		**334.1761**		V	**878.4982**	861.4716	860.4876	8
4	**120.0808**	453.2496		**481.2445**		F	**779.4298**	762.4032	761.4192	7
5	102.0550	**582.2922**	564.2817	**610.2871**	592.2766	E	**632.3613**	615.3348	614.3508	6
6	44.0495	**653.3293**	635.3188	**681.3242**	663.3137	A	**503.3188**	486.2922	**485.3082**	5
7	44.0495	724.3664	706.3559	**752.3613**	734.3508	A	**432.2816**	415.2551	414.2711	4
8	**86.0964**	837.4505	819.4399	**865.4454**	847.4348	L	**361.2445**	344.2180	343.2340	3
9	74.0600	938.4982	920.4876	966.4931	948.4825	T	**248.1605**	231.1339	230.1499	2
10	101.1073					K	**147.1128**	130.0863		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
AV	143.1179	**171.1128**	AVF	290.1863	318.1812	AVFE	**419.2289**	**447.2238**
AVFEA	490.2660	**518.2609**	AVFEAA	561.3031	**589.2980**	AVFEAAL	674.3872	702.3821
VF	219.1492	**247.1441**	VFE	**348.1918**	376.1867	VFEA	**419.2289**	**447.2238**
VFEAA	490.2660	**518.2609**	VFEAAL	603.3501	631.3450	FE	249.1234	**277.1183**
FEA	320.1605	**348.1554**	FEAA	391.1976	**419.1925**	FEAAL	504.2816	532.2766
FEAALT	**605.3293**	633.3242	EA	173.0921	201.0870	EAA	244.1292	272.1241
EAAL	357.2132	385.2081	EAALT	458.2609	486.2558	AA	115.0866	143.0815
AAL	228.1706	256.1656	AALT	329.2183	357.2132	AL	157.1335	185.1284
ALT	258.1812	286.1761	LT	187.1441	215.1390			

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	Accession	Mass	Score	Description
1.	gi|3309043	26252	424	group V allergen Phl p 5.0204 [Phleum pratense]
2.	gi|2851457	28042	420	RecName: Full=Pollen allergen Phl p 5b; AltName: Full=Allergen Phl p Vb; AltName: Allergen=Phl p
3.	gi|3309041	29351	416	group V allergen Phl p 5.0203 precursor [Phleum pratense]
4.	gi|1684718	27903	404	major allergen Phl p 5 [Phleum pratense]
5.	gi|3309045	28869	399	group V allergen Phl p 5.0206 precursor [Phleum pratense]

Results List

1. gi|3309043 **Mass:** 26252 **Score:** 424 **Expect:** 2.4e-037 **Queries matched:** 20

group V allergen Phl p 5.0204 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1087.5786	1086.5713	1086.5743	-0.0030	186	195	0	---	CIPSLEAAVK
1100.5552	1099.5479	1099.5549	-0.0070	76	85	0	---	LDAAYSVAYK
1112.5911	1111.5838	1111.5913	-0.0075	210	219	0	75	YAVFEAALTK
1112.5911	1111.5838	1111.5913	-0.0075	210	219	0	---	YAVFEAALTK
1147.6296	1146.6223	1146.6284	-0.0061	27	36	0	---	LIEDINVGFK
1175.5544	1174.5471	1174.5506	-0.0034	53	63	0	---	TFEAAFTSSSK
1191.5192	1190.5119	1190.5091	0.0028	175	185	0	---	ESTGGAYDTYK
1388.7444	1387.7371	1387.7459	-0.0088	196	209	0	---	QAYAATVAAAPQVK
1455.7498	1454.7425	1454.7405	0.0020	96	108	0	46	FDSFVASLTEALR
1455.7498	1454.7425	1454.7405	0.0020	96	108	0	---	FDSFVASLTEALR
1487.8147	1486.8074	1486.8143	-0.0069	37	52	1	---	AAVAAAASVPAADKFK
1503.7246	1502.7173	1502.7252	-0.0079	172	185	1	---	AIKESTGGAYDTYK
1762.9724	1761.9651	1761.9664	-0.0013	69	85	1	---	APGLVPKLDAAYSVAYK
1842.0344	1841.0271	1841.0298	-0.0026	131	147	1	---	IPAGELQIIDKIDAAFK
1935.0050	1933.9977	1933.9996	-0.0019	20	36	1	---	ATTEEQKLIEDINVGFK
2246.2302	2245.2229	2245.2139	0.0090	109	130	0	---	VIAGALEVHAVKPVTEEPGMAK
2262.2188	2261.2115	2261.2088	0.0027	109	130	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2234	2350.2161	2350.2168	-0.0006	86	108	1	113	AAVGATPEAKFDSFVASLTEALR
2351.2234	2350.2161	2350.2168	-0.0006	86	108	1	---	AAVGATPEAKFDSFVASLTEALR
2427.2263	2426.2190	2426.2117	0.0073	148	171	1	---	VAATAAATAPADDKFTVFEAAFNK

No match to: 713.4093, 724.4933, 750.5203, 768.5222, 838.5289, 1011.6370, 1070.5522, 1179.6053, 1283.6729, 1313.6979, 1326.6823, 1371.7222, 1405.6453, 1448.9188, 1475.7643, 1529.6760, 1572.6864, 1708.7795, 1940.9390, 1987.0693, 2205.2290, 2323.9714, 2566.1936, 2644.3782, 2644.3782, 2662.3860, 2825.3403, 3087.6477, 3349.6311, 3607.8674, 3679.8777, 3679.8777, 3809.8191, 3814.9424

2. gi|2851457 **Mass:** 28042 **Score:** 420 **Expect:** 6e-037 **Queries matched:** 20

RecName: Full=Pollen allergen Phl p 5b; AltName: Full=Allergen Phl p Vb; AltName: Allergen=Phl p 5b

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1087.5786	1086.5713	1086.5743	-0.0030	205	214	0	---	CIPSLEAAVK
1100.5552	1099.5479	1099.5549	-0.0070	95	104	0	---	LDAAYSVAYK
1112.5911	1111.5838	1111.5913	-0.0075	229	238	0	75	YAVFEAALTK
1112.5911	1111.5838	1111.5913	-0.0075	229	238	0	---	YAVFEAALTK
1147.6296	1146.6223	1146.6284	-0.0061	46	55	0	---	LIEDINVGFK
1175.5544	1174.5471	1174.5506	-0.0034	72	82	0	---	TFEAAFTSSSK
1191.5192	1190.5119	1190.5091	0.0028	194	204	0	---	ESTGGAYDTYK
1388.7444	1387.7371	1387.7459	-0.0088	215	228	0	---	QAYAATVAAAPQVK
1455.7498	1454.7425	1454.7405	0.0020	115	127	0	46	FDSFVASLTEALR
1455.7498	1454.7425	1454.7405	0.0020	115	127	0	---	FDSFVASLTEALR
1487.8147	1486.8074	1486.8143	-0.0069	56	71	1	---	AAVAAAASVPAADKFK
1503.7246	1502.7173	1502.7252	-0.0079	191	204	1	---	AIKESTGGAYDTYK
1762.9724	1761.9651	1761.9664	-0.0013	88	104	1	---	APGLVPKLDAAYSVAYK
1842.0344	1841.0271	1841.0298	-0.0026	150	166	1	---	IPAGELQIIDKIDAAFK
1935.0050	1933.9977	1933.9996	-0.0019	39	55	1	---	ATTEEQKLIEDINVGFK
2246.2302	2245.2229	2245.2139	0.0090	128	149	0	---	VIAGALEVHAVKPVTEEPGMAK
2262.2188	2261.2115	2261.2088	0.0027	128	149	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2234	2350.2161	2350.2168	-0.0006	105	127	1	113	AAVGATPEAKFDSFVASLTEALR
2351.2234	2350.2161	2350.2168	-0.0006	105	127	1	---	AAVGATPEAKFDSFVASLTEALR
2427.2263	2426.2190	2426.2117	0.0073	167	190	1	---	VAATAAATAPADDKFTVFEAAFNK

No match to: 713.4093, 724.4933, 750.5203, 768.5222, 838.5289, 1011.6370, 1070.5522, 1179.6053, 1283.6729, 1313.6979, 1326.6823, 1371.7222, 1405.6453, 1448.9188, 1475.7643, 1529.6760, 1572.6864, 1708.7795, 1940.9390, 1987.0693, 2205.2290, 2323.9714, 2566.1936, 2644.3782, 2644.3782, 2662.3860, 2825.3403, 3087.6477, 3349.6311, 3607.8674, 3679.8777, 3679.8777, 3809.8191, 3814.9424

3. gi|3309041 **Mass:** 29351 **Score:** 416 **Expect:** 1.5e-036 **Queries matched:** 20

group V allergen Phl p 5.0203 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1087.5786	1086.5713	1086.5743	-0.0030	216	225	0	---	CIPSLEAAVK
1100.5552	1099.5479	1099.5549	-0.0070	106	115	0	---	LDAAYSVAYK
1112.5911	1111.5838	1111.5913	-0.0075	240	249	0	75	YAVFEAALTK
1112.5911	1111.5838	1111.5913	-0.0075	240	249	0	---	YAVFEAALTK
1147.6296	1146.6223	1146.6284	-0.0061	57	66	0	---	LIEDINVGFK
1175.5544	1174.5471	1174.5506	-0.0034	83	93	0	---	TFEAAFTSSSK
1191.5192	1190.5119	1190.5091	0.0028	205	215	0	---	ESTGGAYDTYK
1388.7444	1387.7371	1387.7459	-0.0088	226	239	0	---	QAYAATVAAAPQVK
1455.7498	1454.7425	1454.7405	0.0020	126	138	0	46	FDSFVASLTEALR
1455.7498	1454.7425	1454.7405	0.0020	126	138	0	---	FDSFVASLTEALR
1487.8147	1486.8074	1486.8143	-0.0069	67	82	1	---	AAVAAAASVPAADKFK

1503.7246	1502.7173	1502.7252	-0.0079	202 - 215	1	---	AIKESTGGAYDTYK
1762.9724	1761.9651	1761.9664	-0.0013	99 - 115	1	---	APGLVPKLDAAYSVAYK
1842.0344	1841.0271	1841.0298	-0.0026	161 - 177	1	---	IPAGELQIIDKIDAAFK
1935.0050	1933.9977	1933.9996	-0.0019	50 - 66	1	---	ATTEEQKLIEDINVGFK
2246.2302	2245.2229	2245.2139	0.0090	139 - 160	0	---	VIAGALEVHAVKPVTEEPGMAK
2262.2188	2261.2115	2261.2088	0.0027	139 - 160	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2234	2350.2161	2350.2168	-0.0006	116 - 138	1	113	AAVGATPEAKFDSFVASLTEALR
2351.2234	2350.2161	2350.2168	-0.0006	116 - 138	1	---	AAVGATPEAKFDSFVASLTEALR
2427.2263	2426.2190	2426.2117	0.0073	178 - 201	1	---	VAATAAATAPADDKFTVFEAAFNK

No match to: 713.4093, 724.4933, 750.5203, 768.5222, 838.5289, 1011.6370, 1070.5522, 1179.6053, 1283.6729, 1313.6979, 1326.6823, 1371.7222, 1405.6453, 1448.9188, 1475.7643, 1529.6760, 1572.6864, 1708.7795, 1940.9390, 1987.0693, 2205.2290, 2323.9714, 2566.1936, 2644.3782, 2644.3782, 2662.3860, 2825.3403, 3087.6477, 3349.6311, 3607.8674, 3679.8777, 3679.8777, 3809.8191, 3814.9424

4. gi|1684718 **Mass:** 27903 **Score:** 404 **Expect:** 2.4e-035 **Queries matched:** 19

major allergen Phl p 5 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1087.5786	1086.5713	1086.5743	-0.0030	202 - 211	0	---	CIPSLEAAVK
1100.5552	1099.5479	1099.5549	-0.0070	92 - 101	0	---	LDAAYSVAYK
1112.5911	1111.5838	1111.5913	-0.0075	226 - 235	0	75	YAVFEAALTK
1112.5911	1111.5838	1111.5913	-0.0075	226 - 235	0	---	YAVFEAALTK
1147.6296	1146.6223	1146.6284	-0.0061	43 - 52	0	---	LIEDINVGFK
1175.5544	1174.5471	1174.5506	-0.0034	69 - 79	0	---	TFEAAFTSSSK
1191.5192	1190.5119	1190.5091	0.0028	191 - 201	0	---	ESTGGAYDTYK
1388.7444	1387.7371	1387.7459	-0.0088	212 - 225	0	---	QAYAATVAAAPQVK
1455.7498	1454.7425	1454.7405	0.0020	112 - 124	0	46	FDSFVASLTEALR
1455.7498	1454.7425	1454.7405	0.0020	112 - 124	0	---	FDSFVASLTEALR
1503.7246	1502.7173	1502.7252	-0.0079	188 - 201	1	---	AIKESTGGAYDTYK
1762.9724	1761.9651	1761.9664	-0.0013	85 - 101	1	---	APGLVPKLDAAYSVAYK
1842.0344	1841.0271	1841.0298	-0.0026	147 - 163	1	---	IPAGELQIIDKIDAAFK
1935.0050	1933.9977	1933.9996	-0.0019	36 - 52	1	---	ATTEEQKLIEDINVGFK
2246.2302	2245.2229	2245.2139	0.0090	125 - 146	0	---	VIAGALEVHAVKPVTEEPGMAK
2262.2188	2261.2115	2261.2088	0.0027	125 - 146	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2234	2350.2161	2350.2168	-0.0006	102 - 124	1	113	AAVGATPEAKFDSFVASLTEALR
2351.2234	2350.2161	2350.2168	-0.0006	102 - 124	1	---	AAVGATPEAKFDSFVASLTEALR
2427.2263	2426.2190	2426.2117	0.0073	164 - 187	1	---	VAATAAATAPADDKFTVFEAAFNK

No match to: 713.4093, 724.4933, 750.5203, 768.5222, 838.5289, 1011.6370, 1070.5522, 1179.6053, 1283.6729, 1313.6979, 1326.6823, 1371.7222, 1405.6453, 1448.9188, 1475.7643, 1487.8147, 1529.6760, 1572.6864, 1708.7795, 1940.9390, 1987.0693, 2205.2290, 2323.9714, 2566.1936, 2644.3782, 2644.3782, 2662.3860, 2825.3403, 3087.6477, 3349.6311, 3607.8674, 3679.8777, 3679.8777, 3809.8191, 3814.9424

5. gi|3309045 **Mass:** 28869 **Score:** 399 **Expect:** 7.6e-035 **Queries matched:** 18

group V allergen Phl p 5.0206 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1087.5786	1086.5713	1086.5743	-0.0030	211	220	0	---	CIPSLEAAVK
1100.5552	1099.5479	1099.5549	-0.0070	101	110	0	---	LDAAYSVAYK
1112.5911	1111.5838	1111.5913	-0.0075	235	244	0	75	YAVFEAALTK
1112.5911	1111.5838	1111.5913	-0.0075	235	244	0	---	YAVFEAALTK
1147.6296	1146.6223	1146.6284	-0.0061	52	61	0	---	LIEDINVGFK
1175.5544	1174.5471	1174.5506	-0.0034	78	88	0	---	TFEAAFTSSSK
1191.5192	1190.5119	1190.5091	0.0028	200	210	0	---	ESTGGAYDTYK
1388.7444	1387.7371	1387.7459	-0.0088	221	234	0	---	QAYAATVAAAPQVK
1455.7498	1454.7425	1454.7405	0.0020	121	133	0	46	FDSFVASLTEALR
1455.7498	1454.7425	1454.7405	0.0020	121	133	0	---	FDSFVASLTEALR
1487.8147	1486.8074	1486.8143	-0.0069	62	77	1	---	AAVAAAASVPAADKFK
1503.7246	1502.7173	1502.7252	-0.0079	197	210	1	---	AIKESTGGAYDTYK
1762.9724	1761.9651	1761.9664	-0.0013	94	110	1	---	APGLVPKLDAAYSVAYK
1842.0344	1841.0271	1841.0298	-0.0026	156	172	1	---	IPAGELQIIDKIDAAFK
1935.0050	1933.9977	1933.9996	-0.0019	45	61	1	---	ATTEEQKLIEDINVGFK
2351.2234	2350.2161	2350.2168	-0.0006	111	133	1	113	AAVGATPEAKFDSFVASLTEALR
2351.2234	2350.2161	2350.2168	-0.0006	111	133	1	---	AAVGATPEAKFDSFVASLTEALR
2427.2263	2426.2190	2426.2117	0.0073	173	196	1	---	VAATAAATAPADDKFTVFEAAFNK

No match to: 713.4093, 724.4933, 750.5203, 768.5222, 838.5289, 1011.6370, 1070.5522, 1179.6053, 1283.6729, 1313.6979, 1326.6823, 1371.7222, 1405.6453, 1448.9188, 1475.7643, 1529.6760, 1572.6864, 1708.7795, 1940.9390, 1987.0693, 2205.2290, 2246.2302, 2262.2188, 2323.9714, 2566.1936, 2644.3782, 2644.3782, 2662.3860, 2825.3403, 3087.6477, 3349.6311, 3607.8674, 3679.8777, 3679.8777, 3809.8191, 3814.9424

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 54

Protein View

Match to: **gi|3309043** Score: **424** Expect: **2.4e-037**
group V allergen Phl p 5.0204 [Phleum pratense]

Nominal mass (M_r): **26252**; Calculated pI value: **5.61**
NCBI BLAST search of gi|3309043 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **73%**

Matched peptides shown in **Bold Red**

```
   1 ADAGYAPATP AAAGAEAGKA TTEEQKLIED INVGFKAAVA AAASVPAADK
  51 FKTFEAAFTS SSKAATAKAP GLVPKLDAAY SVAYKAAVGA TPEAKFDSFV
 101 ASLTEALRVI AGALEVHAVK PVTEEPGMAK IPAGELQIID KIDAAFKVAA
 151 TAAATAPADD KFTVFEAAFN KAIKESTGGA YDTYKCIPSL EAAVKQAYAA
 201 TVAAAPQVKY AVFEAALTKA ITAMSEVQKV SQPATGAATV AAGAATTAAG
 251 AASGAATVAA GGYKV
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
20 - 36	1935.0050	1933.9977	1933.9996	-0.0019	1	ATTEEQKLIEDINVGFK (No match)
27 - 36	1147.6296	1146.6223	1146.6284	-0.0061	0	LIEDINVGFK (No match)
37 - 52	1487.8147	1486.8074	1486.8143	-0.0069	1	AAVAAAASVPAADKFK (No match)
53 - 63	1175.5544	1174.5471	1174.5506	-0.0034	0	TFEAAFTSSSK (No match)
69 - 85	1762.9724	1761.9651	1761.9664	-0.0013	1	APGLVPKLDAAYSVAYK (No match)
76 - 85	1100.5552	1099.5479	1099.5549	-0.0070	0	LDAAYSVAYK (No match)
86 - 108	2351.2234	2350.2161	2350.2168	-0.0006	1	AAVGATPEAKFDSFVASLTEALR (Ions score 113)
86 - 108	2351.2234	2350.2161	2350.2168	-0.0006	1	AAVGATPEAKFDSFVASLTEALR (No match)
96 - 108	1455.7498	1454.7425	1454.7405	0.0020	0	FDSFVASLTEALR (Ions score 46)
96 - 108	1455.7498	1454.7425	1454.7405	0.0020	0	FDSFVASLTEALR (No match)
109 - 130	2246.2302	2245.2229	2245.2139	0.0090	0	VIAGALEVHAVKPVTEEPGMAK (No match)
109 - 130	2262.2188	2261.2115	2261.2088	0.0027	0	VIAGALEVHAVKPVTEEPGMAK Oxidation (M) (No match)
131 - 147	1842.0344	1841.0271	1841.0298	-0.0026	1	IPAGELQIIDKIDAAFK (No match)
148 - 171	2427.2263	2426.2190	2426.2117	0.0073	1	VAATAAATAPADDKFTVFEAAFNK (No match)
172 - 185	1503.7246	1502.7173	1502.7252	-0.0079	1	AIKESTGGAYDTYK (No match)
175 - 185	1191.5192	1190.5119	1190.5091	0.0028	0	ESTGGAYDTYK (No match)
186 - 195	1087.5786	1086.5713	1086.5743	-0.0030	0	CIPSLEAAVK (No match)
196 - 209	1388.7444	1387.7371	1387.7459	-0.0088	0	QAYAATVAAAPQVK (No match)
210 - 219	1112.5911	1111.5838	1111.5913	-0.0075	0	YAVFEAALTK (Ions score 75)
210 - 219	1112.5911	1111.5838	1111.5913	-0.0075	0	YAVFEAALTK (No match)

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	Accession	Mass	Score	Description
1.	gi|3309043	26252	871	group V allergen Phl p 5.0204 [Phleum pratense]
2.	gi|2851457	28042	867	RecName: Full=Pollen allergen Phl p 5b; AltName: Full=Allergen Phl p Vb; AltName: Allergen=Phl
3.	gi|3309041	29351	865	group V allergen Phl p 5.0203 precursor [Phleum pratense]
4.	gi|1684718	27903	845	major allergen Phl p 5 [Phleum pratense]
5.	gi|3309045	28869	842	group V allergen Phl p 5.0206 precursor [Phleum pratense]
6.	gi|481397	28182	823	allergen Phl p Vb - common timothy
7.	gi|3309047	28384	713	group V allergen Phl p 5.0207 precursor [Phleum pratense]
8.	gi|28948464	10653	320	Chain A, Crystal Structure Of The Functional Domain Of The Major Grass Pollen Allergen Phl P 5b
9.	gi|11991229	29216	188	pollen allergen Hol l 5b [Holcus lanatus]
10.	gi|897626	5802	48	unknown protein

Results List

1. gi|3309043 **Mass:** 26252 **Score:** 871 **Expect:** 4.8e-082 **Queries matched:** 18

group V allergen Phl p 5.0204 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1087.5754	1086.5681	1086.5743	-0.0062	186	195	0	---	CIPSLEAAVK
1100.5471	1099.5398	1099.5549	-0.0151	76	85	0	---	LDAAYSVAYK
1112.5883	1111.5810	1111.5913	-0.0103	210	219	0	---	YAVFEAALTK
1147.6279	1146.6206	1146.6284	-0.0078	27	36	0	---	LIEDINVGFK
1175.5482	1174.5409	1174.5506	-0.0096	53	63	0	---	TFEAAFTSSSK
1455.7458	1454.7385	1454.7405	-0.0020	96	108	0	109	FDSFVASLTEALR
1455.7458	1454.7385	1454.7405	-0.0020	96	108	0	---	FDSFVASLTEALR
1487.8081	1486.8008	1486.8143	-0.0135	37	52	1	---	AAVAAAASVPAADKFK
1503.7310	1502.7237	1502.7252	-0.0015	172	185	1	---	AIKESTGGAYDTYK
1842.0339	1841.0266	1841.0298	-0.0031	131	147	1	158	IPAGELQIIDKIDAAFK
1842.0339	1841.0266	1841.0298	-0.0031	131	147	1	---	IPAGELQIIDKIDAAFK
1935.0024	1933.9951	1933.9996	-0.0045	20	36	1	---	ATTEEQKLIEDINVGFK
1935.0024	1933.9951	1933.9996	-0.0045	20	36	1	131	ATTEEQKLIEDINVGFK
2262.2273	2261.2200	2261.2088	0.0112	109	130	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2207	2350.2134	2350.2168	-0.0033	86	108	1	---	AAVGATPEAKFDSFVASLTEALR
2351.2207	2350.2134	2350.2168	-0.0033	86	108	1	148	AAVGATPEAKFDSFVASLTEALR
2427.2327	2426.2254	2426.2117	0.0137	148	171	1	---	VAATAAATAPADDKFTVFEAAFNK
2427.2327	2426.2254	2426.2117	0.0137	148	171	1	104	VAATAAATAPADDKFTVFEAAFNK

No match to: 713.4184, 1469.7655, 2644.3872, 3607.8345

2. gi|2851457 **Mass:** 28042 **Score:** 867 **Expect:** 1.2e-081 **Queries matched:** 18

RecName: Full=Pollen allergen Phl p 5b; AltName: Full=Allergen Phl p Vb; AltName: Allergen=Phl p 5b

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1087.5754	1086.5681	1086.5743	-0.0062	205	214	0	---	CIPSLEAAVK
1100.5471	1099.5398	1099.5549	-0.0151	95	104	0	---	LDAAYSVAYK
1112.5883	1111.5810	1111.5913	-0.0103	229	238	0	---	YAVFEAALTK
1147.6279	1146.6206	1146.6284	-0.0078	46	55	0	---	LIEDINVGFK
1175.5482	1174.5409	1174.5506	-0.0096	72	82	0	---	TFEAAFTSSSK
1455.7458	1454.7385	1454.7405	-0.0020	115	127	0	109	FDSFVASLTEALR
1455.7458	1454.7385	1454.7405	-0.0020	115	127	0	---	FDSFVASLTEALR
1487.8081	1486.8008	1486.8143	-0.0135	56	71	1	---	AAVAAAASVPAADKFK
1503.7310	1502.7237	1502.7252	-0.0015	191	204	1	---	AIKESTGGAYDTYK
1842.0339	1841.0266	1841.0298	-0.0031	150	166	1	158	IPAGELQIIDKIDAAFK
1842.0339	1841.0266	1841.0298	-0.0031	150	166	1	---	IPAGELQIIDKIDAAFK
1935.0024	1933.9951	1933.9996	-0.0045	39	55	1	---	ATTEEQKLIEDINVGFK
1935.0024	1933.9951	1933.9996	-0.0045	39	55	1	131	ATTEEQKLIEDINVGFK
2262.2273	2261.2200	2261.2088	0.0112	128	149	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2207	2350.2134	2350.2168	-0.0033	105	127	1	---	AAVGATPEAKFDSFVASLTEALR
2351.2207	2350.2134	2350.2168	-0.0033	105	127	1	148	AAVGATPEAKFDSFVASLTEALR
2427.2327	2426.2254	2426.2117	0.0137	167	190	1	---	VAATAAATAPADDKFTVFEAAFNK
2427.2327	2426.2254	2426.2117	0.0137	167	190	1	104	VAATAAATAPADDKFTVFEAAFNK

No match to: 713.4184, 1469.7655, 2644.3872, 3607.8345

3. gi|3309041 **Mass:** 29351 **Score:** 865 **Expect:** 1.9e-081 **Queries matched:** 18

group V allergen Phl p 5.0203 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1087.5754	1086.5681	1086.5743	-0.0062	216	225	0	---	CIPSLEAAVK
1100.5471	1099.5398	1099.5549	-0.0151	106	115	0	---	LDAAYSVAYK
1112.5883	1111.5810	1111.5913	-0.0103	240	249	0	---	YAVFEAALTK
1147.6279	1146.6206	1146.6284	-0.0078	57	66	0	---	LIEDINVGFK
1175.5482	1174.5409	1174.5506	-0.0096	83	93	0	---	TFEAAFTSSSK
1455.7458	1454.7385	1454.7405	-0.0020	126	138	0	109	FDSFVASLTEALR
1455.7458	1454.7385	1454.7405	-0.0020	126	138	0	---	FDSFVASLTEALR
1487.8081	1486.8008	1486.8143	-0.0135	67	82	1	---	AAVAAAASVPAADKFK
1503.7310	1502.7237	1502.7252	-0.0015	202	215	1	---	AIKESTGGAYDTYK
1842.0339	1841.0266	1841.0298	-0.0031	161	177	1	158	IPAGELQIIDKIDAAFK
1842.0339	1841.0266	1841.0298	-0.0031	161	177	1	---	IPAGELQIIDKIDAAFK
1935.0024	1933.9951	1933.9996	-0.0045	50	66	1	---	ATTEEQKLIEDINVGFK
1935.0024	1933.9951	1933.9996	-0.0045	50	66	1	131	ATTEEQKLIEDINVGFK
2262.2273	2261.2200	2261.2088	0.0112	139	160	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2207	2350.2134	2350.2168	-0.0033	116	138	1	---	AAVGATPEAKFDSFVASLTEALR
2351.2207	2350.2134	2350.2168	-0.0033	116	138	1	148	AAVGATPEAKFDSFVASLTEALR

2427.2327	2426.2254	2426.2117	0.0137	178 - 201	1	---	VAATAAATAPADDKFTVFEAAFNK
2427.2327	2426.2254	2426.2117	0.0137	178 - 201	1	104	VAATAAATAPADDKFTVFEAAFNK

No match to: 713.4184, 1469.7655, 2644.3872, 3607.8345

4. gi|1684718 **Mass:** 27903 **Score:** 845 **Expect:** 1.9e-079 **Queries matched:** 17

major allergen Phl p 5 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1087.5754	1086.5681	1086.5743	-0.0062	202	211	0	---	CIPSLEAAVK
1100.5471	1099.5398	1099.5549	-0.0151	92	101	0	---	LDAAYSVAYK
1112.5883	1111.5810	1111.5913	-0.0103	226	235	0	---	YAVFEAALTK
1147.6279	1146.6206	1146.6284	-0.0078	43	52	0	---	LIEDINVGFK
1175.5482	1174.5409	1174.5506	-0.0096	69	79	0	---	TFEAAFTSSSK
1455.7458	1454.7385	1454.7405	-0.0020	112	124	0	109	FDSFVASLTEALR
1455.7458	1454.7385	1454.7405	-0.0020	112	124	0	---	FDSFVASLTEALR
1503.7310	1502.7237	1502.7252	-0.0015	188	201	1	---	AIKESTGGAYDTYK
1842.0339	1841.0266	1841.0298	-0.0031	147	163	1	158	IPAGELQIIDKIDAAFK
1842.0339	1841.0266	1841.0298	-0.0031	147	163	1	---	IPAGELQIIDKIDAAFK
1935.0024	1933.9951	1933.9996	-0.0045	36	52	1	---	ATTEEQKLIEDINVGFK
1935.0024	1933.9951	1933.9996	-0.0045	36	52	1	131	ATTEEQKLIEDINVGFK
2262.2273	2261.2200	2261.2088	0.0112	125 - 146	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)	
2351.2207	2350.2134	2350.2168	-0.0033	102 - 124	1	---	AAVGATPEAKFDSFVASLTEALR	
2351.2207	2350.2134	2350.2168	-0.0033	102 - 124	1	148	AAVGATPEAKFDSFVASLTEALR	
2427.2327	2426.2254	2426.2117	0.0137	164 - 187	1	---	VAATAAATAPADDKFTVFEAAFNK	
2427.2327	2426.2254	2426.2117	0.0137	164 - 187	1	104	VAATAAATAPADDKFTVFEAAFNK	

No match to: 713.4184, 1469.7655, 1487.8081, 2644.3872, 3607.8345

5. gi|3309045 **Mass:** 28869 **Score:** 842 **Expect:** 3.8e-079 **Queries matched:** 17

group V allergen Phl p 5.0206 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1087.5754	1086.5681	1086.5743	-0.0062	211	220	0	---	CIPSLEAAVK
1100.5471	1099.5398	1099.5549	-0.0151	101	110	0	---	LDAAYSVAYK
1112.5883	1111.5810	1111.5913	-0.0103	235	244	0	---	YAVFEAALTK
1147.6279	1146.6206	1146.6284	-0.0078	52	61	0	---	LIEDINVGFK
1175.5482	1174.5409	1174.5506	-0.0096	78	88	0	---	TFEAAFTSSSK
1455.7458	1454.7385	1454.7405	-0.0020	121	133	0	109	FDSFVASLTEALR
1455.7458	1454.7385	1454.7405	-0.0020	121	133	0	---	FDSFVASLTEALR
1487.8081	1486.8008	1486.8143	-0.0135	62	77	1	---	AAVAAAASVPAADKFK
1503.7310	1502.7237	1502.7252	-0.0015	197	210	1	---	AIKESTGGAYDTYK
1842.0339	1841.0266	1841.0298	-0.0031	156	172	1	158	IPAGELQIIDKIDAAFK
1842.0339	1841.0266	1841.0298	-0.0031	156	172	1	---	IPAGELQIIDKIDAAFK
1935.0024	1933.9951	1933.9996	-0.0045	45	61	1	---	ATTEEQKLIEDINVGFK

1935.0024	1933.9951	1933.9996	-0.0045	45 - 61	1	131	ATTEEQKLIEDINVGFK
2351.2207	2350.2134	2350.2168	-0.0033	111 - 133	1	---	AAVGATPEAKFDSFVASLTEALR
2351.2207	2350.2134	2350.2168	-0.0033	111 - 133	1	148	AAVGATPEAKFDSFVASLTEALR
2427.2327	2426.2254	2426.2117	0.0137	173 - 196	1	---	VAATAAATAPADDKFTVFEAAFNK
2427.2327	2426.2254	2426.2117	0.0137	173 - 196	1	104	VAATAAATAPADDKFTVFEAAFNK

No match to: 713.4184, 1469.7655, 2262.2273, 2644.3872, 3607.8345

6. gi|481397 **Mass:** 28182 **Score:** 823 **Expect:** 3e-077 **Queries matched:** 16

allergen Phl p Vb - common timothy

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1087.5754	1086.5681	1086.5743	-0.0062	201 - 210		0	---	CIPSLEAAVK
1100.5471	1099.5398	1099.5549	-0.0151	91 - 100		0	---	LDAAYSVAYK
1112.5883	1111.5810	1111.5913	-0.0103	225 - 234		0	---	YAVFEAALTK
1147.6279	1146.6206	1146.6284	-0.0078	44 - 53		0	---	LIEDINVGFK
1455.7458	1454.7385	1454.7405	-0.0020	111 - 123		0	109	FDSFVASLTEALR
1455.7458	1454.7385	1454.7405	-0.0020	111 - 123		0	---	FDSFVASLTEALR
1503.7310	1502.7237	1502.7252	-0.0015	187 - 200		1	---	AIKESTGGAYDTYK
1842.0339	1841.0266	1841.0298	-0.0031	146 - 162		1	158	IPAGELQIIDKIDAAFK
1842.0339	1841.0266	1841.0298	-0.0031	146 - 162		1	---	IPAGELQIIDKIDAAFK
1935.0024	1933.9951	1933.9996	-0.0045	37 - 53		1	---	ATTEEQKLIEDINVGFK
1935.0024	1933.9951	1933.9996	-0.0045	37 - 53		1	131	ATTEEQKLIEDINVGFK
2262.2273	2261.2200	2261.2088	0.0112	124 - 145		0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2207	2350.2134	2350.2168	-0.0033	101 - 123		1	---	AAVGATPEAKFDSFVASLTEALR
2351.2207	2350.2134	2350.2168	-0.0033	101 - 123		1	148	AAVGATPEAKFDSFVASLTEALR
2427.2327	2426.2254	2426.2117	0.0137	163 - 186		1	---	VAATAAATAPADDKFTVFEAAFNK
2427.2327	2426.2254	2426.2117	0.0137	163 - 186		1	104	VAATAAATAPADDKFTVFEAAFNK

No match to: 713.4184, 1175.5482, 1469.7655, 1487.8081, 2644.3872, 3607.8345

7. gi|3309047 **Mass:** 28384 **Score:** 713 **Expect:** 3e-066 **Queries matched:** 15

group V allergen Phl p 5.0207 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1087.5754	1086.5681	1086.5743	-0.0062	208 - 217		0	---	CIPSLEAAVK
1112.5883	1111.5810	1111.5913	-0.0103	232 - 241		0	---	YAVFEAALTK
1147.6279	1146.6206	1146.6284	-0.0078	52 - 61		0	---	LIEDINVGFK
1175.5482	1174.5409	1174.5506	-0.0096	78 - 88		0	---	TFEAAFTSSSK
1455.7458	1454.7385	1454.7405	-0.0020	121 - 133		0	109	FDSFVASLTEALR
1455.7458	1454.7385	1454.7405	-0.0020	121 - 133		0	---	FDSFVASLTEALR
1487.8081	1486.8008	1486.8143	-0.0135	62 - 77		1	---	AAVAAAASVPAADKFK
1503.7310	1502.7237	1502.7252	-0.0015	194 - 207		1	---	AIKESTGGAYDTYK
1842.0339	1841.0266	1841.0298	-0.0031	156 - 172		1	158	IPAGELQIIDKIDAAFK
1842.0339	1841.0266	1841.0298	-0.0031	156 - 172		1	---	IPAGELQIIDKIDAAFK

1935.0024	1933.9951	1933.9996	-0.0045	45 - 61	1	---	ATTEEQKLIEDINVGFK
1935.0024	1933.9951	1933.9996	-0.0045	45 - 61	1	131	ATTEEQKLIEDINVGFK
2262.2273	2261.2200	2261.2088	0.0112	134 - 155	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2207	2350.2134	2350.2168	-0.0033	111 - 133	1	---	AAVGATPEAKFDSFVASLTEALR
2351.2207	2350.2134	2350.2168	-0.0033	111 - 133	1	148	AAVGATPEAKFDSFVASLTEALR

No match to: 713.4184, 1100.5471, 1469.7655, 2427.2327, 2427.2327, 2644.3872, 3607.8345

8. gi|28948464 **Mass:** 10653 **Score:** 320 **Expect:** 6e-027 **Queries matched:** 6

Chain A, Crystal Structure Of The Functional Domain Of The Major Grass Pollen Allergen Phl P 5b

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1087.5754	1086.5681	1086.5743	-0.0062	56 -	65	0	---	CIPSLEAAVK
1112.5883	1111.5810	1111.5913	-0.0103	80 -	89	0	---	YAVFEAALTK
1842.0339	1841.0266	1841.0298	-0.0031	1 -	17	1	158	IPAGELQIIDKIDAAFK
1842.0339	1841.0266	1841.0298	-0.0031	1 -	17	1	---	IPAGELQIIDKIDAAFK
2427.2327	2426.2254	2426.2117	0.0137	18 -	41	1	---	VAATAAATAPADDKFTVFEAAFNK
2427.2327	2426.2254	2426.2117	0.0137	18 -	41	1	104	VAATAAATAPADDKFTVFEAAFNK

No match to: 713.4184, 1100.5471, 1147.6279, 1175.5482, 1455.7458, 1455.7458, 1469.7655, 1487.8081, 1503.7310, 1935.0024, 1935.0024, 2262.2273, 2351.2207, 2351.2207, 2644.3872, 3607.8345

9. gi|11991229 **Mass:** 29216 **Score:** 188 **Expect:** 9.6e-014 **Queries matched:** 5

pollen allergen Hol l 5b [Holcus lanatus]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1455.7458	1454.7385	1454.7881	-0.0495	63 -	78	1	---	AAVAAAAGAPPADKFK
1455.7458	1454.7385	1454.7881	-0.0495	63 -	78	1	---	AAVAAAAGAPPADKFK
1842.0339	1841.0266	1841.0298	-0.0031	162 -	178	1	158	IPAGELQIIDKIDAAFK
1842.0339	1841.0266	1841.0298	-0.0031	162 -	178	1	---	IPAGELQIIDKIDAAFK
2644.3872	2643.3799	2643.2492	0.1307	193 -	216	1	---	FTVFEAAFNNAIKESTGGAYDTYK

No match to: 713.4184, 1087.5754, 1100.5471, 1112.5883, 1147.6279, 1175.5482, 1469.7655, 1487.8081, 1503.7310, 1935.0024, 1935.0024, 2262.2273, 2351.2207, 2351.2207, 2427.2327, 2427.2327, 3607.8345

10. gi|897626 **Mass:** 5802 **Score:** 48 **Expect:** 9.2 **Queries matched:** 3

unknown protein

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1175.5482	1174.5409	1174.6016	-0.0606	1 -	11	0	---	MVEPTISSVGR
1487.8081	1486.8008	1486.7966	0.0043	12 -	24	0	---	LNLLACPSPLSFR
2644.3872	2643.3799	2643.3876	-0.0077	1 -	24	1	---	MVEPTISSVGRLNLLACPSPLSFR

No match to: 713.4184, 1087.5754, 1100.5471, 1112.5883, 1147.6279, 1455.7458, 1455.7458, 1469.7655, 1503.7310, 1842.0339, 1842.0339, 1935.0024, 1935.0024, 2262.2273, 2351.2207, 2351.2207, 2427.2327, 2427.2327, 3607.8345

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 22

Protein View

Match to: **gi|3309043** Score: **871** Expect: **4.8e-082**
group V allergen Phl p 5.0204 [Phleum pratense]

Nominal mass (M_r): **26252**; Calculated pI value: **5.61**
NCBI BLAST search of gi|3309043 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **65%**

Matched peptides shown in **Bold Red**

```
     1 ADAGYAPATP AAAGAEAGKA TTEEQKLIED INVGFKAAVA AAASVPAADK
    51 FKTFEAAFTS SSKAATAKAP GLVPKLDAAY SVAYKAAVGA TPEAKFDSFV
   101 ASLTEALRVI AGALEVHAVK PVTEEPGMAK IPAGELQIID KIDAAFKVAA
   151 TAAATAPADD KFTVFEAAFN KAIKESTGGA YDTYKCIPSL EAAVKQAYAA
   201 TVAAAPQVKY AVFEAALTKA ITAMSEVQKV SQPATGAATV AAGAATTAAG
   251 AASGAATVAA GGYKV
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
20 - 36	1935.0024	1933.9951	1933.9996	-0.0045	1	**ATTEEQKLIEDINVGFK** (No match)
20 - 36	1935.0024	1933.9951	1933.9996	-0.0045	1	**ATTEEQKLIEDINVGFK** (Ions score 131)
27 - 36	1147.6279	1146.6206	1146.6284	-0.0078	0	**LIEDINVGFK** (No match)
37 - 52	1487.8081	1486.8008	1486.8143	-0.0135	1	**AAVAAAASVPAADKFK** (No match)
53 - 63	1175.5482	1174.5409	1174.5506	-0.0096	0	**TFEAAFTSSSK** (No match)
76 - 85	1100.5471	1099.5398	1099.5549	-0.0151	0	**LDAAYSVAYK** (No match)
86 - 108	2351.2207	2350.2134	2350.2168	-0.0033	1	**AAVGATPEAKFDSFVASLTEALR** (No match)
86 - 108	2351.2207	2350.2134	2350.2168	-0.0033	1	**AAVGATPEAKFDSFVASLTEALR** (Ions score 148)
96 - 108	1455.7458	1454.7385	1454.7405	-0.0020	0	**FDSFVASLTEALR** (Ions score 109)
96 - 108	1455.7458	1454.7385	1454.7405	-0.0020	0	**FDSFVASLTEALR** (No match)
109 - 130	2262.2273	2261.2200	2261.2088	0.0112	0	**VIAGALEVHAVKPVTEEPGMAK** Oxidation (M) (No match)
131 - 147	1842.0339	1841.0266	1841.0298	-0.0031	1	**IPAGELQIIDKIDAAFK** (Ions score 158)
131 - 147	1842.0339	1841.0266	1841.0298	-0.0031	1	**IPAGELQIIDKIDAAFK** (No match)
148 - 171	2427.2327	2426.2254	2426.2117	0.0137	1	**VAATAAATAPADDKFTVFEAAFNK** (No match)
148 - 171	2427.2327	2426.2254	2426.2117	0.0137	1	**VAATAAATAPADDKFTVFEAAFNK** (Ions score 104)
172 - 185	1503.7310	1502.7237	1502.7252	-0.0015	1	**AIKESTGGAYDTYK** (No match)
186 - 195	1087.5754	1086.5681	1086.5743	-0.0062	0	**CIPSLEAAVK** (No match)
210 - 219	1112.5883	1111.5810	1111.5913	-0.0103	0	**YAVFEAALTK** (No match)

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	Accession	Mass	Score	Description
1.	gi|3309043	26252	390	group V allergen Phl p 5.0204 [Phleum pratense]
2.	gi|2851457	28042	386	RecName: Full=Pollen allergen Phl p 5b; AltName: Full=Allergen Phl p Vb; AltName: Allergen=Phl p
3.	gi|3309041	29351	382	group V allergen Phl p 5.0203 precursor [Phleum pratense]
4.	gi|1684718	27903	350	major allergen Phl p 5 [Phleum pratense]
5.	gi|3309045	28869	347	group V allergen Phl p 5.0206 precursor [Phleum pratense]

Results List

1. gi|3309043 **Mass:** 26252 **Score:** 390 **Expect:** 6e-034 **Queries matched:** 17

group V allergen Phl p 5.0204 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1087.5658	1086.5585	1086.5743	-0.0158	186	195	0	---	CIPSLEAAVK
1100.5566	1099.5493	1099.5549	-0.0056	76	85	0	---	LDAAYSVAYK
1112.5903	1111.5830	1111.5913	-0.0083	210	219	0	72	YAVFEAALTK
1112.5903	1111.5830	1111.5913	-0.0083	210	219	0	---	YAVFEAALTK
1175.5527	1174.5454	1174.5506	-0.0051	53	63	0	---	TFEAAFTSSSK
1388.7395	1387.7322	1387.7459	-0.0137	196	209	0	---	QAYAATVAAAPQVK
1455.7511	1454.7438	1454.7405	0.0033	96	108	0	---	FDSFVASLTEALR
1487.8143	1486.8070	1486.8143	-0.0073	37	52	1	---	AAVAAAASVPAADKFK
1503.7361	1502.7288	1502.7252	0.0036	172	185	1	---	AIKESTGGAYDTYK
1762.9655	1761.9582	1761.9664	-0.0082	69	85	1	137	APGLVPKLDAAYSVAYK
1762.9655	1761.9582	1761.9664	-0.0082	69	85	1	---	APGLVPKLDAAYSVAYK
1842.0275	1841.0202	1841.0298	-0.0095	131	147	1	---	IPAGELQIIDKIDAAFK
1934.9996	1933.9923	1933.9996	-0.0073	20	36	1	---	ATTEEQKLIEDINVGFK
2262.2163	2261.2090	2261.2088	0.0002	109	130	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2217	2350.2144	2350.2168	-0.0023	86	108	1	---	AAVGATPEAKFDSFVASLTEALR
2427.2283	2426.2210	2426.2117	0.0093	148	171	1	---	VAATAAATAPADDKFTVFEAAFNK
3018.5837	3017.5764	3017.5416	0.0348	230	265	1	---	VSQPATGAATVAAGAATTAAGAASGAATVAAGGYKV

No match to: 713.4075, 716.3547, 724.4929, 734.4952, 746.3596, 750.5169, 768.5217, 782.4734, 788.3716, 838.5288, 848.5220, 864.5399, 886.9843, 917.2784, 1007.6766, 1033.6849, 1133.7100, 1279.7639, 1334.8762, 1371.7279, 1448.9077, 1562.9420, 1618.0571, 1732.0874, 2015.2739, 2205.2249, 2205.2249, 2247.2178, 2644.3748, 2644.3748, 2823.3142, 3086.6362, 3607.8152, 3679.8616, 3679.8616, 3811.8735

2. gi|2851457 **Mass:** 28042 **Score:** 386 **Expect:** 1.5e-033 **Queries matched:** 17

RecName: Full=Pollen allergen Phl p 5b; AltName: Full=Allergen Phl p Vb; AltName: Allergen=Phl p 5b

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1087.5658	1086.5585	1086.5743	-0.0158	205	214	0	---	CIPSLEAAVK

1100.5566	1099.5493	1099.5549	-0.0056	95 - 104	0	---	LDAAYSVAYK
1112.5903	1111.5830	1111.5913	-0.0083	229 - 238	0	72	YAVFEAALTK
1112.5903	1111.5830	1111.5913	-0.0083	229 - 238	0	---	YAVFEAALTK
1175.5527	1174.5454	1174.5506	-0.0051	72 - 82	0	---	TFEAAFTSSSK
1388.7395	1387.7322	1387.7459	-0.0137	215 - 228	0	---	QAYAATVAAAPQVK
1455.7511	1454.7438	1454.7405	0.0033	115 - 127	0	---	FDSFVASLTEALR
1487.8143	1486.8070	1486.8143	-0.0073	56 - 71	1	---	AAVAAAASVPAADKFK
1503.7361	1502.7288	1502.7252	0.0036	191 - 204	1	---	AIKESTGGAYDTYK
1762.9655	1761.9582	1761.9664	-0.0082	88 - 104	1	137	APGLVPKLDAAYSVAYK
1762.9655	1761.9582	1761.9664	-0.0082	88 - 104	1	---	APGLVPKLDAAYSVAYK
1842.0275	1841.0202	1841.0298	-0.0095	150 - 166	1	---	IPAGELQIIDKIDAAFK
1934.9996	1933.9923	1933.9996	-0.0073	39 - 55	1	---	ATTEEQKLIEDINVGFK
2262.2163	2261.2090	2261.2088	0.0002	128 - 149	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2217	2350.2144	2350.2168	-0.0023	105 - 127	1	---	AAVGATPEAKFDSFVASLTEALR
2427.2283	2426.2210	2426.2117	0.0093	167 - 190	1	---	VAATAAATAPADDKFTVFEAAFNK
3018.5837	3017.5764	3017.5416	0.0348	249 - 284	1	---	VSQPATGAATVAAGAATTAAGAASGAATVAAGGYKV

No match to: 713.4075, 716.3547, 724.4929, 734.4952, 746.3596, 750.5169, 768.5217, 782.4734, 788.3716, 838.5288, 848.5220, 864.5399, 886.9843, 917.2784, 1007.6766, 1033.6849, 1133.7100, 1279.7639, 1334.8762, 1371.7279, 1448.9077, 1562.9420, 1618.0571, 1732.0874, 2015.2739, 2205.2249, 2205.2249, 2247.2178, 2644.3748, 2644.3748, 2823.3142, 3086.6362, 3607.8152, 3679.8616, 3679.8616, 3811.8735

3. gi|3309041 **Mass:** 29351 **Score:** 382 **Expect:** 3.8e-033 **Queries matched:** 17

group V allergen Phl p 5.0203 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start - End	Miss	Ions	Peptide
1087.5658	1086.5585	1086.5743	-0.0158	216 - 225	0	---	CIPSLEAAVK
1100.5566	1099.5493	1099.5549	-0.0056	106 - 115	0	---	LDAAYSVAYK
1112.5903	1111.5830	1111.5913	-0.0083	240 - 249	0	72	YAVFEAALTK
1112.5903	1111.5830	1111.5913	-0.0083	240 - 249	0	---	YAVFEAALTK
1175.5527	1174.5454	1174.5506	-0.0051	83 - 93	0	---	TFEAAFTSSSK
1388.7395	1387.7322	1387.7459	-0.0137	226 - 239	0	---	QAYAATVAAAPQVK
1455.7511	1454.7438	1454.7405	0.0033	126 - 138	0	---	FDSFVASLTEALR
1487.8143	1486.8070	1486.8143	-0.0073	67 - 82	1	---	AAVAAAASVPAADKFK
1503.7361	1502.7288	1502.7252	0.0036	202 - 215	1	---	AIKESTGGAYDTYK
1762.9655	1761.9582	1761.9664	-0.0082	99 - 115	1	137	APGLVPKLDAAYSVAYK
1762.9655	1761.9582	1761.9664	-0.0082	99 - 115	1	---	APGLVPKLDAAYSVAYK
1842.0275	1841.0202	1841.0298	-0.0095	161 - 177	1	---	IPAGELQIIDKIDAAFK
1934.9996	1933.9923	1933.9996	-0.0073	50 - 66	1	---	ATTEEQKLIEDINVGFK
2262.2163	2261.2090	2261.2088	0.0002	139 - 160	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2217	2350.2144	2350.2168	-0.0023	116 - 138	1	---	AAVGATPEAKFDSFVASLTEALR
2427.2283	2426.2210	2426.2117	0.0093	178 - 201	1	---	VAATAAATAPADDKFTVFEAAFNK
3018.5837	3017.5764	3017.5416	0.0348	260 - 295	1	---	VSQPATGAATVAAGAATTAAGAASGAATVAAGGYKV

No match to: 713.4075, 716.3547, 724.4929, 734.4952, 746.3596, 750.5169, 768.5217, 782.4734, 788.3716, 838.5288,

848.5220, 864.5399, 886.9843, 917.2784, 1007.6766, 1033.6849, 1133.7100, 1279.7639, 1334.8762, 1371.7279, 1448.9077, 1562.9420, 1618.0571, 1732.0874, 2015.2739, 2205.2249, 2205.2249, 2247.2178, 2644.3748, 2644.3748, 2823.3142, 3086.6362, 3607.8152, 3679.8616, 3679.8616, 3811.8735

4. gi|1684718 **Mass:** 27903 **Score:** 350 **Expect:** 6e-030 **Queries matched:** 15

major allergen Phl p 5 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1087.5658	1086.5585	1086.5743	-0.0158	202	211	0	---	CIPSLEAAVK
1100.5566	1099.5493	1099.5549	-0.0056	92	101	0	---	LDAAYSVAYK
1112.5903	1111.5830	1111.5913	-0.0083	226	235	0	72	YAVFEAALTK
1112.5903	1111.5830	1111.5913	-0.0083	226	235	0	---	YAVFEAALTK
1175.5527	1174.5454	1174.5506	-0.0051	69	79	0	---	TFEAAFTSSSK
1388.7395	1387.7322	1387.7459	-0.0137	212	225	0	---	QAYAATVAAAPQVK
1455.7511	1454.7438	1454.7405	0.0033	112	124	0	---	FDSFVASLTEALR
1503.7361	1502.7288	1502.7252	0.0036	188	201	1	---	AIKESTGGAYDTYK
1762.9655	1761.9582	1761.9664	-0.0082	85	101	1	137	APGLVPKLDAAYSVAYK
1762.9655	1761.9582	1761.9664	-0.0082	85	101	1	---	APGLVPKLDAAYSVAYK
1842.0275	1841.0202	1841.0298	-0.0095	147	163	1	---	IPAGELQIIDKIDAAFK
1934.9996	1933.9923	1933.9996	-0.0073	36	52	1	---	ATTEEQKLIEDINVGFK
2262.2163	2261.2090	2261.2088	0.0002	125	146	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2217	2350.2144	2350.2168	-0.0023	102	124	1	---	AAVGATPEAKFDSFVASLTEALR
2427.2283	2426.2210	2426.2117	0.0093	164	187	1	---	VAATAAATAPADDKFTVFEAAFNK

No match to: 713.4075, 716.3547, 724.4929, 734.4952, 746.3596, 750.5169, 768.5217, 782.4734, 788.3716, 838.5288, 848.5220, 864.5399, 886.9843, 917.2784, 1007.6766, 1033.6849, 1133.7100, 1279.7639, 1334.8762, 1371.7279, 1448.9077, 1487.8143, 1562.9420, 1618.0571, 1732.0874, 2015.2739, 2205.2249, 2205.2249, 2247.2178, 2644.3748, 2644.3748, 2823.3142, 3018.5837, 3086.6362, 3607.8152, 3679.8616, 3679.8616, 3811.8735

5. gi|3309045 **Mass:** 28869 **Score:** 347 **Expect:** 1.2e-029 **Queries matched:** 15

group V allergen Phl p 5.0206 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1087.5658	1086.5585	1086.5743	-0.0158	211	220	0	---	CIPSLEAAVK
1100.5566	1099.5493	1099.5549	-0.0056	101	110	0	---	LDAAYSVAYK
1112.5903	1111.5830	1111.5913	-0.0083	235	244	0	72	YAVFEAALTK
1112.5903	1111.5830	1111.5913	-0.0083	235	244	0	---	YAVFEAALTK
1175.5527	1174.5454	1174.5506	-0.0051	78	88	0	---	TFEAAFTSSSK
1388.7395	1387.7322	1387.7459	-0.0137	221	234	0	---	QAYAATVAAAPQVK
1455.7511	1454.7438	1454.7405	0.0033	121	133	0	---	FDSFVASLTEALR
1487.8143	1486.8070	1486.8143	-0.0073	62	77	1	---	AAVAAAASVPAADKFK
1503.7361	1502.7288	1502.7252	0.0036	197	210	1	---	AIKESTGGAYDTYK
1762.9655	1761.9582	1761.9664	-0.0082	94	110	1	137	APGLVPKLDAAYSVAYK
1762.9655	1761.9582	1761.9664	-0.0082	94	110	1	---	APGLVPKLDAAYSVAYK
1842.0275	1841.0202	1841.0298	-0.0095	156	172	1	---	IPAGELQIIDKIDAAFK

1934.9996	1933.9923	1933.9996	-0.0073	45 - 61	1	---	ATTEEQKLIEDINVGFK
2351.2217	2350.2144	2350.2168	-0.0023	111 - 133	1	---	AAVGATPEAKFDSFVASLTEALR
2427.2283	2426.2210	2426.2117	0.0093	173 - 196	1	---	VAATAAATAPADDKFTVFEAAFNK

No match to: 713.4075, 716.3547, 724.4929, 734.4952, 746.3596, 750.5169, 768.5217, 782.4734, 788.3716, 838.5288, 848.5220, 864.5399, 886.9843, 917.2784, 1007.6766, 1033.6849, 1133.7100, 1279.7639, 1334.8762, 1371.7279, 1448.9077, 1562.9420, 1618.0571, 1732.0874, 2015.2739, 2205.2249, 2205.2249, 2247.2178, 2262.2163, 2644.3748, 2644.3748, 2823.3142, 3018.5837, 3086.6362, 3607.8152, 3679.8616, 3679.8616, 3811.8735

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 53

Protein View

Match to: **gi|3309043** Score: **390** Expect: **6e-034**
group V allergen Phl p 5.0204 [Phleum pratense]

Nominal mass (M_r): **26252**; Calculated pI value: **5.61**
NCBI BLAST search of gi|3309043 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **87%**

Matched peptides shown in **Bold Red**

```
   1 ADAGYAPATP AAAGAEAGKA TTEEQKLIED INVGFKAAVA AAASVPAADK
  51 FKTFEAAFTS SSKAATAKAP GLVPKLDAAY SVAYKAAVGA TPEAKFDSFV
 101 ASLTEALRVI AGALEVHAVK PVTEEPGMAK IPAGELQIID KIDAAFKVAA
 151 TAAATAPADD KFTVFEAAFN KAIKESTGGA YDTYKCIPSL EAAVKQAYAA
 201 TVAAAPQVKY AVFEAALTKA ITAMSEVQKV SQPATGAATV AAGAATTAAG
 251 AASGAATVAA GGYKV
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
20 - 36	1934.9996	1933.9923	1933.9996	-0.0073	1	**ATTEEQKLIEDINVGFK** (No match)
37 - 52	1487.8143	1486.8070	1486.8143	-0.0073	1	**AAVAAAASVPAADKFK** (No match)
53 - 63	1175.5527	1174.5454	1174.5506	-0.0051	0	**TFEAAFTSSSK** (No match)
69 - 85	1762.9655	1761.9582	1761.9664	-0.0082	1	**APGLVPKLDAAYSVAYK** (Ions score 137)
69 - 85	1762.9655	1761.9582	1761.9664	-0.0082	1	**APGLVPKLDAAYSVAYK** (No match)
76 - 85	1100.5566	1099.5493	1099.5549	-0.0056	0	**LDAAYSVAYK** (No match)
86 - 108	2351.2217	2350.2144	2350.2168	-0.0023	1	**AAVGATPEAKFDSFVASLTEALR** (No match)
96 - 108	1455.7511	1454.7438	1454.7405	0.0033	0	**FDSFVASLTEALR** (No match)
109 - 130	2262.2163	2261.2090	2261.2088	0.0002	0	**VIAGALEVHAVKPVTEEPGMAK** Oxidation (M) (No match)
131 - 147	1842.0275	1841.0202	1841.0298	-0.0095	1	**IPAGELQIIDKIDAAFK** (No match)
148 - 171	2427.2283	2426.2210	2426.2117	0.0093	1	**VAATAAATAPADDKFTVFEAAFNK** (No match)
172 - 185	1503.7361	1502.7288	1502.7252	0.0036	1	**AIKESTGGAYDTYK** (No match)
186 - 195	1087.5658	1086.5585	1086.5743	-0.0158	0	**CIPSLEAAVK** (No match)
196 - 209	1388.7395	1387.7322	1387.7459	-0.0137	0	**QAYAATVAAAPQVK** (No match)
210 - 219	1112.5903	1111.5830	1111.5913	-0.0083	0	**YAVFEAALTK** (Ions score 72)
210 - 219	1112.5903	1111.5830	1111.5913	-0.0083	0	**YAVFEAALTK** (No match)
230 - 265	3018.5837	3017.5764	3017.5416	0.0348	1	**VSQPATGAATVAAGAATTAAGAASGAATVAAGGYKV** (No match)

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	Accession	Mass	Score	Description
1.	gi|3309043	26252	172	group V allergen Phl p 5.0204 [Phleum pratense]
2.	gi|1684718	27903	172	major allergen Phl p 5 [Phleum pratense]
3.	gi|2851457	28042	172	RecName: Full=Pollen allergen Phl p 5b; AltName: Full=Allergen Phl p Vb; AltName: Allergen=Phl
4.	gi|3309045	28869	171	group V allergen Phl p 5.0206 precursor [Phleum pratense]
5.	gi|3309041	29351	170	group V allergen Phl p 5.0203 precursor [Phleum pratense]
6.	gi|28948464	10653	69	Chain A, Crystal Structure Of The Functional Domain Of The Major Grass Pollen Allergen Phl P 5b
7.	gi|2266623	24693	66	group V grass pollen allergen [Holcus lanatus]
8.	gi|14423120	26342	65	group 5 isoallergen 1 [Dactylis glomerata]
9.	gi|14423122	26281	65	group 5 isoallergen 2 [Dactylis glomerata]
10.	gi|481397	28182	65	allergen Phl p Vb - common timothy

Results List

1. gi|3309043 **Mass:** 26252 **Score:** 172 **Expect:** 3.8e-012 **Queries matched:** 4

group V allergen Phl p 5.0204 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1112.5889	1111.5816	1111.5913	-0.0097	210	219	0	57	YAVFEAALTK
1112.5889	1111.5816	1111.5913	-0.0097	210	219	0	---	YAVFEAALTK
1762.9703	1761.9630	1761.9664	-0.0034	69	85	1	94	APGLVPKLDAAYSVAYK
1762.9703	1761.9630	1761.9664	-0.0034	69	85	1	---	APGLVPKLDAAYSVAYK

No match to: 713.4020, 768.5189, 825.0999, 864.5087, 881.2758, 1936.0068, 2205.2034, 2644.3735, 2644.3735

2. gi|1684718 **Mass:** 27903 **Score:** 172 **Expect:** 3.8e-012 **Queries matched:** 4

major allergen Phl p 5 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1112.5889	1111.5816	1111.5913	-0.0097	226	235	0	57	YAVFEAALTK
1112.5889	1111.5816	1111.5913	-0.0097	226	235	0	---	YAVFEAALTK
1762.9703	1761.9630	1761.9664	-0.0034	85	101	1	94	APGLVPKLDAAYSVAYK
1762.9703	1761.9630	1761.9664	-0.0034	85	101	1	---	APGLVPKLDAAYSVAYK

No match to: 713.4020, 768.5189, 825.0999, 864.5087, 881.2758, 1936.0068, 2205.2034, 2644.3735, 2644.3735

3. gi|2851457 **Mass:** 28042 **Score:** 172 **Expect:** 3.8e-012 **Queries matched:** 4

RecName: Full=Pollen allergen Phl p 5b; AltName: Full=Allergen Phl p Vb; AltName: Allergen=Phl p 5b

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1112.5889	1111.5816	1111.5913	-0.0097	229	238	0	57	YAVFEAALTK
1112.5889	1111.5816	1111.5913	-0.0097	229	238	0	---	YAVFEAALTK
1762.9703	1761.9630	1761.9664	-0.0034	88	104	1	94	APGLVPKLDAAYSVAYK
1762.9703	1761.9630	1761.9664	-0.0034	88	104	1	---	APGLVPKLDAAYSVAYK

No match to: 713.4020, 768.5189, 825.0999, 864.5087, 881.2758, 1936.0068, 2205.2034, 2644.3735, 2644.3735

4. gi|3309045 **Mass:** 28869 **Score:** 171 **Expect:** 4.8e-012 **Queries matched:** 4

group V allergen Phl p 5.0206 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1112.5889	1111.5816	1111.5913	-0.0097	235	244	0	57	YAVFEAALTK
1112.5889	1111.5816	1111.5913	-0.0097	235	244	0	---	YAVFEAALTK
1762.9703	1761.9630	1761.9664	-0.0034	94	110	1	94	APGLVPKLDAAYSVAYK
1762.9703	1761.9630	1761.9664	-0.0034	94	110	1	---	APGLVPKLDAAYSVAYK

No match to: 713.4020, 768.5189, 825.0999, 864.5087, 881.2758, 1936.0068, 2205.2034, 2644.3735, 2644.3735

5. gi|3309041 **Mass:** 29351 **Score:** 170 **Expect:** 6e-012 **Queries matched:** 4

group V allergen Phl p 5.0203 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1112.5889	1111.5816	1111.5913	-0.0097	240	249	0	57	YAVFEAALTK
1112.5889	1111.5816	1111.5913	-0.0097	240	249	0	---	YAVFEAALTK
1762.9703	1761.9630	1761.9664	-0.0034	99	115	1	94	APGLVPKLDAAYSVAYK
1762.9703	1761.9630	1761.9664	-0.0034	99	115	1	---	APGLVPKLDAAYSVAYK

No match to: 713.4020, 768.5189, 825.0999, 864.5087, 881.2758, 1936.0068, 2205.2034, 2644.3735, 2644.3735

6. gi|28948464 **Mass:** 10653 **Score:** 69 **Expect:** 0.078 **Queries matched:** 2

Chain A, Crystal Structure Of The Functional Domain Of The Major Grass Pollen Allergen Phl P 5b

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1112.5889	1111.5816	1111.5913	-0.0097	80	89	0	57	YAVFEAALTK
1112.5889	1111.5816	1111.5913	-0.0097	80	89	0	---	YAVFEAALTK

No match to: 713.4020, 768.5189, 825.0999, 864.5087, 881.2758, 1762.9703, 1762.9703, 1936.0068, 2205.2034, 2644.3735, 2644.3735

7. gi|2266623 **Mass:** 24693 **Score:** 66 **Expect:** 0.17 **Queries matched:** 2

group V grass pollen allergen [Holcus lanatus]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1112.5889	1111.5816	1111.5913	-0.0097	193	202	0	57	YAVFEAALTK
1112.5889	1111.5816	1111.5913	-0.0097	193	202	0	---	YAVFEAALTK

No match to: 713.4020, 768.5189, 825.0999, 864.5087, 881.2758, 1762.9703, 1762.9703, 1936.0068, 2205.2034, 2644.3735, 2644.3735

8. gi|14423120 **Mass:** 26342 **Score:** 65 **Expect:** 0.18 **Queries matched:** 2

group 5 isoallergen 1 [Dactylis glomerata]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1112.5889	1111.5816	1111.5913	-0.0097	214	223	0	57	YAVFEAALTK
1112.5889	1111.5816	1111.5913	-0.0097	214	223	0	---	YAVFEAALTK

No match to: 713.4020, 768.5189, 825.0999, 864.5087, 881.2758, 1762.9703, 1762.9703, 1936.0068, 2205.2034,

2644.3735, 2644.3735

9. gi|14423122 **Mass:** 26281 **Score:** 65 **Expect:** 0.18 **Queries matched:** 2

group 5 isoallergen 2 [Dactylis glomerata]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1112.5889	1111.5816	1111.5913	-0.0097	214	223	0	57	YAVFEAALTK
1112.5889	1111.5816	1111.5913	-0.0097	214	223	0	---	YAVFEAALTK

No match to: 713.4020, 768.5189, 825.0999, 864.5087, 881.2758, 1762.9703, 1762.9703, 1936.0068, 2205.2034, 2644.3735, 2644.3735

10. gi|481397 **Mass:** 28182 **Score:** 65 **Expect:** 0.19 **Queries matched:** 2

allergen Phl p Vb - common timothy

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1112.5889	1111.5816	1111.5913	-0.0097	225	234	0	57	YAVFEAALTK
1112.5889	1111.5816	1111.5913	-0.0097	225	234	0	---	YAVFEAALTK

No match to: 713.4020, 768.5189, 825.0999, 864.5087, 881.2758, 1762.9703, 1762.9703, 1936.0068, 2205.2034, 2644.3735, 2644.3735

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 13

Protein View

Match to: **gi|3309043** Score: **172** Expect: **3.8e-012**
group V allergen Phl p 5.0204 [Phleum pratense]

Nominal mass (M_r): **26252**; Calculated pI value: **5.61**
NCBI BLAST search of gi|3309043 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

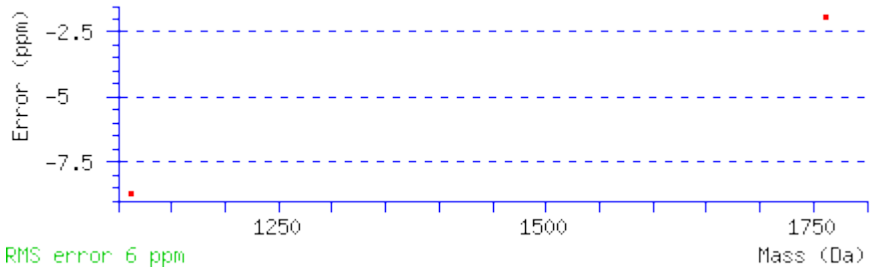
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **10%**

Matched peptides shown in **Bold Red**

```
   1 ADAGYAPATP AAAGAEAGKA TTEEQKLIED INVGFKAAVA AAASVPAADK
  51 FKTFEAAFTS SSKAATAKAP GLVPKLDAAY SVAYKAAVGA TPEAKFDSFV
 101 ASLTEALRVI AGALEVHAVK PVTEEPGMAK IPAGELQIID KIDAAFKVAA
 151 TAAATAPADD KFTVFEAAFN KAIKESTGGA YDTYKCIPSL EAAVKQAYAA
 201 TVAAAPQVKY AVFEAALTKA ITAMSEVQKV SQPATGAATV AAGAATTAAG
 251 AASGAATVAA GGYKV
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
69 - 85	1762.9703	1761.9630	1761.9664	-0.0034	1	APGLVPKLDAAYSVAYK	(Ions score 94)
69 - 85	1762.9703	1761.9630	1761.9664	-0.0034	1	APGLVPKLDAAYSVAYK	(No match)
210 - 219	1112.5889	1111.5816	1111.5913	-0.0097	0	YAVFEAALTK	(Ions score 57)
210 - 219	1112.5889	1111.5816	1111.5913	-0.0097	0	YAVFEAALTK	(No match)



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	Accession	Mass	Score	Description
1.	gi|3309043	26252	508	group V allergen Phl p 5.0204 [Phleum pratense]
2.	gi|2851457	28042	505	RecName: Full=Pollen allergen Phl p 5b; AltName: Full=Allergen Phl p Vb; AltName: Allergen=Phl
3.	gi|3309041	29351	502	group V allergen Phl p 5.0203 precursor [Phleum pratense]
4.	gi|1684718	27903	487	major allergen Phl p 5 [Phleum pratense]
5.	gi|3309045	28869	485	group V allergen Phl p 5.0206 precursor [Phleum pratense]
6.	gi|481397	28182	311	allergen Phl p Vb - common timothy
7.	gi|3309047	28384	309	group V allergen Phl p 5.0207 precursor [Phleum pratense]
8.	gi|28948464	10653	141	Chain A, Crystal Structure Of The Functional Domain Of The Major Grass Pollen Allergen Phl P 5b
9.	gi|2266623	24693	94	group V grass pollen allergen [Holcus lanatus]
10.	gi|14423120	26342	93	group 5 isoallergen 1 [Dactylis glomerata]

Results List

1. gi|3309043 **Mass:** 26252 **Score:** 508 **Expect:** 9.6e-046 **Queries matched:** 15

group V allergen Phl p 5.0204 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1100.5697	1099.5624	1099.5549	0.0075	76	85	0	---	LDAAYSVAYK
1112.5907	1111.5834	1111.5913	-0.0079	210	219	0	88	YAVFEAALTK
1112.5907	1111.5834	1111.5913	-0.0079	210	219	0	---	YAVFEAALTK
1388.7401	1387.7328	1387.7459	-0.0131	196	209	0	---	QAYAATVAAAPQVK
1455.7529	1454.7456	1454.7405	0.0051	96	108	0	---	FDSFVASLTEALR
1455.7529	1454.7456	1454.7405	0.0051	96	108	0	29	FDSFVASLTEALR
1487.8265	1486.8192	1486.8143	0.0049	37	52	1	---	AAVAAAASVPAADKFK
1762.9740	1761.9667	1761.9664	0.0003	69	85	1	---	APGLVPKLDAAYSVAYK
1762.9740	1761.9667	1761.9664	0.0003	69	85	1	141	APGLVPKLDAAYSVAYK
1842.0393	1841.0320	1841.0298	0.0023	131	147	1	---	IPAGELQIIDKIDAAFK
1935.0109	1934.0036	1933.9996	0.0040	20	36	1	---	ATTEEQKLIEDINVGFK
1935.0109	1934.0036	1933.9996	0.0040	20	36	1	97	ATTEEQKLIEDINVGFK
2262.2185	2261.2112	2261.2088	0.0024	109	130	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2207	2350.2134	2350.2168	-0.0033	86	108	1	---	AAVGATPEAKFDSFVASLTEALR
2427.2490	2426.2417	2426.2117	0.0300	148	171	1	---	VAATAAATAPADDKFTVFEAAFNK

No match to: 713.4096, 768.5197, 864.5092, 1134.5851, 1692.7853, 1784.9611, 1957.9978, 2205.2412, 2212.1272, 2644.3765, 2644.3765, 2667.3357, 2825.3110, 3607.8040

2. gi|2851457 **Mass:** 28042 **Score:** 505 **Expect:** 1.9e-045 **Queries matched:** 15

RecName: Full=Pollen allergen Phl p 5b; AltName: Full=Allergen Phl p Vb; AltName: Allergen=Phl p 5b

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1100.5697	1099.5624	1099.5549	0.0075	95	104	0	---	LDAAYSVAYK

1112.5907	1111.5834	1111.5913	-0.0079	229 - 238	0	88	YAVFEAALTK
1112.5907	1111.5834	1111.5913	-0.0079	229 - 238	0	---	YAVFEAALTK
1388.7401	1387.7328	1387.7459	-0.0131	215 - 228	0	---	QAYAATVAAAPQVK
1455.7529	1454.7456	1454.7405	0.0051	115 - 127	0	---	FDSFVASLTEALR
1455.7529	1454.7456	1454.7405	0.0051	115 - 127	0	29	FDSFVASLTEALR
1487.8265	1486.8192	1486.8143	0.0049	56 - 71	1	---	AAVAAAASVPAADKFK
1762.9740	1761.9667	1761.9664	0.0003	88 - 104	1	---	APGLVPKLDAAYSVAYK
1762.9740	1761.9667	1761.9664	0.0003	88 - 104	1	141	APGLVPKLDAAYSVAYK
1842.0393	1841.0320	1841.0298	0.0023	150 - 166	1	---	IPAGELQIIDKIDAAFK
1935.0109	1934.0036	1933.9996	0.0040	39 - 55	1	---	ATTEEQKLIEDINVGFK
1935.0109	1934.0036	1933.9996	0.0040	39 - 55	1	97	ATTEEQKLIEDINVGFK
2262.2185	2261.2112	2261.2088	0.0024	128 - 149	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2207	2350.2134	2350.2168	-0.0033	105 - 127	1	---	AAVGATPEAKFDSFVASLTEALR
2427.2490	2426.2417	2426.2117	0.0300	167 - 190	1	---	VAATAAATAPADDKFTVFEAAFNK

No match to: 713.4096, 768.5197, 864.5092, 1134.5851, 1692.7853, 1784.9611, 1957.9978, 2205.2412, 2212.1272, 2644.3765, 2644.3765, 2667.3357, 2825.3110, 3607.8040

3. gi|3309041 **Mass:** 29351 **Score:** 502 **Expect:** 3.8e-045 **Queries matched:** 15

group V allergen Phl p 5.0203 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1100.5697	1099.5624	1099.5549	0.0075	106 - 115	0	---	LDAAYSVAYK
1112.5907	1111.5834	1111.5913	-0.0079	240 - 249	0	88	YAVFEAALTK
1112.5907	1111.5834	1111.5913	-0.0079	240 - 249	0	---	YAVFEAALTK
1388.7401	1387.7328	1387.7459	-0.0131	226 - 239	0	---	QAYAATVAAAPQVK
1455.7529	1454.7456	1454.7405	0.0051	126 - 138	0	---	FDSFVASLTEALR
1455.7529	1454.7456	1454.7405	0.0051	126 - 138	0	29	FDSFVASLTEALR
1487.8265	1486.8192	1486.8143	0.0049	67 - 82	1	---	AAVAAAASVPAADKFK
1762.9740	1761.9667	1761.9664	0.0003	99 - 115	1	---	APGLVPKLDAAYSVAYK
1762.9740	1761.9667	1761.9664	0.0003	99 - 115	1	141	APGLVPKLDAAYSVAYK
1842.0393	1841.0320	1841.0298	0.0023	161 - 177	1	---	IPAGELQIIDKIDAAFK
1935.0109	1934.0036	1933.9996	0.0040	50 - 66	1	---	ATTEEQKLIEDINVGFK
1935.0109	1934.0036	1933.9996	0.0040	50 - 66	1	97	ATTEEQKLIEDINVGFK
2262.2185	2261.2112	2261.2088	0.0024	139 - 160	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2207	2350.2134	2350.2168	-0.0033	116 - 138	1	---	AAVGATPEAKFDSFVASLTEALR
2427.2490	2426.2417	2426.2117	0.0300	178 - 201	1	---	VAATAAATAPADDKFTVFEAAFNK

No match to: 713.4096, 768.5197, 864.5092, 1134.5851, 1692.7853, 1784.9611, 1957.9978, 2205.2412, 2212.1272, 2644.3765, 2644.3765, 2667.3357, 2825.3110, 3607.8040

4. gi|1684718 **Mass:** 27903 **Score:** 487 **Expect:** 1.2e-043 **Queries matched:** 14

major allergen Phl p 5 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide

1100.5697	1099.5624	1099.5549	0.0075	92 - 101	0	---	LDAAYSVAYK
1112.5907	1111.5834	1111.5913	-0.0079	226 - 235	0	88	YAVFEAALTK
1112.5907	1111.5834	1111.5913	-0.0079	226 - 235	0	---	YAVFEAALTK
1388.7401	1387.7328	1387.7459	-0.0131	212 - 225	0	---	QAYAATVAAAPQVK
1455.7529	1454.7456	1454.7405	0.0051	112 - 124	0	---	FDSFVASLTEALR
1455.7529	1454.7456	1454.7405	0.0051	112 - 124	0	29	FDSFVASLTEALR
1762.9740	1761.9667	1761.9664	0.0003	85 - 101	1	---	APGLVPKLDAAYSVAYK
1762.9740	1761.9667	1761.9664	0.0003	85 - 101	1	141	APGLVPKLDAAYSVAYK
1842.0393	1841.0320	1841.0298	0.0023	147 - 163	1	---	IPAGELQIIDKIDAAFK
1935.0109	1934.0036	1933.9996	0.0040	36 - 52	1	---	ATTEEQKLIEDINVGFK
1935.0109	1934.0036	1933.9996	0.0040	36 - 52	1	97	ATTEEQKLIEDINVGFK
2262.2185	2261.2112	2261.2088	0.0024	125 - 146	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2207	2350.2134	2350.2168	-0.0033	102 - 124	1	---	AAVGATPEAKFDSFVASLTEALR
2427.2490	2426.2417	2426.2117	0.0300	164 - 187	1	---	VAATAAATAPADDKFTVFEAAFNK

No match to: 713.4096, 768.5197, 864.5092, 1134.5851, 1487.8265, 1692.7853, 1784.9611, 1957.9978, 2205.2412, 2212.1272, 2644.3765, 2644.3765, 2667.3357, 2825.3110, 3607.8040

5. gi|3309045 **Mass:** 28869 **Score:** 485 **Expect:** 1.9e-043 **Queries matched:** 14

group V allergen Phl p 5.0206 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start - End	Miss	Ions	Peptide
1100.5697	1099.5624	1099.5549	0.0075	101 - 110	0	---	LDAAYSVAYK
1112.5907	1111.5834	1111.5913	-0.0079	235 - 244	0	88	YAVFEAALTK
1112.5907	1111.5834	1111.5913	-0.0079	235 - 244	0	---	YAVFEAALTK
1388.7401	1387.7328	1387.7459	-0.0131	221 - 234	0	---	QAYAATVAAAPQVK
1455.7529	1454.7456	1454.7405	0.0051	121 - 133	0	---	FDSFVASLTEALR
1455.7529	1454.7456	1454.7405	0.0051	121 - 133	0	29	FDSFVASLTEALR
1487.8265	1486.8192	1486.8143	0.0049	62 - 77	1	---	AAVAAAASVPAADKFK
1762.9740	1761.9667	1761.9664	0.0003	94 - 110	1	---	APGLVPKLDAAYSVAYK
1762.9740	1761.9667	1761.9664	0.0003	94 - 110	1	141	APGLVPKLDAAYSVAYK
1842.0393	1841.0320	1841.0298	0.0023	156 - 172	1	---	IPAGELQIIDKIDAAFK
1935.0109	1934.0036	1933.9996	0.0040	45 - 61	1	---	ATTEEQKLIEDINVGFK
1935.0109	1934.0036	1933.9996	0.0040	45 - 61	1	97	ATTEEQKLIEDINVGFK
2351.2207	2350.2134	2350.2168	-0.0033	111 - 133	1	---	AAVGATPEAKFDSFVASLTEALR
2427.2490	2426.2417	2426.2117	0.0300	173 - 196	1	---	VAATAAATAPADDKFTVFEAAFNK

No match to: 713.4096, 768.5197, 864.5092, 1134.5851, 1692.7853, 1784.9611, 1957.9978, 2205.2412, 2212.1272, 2262.2185, 2644.3765, 2644.3765, 2667.3357, 2825.3110, 3607.8040

6. gi|481397 **Mass:** 28182 **Score:** 311 **Expect:** 4.8e-026 **Queries matched:** 11

allergen Phl p Vb - common timothy

Observed	Mr(expt)	Mr(calc)	Delta	Start - End	Miss	Ions	Peptide
1100.5697	1099.5624	1099.5549	0.0075	91 - 100	0	---	LDAAYSVAYK

1112.5907	1111.5834	1111.5913	-0.0079	225 - 234	0	88	YAVFEAALTK
1112.5907	1111.5834	1111.5913	-0.0079	225 - 234	0	---	YAVFEAALTK
1455.7529	1454.7456	1454.7405	0.0051	111 - 123	0	---	FDSFVASLTEALR
1455.7529	1454.7456	1454.7405	0.0051	111 - 123	0	29	FDSFVASLTEALR
1842.0393	1841.0320	1841.0298	0.0023	146 - 162	1	---	IPAGELQIIDKIDAAFK
1935.0109	1934.0036	1933.9996	0.0040	37 - 53	1	---	ATTEEQKLIEDINVGFK
1935.0109	1934.0036	1933.9996	0.0040	37 - 53	1	97	ATTEEQKLIEDINVGFK
2262.2185	2261.2112	2261.2088	0.0024	124 - 145	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2207	2350.2134	2350.2168	-0.0033	101 - 123	1	---	AAVGATPEAKFDSFVASLTEALR
2427.2490	2426.2417	2426.2117	0.0300	163 - 186	1	---	VAATAAATAPADDKFTVFEAAFNK

No match to: 713.4096, 768.5197, 864.5092, 1134.5851, 1388.7401, 1487.8265, 1692.7853, 1762.9740, 1762.9740, 1784.9611, 1957.9978, 2205.2412, 2212.1272, 2644.3765, 2644.3765, 2667.3357, 2825.3110, 3607.8040

7. gi|3309047 **Mass:** 28384 **Score:** 309 **Expect:** 7.6e-026 **Queries matched:** 11

group V allergen Phl p 5.0207 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1112.5907	1111.5834	1111.5913	-0.0079	232 - 241	0	88	YAVFEAALTK
1112.5907	1111.5834	1111.5913	-0.0079	232 - 241	0	---	YAVFEAALTK
1388.7401	1387.7328	1387.7459	-0.0131	218 - 231	0	---	QAYAATVAAAPQVK
1455.7529	1454.7456	1454.7405	0.0051	121 - 133	0	---	FDSFVASLTEALR
1455.7529	1454.7456	1454.7405	0.0051	121 - 133	0	29	FDSFVASLTEALR
1487.8265	1486.8192	1486.8143	0.0049	62 - 77	1	---	AAVAAAASVPAADKFK
1842.0393	1841.0320	1841.0298	0.0023	156 - 172	1	---	IPAGELQIIDKIDAAFK
1935.0109	1934.0036	1933.9996	0.0040	45 - 61	1	---	ATTEEQKLIEDINVGFK
1935.0109	1934.0036	1933.9996	0.0040	45 - 61	1	97	ATTEEQKLIEDINVGFK
2262.2185	2261.2112	2261.2088	0.0024	134 - 155	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2207	2350.2134	2350.2168	-0.0033	111 - 133	1	---	AAVGATPEAKFDSFVASLTEALR

No match to: 713.4096, 768.5197, 864.5092, 1100.5697, 1134.5851, 1692.7853, 1762.9740, 1762.9740, 1784.9611, 1957.9978, 2205.2412, 2212.1272, 2427.2490, 2644.3765, 2644.3765, 2667.3357, 2825.3110, 3607.8040

8. gi|28948464 **Mass:** 10653 **Score:** 141 **Expect:** 4.8e-009 **Queries matched:** 5

Chain A, Crystal Structure Of The Functional Domain Of The Major Grass Pollen Allergen Phl P 5b

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1112.5907	1111.5834	1111.5913	-0.0079	80 - 89	0	88	YAVFEAALTK
1112.5907	1111.5834	1111.5913	-0.0079	80 - 89	0	---	YAVFEAALTK
1388.7401	1387.7328	1387.7459	-0.0131	66 - 79	0	---	QAYAATVAAAPQVK
1842.0393	1841.0320	1841.0298	0.0023	1 - 17	1	---	IPAGELQIIDKIDAAFK
2427.2490	2426.2417	2426.2117	0.0300	18 - 41	1	---	VAATAAATAPADDKFTVFEAAFNK

No match to: 713.4096, 768.5197, 864.5092, 1100.5697, 1134.5851, 1455.7529, 1455.7529, 1487.8265, 1692.7853, 1762.9740, 1762.9740, 1784.9611, 1935.0109, 1935.0109, 1957.9978, 2205.2412, 2212.1272, 2262.2185, 2351.2207, 2644.3765, 2644.3765, 2667.3357, 2825.3110, 3607.8040

9. gi|2266623 **Mass:** 24693 **Score:** 94 **Expect:** 0.00026 **Queries matched:** 2

group V grass pollen allergen [Holcus lanatus]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1112.5907	1111.5834	1111.5913	-0.0079	193 -	202	0	88	YAVFEAALTK
1112.5907	1111.5834	1111.5913	-0.0079	193 -	202	0	---	YAVFEAALTK

No match to: 713.4096, 768.5197, 864.5092, 1100.5697, 1134.5851, 1388.7401, 1455.7529, 1455.7529, 1487.8265, 1692.7853, 1762.9740, 1762.9740, 1784.9611, 1842.0393, 1935.0109, 1935.0109, 1957.9978, 2205.2412, 2212.1272, 2262.2185, 2351.2207, 2427.2490, 2644.3765, 2644.3765, 2667.3357, 2825.3110, 3607.8040

10. gi|14423120 **Mass:** 26342 **Score:** 93 **Expect:** 0.00028 **Queries matched:** 2

group 5 isoallergen 1 [Dactylis glomerata]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1112.5907	1111.5834	1111.5913	-0.0079	214 -	223	0	88	YAVFEAALTK
1112.5907	1111.5834	1111.5913	-0.0079	214 -	223	0	---	YAVFEAALTK

No match to: 713.4096, 768.5197, 864.5092, 1100.5697, 1134.5851, 1388.7401, 1455.7529, 1455.7529, 1487.8265, 1692.7853, 1762.9740, 1762.9740, 1784.9611, 1842.0393, 1935.0109, 1935.0109, 1957.9978, 2205.2412, 2212.1272, 2262.2185, 2351.2207, 2427.2490, 2644.3765, 2644.3765, 2667.3357, 2825.3110, 3607.8040

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 29

Protein View

Match to: **gi|3309043** Score: **508** Expect: **9.6e-046**
group V allergen Phl p 5.0204 [Phleum pratense]

Nominal mass (M_r): **26252**; Calculated pI value: **5.61**
NCBI BLAST search of gi|3309043 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **60%**

Matched peptides shown in **Bold Red**

```
    1 ADAGYAPATP AAAGAEAGKA TTEEQKLIED INVGFKAAVA AAASVPAADK
   51 FKTFEAAFTS SSKAATAKAP GLVPKLDAAY SVAYKAAVGA TPEAKFDSFV
  101 ASLTEALRVI AGALEVHAVK PVTEEPGMAK IPAGELQIID KIDAAFKVAA
  151 TAAATAPADD KFTVFEAAFN KAIKESTGGA YDTYKCIPSL EAAVKQAYAA
  201 TVAAAPQVKY AVFEAALTKA ITAMSEVQKV SQPATGAATV AAGAATTAAG
  251 AASGAATVAA GGYKV
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
20 - 36	1935.0109	1934.0036	1933.9996	0.0040	1	ATTEEQKLIEDINVGFK	(No match)
20 - 36	1935.0109	1934.0036	1933.9996	0.0040	1	ATTEEQKLIEDINVGFK	(Ions score 97)
37 - 52	1487.8265	1486.8192	1486.8143	0.0049	1	AAVAAAASVPAADKFK	(No match)
69 - 85	1762.9740	1761.9667	1761.9664	0.0003	1	APGLVPKLDAAYSVAYK	(No match)
69 - 85	1762.9740	1761.9667	1761.9664	0.0003	1	APGLVPKLDAAYSVAYK	(Ions score 141)
76 - 85	1100.5697	1099.5624	1099.5549	0.0075	0	LDAAYSVAYK	(No match)
86 - 108	2351.2207	2350.2134	2350.2168	-0.0033	1	AAVGATPEAKFDSFVASLTEALR	(No match)
96 - 108	1455.7529	1454.7456	1454.7405	0.0051	0	FDSFVASLTEALR	(No match)
96 - 108	1455.7529	1454.7456	1454.7405	0.0051	0	FDSFVASLTEALR	(Ions score 29)
109 - 130	2262.2185	2261.2112	2261.2088	0.0024	0	VIAGALEVHAVKPVTEEPGMAK	Oxidation (M) (No match)
131 - 147	1842.0393	1841.0320	1841.0298	0.0023	1	IPAGELQIIDKIDAAFK	(No match)
148 - 171	2427.2490	2426.2417	2426.2117	0.0300	1	VAATAAATAPADDKFTVFEAAFNK	(No match)
196 - 209	1388.7401	1387.7328	1387.7459	-0.0131	0	QAYAATVAAAPQVK	(No match)
210 - 219	1112.5907	1111.5834	1111.5913	-0.0079	0	YAVFEAALTK	(Ions score 88)
210 - 219	1112.5907	1111.5834	1111.5913	-0.0079	0	YAVFEAALTK	(No match)

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	Accession	Mass	Score	Description
1.	gi|3309043	26252	360	group V allergen Phl p 5.0204 [Phleum pratense]
2.	gi|1684718	27903	358	major allergen Phl p 5 [Phleum pratense]
3.	gi|2851457	28042	357	RecName: Full=Pollen allergen Phl p 5b; AltName: Full=Allergen Phl p Vb; AltName: Allergen=Phl
4.	gi|3309041	29351	355	group V allergen Phl p 5.0203 precursor [Phleum pratense]
5.	gi|3309045	28869	308	group V allergen Phl p 5.0206 precursor [Phleum pratense]
6.	gi|3309047	28384	196	group V allergen Phl p 5.0207 precursor [Phleum pratense]
7.	gi|481397	28182	181	allergen Phl p Vb - common timothy
8.	gi|28948464	10653	102	Chain A, Crystal Structure Of The Functional Domain Of The Major Grass Pollen Allergen Phl P 5b
9.	gi|2266623	24693	80	group V grass pollen allergen [Holcus lanatus]
10.	gi|14423120	26342	79	group 5 isoallergen 1 [Dactylis glomerata]

Results List

1. gi|3309043 **Mass:** 26252 **Score:** 360 **Expect:** 6e-031 **Queries matched:** 14

group V allergen Phl p 5.0204 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1112.5939	1111.5866	1111.5913	-0.0047	210	219	0	---	YAVFEAALTK
1112.5939	1111.5866	1111.5913	-0.0047	210	219	0	65	YAVFEAALTK
1388.7510	1387.7437	1387.7459	-0.0022	196	209	0	---	QAYAATVAAAPQVK
1455.7570	1454.7497	1454.7405	0.0092	96	108	0	---	FDSFVASLTEALR
1455.7570	1454.7497	1454.7405	0.0092	96	108	0	4	FDSFVASLTEALR
1503.7540	1502.7467	1502.7252	0.0215	172	185	1	---	AIKESTGGAYDTYK
1762.9725	1761.9652	1761.9664	-0.0012	69	85	1	---	APGLVPKLDAAYSVAYK
1762.9725	1761.9652	1761.9664	-0.0012	69	85	1	141	APGLVPKLDAAYSVAYK
1842.0327	1841.0254	1841.0298	-0.0043	131	147	1	---	IPAGELQIIDKIDAAFK
1935.0103	1934.0030	1933.9996	0.0034	20	36	1	---	ATTEEQKLIEDINVGFK
2246.2219	2245.2146	2245.2139	0.0007	109	130	0	---	VIAGALEVHAVKPVTEEPGMAK
2262.2175	2261.2102	2261.2088	0.0014	109	130	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2262.2175	2261.2102	2261.2088	0.0014	109	130	0	26	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2175	2350.2102	2350.2168	-0.0065	86	108	1	---	AAVGATPEAKFDSFVASLTEALR

No match to: 713.4116, 750.5168, 768.5250, 855.0381, 881.2772, 886.9822, 1334.8931, 1449.9404, 1525.7491, 2153.1096, 2205.2148, 2644.3706, 2644.3706

2. gi|1684718 **Mass:** 27903 **Score:** 358 **Expect:** 9.6e-031 **Queries matched:** 14

major allergen Phl p 5 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1112.5939	1111.5866	1111.5913	-0.0047	226	235	0	---	YAVFEAALTK
1112.5939	1111.5866	1111.5913	-0.0047	226	235	0	65	YAVFEAALTK

1388.7510	1387.7437	1387.7459	-0.0022	212 - 225	0	---	QAYAATVAAAPQVK
1455.7570	1454.7497	1454.7405	0.0092	112 - 124	0	---	FDSFVASLTEALR
1455.7570	1454.7497	1454.7405	0.0092	112 - 124	0	4	FDSFVASLTEALR
1503.7540	1502.7467	1502.7252	0.0215	188 - 201	1	---	AIKESTGGAYDTYK
1762.9725	1761.9652	1761.9664	-0.0012	85 - 101	1	---	APGLVPKLDAAYSVAYK
1762.9725	1761.9652	1761.9664	-0.0012	85 - 101	1	141	APGLVPKLDAAYSVAYK
1842.0327	1841.0254	1841.0298	-0.0043	147 - 163	1	---	IPAGELQIIDKIDAAFK
1935.0103	1934.0030	1933.9996	0.0034	36 - 52	1	---	ATTEEQKLIEDINVGFK
2246.2219	2245.2146	2245.2139	0.0007	125 - 146	0	---	VIAGALEVHAVKPVTEEPGMAK
2262.2175	2261.2102	2261.2088	0.0014	125 - 146	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2262.2175	2261.2102	2261.2088	0.0014	125 - 146	0	26	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2175	2350.2102	2350.2168	-0.0065	102 - 124	1	---	AAVGATPEAKFDSFVASLTEALR

No match to: 713.4116, 750.5168, 768.5250, 855.0381, 881.2772, 886.9822, 1334.8931, 1449.9404, 1525.7491, 2153.1096, 2205.2148, 2644.3706, 2644.3706

3. gi|2851457 **Mass:** 28042 **Score:** 357 **Expect:** 1.2e-030 **Queries matched:** 14

RecName: Full=Pollen allergen Phl p 5b; AltName: Full=Allergen Phl p Vb; AltName: Allergen=Phl p 5b

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1112.5939	1111.5866	1111.5913	-0.0047	229 - 238	0	---	YAVFEAALTK
1112.5939	1111.5866	1111.5913	-0.0047	229 - 238	0	65	YAVFEAALTK
1388.7510	1387.7437	1387.7459	-0.0022	215 - 228	0	---	QAYAATVAAAPQVK
1455.7570	1454.7497	1454.7405	0.0092	115 - 127	0	---	FDSFVASLTEALR
1455.7570	1454.7497	1454.7405	0.0092	115 - 127	0	4	FDSFVASLTEALR
1503.7540	1502.7467	1502.7252	0.0215	191 - 204	1	---	AIKESTGGAYDTYK
1762.9725	1761.9652	1761.9664	-0.0012	88 - 104	1	---	APGLVPKLDAAYSVAYK
1762.9725	1761.9652	1761.9664	-0.0012	88 - 104	1	141	APGLVPKLDAAYSVAYK
1842.0327	1841.0254	1841.0298	-0.0043	150 - 166	1	---	IPAGELQIIDKIDAAFK
1935.0103	1934.0030	1933.9996	0.0034	39 - 55	1	---	ATTEEQKLIEDINVGFK
2246.2219	2245.2146	2245.2139	0.0007	128 - 149	0	---	VIAGALEVHAVKPVTEEPGMAK
2262.2175	2261.2102	2261.2088	0.0014	128 - 149	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2262.2175	2261.2102	2261.2088	0.0014	128 - 149	0	26	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2175	2350.2102	2350.2168	-0.0065	105 - 127	1	---	AAVGATPEAKFDSFVASLTEALR

No match to: 713.4116, 750.5168, 768.5250, 855.0381, 881.2772, 886.9822, 1334.8931, 1449.9404, 1525.7491, 2153.1096, 2205.2148, 2644.3706, 2644.3706

4. gi|3309041 **Mass:** 29351 **Score:** 355 **Expect:** 1.9e-030 **Queries matched:** 14

group V allergen Phl p 5.0203 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1112.5939	1111.5866	1111.5913	-0.0047	240 - 249	0	---	YAVFEAALTK
1112.5939	1111.5866	1111.5913	-0.0047	240 - 249	0	65	YAVFEAALTK
1388.7510	1387.7437	1387.7459	-0.0022	226 - 239	0	---	QAYAATVAAAPQVK

1455.7570	1454.7497	1454.7405	0.0092	126 - 138	0	---	FDSFVASLTEALR
1455.7570	1454.7497	1454.7405	0.0092	126 - 138	0	4	FDSFVASLTEALR
1503.7540	1502.7467	1502.7252	0.0215	202 - 215	1	---	AIKESTGGAYDTYK
1762.9725	1761.9652	1761.9664	-0.0012	99 - 115	1	---	APGLVPKLDAAYSVAYK
1762.9725	1761.9652	1761.9664	-0.0012	99 - 115	1	141	APGLVPKLDAAYSVAYK
1842.0327	1841.0254	1841.0298	-0.0043	161 - 177	1	---	IPAGELQIIDKIDAAFK
1935.0103	1934.0030	1933.9996	0.0034	50 - 66	1	---	ATTEEQKLIEDINVGFK
2246.2219	2245.2146	2245.2139	0.0007	139 - 160	0	---	VIAGALEVHAVKPVTEEPGMAK
2262.2175	2261.2102	2261.2088	0.0014	139 - 160	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2262.2175	2261.2102	2261.2088	0.0014	139 - 160	0	26	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2175	2350.2102	2350.2168	-0.0065	116 - 138	1	---	AAVGATPEAKFDSFVASLTEALR

No match to: 713.4116, 750.5168, 768.5250, 855.0381, 881.2772, 886.9822, 1334.8931, 1449.9404, 1525.7491, 2153.1096, 2205.2148, 2644.3706, 2644.3706

5. gi|3309045 **Mass:** 28869 **Score:** 308 **Expect:** 9.6e-026 **Queries matched:** 11

group V allergen Phl p 5.0206 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start - End	Miss	Ions	Peptide
1112.5939	1111.5866	1111.5913	-0.0047	235 - 244	0	---	YAVFEAALTK
1112.5939	1111.5866	1111.5913	-0.0047	235 - 244	0	65	YAVFEAALTK
1388.7510	1387.7437	1387.7459	-0.0022	221 - 234	0	---	QAYAATVAAAPQVK
1455.7570	1454.7497	1454.7405	0.0092	121 - 133	0	---	FDSFVASLTEALR
1455.7570	1454.7497	1454.7405	0.0092	121 - 133	0	4	FDSFVASLTEALR
1503.7540	1502.7467	1502.7252	0.0215	197 - 210	1	---	AIKESTGGAYDTYK
1762.9725	1761.9652	1761.9664	-0.0012	94 - 110	1	---	APGLVPKLDAAYSVAYK
1762.9725	1761.9652	1761.9664	-0.0012	94 - 110	1	141	APGLVPKLDAAYSVAYK
1842.0327	1841.0254	1841.0298	-0.0043	156 - 172	1	---	IPAGELQIIDKIDAAFK
1935.0103	1934.0030	1933.9996	0.0034	45 - 61	1	---	ATTEEQKLIEDINVGFK
2351.2175	2350.2102	2350.2168	-0.0065	111 - 133	1	---	AAVGATPEAKFDSFVASLTEALR

No match to: 713.4116, 750.5168, 768.5250, 855.0381, 881.2772, 886.9822, 1334.8931, 1449.9404, 1525.7491, 2153.1096, 2205.2148, 2246.2219, 2262.2175, 2262.2175, 2644.3706, 2644.3706

6. gi|3309047 **Mass:** 28384 **Score:** 196 **Expect:** 1.5e-014 **Queries matched:** 12

group V allergen Phl p 5.0207 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start - End	Miss	Ions	Peptide
1112.5939	1111.5866	1111.5913	-0.0047	232 - 241	0	---	YAVFEAALTK
1112.5939	1111.5866	1111.5913	-0.0047	232 - 241	0	65	YAVFEAALTK
1388.7510	1387.7437	1387.7459	-0.0022	218 - 231	0	---	QAYAATVAAAPQVK
1455.7570	1454.7497	1454.7405	0.0092	121 - 133	0	---	FDSFVASLTEALR
1455.7570	1454.7497	1454.7405	0.0092	121 - 133	0	4	FDSFVASLTEALR
1503.7540	1502.7467	1502.7252	0.0215	194 - 207	1	---	AIKESTGGAYDTYK
1842.0327	1841.0254	1841.0298	-0.0043	156 - 172	1	---	IPAGELQIIDKIDAAFK

1935.0103	1934.0030	1933.9996	0.0034	45 - 61	1	---	ATTEEQKLIEDINVGFK
2246.2219	2245.2146	2245.2139	0.0007	134 - 155	0	---	VIAGALEVHAVKPVTEEPGMAK
2262.2175	2261.2102	2261.2088	0.0014	134 - 155	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2262.2175	2261.2102	2261.2088	0.0014	134 - 155	0	26	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2175	2350.2102	2350.2168	-0.0065	111 - 133	1	---	AAVGATPEAKFDSFVASLTEALR

No match to: 713.4116, 750.5168, 768.5250, 855.0381, 881.2772, 886.9822, 1334.8931, 1449.9404, 1525.7491, 1762.9725, 1762.9725, 2153.1096, 2205.2148, 2644.3706, 2644.3706

7. gi|481397 **Mass:** 28182 **Score:** 181 **Expect:** 4.8e-013 **Queries matched:** 11

allergen Phl p Vb - common timothy

Observed	Mr(expt)	Mr(calc)	Delta	Start - End	Miss	Ions	Peptide
1112.5939	1111.5866	1111.5913	-0.0047	225 - 234	0	---	YAVFEAALTK
1112.5939	1111.5866	1111.5913	-0.0047	225 - 234	0	65	YAVFEAALTK
1455.7570	1454.7497	1454.7405	0.0092	111 - 123	0	---	FDSFVASLTEALR
1455.7570	1454.7497	1454.7405	0.0092	111 - 123	0	4	FDSFVASLTEALR
1503.7540	1502.7467	1502.7252	0.0215	187 - 200	1	---	AIKESTGGAYDTYK
1842.0327	1841.0254	1841.0298	-0.0043	146 - 162	1	---	IPAGELQIIDKIDAAFK
1935.0103	1934.0030	1933.9996	0.0034	37 - 53	1	---	ATTEEQKLIEDINVGFK
2246.2219	2245.2146	2245.2139	0.0007	124 - 145	0	---	VIAGALEVHAVKPVTEEPGMAK
2262.2175	2261.2102	2261.2088	0.0014	124 - 145	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2262.2175	2261.2102	2261.2088	0.0014	124 - 145	0	26	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2175	2350.2102	2350.2168	-0.0065	101 - 123	1	---	AAVGATPEAKFDSFVASLTEALR

No match to: 713.4116, 750.5168, 768.5250, 855.0381, 881.2772, 886.9822, 1334.8931, 1388.7510, 1449.9404, 1525.7491, 1762.9725, 1762.9725, 2153.1096, 2205.2148, 2644.3706, 2644.3706

8. gi|28948464 **Mass:** 10653 **Score:** 102 **Expect:** 3.8e-005 **Queries matched:** 4

Chain A, Crystal Structure Of The Functional Domain Of The Major Grass Pollen Allergen Phl P 5b

Observed	Mr(expt)	Mr(calc)	Delta	Start - End	Miss	Ions	Peptide
1112.5939	1111.5866	1111.5913	-0.0047	80 - 89	0	---	YAVFEAALTK
1112.5939	1111.5866	1111.5913	-0.0047	80 - 89	0	65	YAVFEAALTK
1388.7510	1387.7437	1387.7459	-0.0022	66 - 79	0	---	QAYAATVAAAPQVK
1842.0327	1841.0254	1841.0298	-0.0043	1 - 17	1	---	IPAGELQIIDKIDAAFK

No match to: 713.4116, 750.5168, 768.5250, 855.0381, 881.2772, 886.9822, 1334.8931, 1449.9404, 1455.7570, 1455.7570, 1503.7540, 1525.7491, 1762.9725, 1762.9725, 1935.0103, 2153.1096, 2205.2148, 2246.2219, 2262.2175, 2262.2175, 2351.2175, 2644.3706, 2644.3706

9. gi|2266623 **Mass:** 24693 **Score:** 80 **Expect:** 0.006 **Queries matched:** 3

group V grass pollen allergen [Holcus lanatus]

Observed	Mr(expt)	Mr(calc)	Delta	Start - End	Miss	Ions	Peptide
1112.5939	1111.5866	1111.5913	-0.0047	193 - 202	0	---	YAVFEAALTK
1112.5939	1111.5866	1111.5913	-0.0047	193 - 202	0	65	YAVFEAALTK
1503.7540	1502.7467	1502.7252	0.0215	155 - 168	1	---	ALKESTGGAYESYK

No match to: 713.4116, 750.5168, 768.5250, 855.0381, 881.2772, 886.9822, 1334.8931, 1388.7510, 1449.9404, 1455.7570, 1455.7570, 1525.7491, 1762.9725, 1762.9725, 1842.0327, 1935.0103, 2153.1096, 2205.2148, 2246.2219, 2262.2175, 2262.2175, 2351.2175, 2644.3706, 2644.3706

10. gi|14423120 **Mass:** 26342 **Score:** 79 **Expect:** 0.0071 **Queries matched:** 3

group 5 isoallergen 1 [Dactylis glomerata]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1112.5939	1111.5866	1111.5913	-0.0047	214	223	0	---	YAVFEAALTK
1112.5939	1111.5866	1111.5913	-0.0047	214	223	0	65	YAVFEAALTK
1503.7540	1502.7467	1502.7252	0.0215	176	189	1	---	AIKESTGGAYESYK

No match to: 713.4116, 750.5168, 768.5250, 855.0381, 881.2772, 886.9822, 1334.8931, 1388.7510, 1449.9404, 1455.7570, 1455.7570, 1525.7491, 1762.9725, 1762.9725, 1842.0327, 1935.0103, 2153.1096, 2205.2148, 2246.2219, 2262.2175, 2262.2175, 2351.2175, 2644.3706, 2644.3706

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 27

Protein View

Match to: **gi|3309043** Score: **360** Expect: **6e-031**
group V allergen Phl p 5.0204 [Phleum pratense]

Nominal mass (M_r): **26252**; Calculated pI value: **5.61**
NCBI BLAST search of gi|3309043 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **50%**

Matched peptides shown in **Bold Red**

```
   1 ADAGYAPATP AAAGAEAGKA TTEEQKLIED INVGFKAAVA AAASVPAADK
  51 FKTFEAAFTS SSKAATAKAP GLVPKLDAAY SVAYKAAVGA TPEAKFDSFV
 101 ASLTEALRVI AGALEVHAVK PVTEEPGMAK IPAGELQIID KIDAAFKVAA
 151 TAAATAPADD KFTVFEAAFN KAIKESTGGA YDTYKCIPSL EAAVKQAYAA
 201 TVAAAPQVKY AVFEAALTKA ITAMSEVQKV SQPATGAATV AAGAATTAAG
 251 AASGAATVAA GGYKV
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
20 - 36	1935.0103	1934.0030	1933.9996	0.0034	1	ATTEEQKLIEDINVGFK	(No match)
69 - 85	1762.9725	1761.9652	1761.9664	-0.0012	1	APGLVPKLDAAYSVAYK	(No match)
69 - 85	1762.9725	1761.9652	1761.9664	-0.0012	1	APGLVPKLDAAYSVAYK	(Ions score 141)
86 - 108	2351.2175	2350.2102	2350.2168	-0.0065	1	AAVGATPEAKFDSFVASLTEALR	(No match)
96 - 108	1455.7570	1454.7497	1454.7405	0.0092	0	FDSFVASLTEALR	(No match)
96 - 108	1455.7570	1454.7497	1454.7405	0.0092	0	FDSFVASLTEALR	(Ions score 4)
109 - 130	2246.2219	2245.2146	2245.2139	0.0007	0	VIAGALEVHAVKPVTEEPGMAK	(No match)
109 - 130	2262.2175	2261.2102	2261.2088	0.0014	0	VIAGALEVHAVKPVTEEPGMAK	Oxidation (M) (No match)
109 - 130	2262.2175	2261.2102	2261.2088	0.0014	0	VIAGALEVHAVKPVTEEPGMAK	Oxidation (M) (Ions score 26)
131 - 147	1842.0327	1841.0254	1841.0298	-0.0043	1	IPAGELQIIDKIDAAFK	(No match)
172 - 185	1503.7540	1502.7467	1502.7252	0.0215	1	AIKESTGGAYDTYK	(No match)
196 - 209	1388.7510	1387.7437	1387.7459	-0.0022	0	QAYAATVAAAPQVK	(No match)
210 - 219	1112.5939	1111.5866	1111.5913	-0.0047	0	YAVFEAALTK	(No match)
210 - 219	1112.5939	1111.5866	1111.5913	-0.0047	0	YAVFEAALTK	(Ions score 65)

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	Accession	Mass	Score	Description
1.	gi|3309043	26252	92	group V allergen Phl p 5.0204 [Phleum pratense]
2.	gi|1684718	27903	91	major allergen Phl p 5 [Phleum pratense]
3.	gi|2851457	28042	90	RecName: Full=Pollen allergen Phl p 5b; AltName: Full=Allergen Phl p Vb; AltName: Allergen=Phl
4.	gi|3309041	29351	88	group V allergen Phl p 5.0203 precursor [Phleum pratense]
5.	gi|481397	28182	78	allergen Phl p Vb - common timothy
6.	gi|3309047	28384	77	group V allergen Phl p 5.0207 precursor [Phleum pratense]
7.	gi|3309045	28869	76	group V allergen Phl p 5.0206 precursor [Phleum pratense]
8.	gi|224129800	92864	50	predicted protein [Populus trichocarpa]
9.	gi|195612566	10509	46	hypothetical protein [Zea mays]
10.	gi|2266623	24693	46	group V grass pollen allergen [Holcus lanatus]

Results List

1. gi|3309043 **Mass:** 26252 **Score:** 92 **Expect:** 0.00036 **Queries matched:** 9

group V allergen Phl p 5.0204 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1112.5946	1111.5873	1111.5913	-0.0040	210	219	0	25	YAVFEAALTK
1112.5946	1111.5873	1111.5913	-0.0040	210	219	0	---	YAVFEAALTK
1455.7616	1454.7543	1454.7405	0.0138	96	108	0	---	FDSFVASLTEALR
1762.9806	1761.9733	1761.9664	0.0069	69	85	1	---	APGLVPKLDAAYSVAYK
1762.9806	1761.9733	1761.9664	0.0069	69	85	1	---	APGLVPKLDAAYSVAYK
1842.0580	1841.0507	1841.0298	0.0210	131	147	1	---	IPAGELQIIDKIDAAFK
1935.0156	1934.0083	1933.9996	0.0087	20	36	1	---	ATTEEQKLIEDINVGFK
2262.2126	2261.2053	2261.2088	-0.0035	109	130	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2385	2350.2312	2350.2168	0.0145	86	108	1	---	AAVGATPEAKFDSFVASLTEALR

No match to: 713.4016, 734.4894, 750.5089, 768.5162, 782.4797, 848.5251, 864.5333, 1133.7053, 1279.7734, 1291.6953, 1334.8873, 1404.6686, 1405.1724, 1448.9169, 1562.9581, 1572.8828, 1618.0707, 1732.0944, 1940.9624, 2144.0466, 2205.2346, 2230.2224, 2239.1462, 2247.2400, 2564.1963, 2644.3784, 2663.3682, 2780.9858, 2823.3147, 2826.3318, 2909.4304, 2921.3589, 3331.5759, 3348.6199

2. gi|1684718 **Mass:** 27903 **Score:** 91 **Expect:** 0.00053 **Queries matched:** 9

major allergen Phl p 5 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1112.5946	1111.5873	1111.5913	-0.0040	226	235	0	25	YAVFEAALTK
1112.5946	1111.5873	1111.5913	-0.0040	226	235	0	---	YAVFEAALTK
1455.7616	1454.7543	1454.7405	0.0138	112	124	0	---	FDSFVASLTEALR
1762.9806	1761.9733	1761.9664	0.0069	85	101	1	---	APGLVPKLDAAYSVAYK
1762.9806	1761.9733	1761.9664	0.0069	85	101	1	---	APGLVPKLDAAYSVAYK

1842.0580	1841.0507	1841.0298	0.0210	147 - 163	1	---	IPAGELQIIDKIDAAFK
1935.0156	1934.0083	1933.9996	0.0087	36 - 52	1	---	ATTEEQKLIEDINVGFK
2262.2126	2261.2053	2261.2088	-0.0035	125 - 146	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2385	2350.2312	2350.2168	0.0145	102 - 124	1	---	AAVGATPEAKFDSFVASLTEALR

No match to: 713.4016, 734.4894, 750.5089, 768.5162, 782.4797, 848.5251, 864.5333, 1133.7053, 1279.7734, 1291.6953, 1334.8873, 1404.6686, 1405.1724, 1448.9169, 1562.9581, 1572.8828, 1618.0707, 1732.0944, 1940.9624, 2144.0466, 2205.2346, 2230.2224, 2239.1462, 2247.2400, 2564.1963, 2644.3784, 2663.3682, 2780.9858, 2823.3147, 2826.3318, 2909.4304, 2921.3589, 3331.5759, 3348.6199

3. gi|2851457 **Mass:** 28042 **Score:** 90 **Expect:** 0.00057 **Queries matched:** 9

RecName: Full=Pollen allergen Phl p 5b; AltName: Full=Allergen Phl p Vb; AltName: Allergen=Phl p 5b

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1112.5946	1111.5873	1111.5913	-0.0040	229 - 238	0	25	YAVFEAALTK
1112.5946	1111.5873	1111.5913	-0.0040	229 - 238	0	---	YAVFEAALTK
1455.7616	1454.7543	1454.7405	0.0138	115 - 127	0	---	FDSFVASLTEALR
1762.9806	1761.9733	1761.9664	0.0069	88 - 104	1	---	APGLVPKLDAAYSVAYK
1762.9806	1761.9733	1761.9664	0.0069	88 - 104	1	---	APGLVPKLDAAYSVAYK
1842.0580	1841.0507	1841.0298	0.0210	150 - 166	1	---	IPAGELQIIDKIDAAFK
1935.0156	1934.0083	1933.9996	0.0087	39 - 55	1	---	ATTEEQKLIEDINVGFK
2262.2126	2261.2053	2261.2088	-0.0035	128 - 149	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2385	2350.2312	2350.2168	0.0145	105 - 127	1	---	AAVGATPEAKFDSFVASLTEALR

No match to: 713.4016, 734.4894, 750.5089, 768.5162, 782.4797, 848.5251, 864.5333, 1133.7053, 1279.7734, 1291.6953, 1334.8873, 1404.6686, 1405.1724, 1448.9169, 1562.9581, 1572.8828, 1618.0707, 1732.0944, 1940.9624, 2144.0466, 2205.2346, 2230.2224, 2239.1462, 2247.2400, 2564.1963, 2644.3784, 2663.3682, 2780.9858, 2823.3147, 2826.3318, 2909.4304, 2921.3589, 3331.5759, 3348.6199

4. gi|3309041 **Mass:** 29351 **Score:** 88 **Expect:** 0.0009 **Queries matched:** 9

group V allergen Phl p 5.0203 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1112.5946	1111.5873	1111.5913	-0.0040	240 - 249	0	25	YAVFEAALTK
1112.5946	1111.5873	1111.5913	-0.0040	240 - 249	0	---	YAVFEAALTK
1455.7616	1454.7543	1454.7405	0.0138	126 - 138	0	---	FDSFVASLTEALR
1762.9806	1761.9733	1761.9664	0.0069	99 - 115	1	---	APGLVPKLDAAYSVAYK
1762.9806	1761.9733	1761.9664	0.0069	99 - 115	1	---	APGLVPKLDAAYSVAYK
1842.0580	1841.0507	1841.0298	0.0210	161 - 177	1	---	IPAGELQIIDKIDAAFK
1935.0156	1934.0083	1933.9996	0.0087	50 - 66	1	---	ATTEEQKLIEDINVGFK
2262.2126	2261.2053	2261.2088	-0.0035	139 - 160	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2385	2350.2312	2350.2168	0.0145	116 - 138	1	---	AAVGATPEAKFDSFVASLTEALR

No match to: 713.4016, 734.4894, 750.5089, 768.5162, 782.4797, 848.5251, 864.5333, 1133.7053, 1279.7734, 1291.6953, 1334.8873, 1404.6686, 1405.1724, 1448.9169, 1562.9581, 1572.8828, 1618.0707, 1732.0944, 1940.9624, 2144.0466, 2205.2346, 2230.2224, 2239.1462, 2247.2400, 2564.1963, 2644.3784, 2663.3682, 2780.9858, 2823.3147, 2826.3318, 2909.4304, 2921.3589, 3331.5759, 3348.6199

5. gi|481397 **Mass:** 28182 **Score:** 78 **Expect:** 0.011 **Queries matched:** 7

allergen Phl p Vb - common timothy

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1112.5946	1111.5873	1111.5913	-0.0040	225	234	0	25	YAVFEAALTK
1112.5946	1111.5873	1111.5913	-0.0040	225	234	0	---	YAVFEAALTK
1455.7616	1454.7543	1454.7405	0.0138	111	123	0	---	FDSFVASLTEALR
1842.0580	1841.0507	1841.0298	0.0210	146	162	1	---	IPAGELQIIDKIDAAFK
1935.0156	1934.0083	1933.9996	0.0087	37	53	1	---	ATTEEQKLIEDINVGFK
2262.2126	2261.2053	2261.2088	-0.0035	124	145	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2385	2350.2312	2350.2168	0.0145	101	123	1	---	AAVGATPEAKFDSFVASLTEALR

No match to: 713.4016, 734.4894, 750.5089, 768.5162, 782.4797, 848.5251, 864.5333, 1133.7053, 1279.7734, 1291.6953, 1334.8873, 1404.6686, 1405.1724, 1448.9169, 1562.9581, 1572.8828, 1618.0707, 1732.0944, 1762.9806, 1762.9806, 1940.9624, 2144.0466, 2205.2346, 2230.2224, 2239.1462, 2247.2400, 2564.1963, 2644.3784, 2663.3682, 2780.9858, 2823.3147, 2826.3318, 2909.4304, 2921.3589, 3331.5759, 3348.6199

6. gi|3309047 **Mass:** 28384 **Score:** 77 **Expect:** 0.012 **Queries matched:** 7

group V allergen Phl p 5.0207 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1112.5946	1111.5873	1111.5913	-0.0040	232	241	0	25	YAVFEAALTK
1112.5946	1111.5873	1111.5913	-0.0040	232	241	0	---	YAVFEAALTK
1455.7616	1454.7543	1454.7405	0.0138	121	133	0	---	FDSFVASLTEALR
1842.0580	1841.0507	1841.0298	0.0210	156	172	1	---	IPAGELQIIDKIDAAFK
1935.0156	1934.0083	1933.9996	0.0087	45	61	1	---	ATTEEQKLIEDINVGFK
2262.2126	2261.2053	2261.2088	-0.0035	134	155	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2385	2350.2312	2350.2168	0.0145	111	133	1	---	AAVGATPEAKFDSFVASLTEALR

No match to: 713.4016, 734.4894, 750.5089, 768.5162, 782.4797, 848.5251, 864.5333, 1133.7053, 1279.7734, 1291.6953, 1334.8873, 1404.6686, 1405.1724, 1448.9169, 1562.9581, 1572.8828, 1618.0707, 1732.0944, 1762.9806, 1762.9806, 1940.9624, 2144.0466, 2205.2346, 2230.2224, 2239.1462, 2247.2400, 2564.1963, 2644.3784, 2663.3682, 2780.9858, 2823.3147, 2826.3318, 2909.4304, 2921.3589, 3331.5759, 3348.6199

7. gi|3309045 **Mass:** 28869 **Score:** 76 **Expect:** 0.015 **Queries matched:** 8

group V allergen Phl p 5.0206 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1112.5946	1111.5873	1111.5913	-0.0040	235	244	0	25	YAVFEAALTK
1112.5946	1111.5873	1111.5913	-0.0040	235	244	0	---	YAVFEAALTK
1455.7616	1454.7543	1454.7405	0.0138	121	133	0	---	FDSFVASLTEALR
1762.9806	1761.9733	1761.9664	0.0069	94	110	1	---	APGLVPKLDAAYSVAYK
1762.9806	1761.9733	1761.9664	0.0069	94	110	1	---	APGLVPKLDAAYSVAYK
1842.0580	1841.0507	1841.0298	0.0210	156	172	1	---	IPAGELQIIDKIDAAFK
1935.0156	1934.0083	1933.9996	0.0087	45	61	1	---	ATTEEQKLIEDINVGFK
2351.2385	2350.2312	2350.2168	0.0145	111	133	1	---	AAVGATPEAKFDSFVASLTEALR

No match to: 713.4016, 734.4894, 750.5089, 768.5162, 782.4797, 848.5251, 864.5333, 1133.7053, 1279.7734, 1291.6953, 1334.8873, 1404.6686, 1405.1724, 1448.9169, 1562.9581, 1572.8828, 1618.0707, 1732.0944, 1940.9624,

2144.0466, 2205.2346, 2230.2224, 2239.1462, 2247.2400, 2262.2126, 2564.1963, 2644.3784, 2663.3682, 2780.9858, 2823.3147, 2826.3318, 2909.4304, 2921.3589, 3331.5759, 3348.6199

8. gi|224129800 **Mass:** 92864 **Score:** 50 **Expect:** 6.1 **Queries matched:** 9

predicted protein [Populus trichocarpa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1133.7053	1132.6980	1132.6339	0.0641	655 -	665	0	---	STITSLALAEK
1762.9806	1761.9733	1761.9083	0.0650	485 -	500	1	---	GFIADLDSIQMTPARK
1762.9806	1761.9733	1761.9083	0.0650	485 -	500	1	---	GFIADLDSIQMTPARK
2144.0466	2143.0393	2143.0228	0.0165	181 -	199	1	---	LIEGGEVNRHFGETNMNAR
2230.2224	2229.2151	2229.1851	0.0300	733 -	753	1	---	DSLLEKVSESSQNLAAVALQK
2247.2400	2246.2327	2246.1365	0.0963	543 -	561	0	---	HLEQLQLNDHLMGEISELK
2564.1963	2563.1890	2563.1787	0.0103	131 -	151	0	---	VSYMEIYNEEINDLFAVENQK + Oxidation (M)
2909.4304	2908.4231	2908.3589	0.0643	460 -	484	1	---	LPDFSPLPDNYSNVADEDTWLKMNK
3331.5759	3330.5686	3330.4227	0.1460	625 -	652	1	---	FSMAMDDHKSFNENDSLVQENCEVLSER

No match to: 713.4016, 734.4894, 750.5089, 768.5162, 782.4797, 848.5251, 864.5333, 1112.5946, 1112.5946, 1279.7734, 1291.6953, 1334.8873, 1404.6686, 1405.1724, 1448.9169, 1455.7616, 1562.9581, 1572.8828, 1618.0707, 1732.0944, 1842.0580, 1935.0156, 1940.9624, 2205.2346, 2239.1462, 2262.2126, 2351.2385, 2644.3784, 2663.3682, 2780.9858, 2823.3147, 2826.3318, 2921.3589, 3348.6199

9. gi|195612566 **Mass:** 10509 **Score:** 46 **Expect:** 14 **Queries matched:** 6

hypothetical protein [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1112.5946	1111.5873	1111.5185	0.0688	86 -	95	0	---	QFAGEIPYST
1112.5946	1111.5873	1111.5185	0.0688	86 -	95	0	---	QFAGEIPYST
1572.8828	1571.8755	1571.8518	0.0237	7 -	21	1	---	NSLVAEGDVSVQKVK
1762.9806	1761.9733	1761.9260	0.0473	69 -	83	1	---	ALSEQEIINDYIARK
1762.9806	1761.9733	1761.9260	0.0473	69 -	83	1	---	ALSEQEIINDYIARK
2564.1963	2563.1890	2563.3223	-0.1332	22 -	42	1	---	KIEPVYDYDLVTRPWVFGNPR

No match to: 713.4016, 734.4894, 750.5089, 768.5162, 782.4797, 848.5251, 864.5333, 1133.7053, 1279.7734, 1291.6953, 1334.8873, 1404.6686, 1405.1724, 1448.9169, 1455.7616, 1562.9581, 1618.0707, 1732.0944, 1842.0580, 1935.0156, 1940.9624, 2144.0466, 2205.2346, 2230.2224, 2239.1462, 2247.2400, 2262.2126, 2351.2385, 2644.3784, 2663.3682, 2780.9858, 2823.3147, 2826.3318, 2909.4304, 2921.3589, 3331.5759, 3348.6199

10. gi|2266623 **Mass:** 24693 **Score:** 46 **Expect:** 17 **Queries matched:** 4

group V grass pollen allergen [Holcus lanatus]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1112.5946	1111.5873	1111.5913	-0.0040	193 -	202	0	25	YAVFEAALTK
1112.5946	1111.5873	1111.5913	-0.0040	193 -	202	0	---	YAVFEAALTK
1279.7734	1278.7661	1278.7295	0.0366	13 -	26	1	---	AAVAAAAKVPPADK
2247.2400	2246.2327	2246.1106	0.1222	158 -	178	1	---	ESTGGAYESYKFIPSLEAAVK

No match to: 713.4016, 734.4894, 750.5089, 768.5162, 782.4797, 848.5251, 864.5333, 1133.7053, 1291.6953, 1334.8873, 1404.6686, 1405.1724, 1448.9169, 1455.7616, 1562.9581, 1572.8828, 1618.0707, 1732.0944, 1762.9806,

1762.9806, 1842.0580, 1935.0156, 1940.9624, 2144.0466, 2205.2346, 2230.2224, 2239.1462, 2262.2126, 2351.2385, 2564.1963, 2644.3784, 2663.3682, 2780.9858, 2823.3147, 2826.3318, 2909.4304, 2921.3589, 3331.5759, 3348.6199

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 43

Protein View

Match to: **gi|3309043** Score: **92** Expect: **0.00036**
group V allergen Phl p 5.0204 [Phleum pratense]

Nominal mass (M_r): **26252**; Calculated pI value: **5.61**
NCBI BLAST search of gi|3309043 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

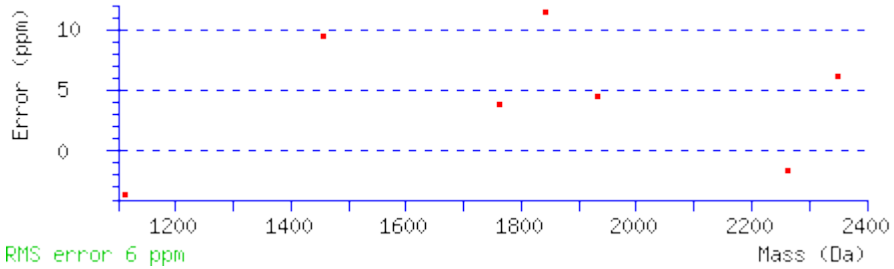
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **40%**

Matched peptides shown in **Bold Red**

```
   1 ADAGYAPATP AAAGAEAGKA TTEEQKLIED INVGFKAAVA AAASVPAADK
  51 FKTFEAAFTS SSKAATAKAP GLVPKLDAAY SVAYKAAVGA TPEAKFDSFV
 101 ASLTEALRVI AGALEVHAVK PVTEEPGMAK IPAGELQIID KIDAAFKVAA
 151 TAAATAPADD KFTVFEAAFN KAIKESTGGA YDTYKCIPSL EAAVKQAYAA
 201 TVAAAPQVKY AVFEAALTKA ITAMSEVQKV SQPATGAATV AAGAATTAAG
 251 AASGAATVAA GGYKV
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
20 - 36	1935.0156	1934.0083	1933.9996	0.0087	1	**ATTEEQKLIEDINVGFK**	(No match)
69 - 85	1762.9806	1761.9733	1761.9664	0.0069	1	**APGLVPKLDAAYSVAYK**	(No match)
69 - 85	1762.9806	1761.9733	1761.9664	0.0069	1	**APGLVPKLDAAYSVAYK**	(No match)
86 - 108	2351.2385	2350.2312	2350.2168	0.0145	1	**AAVGATPEAKFDSFVASLTEALR**	(No match)
96 - 108	1455.7616	1454.7543	1454.7405	0.0138	0	**FDSFVASLTEALR**	(No match)
109 - 130	2262.2126	2261.2053	2261.2088	-0.0035	0	**VIAGALEVHAVKPVTEEPGMAK** Oxidation (M)	(No match)
131 - 147	1842.0580	1841.0507	1841.0298	0.0210	1	**IPAGELQIIDKIDAAFK**	(No match)
210 - 219	1112.5946	1111.5873	1111.5913	-0.0040	0	**YAVFEAALTK**	(Ions score 25)
210 - 219	1112.5946	1111.5873	1111.5913	-0.0040	0	**YAVFEAALTK**	(No match)



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	Accession	Mass	Score	Description
1.	gi|3309043	26252	648	group V allergen Phl p 5.0204 [Phleum pratense]
2.	gi|2851457	28042	643	RecName: Full=Pollen allergen Phl p 5b; AltName: Full=Allergen Phl p Vb; AltName: Allergen=Phl
3.	gi|3309041	29351	639	group V allergen Phl p 5.0203 precursor [Phleum pratense]
4.	gi|1684718	27903	602	major allergen Phl p 5 [Phleum pratense]
5.	gi|3309045	28869	596	group V allergen Phl p 5.0206 precursor [Phleum pratense]
6.	gi|3309047	28384	587	group V allergen Phl p 5.0207 precursor [Phleum pratense]
7.	gi|481397	28182	573	allergen Phl p Vb - common timothy
8.	gi|28948464	10653	139	Chain A, Crystal Structure Of The Functional Domain Of The Major Grass Pollen Allergen Phl P 5b
9.	gi|2266623	24693	107	group V grass pollen allergen [Holcus lanatus]
10.	gi|14423120	26342	96	group 5 isoallergen 1 [Dactylis glomerata]

Results List

1. gi|3309043 **Mass:** 26252 **Score:** 648 **Expect:** 9.6e-060 **Queries matched:** 22

group V allergen Phl p 5.0204 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1087.5717	1086.5644	1086.5743	-0.0099	186	195	0	---	CIPSLEAAVK
1100.5553	1099.5480	1099.5549	-0.0069	76	85	0	---	LDAAYSVAYK
1112.5928	1111.5855	1111.5913	-0.0058	210	219	0	---	YAVFEAALTK
1112.5928	1111.5855	1111.5913	-0.0058	210	219	0	77	YAVFEAALTK
1147.6340	1146.6267	1146.6284	-0.0017	27	36	0	---	LIEDINVGFK
1175.5499	1174.5426	1174.5506	-0.0079	53	63	0	---	TFEAAFTSSSK
1191.5004	1190.4931	1190.5091	-0.0160	175	185	0	---	ESTGGAYDTYK
1388.7478	1387.7405	1387.7459	-0.0054	196	209	0	---	QAYAATVAAAPQVK
1455.7471	1454.7398	1454.7405	-0.0007	96	108	0	---	FDSFVASLTEALR
1455.7471	1454.7398	1454.7405	-0.0007	96	108	0	77	FDSFVASLTEALR
1487.8173	1486.8100	1486.8143	-0.0043	37	52	1	---	AAVAAAASVPAADKFK
1503.7239	1502.7166	1502.7252	-0.0086	172	185	1	---	AIKESTGGAYDTYK
1762.9703	1761.9630	1761.9664	-0.0034	69	85	1	---	APGLVPKLDAAYSVAYK
1842.0336	1841.0263	1841.0298	-0.0034	131	147	1	---	IPAGELQIIDKIDAAFK
1935.0063	1933.9990	1933.9996	-0.0006	20	36	1	---	ATTEEQKLIEDINVGFK
1935.0063	1933.9990	1933.9996	-0.0006	20	36	1	133	ATTEEQKLIEDINVGFK
2246.2207	2245.2134	2245.2139	-0.0005	109	130	0	---	VIAGALEVHAVKPVTEEPGMAK
2262.2173	2261.2100	2261.2088	0.0012	109	130	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2202	2350.2129	2350.2168	-0.0038	86	108	1	---	AAVGATPEAKFDSFVASLTEALR
2351.2202	2350.2129	2350.2168	-0.0038	86	108	1	120	AAVGATPEAKFDSFVASLTEALR
2427.2297	2426.2224	2426.2117	0.0107	148	171	1	---	VAATAAATAPADDKFTVFEAAFNK

3018.5803	3017.5730	3017.5416	0.0314	230 - 265	1	---	VSQPATGAATVAAGAATTAAGAASGAATVAAGGYKV

No match to: 713.4092, 734.4933, 750.5178, 768.5241, 864.5425, 886.9792, 1070.5497, 1279.7671, 1323.6816, 1334.8748, 1371.7266, 1448.9136, 1691.7789, 2205.2263, 2441.3022, 2644.3701, 2644.3701, 2824.2917, 3087.6587, 3607.7864

2. gi|2851457 **Mass:** 28042 **Score:** 643 **Expect:** 3e-059 **Queries matched:** 22

RecName: Full=Pollen allergen Phl p 5b; AltName: Full=Allergen Phl p Vb; AltName: Allergen=Phl p 5b

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1087.5717	1086.5644	1086.5743	-0.0099	205 -	214	0	---	CIPSLEAAVK
1100.5553	1099.5480	1099.5549	-0.0069	95 -	104	0	---	LDAAYSVAYK
1112.5928	1111.5855	1111.5913	-0.0058	229 -	238	0	---	YAVFEAALTK
1112.5928	1111.5855	1111.5913	-0.0058	229 -	238	0	77	YAVFEAALTK
1147.6340	1146.6267	1146.6284	-0.0017	46 -	55	0	---	LIEDINVGFK
1175.5499	1174.5426	1174.5506	-0.0079	72 -	82	0	---	TFEAAFTSSSK
1191.5004	1190.4931	1190.5091	-0.0160	194 -	204	0	---	ESTGGAYDTYK
1388.7478	1387.7405	1387.7459	-0.0054	215 -	228	0	---	QAYAATVAAAPQVK
1455.7471	1454.7398	1454.7405	-0.0007	115 -	127	0	---	FDSFVASLTEALR
1455.7471	1454.7398	1454.7405	-0.0007	115 -	127	0	77	FDSFVASLTEALR
1487.8173	1486.8100	1486.8143	-0.0043	56 -	71	1	---	AAVAAAASVPAADKFK
1503.7239	1502.7166	1502.7252	-0.0086	191 -	204	1	---	AIKESTGGAYDTYK
1762.9703	1761.9630	1761.9664	-0.0034	88 -	104	1	---	APGLVPKLDAAYSVAYK
1842.0336	1841.0263	1841.0298	-0.0034	150 -	166	1	---	IPAGELQIIDKIDAAFK
1935.0063	1933.9990	1933.9996	-0.0006	39 -	55	1	---	ATTEEQKLIEDINVGFK
1935.0063	1933.9990	1933.9996	-0.0006	39 -	55	1	133	ATTEEQKLIEDINVGFK
2246.2207	2245.2134	2245.2139	-0.0005	128 -	149	0	---	VIAGALEVHAVKPVTEEPGMAK
2262.2173	2261.2100	2261.2088	0.0012	128 -	149	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2202	2350.2129	2350.2168	-0.0038	105 -	127	1	---	AAVGATPEAKFDSFVASLTEALR
2351.2202	2350.2129	2350.2168	-0.0038	105 -	127	1	120	AAVGATPEAKFDSFVASLTEALR
2427.2297	2426.2224	2426.2117	0.0107	167 -	190	1	---	VAATAAATAPADDKFTVFEAAFNK
3018.5803	3017.5730	3017.5416	0.0314	249 -	284	1	---	VSQPATGAATVAAGAATTAAGAASGAATVAAGGYKV

No match to: 713.4092, 734.4933, 750.5178, 768.5241, 864.5425, 886.9792, 1070.5497, 1279.7671, 1323.6816, 1334.8748, 1371.7266, 1448.9136, 1691.7789, 2205.2263, 2441.3022, 2644.3701, 2644.3701, 2824.2917, 3087.6587, 3607.7864

3. gi|3309041 **Mass:** 29351 **Score:** 639 **Expect:** 7.6e-059 **Queries matched:** 22

group V allergen Phl p 5.0203 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1087.5717	1086.5644	1086.5743	-0.0099	216 -	225	0	---	CIPSLEAAVK
1100.5553	1099.5480	1099.5549	-0.0069	106 -	115	0	---	LDAAYSVAYK
1112.5928	1111.5855	1111.5913	-0.0058	240 -	249	0	---	YAVFEAALTK
1112.5928	1111.5855	1111.5913	-0.0058	240 -	249	0	77	YAVFEAALTK
1147.6340	1146.6267	1146.6284	-0.0017	57 -	66	0	---	LIEDINVGFK

1175.5499	1174.5426	1174.5506	-0.0079	83 - 93	0	---	TFEAAFTSSSK
1191.5004	1190.4931	1190.5091	-0.0160	205 - 215	0	---	ESTGGAYDTYK
1388.7478	1387.7405	1387.7459	-0.0054	226 - 239	0	---	QAYAATVAAAPQVK
1455.7471	1454.7398	1454.7405	-0.0007	126 - 138	0	---	FDSFVASLTEALR
1455.7471	1454.7398	1454.7405	-0.0007	126 - 138	0	77	FDSFVASLTEALR
1487.8173	1486.8100	1486.8143	-0.0043	67 - 82	1	---	AAVAAAASVPAADKFK
1503.7239	1502.7166	1502.7252	-0.0086	202 - 215	1	---	AIKESTGGAYDTYK
1762.9703	1761.9630	1761.9664	-0.0034	99 - 115	1	---	APGLVPKLDAAYSVAYK
1842.0336	1841.0263	1841.0298	-0.0034	161 - 177	1	---	IPAGELQIIDKIDAAFK
1935.0063	1933.9990	1933.9996	-0.0006	50 - 66	1	---	ATTEEQKLIEDINVGFK
1935.0063	1933.9990	1933.9996	-0.0006	50 - 66	1	133	ATTEEQKLIEDINVGFK
2246.2207	2245.2134	2245.2139	-0.0005	139 - 160	0	---	VIAGALEVHAVKPVTEEPGMAK
2262.2173	2261.2100	2261.2088	0.0012	139 - 160	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2202	2350.2129	2350.2168	-0.0038	116 - 138	1	---	AAVGATPEAKFDSFVASLTEALR
2351.2202	2350.2129	2350.2168	-0.0038	116 - 138	1	120	AAVGATPEAKFDSFVASLTEALR
2427.2297	2426.2224	2426.2117	0.0107	178 - 201	1	---	VAATAAATAPADDKFTVFEAAFNK
3018.5803	3017.5730	3017.5416	0.0314	260 - 295	1	---	VSQPATGAATVAAGAATTAAGAASGAATVAAGGYKV

No match to: 713.4092, 734.4933, 750.5178, 768.5241, 864.5425, 886.9792, 1070.5497, 1279.7671, 1323.6816, 1334.8748, 1371.7266, 1448.9136, 1691.7789, 2205.2263, 2441.3022, 2644.3701, 2644.3701, 2824.2917, 3087.6587, 3607.7864

4. gi|1684718 **Mass:** 27903 **Score:** 602 **Expect:** 3.8e-055 **Queries matched:** 20

major allergen Phl p 5 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1087.5717	1086.5644	1086.5743	-0.0099	202 - 211	0	---	CIPSLEAAVK
1100.5553	1099.5480	1099.5549	-0.0069	92 - 101	0	---	LDAAYSVAYK
1112.5928	1111.5855	1111.5913	-0.0058	226 - 235	0	---	YAVFEAALTK
1112.5928	1111.5855	1111.5913	-0.0058	226 - 235	0	77	YAVFEAALTK
1147.6340	1146.6267	1146.6284	-0.0017	43 - 52	0	---	LIEDINVGFK
1175.5499	1174.5426	1174.5506	-0.0079	69 - 79	0	---	TFEAAFTSSSK
1191.5004	1190.4931	1190.5091	-0.0160	191 - 201	0	---	ESTGGAYDTYK
1388.7478	1387.7405	1387.7459	-0.0054	212 - 225	0	---	QAYAATVAAAPQVK
1455.7471	1454.7398	1454.7405	-0.0007	112 - 124	0	---	FDSFVASLTEALR
1455.7471	1454.7398	1454.7405	-0.0007	112 - 124	0	77	FDSFVASLTEALR
1503.7239	1502.7166	1502.7252	-0.0086	188 - 201	1	---	AIKESTGGAYDTYK
1762.9703	1761.9630	1761.9664	-0.0034	85 - 101	1	---	APGLVPKLDAAYSVAYK
1842.0336	1841.0263	1841.0298	-0.0034	147 - 163	1	---	IPAGELQIIDKIDAAFK
1935.0063	1933.9990	1933.9996	-0.0006	36 - 52	1	---	ATTEEQKLIEDINVGFK
1935.0063	1933.9990	1933.9996	-0.0006	36 - 52	1	133	ATTEEQKLIEDINVGFK
2246.2207	2245.2134	2245.2139	-0.0005	125 - 146	0	---	VIAGALEVHAVKPVTEEPGMAK
2262.2173	2261.2100	2261.2088	0.0012	125 - 146	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)

2351.2202	2350.2129	2350.2168	-0.0038	102 - 124	1	---	AAVGATPEAKFDSFVASLTEALR
2351.2202	2350.2129	2350.2168	-0.0038	102 - 124	1	120	AAVGATPEAKFDSFVASLTEALR
2427.2297	2426.2224	2426.2117	0.0107	164 - 187	1	---	VAATAAATAPADDKFTVFEAAFNK

No match to: 713.4092, 734.4933, 750.5178, 768.5241, 864.5425, 886.9792, 1070.5497, 1279.7671, 1323.6816, 1334.8748, 1371.7266, 1448.9136, 1487.8173, 1691.7789, 2205.2263, 2441.3022, 2644.3701, 2644.3701, 2824.2917, 3018.5803, 3087.6587, 3607.7864

5. gi|3309045 **Mass:** 28869 **Score:** 596 **Expect:** 1.5e-054 **Queries matched:** 19

group V allergen Phl p 5.0206 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1087.5717	1086.5644	1086.5743	-0.0099	211 - 220	0	---	CIPSLEAAVK
1100.5553	1099.5480	1099.5549	-0.0069	101 - 110	0	---	LDAAYSVAYK
1112.5928	1111.5855	1111.5913	-0.0058	235 - 244	0	---	YAVFEAALTK
1112.5928	1111.5855	1111.5913	-0.0058	235 - 244	0	77	YAVFEAALTK
1147.6340	1146.6267	1146.6284	-0.0017	52 - 61	0	---	LIEDINVGFK
1175.5499	1174.5426	1174.5506	-0.0079	78 - 88	0	---	TFEAAFTSSSK
1191.5004	1190.4931	1190.5091	-0.0160	200 - 210	0	---	ESTGGAYDTYK
1388.7478	1387.7405	1387.7459	-0.0054	221 - 234	0	---	QAYAATVAAAPQVK
1455.7471	1454.7398	1454.7405	-0.0007	121 - 133	0	---	FDSFVASLTEALR
1455.7471	1454.7398	1454.7405	-0.0007	121 - 133	0	77	FDSFVASLTEALR
1487.8173	1486.8100	1486.8143	-0.0043	62 - 77	1	---	AAVAAAASVPAADKFK
1503.7239	1502.7166	1502.7252	-0.0086	197 - 210	1	---	AIKESTGGAYDTYK
1762.9703	1761.9630	1761.9664	-0.0034	94 - 110	1	---	APGLVPKLDAAYSVAYK
1842.0336	1841.0263	1841.0298	-0.0034	156 - 172	1	---	IPAGELQIIDKIDAAFK
1935.0063	1933.9990	1933.9996	-0.0006	45 - 61	1	---	ATTEEQKLIEDINVGFK
1935.0063	1933.9990	1933.9996	-0.0006	45 - 61	1	133	ATTEEQKLIEDINVGFK
2351.2202	2350.2129	2350.2168	-0.0038	111 - 133	1	---	AAVGATPEAKFDSFVASLTEALR
2351.2202	2350.2129	2350.2168	-0.0038	111 - 133	1	120	AAVGATPEAKFDSFVASLTEALR
2427.2297	2426.2224	2426.2117	0.0107	173 - 196	1	---	VAATAAATAPADDKFTVFEAAFNK

No match to: 713.4092, 734.4933, 750.5178, 768.5241, 864.5425, 886.9792, 1070.5497, 1279.7671, 1323.6816, 1334.8748, 1371.7266, 1448.9136, 1691.7789, 2205.2263, 2246.2207, 2262.2173, 2441.3022, 2644.3701, 2644.3701, 2824.2917, 3018.5803, 3087.6587, 3607.7864

6. gi|3309047 **Mass:** 28384 **Score:** 587 **Expect:** 1.2e-053 **Queries matched:** 19

group V allergen Phl p 5.0207 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1087.5717	1086.5644	1086.5743	-0.0099	208 - 217	0	---	CIPSLEAAVK
1112.5928	1111.5855	1111.5913	-0.0058	232 - 241	0	---	YAVFEAALTK
1112.5928	1111.5855	1111.5913	-0.0058	232 - 241	0	77	YAVFEAALTK
1147.6340	1146.6267	1146.6284	-0.0017	52 - 61	0	---	LIEDINVGFK
1175.5499	1174.5426	1174.5506	-0.0079	78 - 88	0	---	TFEAAFTSSSK
1191.5004	1190.4931	1190.5091	-0.0160	197 - 207	0	---	ESTGGAYDTYK

1388.7478	1387.7405	1387.7459	-0.0054	218 - 231	0	---	QAYAATVAAAPQVK
1455.7471	1454.7398	1454.7405	-0.0007	121 - 133	0	---	FDSFVASLTEALR
1455.7471	1454.7398	1454.7405	-0.0007	121 - 133	0	77	FDSFVASLTEALR
1487.8173	1486.8100	1486.8143	-0.0043	62 - 77	1	---	AAVAAAASVPAADKFK
1503.7239	1502.7166	1502.7252	-0.0086	194 - 207	1	---	AIKESTGGAYDTYK
1842.0336	1841.0263	1841.0298	-0.0034	156 - 172	1	---	IPAGELQIIDKIDAAFK
1935.0063	1933.9990	1933.9996	-0.0006	45 - 61	1	---	ATTEEQKLIEDINVGFK
1935.0063	1933.9990	1933.9996	-0.0006	45 - 61	1	133	ATTEEQKLIEDINVGFK
2246.2207	2245.2134	2245.2139	-0.0005	134 - 155	0	---	VIAGALEVHAVKPVTEEPGMAK
2262.2173	2261.2100	2261.2088	0.0012	134 - 155	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2202	2350.2129	2350.2168	-0.0038	111 - 133	1	---	AAVGATPEAKFDSFVASLTEALR
2351.2202	2350.2129	2350.2168	-0.0038	111 - 133	1	120	AAVGATPEAKFDSFVASLTEALR
3018.5803	3017.5730	3017.5416	0.0314	252 - 287	1	---	VSQPATGAATVAAGAATTAAGAASGAATVAAGGYKV

No match to: 713.4092, 734.4933, 750.5178, 768.5241, 864.5425, 886.9792, 1070.5497, 1100.5553, 1279.7671, 1323.6816, 1334.8748, 1371.7266, 1448.9136, 1691.7789, 1762.9703, 2205.2263, 2427.2297, 2441.3022, 2644.3701, 2644.3701, 2824.2917, 3087.6587, 3607.7864

7. gi|481397 **Mass:** 28182 **Score:** 573 **Expect:** 3e-052 **Queries matched:** 18

allergen Phl p Vb - common timothy

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1087.5717	1086.5644	1086.5743	-0.0099	201 - 210	0	---	CIPSLEAAVK
1100.5553	1099.5480	1099.5549	-0.0069	91 - 100	0	---	LDAAYSVAYK
1112.5928	1111.5855	1111.5913	-0.0058	225 - 234	0	---	YAVFEAALTK
1112.5928	1111.5855	1111.5913	-0.0058	225 - 234	0	77	YAVFEAALTK
1147.6340	1146.6267	1146.6284	-0.0017	44 - 53	0	---	LIEDINVGFK
1191.5004	1190.4931	1190.5091	-0.0160	190 - 200	0	---	ESTGGAYDTYK
1455.7471	1454.7398	1454.7405	-0.0007	111 - 123	0	---	FDSFVASLTEALR
1455.7471	1454.7398	1454.7405	-0.0007	111 - 123	0	77	FDSFVASLTEALR
1503.7239	1502.7166	1502.7252	-0.0086	187 - 200	1	---	AIKESTGGAYDTYK
1842.0336	1841.0263	1841.0298	-0.0034	146 - 162	1	---	IPAGELQIIDKIDAAFK
1935.0063	1933.9990	1933.9996	-0.0006	37 - 53	1	---	ATTEEQKLIEDINVGFK
1935.0063	1933.9990	1933.9996	-0.0006	37 - 53	1	133	ATTEEQKLIEDINVGFK
2246.2207	2245.2134	2245.2139	-0.0005	124 - 145	0	---	VIAGALEVHAVKPVTEEPGMAK
2262.2173	2261.2100	2261.2088	0.0012	124 - 145	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2202	2350.2129	2350.2168	-0.0038	101 - 123	1	---	AAVGATPEAKFDSFVASLTEALR
2351.2202	2350.2129	2350.2168	-0.0038	101 - 123	1	120	AAVGATPEAKFDSFVASLTEALR
2427.2297	2426.2224	2426.2117	0.0107	163 - 186	1	---	VAATAAATAPADDKFTVFEAAFNK
3018.5803	3017.5730	3017.5416	0.0314	245 - 280	1	---	VSQPATGAATVAAGAATTAAGAASGAATVAAGGYKV

No match to: 713.4092, 734.4933, 750.5178, 768.5241, 864.5425, 886.9792, 1070.5497, 1175.5499, 1279.7671, 1323.6816, 1334.8748, 1371.7266, 1388.7478, 1448.9136, 1487.8173, 1691.7789, 1762.9703, 2205.2263, 2441.3022, 2644.3701, 2644.3701, 2824.2917, 3087.6587, 3607.7864

8. gi|28948464 **Mass:** 10653 **Score:** 139 **Expect:** 7.6e-009 **Queries matched:** 6

Chain A, Crystal Structure Of The Functional Domain Of The Major Grass Pollen Allergen Phl P 5b

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1087.5717	1086.5644	1086.5743	-0.0099	56 -	65	0	---	CIPSLEAAVK
1112.5928	1111.5855	1111.5913	-0.0058	80 -	89	0	---	YAVFEAALTK
1112.5928	1111.5855	1111.5913	-0.0058	80 -	89	0	77	YAVFEAALTK
1388.7478	1387.7405	1387.7459	-0.0054	66 -	79	0	---	QAYAATVAAAPQVK
1842.0336	1841.0263	1841.0298	-0.0034	1 -	17	1	---	IPAGELQIIDKIDAAFK
2427.2297	2426.2224	2426.2117	0.0107	18 -	41	1	---	VAATAAATAPADDKFTVFEAAFNK

No match to: 713.4092, 734.4933, 750.5178, 768.5241, 864.5425, 886.9792, 1070.5497, 1100.5553, 1147.6340, 1175.5499, 1191.5004, 1279.7671, 1323.6816, 1334.8748, 1371.7266, 1448.9136, 1455.7471, 1455.7471, 1487.8173, 1503.7239, 1691.7789, 1762.9703, 1935.0063, 1935.0063, 2205.2263, 2246.2207, 2262.2173, 2351.2202, 2351.2202, 2441.3022, 2644.3701, 2644.3701, 2824.2917, 3018.5803, 3087.6587, 3607.7864

9. gi|2266623 **Mass:** 24693 **Score:** 107 **Expect:** 1.2e-005 **Queries matched:** 5

group V grass pollen allergen [Holcus lanatus]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1112.5928	1111.5855	1111.5913	-0.0058	193 -	202	0	---	YAVFEAALTK
1112.5928	1111.5855	1111.5913	-0.0058	193 -	202	0	77	YAVFEAALTK
1191.5004	1190.4931	1190.5091	-0.0160	158 -	168	0	---	ESTGGAYESYK
1279.7671	1278.7598	1278.7295	0.0303	13 -	26	1	---	AAVAAAAKVPPADK
1503.7239	1502.7166	1502.7252	-0.0086	155 -	168	1	---	ALKESTGGAYESYK

No match to: 713.4092, 734.4933, 750.5178, 768.5241, 864.5425, 886.9792, 1070.5497, 1087.5717, 1100.5553, 1147.6340, 1175.5499, 1323.6816, 1334.8748, 1371.7266, 1388.7478, 1448.9136, 1455.7471, 1455.7471, 1487.8173, 1691.7789, 1762.9703, 1842.0336, 1935.0063, 1935.0063, 2205.2263, 2246.2207, 2262.2173, 2351.2202, 2351.2202, 2427.2297, 2441.3022, 2644.3701, 2644.3701, 2824.2917, 3018.5803, 3087.6587, 3607.7864

10. gi|14423120 **Mass:** 26342 **Score:** 96 **Expect:** 0.00016 **Queries matched:** 4

group 5 isoallergen 1 [Dactylis glomerata]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1112.5928	1111.5855	1111.5913	-0.0058	214 -	223	0	---	YAVFEAALTK
1112.5928	1111.5855	1111.5913	-0.0058	214 -	223	0	77	YAVFEAALTK
1191.5004	1190.4931	1190.5091	-0.0160	179 -	189	0	---	ESTGGAYESYK
1503.7239	1502.7166	1502.7252	-0.0086	176 -	189	1	---	AIKESTGGAYESYK

No match to: 713.4092, 734.4933, 750.5178, 768.5241, 864.5425, 886.9792, 1070.5497, 1087.5717, 1100.5553, 1147.6340, 1175.5499, 1279.7671, 1323.6816, 1334.8748, 1371.7266, 1388.7478, 1448.9136, 1455.7471, 1455.7471, 1487.8173, 1691.7789, 1762.9703, 1842.0336, 1935.0063, 1935.0063, 2205.2263, 2246.2207, 2262.2173, 2351.2202, 2351.2202, 2427.2297, 2441.3022, 2644.3701, 2644.3701, 2824.2917, 3018.5803, 3087.6587, 3607.7864

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 42

Protein View

Match to: **gi|3309043** Score: **648** Expect: **9.6e-060**
group V allergen Phl p 5.0204 [Phleum pratense]

Nominal mass (M_r): **26252**; Calculated pI value: **5.61**
NCBI BLAST search of gi|3309043 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **87%**

Matched peptides shown in **Bold Red**

```
     1 ADAGYAPATP AAAGAEAGKA TTEEQKLIED INVGFKAAVA AAASVPAADK
    51 FKTFEAAFTS SSKAATAKAP GLVPKLDAAY SVAYKAAVGA TPEAKFDSFV
   101 ASLTEALRVI AGALEVHAVK PVTEEPGMAK IPAGELQIID KIDAAFKVAA
   151 TAAATAPADD KFTVFEAAFN KAIKESTGGA YDTYKCIPSL EAAVKQAYAA
   201 TVAAAPQVKY AVFEAALTKA ITAMSEVQKV SQPATGAATV AAGAATTAAG
   251 AASGAATVAA GGYKV
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
20 - 36	1935.0063	1933.9990	1933.9996	-0.0006	1	ATTEEQKLIEDINVGFK (No match)
20 - 36	1935.0063	1933.9990	1933.9996	-0.0006	1	ATTEEQKLIEDINVGFK (Ions score 133)
27 - 36	1147.6340	1146.6267	1146.6284	-0.0017	0	LIEDINVGFK (No match)
37 - 52	1487.8173	1486.8100	1486.8143	-0.0043	1	AAVAAAASVPAADKFK (No match)
53 - 63	1175.5499	1174.5426	1174.5506	-0.0079	0	TFEAAFTSSSK (No match)
69 - 85	1762.9703	1761.9630	1761.9664	-0.0034	1	APGLVPKLDAAYSVAYK (No match)
76 - 85	1100.5553	1099.5480	1099.5549	-0.0069	0	LDAAYSVAYK (No match)
86 - 108	2351.2202	2350.2129	2350.2168	-0.0038	1	AAVGATPEAKFDSFVASLTEALR (No match)
86 - 108	2351.2202	2350.2129	2350.2168	-0.0038	1	AAVGATPEAKFDSFVASLTEALR (Ions score 120)
96 - 108	1455.7471	1454.7398	1454.7405	-0.0007	0	FDSFVASLTEALR (No match)
96 - 108	1455.7471	1454.7398	1454.7405	-0.0007	0	FDSFVASLTEALR (Ions score 77)
109 - 130	2246.2207	2245.2134	2245.2139	-0.0005	0	VIAGALEVHAVKPVTEEPGMAK (No match)
109 - 130	2262.2173	2261.2100	2261.2088	0.0012	0	VIAGALEVHAVKPVTEEPGMAK Oxidation (M) (No match)
131 - 147	1842.0336	1841.0263	1841.0298	-0.0034	1	IPAGELQIIDKIDAAFK (No match)
148 - 171	2427.2297	2426.2224	2426.2117	0.0107	1	VAATAAATAPADDKFTVFEAAFNK (No match)
172 - 185	1503.7239	1502.7166	1502.7252	-0.0086	1	AIKESTGGAYDTYK (No match)
175 - 185	1191.5004	1190.4931	1190.5091	-0.0160	0	ESTGGAYDTYK (No match)
186 - 195	1087.5717	1086.5644	1086.5743	-0.0099	0	CIPSLEAAVK (No match)
196 - 209	1388.7478	1387.7405	1387.7459	-0.0054	0	QAYAATVAAAPQVK (No match)
210 - 219	1112.5928	1111.5855	1111.5913	-0.0058	0	YAVFEAALTK (No match)
210 - 219	1112.5928	1111.5855	1111.5913	-0.0058	0	YAVFEAALTK (Ions score 77)
230 - 265	3018.5803	3017.5730	3017.5416	0.0314	1	VSQPATGAATVAAGAATTAAGAASGAATVAAGGYKV (No match)

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	Accession	Mass	Score	Description
1.	gi|3309043	26252	639	group V allergen Phl p 5.0204 [Phleum pratense]
2.	gi|2851457	28042	634	RecName: Full=Pollen allergen Phl p 5b; AltName: Full=Allergen Phl p Vb; AltName: Allergen=Phl
3.	gi|3309041	29351	631	group V allergen Phl p 5.0203 precursor [Phleum pratense]
4.	gi|1684718	27903	598	major allergen Phl p 5 [Phleum pratense]
5.	gi|3309045	28869	593	group V allergen Phl p 5.0206 precursor [Phleum pratense]
6.	gi|3309047	28384	585	group V allergen Phl p 5.0207 precursor [Phleum pratense]
7.	gi|481397	28182	573	allergen Phl p Vb - common timothy
8.	gi|28948464	10653	173	Chain A, Crystal Structure Of The Functional Domain Of The Major Grass Pollen Allergen Phl P 5
9.	gi|11991229	29216	145	pollen allergen Hol l 5b [Holcus lanatus]
10.	gi|224058437	54253	55	predicted protein [Populus trichocarpa]

Results List

1. gi|3309043 **Mass:** 26252 **Score:** 639 **Expect:** 7.6e-059 **Queries matched:** 22

group V allergen Phl p 5.0204 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1087.5670	1086.5597	1086.5743	-0.0146	186	195	0	---	CIPSLEAAVK
1100.5486	1099.5413	1099.5549	-0.0136	76	85	0	---	LDAAYSVAYK
1112.5851	1111.5778	1111.5913	-0.0135	210	219	0	---	YAVFEAALTK
1147.6316	1146.6243	1146.6284	-0.0041	27	36	0	---	LIEDINVGFK
1175.5500	1174.5427	1174.5506	-0.0078	53	63	0	---	TFEAAFTSSSK
1191.5085	1190.5012	1190.5091	-0.0079	175	185	0	---	ESTGGAYDTYK
1388.7405	1387.7332	1387.7459	-0.0127	196	209	0	---	QAYAATVAAAPQVK
1455.7511	1454.7438	1454.7405	0.0033	96	108	0	---	FDSFVASLTEALR
1455.7511	1454.7438	1454.7405	0.0033	96	108	0	85	FDSFVASLTEALR
1487.8107	1486.8034	1486.8143	-0.0109	37	52	1	---	AAVAAAASVPAADKFK
1503.7347	1502.7274	1502.7252	0.0022	172	185	1	---	AIKESTGGAYDTYK
1762.9688	1761.9615	1761.9664	-0.0049	69	85	1	---	APGLVPKLDAAYSVAYK
1842.0338	1841.0265	1841.0298	-0.0032	131	147	1	---	IPAGELQIIDKIDAAFK
1842.0338	1841.0265	1841.0298	-0.0032	131	147	1	119	IPAGELQIIDKIDAAFK
1935.0046	1933.9973	1933.9996	-0.0023	20	36	1	---	ATTEEQKLIEDINVGFK
1935.0046	1933.9973	1933.9996	-0.0023	20	36	1	108	ATTEEQKLIEDINVGFK
2246.2239	2245.2166	2245.2139	0.0027	109	130	0	---	VIAGALEVHAVKPVTEEPGMAK
2262.2192	2261.2119	2261.2088	0.0031	109	130	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2288	2350.2215	2350.2168	0.0048	86	108	1	---	AAVGATPEAKFDSFVASLTEALR
2351.2288	2350.2215	2350.2168	0.0048	86	108	1	119	AAVGATPEAKFDSFVASLTEALR
2427.2258	2426.2185	2426.2117	0.0068	148	171	1	---	VAATAAATAPADDKFTVFEAAFNK

3018.5769	3017.5696	3017.5416	0.0280	230 - 265	1	---	VSQPATGAATVAAGAATTAAGAASGAATVAAGGYKV

No match to: 713.3972, 734.4841, 750.5088, 768.5095, 782.4742, 1004.5108, 1070.5455, 1135.5984, 1279.7509, 1291.6787, 1334.8665, 1371.7194, 1448.9011, 1469.7822, 1571.8846, 1638.8666, 1691.7775, 1957.0104, 2011.0596, 2143.0444, 2205.2319, 2231.2188, 2564.1870, 2644.3696, 2644.3696, 2662.3875, 2666.3557, 2825.3245, 2908.4321, 2922.3618, 3040.5242, 3087.6294, 3339.7727, 3348.6101, 3404.8296

2. gi|2851457 **Mass:** 28042 **Score:** 634 **Expect:** 2.4e-058 **Queries matched:** 22

RecName: Full=Pollen allergen Phl p 5b; AltName: Full=Allergen Phl p Vb; AltName: Allergen=Phl p 5b

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1087.5670	1086.5597	1086.5743	-0.0146	205 -	214	0	---	CIPSLEAAVK
1100.5486	1099.5413	1099.5549	-0.0136	95 -	104	0	---	LDAAYSVAYK
1112.5851	1111.5778	1111.5913	-0.0135	229 -	238	0	---	YAVFEAALTK
1147.6316	1146.6243	1146.6284	-0.0041	46 -	55	0	---	LIEDINVGFK
1175.5500	1174.5427	1174.5506	-0.0078	72 -	82	0	---	TFEAAFTSSSK
1191.5085	1190.5012	1190.5091	-0.0079	194 -	204	0	---	ESTGGAYDTYK
1388.7405	1387.7332	1387.7459	-0.0127	215 -	228	0	---	QAYAATVAAAPQVK
1455.7511	1454.7438	1454.7405	0.0033	115 -	127	0	---	FDSFVASLTEALR
1455.7511	1454.7438	1454.7405	0.0033	115 -	127	0	85	FDSFVASLTEALR
1487.8107	1486.8034	1486.8143	-0.0109	56 -	71	1	---	AAVAAAASVPAADKFK
1503.7347	1502.7274	1502.7252	0.0022	191 -	204	1	---	AIKESTGGAYDTYK
1762.9688	1761.9615	1761.9664	-0.0049	88 -	104	1	---	APGLVPKLDAAYSVAYK
1842.0338	1841.0265	1841.0298	-0.0032	150 -	166	1	---	IPAGELQIIDKIDAAFK
1842.0338	1841.0265	1841.0298	-0.0032	150 -	166	1	119	IPAGELQIIDKIDAAFK
1935.0046	1933.9973	1933.9996	-0.0023	39 -	55	1	---	ATTEEQKLIEDINVGFK
1935.0046	1933.9973	1933.9996	-0.0023	39 -	55	1	108	ATTEEQKLIEDINVGFK
2246.2239	2245.2166	2245.2139	0.0027	128 -	149	0	---	VIAGALEVHAVKPVTEEPGMAK
2262.2192	2261.2119	2261.2088	0.0031	128 -	149	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2288	2350.2215	2350.2168	0.0048	105 -	127	1	---	AAVGATPEAKFDSFVASLTEALR
2351.2288	2350.2215	2350.2168	0.0048	105 -	127	1	119	AAVGATPEAKFDSFVASLTEALR
2427.2258	2426.2185	2426.2117	0.0068	167 -	190	1	---	VAATAAATAPADDKFTVFEAAFNK
3018.5769	3017.5696	3017.5416	0.0280	249 -	284	1	---	VSQPATGAATVAAGAATTAAGAASGAATVAAGGYKV

No match to: 713.3972, 734.4841, 750.5088, 768.5095, 782.4742, 1004.5108, 1070.5455, 1135.5984, 1279.7509, 1291.6787, 1334.8665, 1371.7194, 1448.9011, 1469.7822, 1571.8846, 1638.8666, 1691.7775, 1957.0104, 2011.0596, 2143.0444, 2205.2319, 2231.2188, 2564.1870, 2644.3696, 2644.3696, 2662.3875, 2666.3557, 2825.3245, 2908.4321, 2922.3618, 3040.5242, 3087.6294, 3339.7727, 3348.6101, 3404.8296

3. gi|3309041 **Mass:** 29351 **Score:** 631 **Expect:** 4.8e-058 **Queries matched:** 22

group V allergen Phl p 5.0203 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1087.5670	1086.5597	1086.5743	-0.0146	216 -	225	0	---	CIPSLEAAVK
1100.5486	1099.5413	1099.5549	-0.0136	106 -	115	0	---	LDAAYSVAYK
1112.5851	1111.5778	1111.5913	-0.0135	240 -	249	0	---	YAVFEAALTK

1147.6316	1146.6243	1146.6284	-0.0041	57 - 66	0	---	LIEDINVGFK
1175.5500	1174.5427	1174.5506	-0.0078	83 - 93	0	---	TFEAAFTSSSK
1191.5085	1190.5012	1190.5091	-0.0079	205 - 215	0	---	ESTGGAYDTYK
1388.7405	1387.7332	1387.7459	-0.0127	226 - 239	0	---	QAYAATVAAAPQVK
1455.7511	1454.7438	1454.7405	0.0033	126 - 138	0	---	FDSFVASLTEALR
1455.7511	1454.7438	1454.7405	0.0033	126 - 138	0	85	FDSFVASLTEALR
1487.8107	1486.8034	1486.8143	-0.0109	67 - 82	1	---	AAVAAAASVPAADKFK
1503.7347	1502.7274	1502.7252	0.0022	202 - 215	1	---	AIKESTGGAYDTYK
1762.9688	1761.9615	1761.9664	-0.0049	99 - 115	1	---	APGLVPKLDAAYSVAYK
1842.0338	1841.0265	1841.0298	-0.0032	161 - 177	1	---	IPAGELQIIDKIDAAFK
1842.0338	1841.0265	1841.0298	-0.0032	161 - 177	1	119	IPAGELQIIDKIDAAFK
1935.0046	1933.9973	1933.9996	-0.0023	50 - 66	1	---	ATTEEQKLIEDINVGFK
1935.0046	1933.9973	1933.9996	-0.0023	50 - 66	1	108	ATTEEQKLIEDINVGFK
2246.2239	2245.2166	2245.2139	0.0027	139 - 160	0	---	VIAGALEVHAVKPVTEEPGMAK
2262.2192	2261.2119	2261.2088	0.0031	139 - 160	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2288	2350.2215	2350.2168	0.0048	116 - 138	1	---	AAVGATPEAKFDSFVASLTEALR
2351.2288	2350.2215	2350.2168	0.0048	116 - 138	1	119	AAVGATPEAKFDSFVASLTEALR
2427.2258	2426.2185	2426.2117	0.0068	178 - 201	1	---	VAATAAATAPADDKFTVFEAAFNK
3018.5769	3017.5696	3017.5416	0.0280	260 - 295	1	---	VSQPATGAATVAAGAATTAAGAASGAATVAAGGYKV

No match to: 713.3972, 734.4841, 750.5088, 768.5095, 782.4742, 1004.5108, 1070.5455, 1135.5984, 1279.7509, 1291.6787, 1334.8665, 1371.7194, 1448.9011, 1469.7822, 1571.8846, 1638.8666, 1691.7775, 1957.0104, 2011.0596, 2143.0444, 2205.2319, 2231.2188, 2564.1870, 2644.3696, 2644.3696, 2662.3875, 2666.3557, 2825.3245, 2908.4321, 2922.3618, 3040.5242, 3087.6294, 3339.7727, 3348.6101, 3404.8296

4. gi|1684718 **Mass:** 27903 **Score:** 598 **Expect:** 9.6e-055 **Queries matched:** 20

major allergen Phl p 5 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start - End	Miss	Ions	Peptide
1087.5670	1086.5597	1086.5743	-0.0146	202 - 211	0	---	CIPSLEAAVK
1100.5486	1099.5413	1099.5549	-0.0136	92 - 101	0	---	LDAAYSVAYK
1112.5851	1111.5778	1111.5913	-0.0135	226 - 235	0	---	YAVFEAALTK
1147.6316	1146.6243	1146.6284	-0.0041	43 - 52	0	---	LIEDINVGFK
1175.5500	1174.5427	1174.5506	-0.0078	69 - 79	0	---	TFEAAFTSSSK
1191.5085	1190.5012	1190.5091	-0.0079	191 - 201	0	---	ESTGGAYDTYK
1388.7405	1387.7332	1387.7459	-0.0127	212 - 225	0	---	QAYAATVAAAPQVK
1455.7511	1454.7438	1454.7405	0.0033	112 - 124	0	---	FDSFVASLTEALR
1455.7511	1454.7438	1454.7405	0.0033	112 - 124	0	85	FDSFVASLTEALR
1503.7347	1502.7274	1502.7252	0.0022	188 - 201	1	---	AIKESTGGAYDTYK
1762.9688	1761.9615	1761.9664	-0.0049	85 - 101	1	---	APGLVPKLDAAYSVAYK
1842.0338	1841.0265	1841.0298	-0.0032	147 - 163	1	---	IPAGELQIIDKIDAAFK
1842.0338	1841.0265	1841.0298	-0.0032	147 - 163	1	119	IPAGELQIIDKIDAAFK
1935.0046	1933.9973	1933.9996	-0.0023	36 - 52	1	---	ATTEEQKLIEDINVGFK

1935.0046	1933.9973	1933.9996	-0.0023	36 - 52	1	108	ATTEEQKLIEDINVGFK
2246.2239	2245.2166	2245.2139	0.0027	125 - 146	0	---	VIAGALEVHAVKPVTEEPGMAK
2262.2192	2261.2119	2261.2088	0.0031	125 - 146	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2288	2350.2215	2350.2168	0.0048	102 - 124	1	---	AAVGATPEAKFDSFVASLTEALR
2351.2288	2350.2215	2350.2168	0.0048	102 - 124	1	119	AAVGATPEAKFDSFVASLTEALR
2427.2258	2426.2185	2426.2117	0.0068	164 - 187	1	---	VAATAAATAPADDKFTVFEAAFNK

No match to: 713.3972, 734.4841, 750.5088, 768.5095, 782.4742, 1004.5108, 1070.5455, 1135.5984, 1279.7509, 1291.6787, 1334.8665, 1371.7194, 1448.9011, 1469.7822, 1487.8107, 1571.8846, 1638.8666, 1691.7775, 1957.0104, 2011.0596, 2143.0444, 2205.2319, 2231.2188, 2564.1870, 2644.3696, 2644.3696, 2662.3875, 2666.3557, 2825.3245, 2908.4321, 2922.3618, 3018.5769, 3040.5242, 3087.6294, 3339.7727, 3348.6101, 3404.8296

5. gi|3309045 **Mass:** 28869 **Score:** 593 **Expect:** 3e-054 **Queries matched:** 19

group V allergen Phl p 5.0206 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1087.5670	1086.5597	1086.5743	-0.0146	211 - 220		0	---	CIPSLEAAVK
1100.5486	1099.5413	1099.5549	-0.0136	101 - 110		0	---	LDAAYSVAYK
1112.5851	1111.5778	1111.5913	-0.0135	235 - 244		0	---	YAVFEAALTK
1147.6316	1146.6243	1146.6284	-0.0041	52 - 61		0	---	LIEDINVGFK
1175.5500	1174.5427	1174.5506	-0.0078	78 - 88		0	---	TFEAAFTSSSK
1191.5085	1190.5012	1190.5091	-0.0079	200 - 210		0	---	ESTGGAYDTYK
1388.7405	1387.7332	1387.7459	-0.0127	221 - 234		0	---	QAYAATVAAAPQVK
1455.7511	1454.7438	1454.7405	0.0033	121 - 133		0	---	FDSFVASLTEALR
1455.7511	1454.7438	1454.7405	0.0033	121 - 133		0	85	FDSFVASLTEALR
1487.8107	1486.8034	1486.8143	-0.0109	62 - 77		1	---	AAVAAAASVPAADKFK
1503.7347	1502.7274	1502.7252	0.0022	197 - 210		1	---	AIKESTGGAYDTYK
1762.9688	1761.9615	1761.9664	-0.0049	94 - 110		1	---	APGLVPKLDAAYSVAYK
1842.0338	1841.0265	1841.0298	-0.0032	156 - 172		1	---	IPAGELQIIDKIDAAFK
1842.0338	1841.0265	1841.0298	-0.0032	156 - 172		1	119	IPAGELQIIDKIDAAFK
1935.0046	1933.9973	1933.9996	-0.0023	45 - 61		1	---	ATTEEQKLIEDINVGFK
1935.0046	1933.9973	1933.9996	-0.0023	45 - 61		1	108	ATTEEQKLIEDINVGFK
2351.2288	2350.2215	2350.2168	0.0048	111 - 133		1	---	AAVGATPEAKFDSFVASLTEALR
2351.2288	2350.2215	2350.2168	0.0048	111 - 133		1	119	AAVGATPEAKFDSFVASLTEALR
2427.2258	2426.2185	2426.2117	0.0068	173 - 196		1	---	VAATAAATAPADDKFTVFEAAFNK

No match to: 713.3972, 734.4841, 750.5088, 768.5095, 782.4742, 1004.5108, 1070.5455, 1135.5984, 1279.7509, 1291.6787, 1334.8665, 1371.7194, 1448.9011, 1469.7822, 1571.8846, 1638.8666, 1691.7775, 1957.0104, 2011.0596, 2143.0444, 2205.2319, 2231.2188, 2246.2239, 2262.2192, 2564.1870, 2644.3696, 2644.3696, 2662.3875, 2666.3557, 2825.3245, 2908.4321, 2922.3618, 3018.5769, 3040.5242, 3087.6294, 3339.7727, 3348.6101, 3404.8296

6. gi|3309047 **Mass:** 28384 **Score:** 585 **Expect:** 1.9e-053 **Queries matched:** 19

group V allergen Phl p 5.0207 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1087.5670	1086.5597	1086.5743	-0.0146	208 - 217		0	---	CIPSLEAAVK

1112.5851	1111.5778	1111.5913	-0.0135	232 - 241	0	---	YAVFEAALTK
1147.6316	1146.6243	1146.6284	-0.0041	52 - 61	0	---	LIEDINVGFK
1175.5500	1174.5427	1174.5506	-0.0078	78 - 88	0	---	TFEAAFTSSSK
1191.5085	1190.5012	1190.5091	-0.0079	197 - 207	0	---	ESTGGAYDTYK
1388.7405	1387.7332	1387.7459	-0.0127	218 - 231	0	---	QAYAATVAAAPQVK
1455.7511	1454.7438	1454.7405	0.0033	121 - 133	0	---	FDSFVASLTEALR
1455.7511	1454.7438	1454.7405	0.0033	121 - 133	0	85	FDSFVASLTEALR
1487.8107	1486.8034	1486.8143	-0.0109	62 - 77	1	---	AAVAAAASVPAADKFK
1503.7347	1502.7274	1502.7252	0.0022	194 - 207	1	---	AIKESTGGAYDTYK
1842.0338	1841.0265	1841.0298	-0.0032	156 - 172	1	---	IPAGELQIIDKIDAAFK
1842.0338	1841.0265	1841.0298	-0.0032	156 - 172	1	119	IPAGELQIIDKIDAAFK
1935.0046	1933.9973	1933.9996	-0.0023	45 - 61	1	---	ATTEEQKLIEDINVGFK
1935.0046	1933.9973	1933.9996	-0.0023	45 - 61	1	108	ATTEEQKLIEDINVGFK
2246.2239	2245.2166	2245.2139	0.0027	134 - 155	0	---	VIAGALEVHAVKPVTEEPGMAK
2262.2192	2261.2119	2261.2088	0.0031	134 - 155	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2288	2350.2215	2350.2168	0.0048	111 - 133	1	---	AAVGATPEAKFDSFVASLTEALR
2351.2288	2350.2215	2350.2168	0.0048	111 - 133	1	119	AAVGATPEAKFDSFVASLTEALR
3018.5769	3017.5696	3017.5416	0.0280	252 - 287	1	---	VSQPATGAATVAAGAATTAAGAASGAATVAAGGYKV

No match to: 713.3972, 734.4841, 750.5088, 768.5095, 782.4742, 1004.5108, 1070.5455, 1100.5486, 1135.5984, 1279.7509, 1291.6787, 1334.8665, 1371.7194, 1448.9011, 1469.7822, 1571.8846, 1638.8666, 1691.7775, 1762.9688, 1957.0104, 2011.0596, 2143.0444, 2205.2319, 2231.2188, 2427.2258, 2564.1870, 2644.3696, 2644.3696, 2662.3875, 2666.3557, 2825.3245, 2908.4321, 2922.3618, 3040.5242, 3087.6294, 3339.7727, 3348.6101, 3404.8296

7. gi|481397 **Mass:** 28182 **Score:** 573 **Expect:** 3e-052 **Queries matched:** 18

allergen Phl p Vb - common timothy

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1087.5670	1086.5597	1086.5743	-0.0146	201 - 210	0	---	CIPSLEAAVK
1100.5486	1099.5413	1099.5549	-0.0136	91 - 100	0	---	LDAAYSVAYK
1112.5851	1111.5778	1111.5913	-0.0135	225 - 234	0	---	YAVFEAALTK
1147.6316	1146.6243	1146.6284	-0.0041	44 - 53	0	---	LIEDINVGFK
1191.5085	1190.5012	1190.5091	-0.0079	190 - 200	0	---	ESTGGAYDTYK
1455.7511	1454.7438	1454.7405	0.0033	111 - 123	0	---	FDSFVASLTEALR
1455.7511	1454.7438	1454.7405	0.0033	111 - 123	0	85	FDSFVASLTEALR
1503.7347	1502.7274	1502.7252	0.0022	187 - 200	1	---	AIKESTGGAYDTYK
1842.0338	1841.0265	1841.0298	-0.0032	146 - 162	1	---	IPAGELQIIDKIDAAFK
1842.0338	1841.0265	1841.0298	-0.0032	146 - 162	1	119	IPAGELQIIDKIDAAFK
1935.0046	1933.9973	1933.9996	-0.0023	37 - 53	1	---	ATTEEQKLIEDINVGFK
1935.0046	1933.9973	1933.9996	-0.0023	37 - 53	1	108	ATTEEQKLIEDINVGFK
2246.2239	2245.2166	2245.2139	0.0027	124 - 145	0	---	VIAGALEVHAVKPVTEEPGMAK
2262.2192	2261.2119	2261.2088	0.0031	124 - 145	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2288	2350.2215	2350.2168	0.0048	101 - 123	1	---	AAVGATPEAKFDSFVASLTEALR

2351.2288	2350.2215	2350.2168	0.0048	101 - 123	1	119	AAVGATPEAKFDSFVASLTEALR
2427.2258	2426.2185	2426.2117	0.0068	163 - 186	1	---	VAATAAATAPADDKFTVFEAAFNK
3018.5769	3017.5696	3017.5416	0.0280	245 - 280	1	---	VSQPATGAATVAAGAATTAAGAASGAATVAAGGYKV

No match to: 713.3972, 734.4841, 750.5088, 768.5095, 782.4742, 1004.5108, 1070.5455, 1135.5984, 1175.5500, 1279.7509, 1291.6787, 1334.8665, 1371.7194, 1388.7405, 1448.9011, 1469.7822, 1487.8107, 1571.8846, 1638.8666, 1691.7775, 1762.9688, 1957.0104, 2011.0596, 2143.0444, 2205.2319, 2231.2188, 2564.1870, 2644.3696, 2644.3696, 2662.3875, 2666.3557, 2825.3245, 2908.4321, 2922.3618, 3040.5242, 3087.6294, 3339.7727, 3348.6101, 3404.8296

8. gi|28948464 **Mass:** 10653 **Score:** 173 **Expect:** 3e-012 **Queries matched:** 6

Chain A, Crystal Structure Of The Functional Domain Of The Major Grass Pollen Allergen Phl P 5b

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1087.5670	1086.5597	1086.5743	-0.0146	56 -	65	0	---	CIPSLEAAVK
1112.5851	1111.5778	1111.5913	-0.0135	80 -	89	0	---	YAVFEAALTK
1388.7405	1387.7332	1387.7459	-0.0127	66 -	79	0	---	QAYAATVAAAPQVK
1842.0338	1841.0265	1841.0298	-0.0032	1 -	17	1	---	IPAGELQIIDKIDAAFK
1842.0338	1841.0265	1841.0298	-0.0032	1 -	17	1	119	IPAGELQIIDKIDAAFK
2427.2258	2426.2185	2426.2117	0.0068	18 -	41	1	---	VAATAAATAPADDKFTVFEAAFNK

No match to: 713.3972, 734.4841, 750.5088, 768.5095, 782.4742, 1004.5108, 1070.5455, 1100.5486, 1135.5984, 1147.6316, 1175.5500, 1191.5085, 1279.7509, 1291.6787, 1334.8665, 1371.7194, 1448.9011, 1455.7511, 1455.7511, 1469.7822, 1487.8107, 1503.7347, 1571.8846, 1638.8666, 1691.7775, 1762.9688, 1935.0046, 1935.0046, 1957.0104, 2011.0596, 2143.0444, 2205.2319, 2231.2188, 2246.2239, 2262.2192, 2351.2288, 2351.2288, 2564.1870, 2644.3696, 2644.3696, 2662.3875, 2666.3557, 2825.3245, 2908.4321, 2922.3618, 3018.5769, 3040.5242, 3087.6294, 3339.7727, 3348.6101, 3404.8296

9. gi|11991229 **Mass:** 29216 **Score:** 145 **Expect:** 1.9e-009 **Queries matched:** 7

pollen allergen Hol l 5b [Holcus lanatus]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1191.5085	1190.5012	1190.5091	-0.0079	206 -	216	0	---	ESTGGAYDTYK
1455.7511	1454.7438	1454.7881	-0.0442	63 -	78	1	---	AAVAAAAGAPPADKFK
1455.7511	1454.7438	1454.7881	-0.0442	63 -	78	1	---	AAVAAAAGAPPADKFK
1842.0338	1841.0265	1841.0298	-0.0032	162 -	178	1	---	IPAGELQIIDKIDAAFK
1842.0338	1841.0265	1841.0298	-0.0032	162 -	178	1	119	IPAGELQIIDKIDAAFK
2644.3696	2643.3623	2643.2492	0.1131	193 -	216	1	---	FTVFEAAFNNAIKESTGGAYDTYK
2644.3696	2643.3623	2643.2492	0.1131	193 -	216	1	---	FTVFEAAFNNAIKESTGGAYDTYK

No match to: 713.3972, 734.4841, 750.5088, 768.5095, 782.4742, 1004.5108, 1070.5455, 1087.5670, 1100.5486, 1112.5851, 1135.5984, 1147.6316, 1175.5500, 1279.7509, 1291.6787, 1334.8665, 1371.7194, 1388.7405, 1448.9011, 1469.7822, 1487.8107, 1503.7347, 1571.8846, 1638.8666, 1691.7775, 1762.9688, 1935.0046, 1935.0046, 1957.0104, 2011.0596, 2143.0444, 2205.2319, 2231.2188, 2246.2239, 2262.2192, 2351.2288, 2351.2288, 2427.2258, 2564.1870, 2662.3875, 2666.3557, 2825.3245, 2908.4321, 2922.3618, 3018.5769, 3040.5242, 3087.6294, 3339.7727, 3348.6101, 3404.8296

10. gi|224058437 **Mass:** 54253 **Score:** 55 **Expect:** 2 **Queries matched:** 10

predicted protein [Populus trichocarpa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide

1004.5108	1003.5035	1003.5702	-0.0667	257 - 265	0	---	LFTPSLAQK
1371.7194	1370.7121	1370.6353	0.0768	266 - 276	0	---	YEELYQENGVK
1455.7511	1454.7438	1454.7187	0.0251	174 - 187	0	---	YGTLIVATGCSASR
1455.7511	1454.7438	1454.7187	0.0251	174 - 187	0	---	YGTLIVATGCSASR
1957.0104	1956.0031	1955.9774	0.0257	174 - 191	1	---	YGTLIVATGCSASRFPEK
2351.2288	2350.2215	2350.2507	-0.0291	343 - 364	1	---	TGIPGIFAIGDVAAFPLKMYNR
2351.2288	2350.2215	2350.2507	-0.0291	343 - 364	1	---	TGIPGIFAIGDVAAFPLKMYNR
2427.2258	2426.2185	2426.3143	-0.0957	218 - 241	1	---	AHKLVIVGGGYIGMEVAAAAVAWK + Oxidation (M)
2825.3245	2824.3172	2824.4051	-0.0879	145 - 170	1	---	GIEMLYEDPVTGIDIEKQTATTISGK + Oxidation (M)
3348.6101	3347.6028	3347.5774	0.0254	384 - 411	1	---	SLLTAHTSSYDYLPYFYSRVFEYEGSPR

No match to: 713.3972, 734.4841, 750.5088, 768.5095, 782.4742, 1070.5455, 1087.5670, 1100.5486, 1112.5851, 1135.5984, 1147.6316, 1175.5500, 1191.5085, 1279.7509, 1291.6787, 1334.8665, 1388.7405, 1448.9011, 1469.7822, 1487.8107, 1503.7347, 1571.8846, 1638.8666, 1691.7775, 1762.9688, 1842.0338, 1842.0338, 1935.0046, 1935.0046, 2011.0596, 2143.0444, 2205.2319, 2231.2188, 2246.2239, 2262.2192, 2564.1870, 2644.3696, 2644.3696, 2662.3875, 2666.3557, 2908.4321, 2922.3618, 3018.5769, 3040.5242, 3087.6294, 3339.7727, 3404.8296

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 57

Protein View

Match to: **gi|3309043** Score: **639** Expect: **7.6e-059**
group V allergen Phl p 5.0204 [Phleum pratense]

Nominal mass (M_r): **26252**; Calculated pI value: **5.61**
NCBI BLAST search of gi|3309043 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **87%**

Matched peptides shown in **Bold Red**

```
    1 ADAGYAPATP AAAGAEAGKA TTEEQKLIED INVGFKAAVA AAASVPAADK
   51 FKTFEAAFTS SSKAATAKAP GLVPKLDAAY SVAYKAAVGA TPEAKFDSFV
  101 ASLTEALRVI AGALEVHAVK PVTEEPGMAK IPAGELQIID KIDAAFKVAA
  151 TAAATAPADD KFTVFEAAFN KAIKESTGGA YDTYKCIPSL EAAVKQAYAA
  201 TVAAAPQVKY AVFEAALTKA ITAMSEVQKV SQPATGAATV AAGAATTAAG
  251 AASGAATVAA GGYKV
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
20 - 36	1935.0046	1933.9973	1933.9996	-0.0023	1	ATTEEQKLIEDINVGFK (No match)
20 - 36	1935.0046	1933.9973	1933.9996	-0.0023	1	ATTEEQKLIEDINVGFK (Ions score 108)
27 - 36	1147.6316	1146.6243	1146.6284	-0.0041	0	LIEDINVGFK (No match)
37 - 52	1487.8107	1486.8034	1486.8143	-0.0109	1	AAVAAAASVPAADKFK (No match)
53 - 63	1175.5500	1174.5427	1174.5506	-0.0078	0	TFEAAFTSSSK (No match)
69 - 85	1762.9688	1761.9615	1761.9664	-0.0049	1	APGLVPKLDAAYSVAYK (No match)
76 - 85	1100.5486	1099.5413	1099.5549	-0.0136	0	LDAAYSVAYK (No match)
86 - 108	2351.2288	2350.2215	2350.2168	0.0048	1	AAVGATPEAKFDSFVASLTEALR (No match)
86 - 108	2351.2288	2350.2215	2350.2168	0.0048	1	AAVGATPEAKFDSFVASLTEALR (Ions score 119)
96 - 108	1455.7511	1454.7438	1454.7405	0.0033	0	FDSFVASLTEALR (No match)
96 - 108	1455.7511	1454.7438	1454.7405	0.0033	0	FDSFVASLTEALR (Ions score 85)
109 - 130	2246.2239	2245.2166	2245.2139	0.0027	0	VIAGALEVHAVKPVTEEPGMAK (No match)
109 - 130	2262.2192	2261.2119	2261.2088	0.0031	0	VIAGALEVHAVKPVTEEPGMAK Oxidation (M) (No match)
131 - 147	1842.0338	1841.0265	1841.0298	-0.0032	1	IPAGELQIIDKIDAAFK (No match)
131 - 147	1842.0338	1841.0265	1841.0298	-0.0032	1	IPAGELQIIDKIDAAFK (Ions score 119)
148 - 171	2427.2258	2426.2185	2426.2117	0.0068	1	VAATAAATAPADDKFTVFEAAFNK (No match)

172 - 185	**1503.7347**	**1502.7274**	**1502.7252**	**0.0022**	**1**	**AIKESTGGAYDTYK** (No match)
175 - 185	**1191.5085**	**1190.5012**	**1190.5091**	**-0.0079**	**0**	**ESTGGAYDTYK** (No match)
186 - 195	**1087.5670**	**1086.5597**	**1086.5743**	**-0.0146**	**0**	**CIPSLEAAVK** (No match)
196 - 209	**1388.7405**	**1387.7332**	**1387.7459**	**-0.0127**	**0**	**QAYAATVAAAPQVK** (No match)
210 - 219	**1112.5851**	**1111.5778**	**1111.5913**	**-0.0135**	**0**	**YAVFEAALTK** (No match)
230 - 265	**3018.5769**	**3017.5696**	**3017.5416**	**0.0280**	**1**	**VSQPATGAATVAAGAATTAAGAASGAATVAAGGYKV** (No match)

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	Accession	Mass	Score	Description
1.	gi|3309043	26252	928	group V allergen Phl p 5.0204 [Phleum pratense]
2.	gi|2851457	28042	923	RecName: Full=Pollen allergen Phl p 5b; AltName: Full=Allergen Phl p Vb; AltName: Allergen=Phl p
3.	gi|3309041	29351	918	group V allergen Phl p 5.0203 precursor [Phleum pratense]
4.	gi|1684718	27903	883	major allergen Phl p 5 [Phleum pratense]
5.	gi|3309045	28869	877	group V allergen Phl p 5.0206 precursor [Phleum pratense]

Results List

1. gi|3309043 **Mass:** 26252 **Score:** 928 **Expect:** 9.6e-088 **Queries matched:** 26

group V allergen Phl p 5.0204 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1077.5546	1076.5473	1076.5536	-0.0062	220	229	0	---	AITAMSEVQK
1087.5743	1086.5670	1086.5743	-0.0073	186	195	0	---	CIPSLEAAVK
1093.5492	1092.5419	1092.5485	-0.0065	220	229	0	---	AITAMSEVQK + Oxidation (M)
1100.5569	1099.5496	1099.5549	-0.0053	76	85	0	---	LDAAYSVAYK
1112.5918	1111.5845	1111.5913	-0.0068	210	219	0	72	YAVFEAALTK
1112.5918	1111.5845	1111.5913	-0.0068	210	219	0	---	YAVFEAALTK
1147.6309	1146.6236	1146.6284	-0.0048	27	36	0	---	LIEDINVGFK
1175.5522	1174.5449	1174.5506	-0.0056	53	63	0	---	TFEAAFTSSSK
1191.5122	1190.5049	1190.5091	-0.0042	175	185	0	---	ESTGGAYDTYK
1388.7468	1387.7395	1387.7459	-0.0064	196	209	0	---	QAYAATVAAAPQVK
1450.7211	1449.7138	1449.7139	-0.0001	51	63	1	---	FKTFEAAFTSSSK
1455.7477	1454.7404	1454.7405	-0.0001	96	108	0	124	FDSFVASLTEALR
1455.7477	1454.7404	1454.7405	-0.0001	96	108	0	---	FDSFVASLTEALR
1487.8168	1486.8095	1486.8143	-0.0048	37	52	1	---	AAVAAAASVPAADKFK
1503.7284	1502.7211	1502.7252	-0.0041	172	185	1	---	AIKESTGGAYDTYK
1762.9708	1761.9635	1761.9664	-0.0029	69	85	1	---	APGLVPKLDAAYSVAYK
1842.0359	1841.0286	1841.0298	-0.0011	131	147	1	171	IPAGELQIIDKIDAAFK
1842.0359	1841.0286	1841.0298	-0.0011	131	147	1	---	IPAGELQIIDKIDAAFK
1935.0057	1933.9984	1933.9996	-0.0012	20	36	1	---	ATTEEQKLIEDINVGFK
1935.0057	1933.9984	1933.9996	-0.0012	20	36	1	150	ATTEEQKLIEDINVGFK
2246.2266	2245.2193	2245.2139	0.0054	109	130	0	---	VIAGALEVHAVKPVTEEPGMAK
2262.2263	2261.2190	2261.2088	0.0102	109	130	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2190	2350.2117	2350.2168	-0.0050	86	108	1	---	AAVGATPEAKFDSFVASLTEALR
2427.2322	2426.2249	2426.2117	0.0132	148	171	1	159	VAATAAATAPADDKFTVFEAAFNK
2427.2322	2426.2249	2426.2117	0.0132	148	171	1	---	VAATAAATAPADDKFTVFEAAFNK

3018.5952	3017.5879	3017.5416	0.0463	230 - 265	1	---	VSQPATGAATVAAGAATTAAGAASGAATVAAGGYKV

No match to: 713.4117, 736.5052, 750.5187, 768.5241, 1070.5498, 1279.7601, 1334.8713, 1371.7246, 1412.7679, 1438.2178, 1438.7498, 1448.9061, 1469.7628, 1691.7839, 2199.8716, 2205.2388, 2443.2139, 2479.1580, 2644.3789, 2662.3916, 2825.3384, 2920.5154, 2922.4004, 3349.6355, 3404.8350, 3607.8394, 3739.9097, 3809.8533

2. gi|2851457 **Mass:** 28042 **Score:** 923 **Expect:** 3e-087 **Queries matched:** 26

RecName: Full=Pollen allergen Phl p 5b; AltName: Full=Allergen Phl p Vb; AltName: Allergen=Phl p 5b

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1077.5546	1076.5473	1076.5536	-0.0062	239 -	248	0	---	AITAMSEVQK
1087.5743	1086.5670	1086.5743	-0.0073	205 -	214	0	---	CIPSLEAAVK
1093.5492	1092.5419	1092.5485	-0.0065	239 -	248	0	---	AITAMSEVQK + Oxidation (M)
1100.5569	1099.5496	1099.5549	-0.0053	95 -	104	0	---	LDAAYSVAYK
1112.5918	1111.5845	1111.5913	-0.0068	229 -	238	0	72	YAVFEAALTK
1112.5918	1111.5845	1111.5913	-0.0068	229 -	238	0	---	YAVFEAALTK
1147.6309	1146.6236	1146.6284	-0.0048	46 -	55	0	---	LIEDINVGFK
1175.5522	1174.5449	1174.5506	-0.0056	72 -	82	0	---	TFEAAFTSSSK
1191.5122	1190.5049	1190.5091	-0.0042	194 -	204	0	---	ESTGGAYDTYK
1388.7468	1387.7395	1387.7459	-0.0064	215 -	228	0	---	QAYAATVAAAPQVK
1450.7211	1449.7138	1449.7139	-0.0001	70 -	82	1	---	FKTFEAAFTSSSK
1455.7477	1454.7404	1454.7405	-0.0001	115 -	127	0	124	FDSFVASLTEALR
1455.7477	1454.7404	1454.7405	-0.0001	115 -	127	0	---	FDSFVASLTEALR
1487.8168	1486.8095	1486.8143	-0.0048	56 -	71	1	---	AAVAAAASVPAADKFK
1503.7284	1502.7211	1502.7252	-0.0041	191 -	204	1	---	AIKESTGGAYDTYK
1762.9708	1761.9635	1761.9664	-0.0029	88 -	104	1	---	APGLVPKLDAAYSVAYK
1842.0359	1841.0286	1841.0298	-0.0011	150 -	166	1	171	IPAGELQIIDKIDAAFK
1842.0359	1841.0286	1841.0298	-0.0011	150 -	166	1	---	IPAGELQIIDKIDAAFK
1935.0057	1933.9984	1933.9996	-0.0012	39 -	55	1	---	ATTEEQKLIEDINVGFK
1935.0057	1933.9984	1933.9996	-0.0012	39 -	55	1	150	ATTEEQKLIEDINVGFK
2246.2266	2245.2193	2245.2139	0.0054	128 -	149	0	---	VIAGALEVHAVKPVTEEPGMAK
2262.2263	2261.2190	2261.2088	0.0102	128 -	149	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2190	2350.2117	2350.2168	-0.0050	105 -	127	1	---	AAVGATPEAKFDSFVASLTEALR
2427.2322	2426.2249	2426.2117	0.0132	167 -	190	1	159	VAATAAATAPADDKFTVFEAAFNK
2427.2322	2426.2249	2426.2117	0.0132	167 -	190	1	---	VAATAAATAPADDKFTVFEAAFNK
3018.5952	3017.5879	3017.5416	0.0463	249 -	284	1	---	VSQPATGAATVAAGAATTAAGAASGAATVAAGGYKV

No match to: 713.4117, 736.5052, 750.5187, 768.5241, 1070.5498, 1279.7601, 1334.8713, 1371.7246, 1412.7679, 1438.2178, 1438.7498, 1448.9061, 1469.7628, 1691.7839, 2199.8716, 2205.2388, 2443.2139, 2479.1580, 2644.3789, 2662.3916, 2825.3384, 2920.5154, 2922.4004, 3349.6355, 3404.8350, 3607.8394, 3739.9097, 3809.8533

3. gi|3309041 **Mass:** 29351 **Score:** 918 **Expect:** 9.6e-087 **Queries matched:** 26

group V allergen Phl p 5.0203 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1077.5546	1076.5473	1076.5536	-0.0062	250 -	259	0	---	AITAMSEVQK

1087.5743	1086.5670	1086.5743	-0.0073	216 - 225	0	---	CIPSLEAAVK
1093.5492	1092.5419	1092.5485	-0.0065	250 - 259	0	---	AITAMSEVQK + Oxidation (M)
1100.5569	1099.5496	1099.5549	-0.0053	106 - 115	0	---	LDAAYSVAYK
1112.5918	1111.5845	1111.5913	-0.0068	240 - 249	0	72	YAVFEAALTK
1112.5918	1111.5845	1111.5913	-0.0068	240 - 249	0	---	YAVFEAALTK
1147.6309	1146.6236	1146.6284	-0.0048	57 - 66	0	---	LIEDINVGFK
1175.5522	1174.5449	1174.5506	-0.0056	83 - 93	0	---	TFEAAFTSSSK
1191.5122	1190.5049	1190.5091	-0.0042	205 - 215	0	---	ESTGGAYDTYK
1388.7468	1387.7395	1387.7459	-0.0064	226 - 239	0	---	QAYAATVAAAPQVK
1450.7211	1449.7138	1449.7139	-0.0001	81 - 93	1	---	FKTFEAAFTSSSK
1455.7477	1454.7404	1454.7405	-0.0001	126 - 138	0	124	FDSFVASLTEALR
1455.7477	1454.7404	1454.7405	-0.0001	126 - 138	0	---	FDSFVASLTEALR
1487.8168	1486.8095	1486.8143	-0.0048	67 - 82	1	---	AAVAAAASVPAADKFK
1503.7284	1502.7211	1502.7252	-0.0041	202 - 215	1	---	AIKESTGGAYDTYK
1762.9708	1761.9635	1761.9664	-0.0029	99 - 115	1	---	APGLVPKLDAAYSVAYK
1842.0359	1841.0286	1841.0298	-0.0011	161 - 177	1	171	IPAGELQIIDKIDAAFK
1842.0359	1841.0286	1841.0298	-0.0011	161 - 177	1	---	IPAGELQIIDKIDAAFK
1935.0057	1933.9984	1933.9996	-0.0012	50 - 66	1	---	ATTEEQKLIEDINVGFK
1935.0057	1933.9984	1933.9996	-0.0012	50 - 66	1	150	ATTEEQKLIEDINVGFK
2246.2266	2245.2193	2245.2139	0.0054	139 - 160	0	---	VIAGALEVHAVKPVTEEPGMAK
2262.2263	2261.2190	2261.2088	0.0102	139 - 160	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2190	2350.2117	2350.2168	-0.0050	116 - 138	1	---	AAVGATPEAKFDSFVASLTEALR
2427.2322	2426.2249	2426.2117	0.0132	178 - 201	1	159	VAATAAATAPADDKFTVFEAAFNK
2427.2322	2426.2249	2426.2117	0.0132	178 - 201	1	---	VAATAAATAPADDKFTVFEAAFNK
3018.5952	3017.5879	3017.5416	0.0463	260 - 295	1	---	VSQPATGAATVAAGAATTAAGAASGAATVAAGGYKV

No match to: 713.4117, 736.5052, 750.5187, 768.5241, 1070.5498, 1279.7601, 1334.8713, 1371.7246, 1412.7679, 1438.2178, 1438.7498, 1448.9061, 1469.7628, 1691.7839, 2199.8716, 2205.2388, 2443.2139, 2479.1580, 2644.3789, 2662.3916, 2825.3384, 2920.5154, 2922.4004, 3349.6355, 3404.8350, 3607.8394, 3739.9097, 3809.8533

4. gi|1684718 **Mass:** 27903 **Score:** 883 **Expect:** 3e-083 **Queries matched:** 24

major allergen Phl p 5 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start - End	Miss	Ions	Peptide
1077.5546	1076.5473	1076.5536	-0.0062	236 - 245	0	---	AITAMSEVQK
1087.5743	1086.5670	1086.5743	-0.0073	202 - 211	0	---	CIPSLEAAVK
1093.5492	1092.5419	1092.5485	-0.0065	236 - 245	0	---	AITAMSEVQK + Oxidation (M)
1100.5569	1099.5496	1099.5549	-0.0053	92 - 101	0	---	LDAAYSVAYK
1112.5918	1111.5845	1111.5913	-0.0068	226 - 235	0	72	YAVFEAALTK
1112.5918	1111.5845	1111.5913	-0.0068	226 - 235	0	---	YAVFEAALTK
1147.6309	1146.6236	1146.6284	-0.0048	43 - 52	0	---	LIEDINVGFK
1175.5522	1174.5449	1174.5506	-0.0056	69 - 79	0	---	TFEAAFTSSSK
1191.5122	1190.5049	1190.5091	-0.0042	191 - 201	0	---	ESTGGAYDTYK

1388.7468	1387.7395	1387.7459	-0.0064	212 - 225	0	---	QAYAATVAAAPQVK
1450.7211	1449.7138	1449.7139	-0.0001	67 - 79	1	---	FKTFEAAFTSSSK
1455.7477	1454.7404	1454.7405	-0.0001	112 - 124	0	124	FDSFVASLTEALR
1455.7477	1454.7404	1454.7405	-0.0001	112 - 124	0	---	FDSFVASLTEALR
1503.7284	1502.7211	1502.7252	-0.0041	188 - 201	1	---	AIKESTGGAYDTYK
1762.9708	1761.9635	1761.9664	-0.0029	85 - 101	1	---	APGLVPKLDAAYSVAYK
1842.0359	1841.0286	1841.0298	-0.0011	147 - 163	1	171	IPAGELQIIDKIDAAFK
1842.0359	1841.0286	1841.0298	-0.0011	147 - 163	1	---	IPAGELQIIDKIDAAFK
1935.0057	1933.9984	1933.9996	-0.0012	36 - 52	1	---	ATTEEQKLIEDINVGFK
1935.0057	1933.9984	1933.9996	-0.0012	36 - 52	1	150	ATTEEQKLIEDINVGFK
2246.2266	2245.2193	2245.2139	0.0054	125 - 146	0	---	VIAGALEVHAVKPVTEEPGMAK
2262.2263	2261.2190	2261.2088	0.0102	125 - 146	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2190	2350.2117	2350.2168	-0.0050	102 - 124	1	---	AAVGATPEAKFDSFVASLTEALR
2427.2322	2426.2249	2426.2117	0.0132	164 - 187	1	159	VAATAAATAPADDKFTVFEAAFNK
2427.2322	2426.2249	2426.2117	0.0132	164 - 187	1	---	VAATAAATAPADDKFTVFEAAFNK

No match to: 713.4117, 736.5052, 750.5187, 768.5241, 1070.5498, 1279.7601, 1334.8713, 1371.7246, 1412.7679, 1438.2178, 1438.7498, 1448.9061, 1469.7628, 1487.8168, 1691.7839, 2199.8716, 2205.2388, 2443.2139, 2479.1580, 2644.3789, 2662.3916, 2825.3384, 2920.5154, 2922.4004, 3018.5952, 3349.6355, 3404.8350, 3607.8394, 3739.9097, 3809.8533

5. gi|3309045 **Mass:** 28869 **Score:** 877 **Expect:** 1.2e-082 **Queries matched:** 23

group V allergen Phl p 5.0206 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1077.5546	1076.5473	1076.5536	-0.0062	245 - 254	0	---	AITAMSEVQK
1087.5743	1086.5670	1086.5743	-0.0073	211 - 220	0	---	CIPSLEAAVK
1093.5492	1092.5419	1092.5485	-0.0065	245 - 254	0	---	AITAMSEVQK + Oxidation (M)
1100.5569	1099.5496	1099.5549	-0.0053	101 - 110	0	---	LDAAYSVAYK
1112.5918	1111.5845	1111.5913	-0.0068	235 - 244	0	72	YAVFEAALTK
1112.5918	1111.5845	1111.5913	-0.0068	235 - 244	0	---	YAVFEAALTK
1147.6309	1146.6236	1146.6284	-0.0048	52 - 61	0	---	LIEDINVGFK
1175.5522	1174.5449	1174.5506	-0.0056	78 - 88	0	---	TFEAAFTSSSK
1191.5122	1190.5049	1190.5091	-0.0042	200 - 210	0	---	ESTGGAYDTYK
1388.7468	1387.7395	1387.7459	-0.0064	221 - 234	0	---	QAYAATVAAAPQVK
1450.7211	1449.7138	1449.7139	-0.0001	76 - 88	1	---	FKTFEAAFTSSSK
1455.7477	1454.7404	1454.7405	-0.0001	121 - 133	0	124	FDSFVASLTEALR
1455.7477	1454.7404	1454.7405	-0.0001	121 - 133	0	---	FDSFVASLTEALR
1487.8168	1486.8095	1486.8143	-0.0048	62 - 77	1	---	AAVAAAASVPAADKFK
1503.7284	1502.7211	1502.7252	-0.0041	197 - 210	1	---	AIKESTGGAYDTYK
1762.9708	1761.9635	1761.9664	-0.0029	94 - 110	1	---	APGLVPKLDAAYSVAYK
1842.0359	1841.0286	1841.0298	-0.0011	156 - 172	1	171	IPAGELQIIDKIDAAFK
1842.0359	1841.0286	1841.0298	-0.0011	156 - 172	1	---	IPAGELQIIDKIDAAFK

1935.0057	1933.9984	1933.9996	-0.0012	45 - 61	1	---	ATTEEQKLIEDINVGFK
1935.0057	1933.9984	1933.9996	-0.0012	45 - 61	1	150	ATTEEQKLIEDINVGFK
2351.2190	2350.2117	2350.2168	-0.0050	111 - 133	1	---	AAVGATPEAKFDSFVASLTEALR
2427.2322	2426.2249	2426.2117	0.0132	173 - 196	1	159	VAATAAATAPADDKFTVFEAAFNK
2427.2322	2426.2249	2426.2117	0.0132	173 - 196	1	---	VAATAAATAPADDKFTVFEAAFNK

No match to: 713.4117, 736.5052, 750.5187, 768.5241, 1070.5498, 1279.7601, 1334.8713, 1371.7246, 1412.7679, 1438.2178, 1438.7498, 1448.9061, 1469.7628, 1691.7839, 2199.8716, 2205.2388, 2246.2266, 2262.2263, 2443.2139, 2479.1580, 2644.3789, 2662.3916, 2825.3384, 2920.5154, 2922.4004, 3018.5952, 3349.6355, 3404.8350, 3607.8394, 3739.9097, 3809.8533

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 54

Protein View

Match to: **gi|3309043** Score: **928** Expect: **9.6e-088**
group V allergen Phl p 5.0204 [Phleum pratense]

Nominal mass (M_r): **26252;** Calculated pI value: **5.61**
NCBI BLAST search of gi|3309043 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **90%**

Matched peptides shown in **Bold Red**

```
    1 ADAGYAPATP AAAGAEAGKA TTEEQKLIED INVGFKAAVA AAASVPAADK
   51 FKTFEAAFTS SSKAATAKAP GLVPKLDAAY SVAYKAAVGA TPEAKFDSFV
  101 ASLTEALRVI AGALEVHAVK PVTEEPGMAK IPAGELQIID KIDAAFKVAA
  151 TAAATAPADD KFTVFEAAFN KAIKESTGGA YDTYKCIPSL EAAVKQAYAA
  201 TVAAAPQVKY AVFEAALTKA ITAMSEVQKV SQPATGAATV AAGAATTAAG
  251 AASGAATVAA GGYKV
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
20 - 36	1935.0057	1933.9984	1933.9996	-0.0012	1	**ATTEEQKLIEDINVGFK** (No match)
20 - 36	1935.0057	1933.9984	1933.9996	-0.0012	1	**ATTEEQKLIEDINVGFK** (Ions score 150)
27 - 36	1147.6309	1146.6236	1146.6284	-0.0048	0	**LIEDINVGFK** (No match)
37 - 52	1487.8168	1486.8095	1486.8143	-0.0048	1	**AAVAAAASVPAADKFK** (No match)
51 - 63	1450.7211	1449.7138	1449.7139	-0.0001	1	**FKTFEAAFTSSSK** (No match)
53 - 63	1175.5522	1174.5449	1174.5506	-0.0056	0	**TFEAAFTSSSK** (No match)
69 - 85	1762.9708	1761.9635	1761.9664	-0.0029	1	**APGLVPKLDAAYSVAYK** (No match)
76 - 85	1100.5569	1099.5496	1099.5549	-0.0053	0	**LDAAYSVAYK** (No match)
86 - 108	2351.2190	2350.2117	2350.2168	-0.0050	1	**AAVGATPEAKFDSFVASLTEALR** (No match)
96 - 108	1455.7477	1454.7404	1454.7405	-0.0001	0	**FDSFVASLTEALR** (Ions score 124)
96 - 108	1455.7477	1454.7404	1454.7405	-0.0001	0	**FDSFVASLTEALR** (No match)
109 - 130	2246.2266	2245.2193	2245.2139	0.0054	0	**VIAGALEVHAVKPVTEEPGMAK** (No match)
109 - 130	2262.2263	2261.2190	2261.2088	0.0102	0	**VIAGALEVHAVKPVTEEPGMAK** Oxidation (M) (No match)
131 - 147	1842.0359	1841.0286	1841.0298	-0.0011	1	**IPAGELQIIDKIDAAFK** (Ions score 171)
131 - 147	1842.0359	1841.0286	1841.0298	-0.0011	1	**IPAGELQIIDKIDAAFK** (No match)
148 - 171	2427.2322	2426.2249	2426.2117	0.0132	1	**VAATAAATAPADDKFTVFEAAFNK** (Ions score 159)
148 - 171	2427.2322	2426.2249	2426.2117	0.0132	1	**VAATAAATAPADDKFTVFEAAFNK** (No match)
172 - 185	1503.7284	1502.7211	1502.7252	-0.0041	1	**AIKESTGGAYDTYK** (No match)
175 - 185	1191.5122	1190.5049	1190.5091	-0.0042	0	**ESTGGAYDTYK** (No match)
186 - 195	1087.5743	1086.5670	1086.5743	-0.0073	0	**CIPSLEAAVK** (No match)
196 - 209	1388.7468	1387.7395	1387.7459	-0.0064	0	**QAYAATVAAAPQVK** (No match)
210 - 219	1112.5918	1111.5845	1111.5913	-0.0068	0	**YAVFEAALTK** (Ions score 72)
210 - 219	1112.5918	1111.5845	1111.5913	-0.0068	0	**YAVFEAALTK** (No match)
220 - 229	1077.5546	1076.5473	1076.5536	-0.0062	0	**AITAMSEVQK** (No match)
220 - 229	1093.5492	1092.5419	1092.5485	-0.0065	0	**AITAMSEVQK** Oxidation (M) (No match)
230 - 265	3018.5952	3017.5879	3017.5416	0.0463	1	**VSQPATGAATVAAGAATTAAGAASGAATVAAGGYKV** (No match)

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	Accession	Mass	Score	Description
1.	gi|3309043	26252	258	group V allergen Phl p 5.0204 [Phleum pratense]
2.	gi|1684718	27903	257	major allergen Phl p 5 [Phleum pratense]
3.	gi|2851457	28042	257	RecName: Full=Pollen allergen Phl p 5b; AltName: Full=Allergen Phl p Vb; AltName: Allergen=Phl
4.	gi|3309045	28869	257	group V allergen Phl p 5.0206 precursor [Phleum pratense]
5.	gi|3309041	29351	256	group V allergen Phl p 5.0203 precursor [Phleum pratense]
6.	gi|481397	28182	109	allergen Phl p Vb - common timothy
7.	gi|3309047	28384	109	group V allergen Phl p 5.0207 precursor [Phleum pratense]
8.	gi|28948464	10653	79	Chain A, Crystal Structure Of The Functional Domain Of The Major Grass Pollen Allergen Phl P 5b
9.	gi|2266623	24693	75	group V grass pollen allergen [Holcus lanatus]
10.	gi|14423120	26342	75	group 5 isoallergen 1 [Dactylis glomerata]

Results List

1. gi|3309043 **Mass:** 26252 **Score:** 258 **Expect:** 9.6e-021 **Queries matched:** 6

group V allergen Phl p 5.0204 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1112.5928	1111.5855	1111.5913	-0.0058	210	-	219	0	66	YAVFEAALTK
1112.5928	1111.5855	1111.5913	-0.0058	210	-	219	0	---	YAVFEAALTK
1762.9777	1761.9704	1761.9664	0.0040	69	-	85	1	---	APGLVPKLDAAYSVAYK
1762.9777	1761.9704	1761.9664	0.0040	69	-	85	1	131	APGLVPKLDAAYSVAYK
1935.0142	1934.0069	1933.9996	0.0073	20	-	36	1	---	ATTEEQKLIEDINVGFK
1935.0142	1934.0069	1933.9996	0.0073	20	-	36	1	20	ATTEEQKLIEDINVGFK

No match to: 713.4103, 768.5247, 1292.6829, 1607.8215, 1633.7937

2. gi|1684718 **Mass:** 27903 **Score:** 257 **Expect:** 1.2e-020 **Queries matched:** 6

major allergen Phl p 5 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1112.5928	1111.5855	1111.5913	-0.0058	226	-	235	0	66	YAVFEAALTK
1112.5928	1111.5855	1111.5913	-0.0058	226	-	235	0	---	YAVFEAALTK
1762.9777	1761.9704	1761.9664	0.0040	85	-	101	1	---	APGLVPKLDAAYSVAYK
1762.9777	1761.9704	1761.9664	0.0040	85	-	101	1	131	APGLVPKLDAAYSVAYK
1935.0142	1934.0069	1933.9996	0.0073	36	-	52	1	---	ATTEEQKLIEDINVGFK
1935.0142	1934.0069	1933.9996	0.0073	36	-	52	1	20	ATTEEQKLIEDINVGFK

No match to: 713.4103, 768.5247, 1292.6829, 1607.8215, 1633.7937

3. gi|2851457 **Mass:** 28042 **Score:** 257 **Expect:** 1.2e-020 **Queries matched:** 6

RecName: Full=Pollen allergen Phl p 5b; AltName: Full=Allergen Phl p Vb; AltName: Allergen=Phl p 5b

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide

1112.5928	1111.5855	1111.5913	-0.0058	229 - 238	0	66	YAVFEAALTK
1112.5928	1111.5855	1111.5913	-0.0058	229 - 238	0	---	YAVFEAALTK
1762.9777	1761.9704	1761.9664	0.0040	88 - 104	1	---	APGLVPKLDAAYSVAYK
1762.9777	1761.9704	1761.9664	0.0040	88 - 104	1	131	APGLVPKLDAAYSVAYK
1935.0142	1934.0069	1933.9996	0.0073	39 - 55	1	---	ATTEEQKLIEDINVGFK
1935.0142	1934.0069	1933.9996	0.0073	39 - 55	1	20	ATTEEQKLIEDINVGFK

No match to: 713.4103, 768.5247, 1292.6829, 1607.8215, 1633.7937

4. gi|3309045 **Mass:** 28869 **Score:** 257 **Expect:** 1.2e-020 **Queries matched:** 6

group V allergen Phl p 5.0206 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start - End	Miss	Ions	Peptide
1112.5928	1111.5855	1111.5913	-0.0058	235 - 244	0	66	YAVFEAALTK
1112.5928	1111.5855	1111.5913	-0.0058	235 - 244	0	---	YAVFEAALTK
1762.9777	1761.9704	1761.9664	0.0040	94 - 110	1	---	APGLVPKLDAAYSVAYK
1762.9777	1761.9704	1761.9664	0.0040	94 - 110	1	131	APGLVPKLDAAYSVAYK
1935.0142	1934.0069	1933.9996	0.0073	45 - 61	1	---	ATTEEQKLIEDINVGFK
1935.0142	1934.0069	1933.9996	0.0073	45 - 61	1	20	ATTEEQKLIEDINVGFK

No match to: 713.4103, 768.5247, 1292.6829, 1607.8215, 1633.7937

5. gi|3309041 **Mass:** 29351 **Score:** 256 **Expect:** 1.5e-020 **Queries matched:** 6

group V allergen Phl p 5.0203 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start - End	Miss	Ions	Peptide
1112.5928	1111.5855	1111.5913	-0.0058	240 - 249	0	66	YAVFEAALTK
1112.5928	1111.5855	1111.5913	-0.0058	240 - 249	0	---	YAVFEAALTK
1762.9777	1761.9704	1761.9664	0.0040	99 - 115	1	---	APGLVPKLDAAYSVAYK
1762.9777	1761.9704	1761.9664	0.0040	99 - 115	1	131	APGLVPKLDAAYSVAYK
1935.0142	1934.0069	1933.9996	0.0073	50 - 66	1	---	ATTEEQKLIEDINVGFK
1935.0142	1934.0069	1933.9996	0.0073	50 - 66	1	20	ATTEEQKLIEDINVGFK

No match to: 713.4103, 768.5247, 1292.6829, 1607.8215, 1633.7937

6. gi|481397 **Mass:** 28182 **Score:** 109 **Expect:** 7.6e-006 **Queries matched:** 4

allergen Phl p Vb - common timothy

Observed	Mr(expt)	Mr(calc)	Delta	Start - End	Miss	Ions	Peptide
1112.5928	1111.5855	1111.5913	-0.0058	225 - 234	0	66	YAVFEAALTK
1112.5928	1111.5855	1111.5913	-0.0058	225 - 234	0	---	YAVFEAALTK
1935.0142	1934.0069	1933.9996	0.0073	37 - 53	1	---	ATTEEQKLIEDINVGFK
1935.0142	1934.0069	1933.9996	0.0073	37 - 53	1	20	ATTEEQKLIEDINVGFK

No match to: 713.4103, 768.5247, 1292.6829, 1607.8215, 1633.7937, 1762.9777, 1762.9777

7. gi|3309047 **Mass:** 28384 **Score:** 109 **Expect:** 7.6e-006 **Queries matched:** 4

group V allergen Phl p 5.0207 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start - End	Miss	Ions	Peptide

1112.5928	1111.5855	1111.5913	-0.0058	232 - 241	0	66	YAVFEAALTK
1112.5928	1111.5855	1111.5913	-0.0058	232 - 241	0	---	YAVFEAALTK
1935.0142	1934.0069	1933.9996	0.0073	45 - 61	1	---	ATTEEQKLIEDINVGFK
1935.0142	1934.0069	1933.9996	0.0073	45 - 61	1	20	ATTEEQKLIEDINVGFK

No match to: 713.4103, 768.5247, 1292.6829, 1607.8215, 1633.7937, 1762.9777, 1762.9777

8. gi|28948464 **Mass:** 10653 **Score:** 79 **Expect:** 0.0083 **Queries matched:** 2

Chain A, Crystal Structure Of The Functional Domain Of The Major Grass Pollen Allergen Phl P 5b

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1112.5928	1111.5855	1111.5913	-0.0058	80 - 89		0	66	YAVFEAALTK
1112.5928	1111.5855	1111.5913	-0.0058	80 - 89		0	---	YAVFEAALTK

No match to: 713.4103, 768.5247, 1292.6829, 1607.8215, 1633.7937, 1762.9777, 1762.9777, 1935.0142, 1935.0142

9. gi|2266623 **Mass:** 24693 **Score:** 75 **Expect:** 0.018 **Queries matched:** 2

group V grass pollen allergen [Holcus lanatus]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1112.5928	1111.5855	1111.5913	-0.0058	193 - 202		0	66	YAVFEAALTK
1112.5928	1111.5855	1111.5913	-0.0058	193 - 202		0	---	YAVFEAALTK

No match to: 713.4103, 768.5247, 1292.6829, 1607.8215, 1633.7937, 1762.9777, 1762.9777, 1935.0142, 1935.0142

10. gi|14423120 **Mass:** 26342 **Score:** 75 **Expect:** 0.02 **Queries matched:** 2

group 5 isoallergen 1 [Dactylis glomerata]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1112.5928	1111.5855	1111.5913	-0.0058	214 - 223		0	66	YAVFEAALTK
1112.5928	1111.5855	1111.5913	-0.0058	214 - 223		0	---	YAVFEAALTK

No match to: 713.4103, 768.5247, 1292.6829, 1607.8215, 1633.7937, 1762.9777, 1762.9777, 1935.0142, 1935.0142

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 11

Protein View

Match to: **gi|3309043** Score: **258** Expect: **9.6e-021**
group V allergen Phl p 5.0204 [Phleum pratense]

Nominal mass (M_r): **26252**; Calculated pI value: **5.61**
NCBI BLAST search of gi|3309043 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

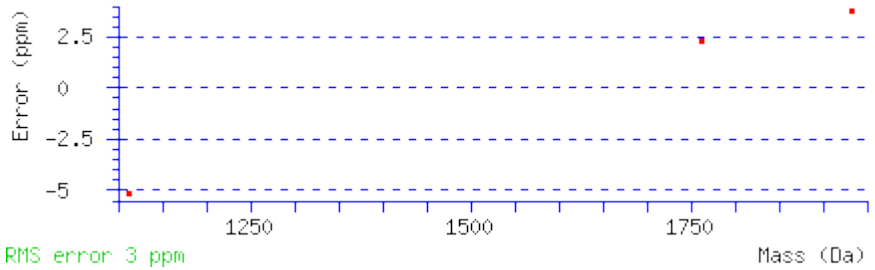
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **16%**

Matched peptides shown in **Bold Red**

```
   1 ADAGYAPATP AAAGAEAGKA TTEEQKLIED INVGFKAAVA AAASVPAADK
  51 FKTFEAAFTS SSKAATAKAP GLVPKLDAAY SVAYKAAVGA TPEAKFDSFV
 101 ASLTEALRVI AGALEVHAVK PVTEEPGMAK IPAGELQIID KIDAAFKVAA
 151 TAAATAPADD KFTVFEAAFN KAIKESTGGA YDTYKCIPSL EAAVKQAYAA
 201 TVAAAPQVKY AVFEAALTKA ITAMSEVQKV SQPATGAATV AAGAATTAAG
 251 AASGAATVAA GGYKV
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
20 - 36	1935.0142	1934.0069	1933.9996	0.0073	1	ATTEEQKLIEDINVGFK	(No match)
20 - 36	1935.0142	1934.0069	1933.9996	0.0073	1	ATTEEQKLIEDINVGFK	(Ions score 20)
69 - 85	1762.9777	1761.9704	1761.9664	0.0040	1	APGLVPKLDAAYSVAYK	(No match)
69 - 85	1762.9777	1761.9704	1761.9664	0.0040	1	APGLVPKLDAAYSVAYK	(Ions score 131)
210 - 219	1112.5928	1111.5855	1111.5913	-0.0058	0	YAVFEAALTK	(Ions score 66)
210 - 219	1112.5928	1111.5855	1111.5913	-0.0058	0	YAVFEAALTK	(No match)



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	Accession	Mass	Score	Description
1.	gi|2851457	28042	255	RecName: Full=Pollen allergen Phl p 5b; AltName: Full=Allergen Phl p Vb; AltName: Allergen=Phl
2.	gi|3309043	26252	244	group V allergen Phl p 5.0204 [Phleum pratense]
3.	gi|1684718	27903	241	major allergen Phl p 5 [Phleum pratense]
4.	gi|3309041	29351	238	group V allergen Phl p 5.0203 precursor [Phleum pratense]
5.	gi|481397	28182	229	allergen Phl p Vb - common timothy
6.	gi|3309045	28869	225	group V allergen Phl p 5.0206 precursor [Phleum pratense]
7.	gi|3309047	28384	212	group V allergen Phl p 5.0207 precursor [Phleum pratense]
8.	gi|28948464	10653	102	Chain A, Crystal Structure Of The Functional Domain Of The Major Grass Pollen Allergen Phl P 5
9.	gi|2266623	24693	65	group V grass pollen allergen [Holcus lanatus]
10.	gi|159467643	91431	60	predicted protein [Chlamydomonas reinhardtii]

Results List

1. gi|2851457 **Mass:** 28042 **Score:** 255 **Expect:** 1.9e-020 **Queries matched:** 17

RecName: Full=Pollen allergen Phl p 5b; AltName: Full=Allergen Phl p Vb; AltName: Allergen=Phl p 5b

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1087.5686	1086.5613	1086.5743	-0.0130	205	214	0	---	CIPSLEAAVK
1112.5883	1111.5810	1111.5913	-0.0103	229	238	0	---	YAVFEAALTK
1112.5883	1111.5810	1111.5913	-0.0103	229	238	0	50	YAVFEAALTK
1388.7413	1387.7340	1387.7459	-0.0119	215	228	0	---	QAYAATVAAAPQVK
1455.7559	1454.7486	1454.7405	0.0081	115	127	0	19	FDSFVASLTEALR
1455.7559	1454.7486	1454.7405	0.0081	115	127	0	---	FDSFVASLTEALR
1503.7390	1502.7317	1502.7252	0.0065	191	204	1	---	AIKESTGGAYDTYK
1762.9752	1761.9679	1761.9664	0.0015	88	104	1	---	APGLVPKLDAAYSVAYK
1842.0369	1841.0296	1841.0298	-0.0001	150	166	1	---	IPAGELQIIDKIDAAFK
1935.0068	1933.9995	1933.9996	-0.0001	39	55	1	39	ATTEEQKLIEDINVGFK
1935.0068	1933.9995	1933.9996	-0.0001	39	55	1	---	ATTEEQKLIEDINVGFK
1952.9865	1951.9792	1951.9275	0.0517	17	38	0	---	SYTADAGYAPATPAAAGAAAGK
2246.2188	2245.2115	2245.2139	-0.0024	128	149	0	---	VIAGALEVHAVKPVTEEPGMAK
2262.2065	2261.1992	2261.2088	-0.0096	128	149	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2271	2350.2198	2350.2168	0.0031	105	127	1	27	AAVGATPEAKFDSFVASLTEALR
2351.2271	2350.2198	2350.2168	0.0031	105	127	1	---	AAVGATPEAKFDSFVASLTEALR
2427.2180	2426.2107	2426.2117	-0.0010	167	190	1	---	VAATAAATAPADDKFTVFEAAFNK

No match to: 713.4021, 724.4802, 734.4965, 750.5103, 768.5143, 782.4732, 838.5202, 845.0931, 854.0439, 864.5125, 881.2834, 886.9861, 1134.6056, 1176.6227, 1279.7474, 1291.6895, 1320.5994, 1334.8694, 1446.7947, 1448.8540, 1525.7544, 1571.8801, 1615.8718, 1633.8181, 1646.9309, 1707.7874, 1827.8575, 1957.0007, 2056.0417, 2152.1138, 2175.2144, 2203.0588, 2231.2092, 2383.9692, 2400.0342, 2565.1919, 2644.3660, 2644.3660, 2666.3528, 2824.3076, 2908.4368, 2923.3738, 3333.5613, 3351.5847

2. gi|3309043 **Mass:** 26252 **Score:** 244 **Expect:** 2.4e-019 **Queries matched:** 16

group V allergen Phl p 5.0204 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1087.5686	1086.5613	1086.5743	-0.0130	186	195	0	---	CIPSLEAAVK
1112.5883	1111.5810	1111.5913	-0.0103	210	219	0	---	YAVFEAALTK
1112.5883	1111.5810	1111.5913	-0.0103	210	219	0	50	YAVFEAALTK
1388.7413	1387.7340	1387.7459	-0.0119	196	209	0	---	QAYAATVAAAPQVK
1455.7559	1454.7486	1454.7405	0.0081	96	108	0	19	FDSFVASLTEALR
1455.7559	1454.7486	1454.7405	0.0081	96	108	0	---	FDSFVASLTEALR
1503.7390	1502.7317	1502.7252	0.0065	172	185	1	---	AIKESTGGAYDTYK
1762.9752	1761.9679	1761.9664	0.0015	69	85	1	---	APGLVPKLDAAYSVAYK
1842.0369	1841.0296	1841.0298	-0.0001	131	147	1	---	IPAGELQIIDKIDAAFK
1935.0068	1933.9995	1933.9996	-0.0001	20	36	1	39	ATTEEQKLIEDINVGFK
1935.0068	1933.9995	1933.9996	-0.0001	20	36	1	---	ATTEEQKLIEDINVGFK
2246.2188	2245.2115	2245.2139	-0.0024	109	130	0	---	VIAGALEVHAVKPVTEEPGMAK
2262.2065	2261.1992	2261.2088	-0.0096	109	130	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2271	2350.2198	2350.2168	0.0031	86	108	1	27	AAVGATPEAKFDSFVASLTEALR
2351.2271	2350.2198	2350.2168	0.0031	86	108	1	---	AAVGATPEAKFDSFVASLTEALR
2427.2180	2426.2107	2426.2117	-0.0010	148	171	1	---	VAATAAATAPADDKFTVFEAAFNK

No match to: 713.4021, 724.4802, 734.4965, 750.5103, 768.5143, 782.4732, 838.5202, 845.0931, 854.0439, 864.5125, 881.2834, 886.9861, 1134.6056, 1176.6227, 1279.7474, 1291.6895, 1320.5994, 1334.8694, 1446.7947, 1448.8540, 1525.7544, 1571.8801, 1615.8718, 1633.8181, 1646.9309, 1707.7874, 1827.8575, 1952.9865, 1957.0007, 2056.0417, 2152.1138, 2175.2144, 2203.0588, 2231.2092, 2383.9692, 2400.0342, 2565.1919, 2644.3660, 2644.3660, 2666.3528, 2824.3076, 2908.4368, 2923.3738, 3333.5613, 3351.5847

3. gi|1684718 **Mass:** 27903 **Score:** 241 **Expect:** 4.8e-019 **Queries matched:** 16

major allergen Phl p 5 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1087.5686	1086.5613	1086.5743	-0.0130	202	211	0	---	CIPSLEAAVK
1112.5883	1111.5810	1111.5913	-0.0103	226	235	0	---	YAVFEAALTK
1112.5883	1111.5810	1111.5913	-0.0103	226	235	0	50	YAVFEAALTK
1388.7413	1387.7340	1387.7459	-0.0119	212	225	0	---	QAYAATVAAAPQVK
1455.7559	1454.7486	1454.7405	0.0081	112	124	0	19	FDSFVASLTEALR
1455.7559	1454.7486	1454.7405	0.0081	112	124	0	---	FDSFVASLTEALR
1503.7390	1502.7317	1502.7252	0.0065	188	201	1	---	AIKESTGGAYDTYK
1762.9752	1761.9679	1761.9664	0.0015	85	101	1	---	APGLVPKLDAAYSVAYK
1842.0369	1841.0296	1841.0298	-0.0001	147	163	1	---	IPAGELQIIDKIDAAFK
1935.0068	1933.9995	1933.9996	-0.0001	36	52	1	39	ATTEEQKLIEDINVGFK
1935.0068	1933.9995	1933.9996	-0.0001	36	52	1	---	ATTEEQKLIEDINVGFK
2246.2188	2245.2115	2245.2139	-0.0024	125	146	0	---	VIAGALEVHAVKPVTEEPGMAK
2262.2065	2261.1992	2261.2088	-0.0096	125	146	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)

2351.2271	2350.2198	2350.2168	0.0031	102 - 124	1	27	AAVGATPEAKFDSFVASLTEALR
2351.2271	2350.2198	2350.2168	0.0031	102 - 124	1	---	AAVGATPEAKFDSFVASLTEALR
2427.2180	2426.2107	2426.2117	-0.0010	164 - 187	1	---	VAATAAATAPADDKFTVFEAAFNK

No match to: 713.4021, 724.4802, 734.4965, 750.5103, 768.5143, 782.4732, 838.5202, 845.0931, 854.0439, 864.5125, 881.2834, 886.9861, 1134.6056, 1176.6227, 1279.7474, 1291.6895, 1320.5994, 1334.8694, 1446.7947, 1448.8540, 1525.7544, 1571.8801, 1615.8718, 1633.8181, 1646.9309, 1707.7874, 1827.8575, 1952.9865, 1957.0007, 2056.0417, 2152.1138, 2175.2144, 2203.0588, 2231.2092, 2383.9692, 2400.0342, 2565.1919, 2644.3660, 2644.3660, 2666.3528, 2824.3076, 2908.4368, 2923.3738, 3333.5613, 3351.5847

4. gi|3309041 **Mass:** 29351 **Score:** 238 **Expect:** 9.6e-019 **Queries matched:** 16

group V allergen Phl p 5.0203 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1087.5686	1086.5613	1086.5743	-0.0130	216 - 225		0	---	CIPSLEAAVK
1112.5883	1111.5810	1111.5913	-0.0103	240 - 249		0	---	YAVFEAALTK
1112.5883	1111.5810	1111.5913	-0.0103	240 - 249		0	50	YAVFEAALTK
1388.7413	1387.7340	1387.7459	-0.0119	226 - 239		0	---	QAYAATVAAAPQVK
1455.7559	1454.7486	1454.7405	0.0081	126 - 138		0	19	FDSFVASLTEALR
1455.7559	1454.7486	1454.7405	0.0081	126 - 138		0	---	FDSFVASLTEALR
1503.7390	1502.7317	1502.7252	0.0065	202 - 215		1	---	AIKESTGGAYDTYK
1762.9752	1761.9679	1761.9664	0.0015	99 - 115		1	---	APGLVPKLDAAYSVAYK
1842.0369	1841.0296	1841.0298	-0.0001	161 - 177		1	---	IPAGELQIIDKIDAAFK
1935.0068	1933.9995	1933.9996	-0.0001	50 - 66		1	39	ATTEEQKLIEDINVGFK
1935.0068	1933.9995	1933.9996	-0.0001	50 - 66		1	---	ATTEEQKLIEDINVGFK
2246.2188	2245.2115	2245.2139	-0.0024	139 - 160		0	---	VIAGALEVHAVKPVTEEPGMAK
2262.2065	2261.1992	2261.2088	-0.0096	139 - 160		0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2271	2350.2198	2350.2168	0.0031	116 - 138		1	27	AAVGATPEAKFDSFVASLTEALR
2351.2271	2350.2198	2350.2168	0.0031	116 - 138		1	---	AAVGATPEAKFDSFVASLTEALR
2427.2180	2426.2107	2426.2117	-0.0010	178 - 201		1	---	VAATAAATAPADDKFTVFEAAFNK

No match to: 713.4021, 724.4802, 734.4965, 750.5103, 768.5143, 782.4732, 838.5202, 845.0931, 854.0439, 864.5125, 881.2834, 886.9861, 1134.6056, 1176.6227, 1279.7474, 1291.6895, 1320.5994, 1334.8694, 1446.7947, 1448.8540, 1525.7544, 1571.8801, 1615.8718, 1633.8181, 1646.9309, 1707.7874, 1827.8575, 1952.9865, 1957.0007, 2056.0417, 2152.1138, 2175.2144, 2203.0588, 2231.2092, 2383.9692, 2400.0342, 2565.1919, 2644.3660, 2644.3660, 2666.3528, 2824.3076, 2908.4368, 2923.3738, 3333.5613, 3351.5847

5. gi|481397 **Mass:** 28182 **Score:** 229 **Expect:** 7.6e-018 **Queries matched:** 15

allergen Phl p Vb - common timothy

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1087.5686	1086.5613	1086.5743	-0.0130	201 - 210		0	---	CIPSLEAAVK
1112.5883	1111.5810	1111.5913	-0.0103	225 - 234		0	---	YAVFEAALTK
1112.5883	1111.5810	1111.5913	-0.0103	225 - 234		0	50	YAVFEAALTK
1455.7559	1454.7486	1454.7405	0.0081	111 - 123		0	19	FDSFVASLTEALR
1455.7559	1454.7486	1454.7405	0.0081	111 - 123		0	---	FDSFVASLTEALR
1503.7390	1502.7317	1502.7252	0.0065	187 - 200		1	---	AIKESTGGAYDTYK

1842.0369	1841.0296	1841.0298	-0.0001	146 - 162	1	---	IPAGELQIIDKIDAAFK
1935.0068	1933.9995	1933.9996	-0.0001	37 - 53	1	39	ATTEEQKLIEDINVGFK
1935.0068	1933.9995	1933.9996	-0.0001	37 - 53	1	---	ATTEEQKLIEDINVGFK
1952.9865	1951.9792	1951.9275	0.0517	15 - 36	0	---	SYTADAGYAPATPAAAGAAAGK
2246.2188	2245.2115	2245.2139	-0.0024	124 - 145	0	---	VIAGALEVHAVKPVTEEPGMAK
2262.2065	2261.1992	2261.2088	-0.0096	124 - 145	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2271	2350.2198	2350.2168	0.0031	101 - 123	1	27	AAVGATPEAKFDSFVASLTEALR
2351.2271	2350.2198	2350.2168	0.0031	101 - 123	1	---	AAVGATPEAKFDSFVASLTEALR
2427.2180	2426.2107	2426.2117	-0.0010	163 - 186	1	---	VAATAAATAPADDKFTVFEAAFNK

No match to: 713.4021, 724.4802, 734.4965, 750.5103, 768.5143, 782.4732, 838.5202, 845.0931, 854.0439, 864.5125, 881.2834, 886.9861, 1134.6056, 1176.6227, 1279.7474, 1291.6895, 1320.5994, 1334.8694, 1388.7413, 1446.7947, 1448.8540, 1525.7544, 1571.8801, 1615.8718, 1633.8181, 1646.9309, 1707.7874, 1762.9752, 1827.8575, 1957.0007, 2056.0417, 2152.1138, 2175.2144, 2203.0588, 2231.2092, 2383.9692, 2400.0342, 2565.1919, 2644.3660, 2644.3660, 2666.3528, 2824.3076, 2908.4368, 2923.3738, 3333.5613, 3351.5847

6. gi|3309045 **Mass:** 28869 **Score:** 225 **Expect:** 1.9e-017 **Queries matched:** 14

group V allergen Phl p 5.0206 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1087.5686	1086.5613	1086.5743	-0.0130	211 - 220	0	---	CIPSLEAAVK
1112.5883	1111.5810	1111.5913	-0.0103	235 - 244	0	---	YAVFEAALTK
1112.5883	1111.5810	1111.5913	-0.0103	235 - 244	0	50	YAVFEAALTK
1388.7413	1387.7340	1387.7459	-0.0119	221 - 234	0	---	QAYAATVAAAPQVK
1455.7559	1454.7486	1454.7405	0.0081	121 - 133	0	19	FDSFVASLTEALR
1455.7559	1454.7486	1454.7405	0.0081	121 - 133	0	---	FDSFVASLTEALR
1503.7390	1502.7317	1502.7252	0.0065	197 - 210	1	---	AIKESTGGAYDTYK
1762.9752	1761.9679	1761.9664	0.0015	94 - 110	1	---	APGLVPKLDAAYSVAYK
1842.0369	1841.0296	1841.0298	-0.0001	156 - 172	1	---	IPAGELQIIDKIDAAFK
1935.0068	1933.9995	1933.9996	-0.0001	45 - 61	1	39	ATTEEQKLIEDINVGFK
1935.0068	1933.9995	1933.9996	-0.0001	45 - 61	1	---	ATTEEQKLIEDINVGFK
2351.2271	2350.2198	2350.2168	0.0031	111 - 133	1	27	AAVGATPEAKFDSFVASLTEALR
2351.2271	2350.2198	2350.2168	0.0031	111 - 133	1	---	AAVGATPEAKFDSFVASLTEALR
2427.2180	2426.2107	2426.2117	-0.0010	173 - 196	1	---	VAATAAATAPADDKFTVFEAAFNK

No match to: 713.4021, 724.4802, 734.4965, 750.5103, 768.5143, 782.4732, 838.5202, 845.0931, 854.0439, 864.5125, 881.2834, 886.9861, 1134.6056, 1176.6227, 1279.7474, 1291.6895, 1320.5994, 1334.8694, 1446.7947, 1448.8540, 1525.7544, 1571.8801, 1615.8718, 1633.8181, 1646.9309, 1707.7874, 1827.8575, 1952.9865, 1957.0007, 2056.0417, 2152.1138, 2175.2144, 2203.0588, 2231.2092, 2246.2188, 2262.2065, 2383.9692, 2400.0342, 2565.1919, 2644.3660, 2644.3660, 2666.3528, 2824.3076, 2908.4368, 2923.3738, 3333.5613, 3351.5847

7. gi|3309047 **Mass:** 28384 **Score:** 212 **Expect:** 3.8e-016 **Queries matched:** 14

group V allergen Phl p 5.0207 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1087.5686	1086.5613	1086.5743	-0.0130	208 - 217	0	---	CIPSLEAAVK
1112.5883	1111.5810	1111.5913	-0.0103	232 - 241	0	---	YAVFEAALTK

1112.5883	1111.5810	1111.5913	-0.0103	232 - 241	0	50	YAVFEAALTK
1388.7413	1387.7340	1387.7459	-0.0119	218 - 231	0	---	QAYAATVAAAPQVK
1455.7559	1454.7486	1454.7405	0.0081	121 - 133	0	19	FDSFVASLTEALR
1455.7559	1454.7486	1454.7405	0.0081	121 - 133	0	---	FDSFVASLTEALR
1503.7390	1502.7317	1502.7252	0.0065	194 - 207	1	---	AIKESTGGAYDTYK
1842.0369	1841.0296	1841.0298	-0.0001	156 - 172	1	---	IPAGELQIIDKIDAAFK
1935.0068	1933.9995	1933.9996	-0.0001	45 - 61	1	39	ATTEEQKLIEDINVGFK
1935.0068	1933.9995	1933.9996	-0.0001	45 - 61	1	---	ATTEEQKLIEDINVGFK
2246.2188	2245.2115	2245.2139	-0.0024	134 - 155	0	---	VIAGALEVHAVKPVTEEPGMAK
2262.2065	2261.1992	2261.2088	-0.0096	134 - 155	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2271	2350.2198	2350.2168	0.0031	111 - 133	1	27	AAVGATPEAKFDSFVASLTEALR
2351.2271	2350.2198	2350.2168	0.0031	111 - 133	1	---	AAVGATPEAKFDSFVASLTEALR

No match to: 713.4021, 724.4802, 734.4965, 750.5103, 768.5143, 782.4732, 838.5202, 845.0931, 854.0439, 864.5125, 881.2834, 886.9861, 1134.6056, 1176.6227, 1279.7474, 1291.6895, 1320.5994, 1334.8694, 1446.7947, 1448.8540, 1525.7544, 1571.8801, 1615.8718, 1633.8181, 1646.9309, 1707.7874, 1762.9752, 1827.8575, 1952.9865, 1957.0007, 2056.0417, 2152.1138, 2175.2144, 2203.0588, 2231.2092, 2383.9692, 2400.0342, 2427.2180, 2565.1919, 2644.3660, 2644.3660, 2666.3528, 2824.3076, 2908.4368, 2923.3738, 3333.5613, 3351.5847

8. gi|28948464 **Mass:** 10653 **Score:** 102 **Expect:** 3.8e-005 **Queries matched:** 6

Chain A, Crystal Structure Of The Functional Domain Of The Major Grass Pollen Allergen Phl P 5b

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1087.5686	1086.5613	1086.5743	-0.0130	56 -	65	0	---	CIPSLEAAVK
1112.5883	1111.5810	1111.5913	-0.0103	80 -	89	0	---	YAVFEAALTK
1112.5883	1111.5810	1111.5913	-0.0103	80 -	89	0	50	YAVFEAALTK
1388.7413	1387.7340	1387.7459	-0.0119	66 -	79	0	---	QAYAATVAAAPQVK
1842.0369	1841.0296	1841.0298	-0.0001	1 -	17	1	---	IPAGELQIIDKIDAAFK
2427.2180	2426.2107	2426.2117	-0.0010	18 -	41	1	---	VAATAAATAPADDKFTVFEAAFNK

No match to: 713.4021, 724.4802, 734.4965, 750.5103, 768.5143, 782.4732, 838.5202, 845.0931, 854.0439, 864.5125, 881.2834, 886.9861, 1134.6056, 1176.6227, 1279.7474, 1291.6895, 1320.5994, 1334.8694, 1446.7947, 1448.8540, 1455.7559, 1455.7559, 1503.7390, 1525.7544, 1571.8801, 1615.8718, 1633.8181, 1646.9309, 1707.7874, 1762.9752, 1827.8575, 1935.0068, 1935.0068, 1952.9865, 1957.0007, 2056.0417, 2152.1138, 2175.2144, 2203.0588, 2231.2092, 2246.2188, 2262.2065, 2351.2271, 2351.2271, 2383.9692, 2400.0342, 2565.1919, 2644.3660, 2644.3660, 2666.3528, 2824.3076, 2908.4368, 2923.3738, 3333.5613, 3351.5847

9. gi|2266623 **Mass:** 24693 **Score:** 65 **Expect:** 0.18 **Queries matched:** 4

group V grass pollen allergen [Holcus lanatus]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1112.5883	1111.5810	1111.5913	-0.0103	193 -	202	0	---	YAVFEAALTK
1112.5883	1111.5810	1111.5913	-0.0103	193 -	202	0	50	YAVFEAALTK
1279.7474	1278.7401	1278.7295	0.0106	13 -	26	1	---	AAVAAAAKVPPADK
1503.7390	1502.7317	1502.7252	0.0065	155 -	168	1	---	ALKESTGGAYESYK

No match to: 713.4021, 724.4802, 734.4965, 750.5103, 768.5143, 782.4732, 838.5202, 845.0931, 854.0439, 864.5125, 881.2834, 886.9861, 1087.5686, 1134.6056, 1176.6227, 1291.6895, 1320.5994, 1334.8694, 1388.7413, 1446.7947,

1448.8540, 1455.7559, 1455.7559, 1525.7544, 1571.8801, 1615.8718, 1633.8181, 1646.9309, 1707.7874, 1762.9752, 1827.8575, 1842.0369, 1935.0068, 1935.0068, 1952.9865, 1957.0007, 2056.0417, 2152.1138, 2175.2144, 2203.0588, 2231.2092, 2246.2188, 2262.2065, 2351.2271, 2351.2271, 2383.9692, 2400.0342, 2427.2180, 2565.1919, 2644.3660, 2644.3660, 2666.3528, 2824.3076, 2908.4368, 2923.3738, 3333.5613, 3351.5847

10. gi|159467643 **Mass:** 91431 **Score:** 60 **Expect:** 0.58 **Queries matched:** 11

predicted protein [Chlamydomonas reinhardtii]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
713.4021	712.3948	712.4231	-0.0283	46	51	0	---	VPLTQR
864.5125	863.5052	863.4864	0.0188	712	719	1	---	KVFNSAAK
1087.5686	1086.5613	1086.6219	-0.0606	591	599	1	---	KMRPEALVK + Oxidation (M)
1446.7947	1445.7874	1445.7374	0.0500	720	733	1	---	RVGGTDAAAYVNPR
2152.1138	2151.1065	2151.0378	0.0688	6	28	0	---	ISNSGGAPLYSGAGGMVAGTTQR
2231.2092	2230.2019	2230.0872	0.1147	85	107	0	---	AAASSTMRPGTSGGGARPQTPTR + Oxidation (M)
2351.2271	2350.2198	2350.1674	0.0525	189	208	1	---	VSLVGCPICARTFRPDAFER
2351.2271	2350.2198	2350.1674	0.0525	355	374	1	---	VSLVGCPICARTFRPDAFER
2427.2180	2426.2107	2426.1038	0.1069	537	565	0	---	ACTADRPMARPGAGAGGGGGGGGGGGAAR
2824.3076	2823.3003	2823.2778	0.0226	275	298	0	---	EGQRPIGFTCYLCGQQYGSQSLMK + Oxidation (M)
3333.5613	3332.5540	3332.6346	-0.0806	318	347	0	---	EQRPLPPMPPELEAGELPTTAAGIEEFNQR + Oxidation (M)

No match to: 724.4802, 734.4965, 750.5103, 768.5143, 782.4732, 838.5202, 845.0931, 854.0439, 881.2834, 886.9861, 1112.5883, 1112.5883, 1134.6056, 1176.6227, 1279.7474, 1291.6895, 1320.5994, 1334.8694, 1388.7413, 1448.8540, 1455.7559, 1455.7559, 1503.7390, 1525.7544, 1571.8801, 1615.8718, 1633.8181, 1646.9309, 1707.7874, 1762.9752, 1827.8575, 1842.0369, 1935.0068, 1935.0068, 1952.9865, 1957.0007, 2056.0417, 2175.2144, 2203.0588, 2246.2188, 2262.2065, 2383.9692, 2400.0342, 2565.1919, 2644.3660, 2644.3660, 2666.3528, 2908.4368, 2923.3738, 3351.5847

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 61

Protein View

Match to: **gi|2851457** Score: **255** Expect: **1.9e-020**
RecName: Full=Pollen allergen Phl p 5b; AltName: Full=Allergen Phl p Vb; AltName: Allergen=Phl p 5b

Nominal mass (M_r): **28042**; Calculated pI value: **8.75**
NCBI BLAST search of gi|2851457 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|2398759 from Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **66%**

Matched peptides shown in **Bold Red**

```
    1 AAAAVPRRGP RGGPGRSYTA DAGYAPATPA AAGAAAGKAT TEEQKLIEDI
   51 NVGFKAAVAA AASVPAADKF KTFEAAFTSS SKAAAAKAPG LVPKLDAAYS
  101 VAYKAAVGAT PEAKFDSFVA SLTEALRVIA GALEVHAVKP VTEEPGMAKI
  151 PAGELQIIDK IDAAFKVAAT AAATAPADDK FTVFEAAFNK AIKESTGGAY
  201 DTYKCIPSLE AAVKQAYAAT VAAAPQVKYA VFEAALTKAI TAMSEVQKVS
  251 QPATGAATVA AGAATTAAGA ASGAATVAAG GYKV
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
17 - 38	1952.9865	1951.9792	1951.9275	0.0517	0	SYTADAGYAPATPAAAGAAAGK	(No match)
39 - 55	1935.0068	1933.9995	1933.9996	-0.0001	1	ATTEEQKLIEDINVGFK	(Ions score 39)
39 - 55	1935.0068	1933.9995	1933.9996	-0.0001	1	ATTEEQKLIEDINVGFK	(No match)
88 - 104	1762.9752	1761.9679	1761.9664	0.0015	1	APGLVPKLDAAYSVAYK	(No match)
105 - 127	2351.2271	2350.2198	2350.2168	0.0031	1	AAVGATPEAKFDSFVASLTEALR	(Ions score 27)
105 - 127	2351.2271	2350.2198	2350.2168	0.0031	1	AAVGATPEAKFDSFVASLTEALR	(No match)
115 - 127	1455.7559	1454.7486	1454.7405	0.0081	0	FDSFVASLTEALR	(Ions score 19)
115 - 127	1455.7559	1454.7486	1454.7405	0.0081	0	FDSFVASLTEALR	(No match)
128 - 149	2246.2188	2245.2115	2245.2139	-0.0024	0	VIAGALEVHAVKPVTEEPGMAK	(No match)
128 - 149	2262.2065	2261.1992	2261.2088	-0.0096	0	VIAGALEVHAVKPVTEEPGMAK	Oxidation (M) (No match)
150 - 166	1842.0369	1841.0296	1841.0298	-0.0001	1	IPAGELQIIDKIDAAFK	(No match)
167 - 190	2427.2180	2426.2107	2426.2117	-0.0010	1	VAATAAATAPADDKFTVFEAAFNK	(No match)
191 - 204	1503.7390	1502.7317	1502.7252	0.0065	1	AIKESTGGAYDTYK	(No match)
205 - 214	1087.5686	1086.5613	1086.5743	-0.0130	0	CIPSLEAAVK	(No match)
215 - 228	1388.7413	1387.7340	1387.7459	-0.0119	0	QAYAATVAAAPQVK	(No match)
229 - 238	1112.5883	1111.5810	1111.5913	-0.0103	0	YAVFEAALTK	(No match)
229 - 238	1112.5883	1111.5810	1111.5913	-0.0103	0	YAVFEAALTK	(Ions score 50)

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	Accession	Mass	Score	Description
1.	gi|3309043	26252	512	group V allergen Phl p 5.0204 [Phleum pratense]
2.	gi|2851457	28042	507	RecName: Full=Pollen allergen Phl p 5b; AltName: Full=Allergen Phl p Vb; AltName: Allergen=Phl p
3.	gi|3309041	29351	504	group V allergen Phl p 5.0203 precursor [Phleum pratense]
4.	gi|1684718	27903	470	major allergen Phl p 5 [Phleum pratense]
5.	gi|3309045	28869	465	group V allergen Phl p 5.0206 precursor [Phleum pratense]

Results List

1. gi|3309043 **Mass:** 26252 **Score:** 512 **Expect:** 3.8e-046 **Queries matched:** 19

group V allergen Phl p 5.0204 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1087.5833	1086.5760	1086.5743	0.0017	186	195	0	---	CIPSLEAAVK
1100.5532	1099.5459	1099.5549	-0.0090	76	85	0	---	LDAAYSVAYK
1112.5931	1111.5858	1111.5913	-0.0055	210	219	0	---	YAVFEAALTK
1112.5931	1111.5858	1111.5913	-0.0055	210	219	0	62	YAVFEAALTK
1175.5554	1174.5481	1174.5506	-0.0024	53	63	0	---	TFEAAFTSSSK
1388.7521	1387.7448	1387.7459	-0.0011	196	209	0	---	QAYAATVAAAPQVK
1455.7543	1454.7470	1454.7405	0.0065	96	108	0	---	FDSFVASLTEALR
1487.8123	1486.8050	1486.8143	-0.0093	37	52	1	---	AAVAAAASVPAADKFK
1503.7361	1502.7288	1502.7252	0.0036	172	185	1	---	AIKESTGGAYDTYK
1762.9734	1761.9661	1761.9664	-0.0003	69	85	1	122	APGLVPKLDAAYSVAYK
1762.9734	1761.9661	1761.9664	-0.0003	69	85	1	---	APGLVPKLDAAYSVAYK
1842.0361	1841.0288	1841.0298	-0.0009	131	147	1	---	IPAGELQIIDKIDAAFK
1935.0093	1934.0020	1933.9996	0.0024	20	36	1	135	ATTEEQKLIEDINVGFK
1935.0093	1934.0020	1933.9996	0.0024	20	36	1	---	ATTEEQKLIEDINVGFK
2246.2229	2245.2156	2245.2139	0.0017	109	130	0	---	VIAGALEVHAVKPVTEEPGMAK
2262.2087	2261.2014	2261.2088	-0.0074	109	130	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2246	2350.2173	2350.2168	0.0006	86	108	1	---	AAVGATPEAKFDSFVASLTEALR
2427.2354	2426.2281	2426.2117	0.0164	148	171	1	---	VAATAAATAPADDKFTVFEAAFNK
3018.6018	3017.5945	3017.5416	0.0529	230	265	1	---	VSQPATGAATVAAGAATTAAGAASGAATVAAGGYKV

No match to: 713.4073, 724.4956, 750.5117, 768.5206, 838.5239, 864.5336, 886.9843, 1070.5500, 1279.7690, 1323.6825, 1334.8890, 1404.6632, 1405.1652, 1448.9133, 1633.7836, 2175.2192, 2175.2192, 2205.2314, 2230.2114, 2456.2300, 2564.1760, 2644.3767, 2644.3767, 2824.3022, 2922.3586, 3057.5989, 3348.6033, 3549.8191, 3810.8413

2. gi|2851457 **Mass:** 28042 **Score:** 507 **Expect:** 1.2e-045 **Queries matched:** 19

RecName: Full=Pollen allergen Phl p 5b; AltName: Full=Allergen Phl p Vb; AltName: Allergen=Phl p 5b

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide

1087.5833	1086.5760	1086.5743	0.0017	205 - 214	0	---	CIPSLEAAVK
1100.5532	1099.5459	1099.5549	-0.0090	95 - 104	0	---	LDAAYSVAYK
1112.5931	1111.5858	1111.5913	-0.0055	229 - 238	0	---	YAVFEAALTK
1112.5931	1111.5858	1111.5913	-0.0055	229 - 238	0	62	YAVFEAALTK
1175.5554	1174.5481	1174.5506	-0.0024	72 - 82	0	---	TFEAAFTSSSK
1388.7521	1387.7448	1387.7459	-0.0011	215 - 228	0	---	QAYAATVAAAPQVK
1455.7543	1454.7470	1454.7405	0.0065	115 - 127	0	---	FDSFVASLTEALR
1487.8123	1486.8050	1486.8143	-0.0093	56 - 71	1	---	AAVAAAASVPAADKFK
1503.7361	1502.7288	1502.7252	0.0036	191 - 204	1	---	AIKESTGGAYDTYK
1762.9734	1761.9661	1761.9664	-0.0003	88 - 104	1	122	APGLVPKLDAAYSVAYK
1762.9734	1761.9661	1761.9664	-0.0003	88 - 104	1	---	APGLVPKLDAAYSVAYK
1842.0361	1841.0288	1841.0298	-0.0009	150 - 166	1	---	IPAGELQIIDKIDAAFK
1935.0093	1934.0020	1933.9996	0.0024	39 - 55	1	135	ATTEEQKLIEDINVGFK
1935.0093	1934.0020	1933.9996	0.0024	39 - 55	1	---	ATTEEQKLIEDINVGFK
2246.2229	2245.2156	2245.2139	0.0017	128 - 149	0	---	VIAGALEVHAVKPVTEEPGMAK
2262.2087	2261.2014	2261.2088	-0.0074	128 - 149	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2246	2350.2173	2350.2168	0.0006	105 - 127	1	---	AAVGATPEAKFDSFVASLTEALR
2427.2354	2426.2281	2426.2117	0.0164	167 - 190	1	---	VAATAAATAPADDKFTVFEAAFNK
3018.6018	3017.5945	3017.5416	0.0529	249 - 284	1	---	VSQPATGAATVAAGAATTAAGAASGAATVAAGGYKV

No match to: 713.4073, 724.4956, 750.5117, 768.5206, 838.5239, 864.5336, 886.9843, 1070.5500, 1279.7690, 1323.6825, 1334.8890, 1404.6632, 1405.1652, 1448.9133, 1633.7836, 2175.2192, 2175.2192, 2205.2314, 2230.2114, 2456.2300, 2564.1760, 2644.3767, 2644.3767, 2824.3022, 2922.3586, 3057.5989, 3348.6033, 3549.8191, 3810.8413

3. gi|3309041 **Mass:** 29351 **Score:** 504 **Expect:** 2.4e-045 **Queries matched:** 19

group V allergen Phl p 5.0203 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1087.5833	1086.5760	1086.5743	0.0017	216 - 225		0	---	CIPSLEAAVK
1100.5532	1099.5459	1099.5549	-0.0090	106 - 115		0	---	LDAAYSVAYK
1112.5931	1111.5858	1111.5913	-0.0055	240 - 249		0	---	YAVFEAALTK
1112.5931	1111.5858	1111.5913	-0.0055	240 - 249		0	62	YAVFEAALTK
1175.5554	1174.5481	1174.5506	-0.0024	83 - 93		0	---	TFEAAFTSSSK
1388.7521	1387.7448	1387.7459	-0.0011	226 - 239		0	---	QAYAATVAAAPQVK
1455.7543	1454.7470	1454.7405	0.0065	126 - 138		0	---	FDSFVASLTEALR
1487.8123	1486.8050	1486.8143	-0.0093	67 - 82		1	---	AAVAAAASVPAADKFK
1503.7361	1502.7288	1502.7252	0.0036	202 - 215		1	---	AIKESTGGAYDTYK
1762.9734	1761.9661	1761.9664	-0.0003	99 - 115		1	122	APGLVPKLDAAYSVAYK
1762.9734	1761.9661	1761.9664	-0.0003	99 - 115		1	---	APGLVPKLDAAYSVAYK
1842.0361	1841.0288	1841.0298	-0.0009	161 - 177		1	---	IPAGELQIIDKIDAAFK
1935.0093	1934.0020	1933.9996	0.0024	50 - 66		1	135	ATTEEQKLIEDINVGFK
1935.0093	1934.0020	1933.9996	0.0024	50 - 66		1	---	ATTEEQKLIEDINVGFK
2246.2229	2245.2156	2245.2139	0.0017	139 - 160		0	---	VIAGALEVHAVKPVTEEPGMAK

2262.2087	2261.2014	2261.2088	-0.0074	139 - 160	0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2246	2350.2173	2350.2168	0.0006	116 - 138	1	---	AAVGATPEAKFDSFVASLTEALR
2427.2354	2426.2281	2426.2117	0.0164	178 - 201	1	---	VAATAAATAPADDKFTVFEAAFNK
3018.6018	3017.5945	3017.5416	0.0529	260 - 295	1	---	VSQPATGAATVAAGAATTAAGAASGAATVAAGGYKV

No match to: 713.4073, 724.4956, 750.5117, 768.5206, 838.5239, 864.5336, 886.9843, 1070.5500, 1279.7690, 1323.6825, 1334.8890, 1404.6632, 1405.1652, 1448.9133, 1633.7836, 2175.2192, 2175.2192, 2205.2314, 2230.2114, 2456.2300, 2564.1760, 2644.3767, 2644.3767, 2824.3022, 2922.3586, 3057.5989, 3348.6033, 3549.8191, 3810.8413

4. gi|1684718 **Mass:** 27903 **Score:** 470 **Expect:** 6e-042 **Queries matched:** 17

major allergen Phl p 5 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1087.5833	1086.5760	1086.5743	0.0017	202 - 211		0	---	CIPSLEAAVK
1100.5532	1099.5459	1099.5549	-0.0090	92 - 101		0	---	LDAAYSVAYK
1112.5931	1111.5858	1111.5913	-0.0055	226 - 235		0	---	YAVFEAALTK
1112.5931	1111.5858	1111.5913	-0.0055	226 - 235		0	62	YAVFEAALTK
1175.5554	1174.5481	1174.5506	-0.0024	69 - 79		0	---	TFEAAFTSSSK
1388.7521	1387.7448	1387.7459	-0.0011	212 - 225		0	---	QAYAATVAAAPQVK
1455.7543	1454.7470	1454.7405	0.0065	112 - 124		0	---	FDSFVASLTEALR
1503.7361	1502.7288	1502.7252	0.0036	188 - 201		1	---	AIKESTGGAYDTYK
1762.9734	1761.9661	1761.9664	-0.0003	85 - 101		1	122	APGLVPKLDAAYSVAYK
1762.9734	1761.9661	1761.9664	-0.0003	85 - 101		1	---	APGLVPKLDAAYSVAYK
1842.0361	1841.0288	1841.0298	-0.0009	147 - 163		1	---	IPAGELQIIDKIDAAFK
1935.0093	1934.0020	1933.9996	0.0024	36 - 52		1	135	ATTEEQKLIEDINVGFK
1935.0093	1934.0020	1933.9996	0.0024	36 - 52		1	---	ATTEEQKLIEDINVGFK
2246.2229	2245.2156	2245.2139	0.0017	125 - 146		0	---	VIAGALEVHAVKPVTEEPGMAK
2262.2087	2261.2014	2261.2088	-0.0074	125 - 146		0	---	VIAGALEVHAVKPVTEEPGMAK + Oxidation (M)
2351.2246	2350.2173	2350.2168	0.0006	102 - 124		1	---	AAVGATPEAKFDSFVASLTEALR
2427.2354	2426.2281	2426.2117	0.0164	164 - 187		1	---	VAATAAATAPADDKFTVFEAAFNK

No match to: 713.4073, 724.4956, 750.5117, 768.5206, 838.5239, 864.5336, 886.9843, 1070.5500, 1279.7690, 1323.6825, 1334.8890, 1404.6632, 1405.1652, 1448.9133, 1487.8123, 1633.7836, 2175.2192, 2175.2192, 2205.2314, 2230.2114, 2456.2300, 2564.1760, 2644.3767, 2644.3767, 2824.3022, 2922.3586, 3018.6018, 3057.5989, 3348.6033, 3549.8191, 3810.8413

5. gi|3309045 **Mass:** 28869 **Score:** 465 **Expect:** 1.9e-041 **Queries matched:** 16

group V allergen Phl p 5.0206 precursor [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1087.5833	1086.5760	1086.5743	0.0017	211 - 220		0	---	CIPSLEAAVK
1100.5532	1099.5459	1099.5549	-0.0090	101 - 110		0	---	LDAAYSVAYK
1112.5931	1111.5858	1111.5913	-0.0055	235 - 244		0	---	YAVFEAALTK
1112.5931	1111.5858	1111.5913	-0.0055	235 - 244		0	62	YAVFEAALTK
1175.5554	1174.5481	1174.5506	-0.0024	78 - 88		0	---	TFEAAFTSSSK
1388.7521	1387.7448	1387.7459	-0.0011	221 - 234		0	---	QAYAATVAAAPQVK

1455.7543	1454.7470	1454.7405	0.0065	121 - 133	0	---	FDSFVASLTEALR
1487.8123	1486.8050	1486.8143	-0.0093	62 - 77	1	---	AAVAAAASVPAADKFK
1503.7361	1502.7288	1502.7252	0.0036	197 - 210	1	---	AIKESTGGAYDTYK
1762.9734	1761.9661	1761.9664	-0.0003	94 - 110	1	122	APGLVPKLDAAYSVAYK
1762.9734	1761.9661	1761.9664	-0.0003	94 - 110	1	---	APGLVPKLDAAYSVAYK
1842.0361	1841.0288	1841.0298	-0.0009	156 - 172	1	---	IPAGELQIIDKIDAAFK
1935.0093	1934.0020	1933.9996	0.0024	45 - 61	1	135	ATTEEQKLIEDINVGFK
1935.0093	1934.0020	1933.9996	0.0024	45 - 61	1	---	ATTEEQKLIEDINVGFK
2351.2246	2350.2173	2350.2168	0.0006	111 - 133	1	---	AAVGATPEAKFDSFVASLTEALR
2427.2354	2426.2281	2426.2117	0.0164	173 - 196	1	---	VAATAAATAPADDKFTVFEAAFNK

No match to: 713.4073, 724.4956, 750.5117, 768.5206, 838.5239, 864.5336, 886.9843, 1070.5500, 1279.7690, 1323.6825, 1334.8890, 1404.6632, 1405.1652, 1448.9133, 1633.7836, 2175.2192, 2175.2192, 2205.2314, 2230.2114, 2246.2229, 2262.2087, 2456.2300, 2564.1760, 2644.3767, 2644.3767, 2824.3022, 2922.3586, 3018.6018, 3057.5989, 3348.6033, 3549.8191, 3810.8413

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 48

Protein View

Match to: **gi|3309043** Score: **512** Expect: **3.8e-046**
group V allergen Phl p 5.0204 [Phleum pratense]

Nominal mass (M_r): **26252**; Calculated pI value: **5.61**
NCBI BLAST search of gi|3309043 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **87%**

Matched peptides shown in **Bold Red**

```
    1 ADAGYAPATP AAAGAEAGKA TTEEQKLIED INVGFKAAVA AAASVPAADK
   51 FKTFEAAFTS SSKAATAKAP GLVPKLDAAY SVAYKAAVGA TPEAKFDSFV
  101 ASLTEALRVI AGALEVHAVK PVTEEPGMAK IPAGELQIID KIDAAFKVAA
  151 TAAATAPADD KFTVFEAAFN KAIKESTGGA YDTYKCIPSL EAAVKQAYAA
  201 TVAAAPQVKY AVFEAALTKA ITAMSEVQKV SQPATGAATV AAGAATTAAG
  251 AASGAATVAA GGYKV
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
20 - 36	1935.0093	1934.0020	1933.9996	0.0024	1	ATTEEQKLIEDINVGFK	(Ions score 135)
20 - 36	1935.0093	1934.0020	1933.9996	0.0024	1	ATTEEQKLIEDINVGFK	(No match)
37 - 52	1487.8123	1486.8050	1486.8143	-0.0093	1	AAVAAAASVPAADKFK	(No match)
53 - 63	1175.5554	1174.5481	1174.5506	-0.0024	0	TFEAAFTSSSK	(No match)
69 - 85	1762.9734	1761.9661	1761.9664	-0.0003	1	APGLVPKLDAAYSVAYK	(Ions score 122)
69 - 85	1762.9734	1761.9661	1761.9664	-0.0003	1	APGLVPKLDAAYSVAYK	(No match)
76 - 85	1100.5532	1099.5459	1099.5549	-0.0090	0	LDAAYSVAYK	(No match)
86 - 108	2351.2246	2350.2173	2350.2168	0.0006	1	AAVGATPEAKFDSFVASLTEALR	(No match)
96 - 108	1455.7543	1454.7470	1454.7405	0.0065	0	FDSFVASLTEALR	(No match)
109 - 130	2246.2229	2245.2156	2245.2139	0.0017	0	VIAGALEVHAVKPVTEEPGMAK	(No match)
109 - 130	2262.2087	2261.2014	2261.2088	-0.0074	0	VIAGALEVHAVKPVTEEPGMAK Oxidation (M)	(No match)
131 - 147	1842.0361	1841.0288	1841.0298	-0.0009	1	IPAGELQIIDKIDAAFK	(No match)
148 - 171	2427.2354	2426.2281	2426.2117	0.0164	1	VAATAAATAPADDKFTVFEAAFNK	(No match)
172 - 185	1503.7361	1502.7288	1502.7252	0.0036	1	AIKESTGGAYDTYK	(No match)
186 - 195	1087.5833	1086.5760	1086.5743	0.0017	0	CIPSLEAAVK	(No match)
196 - 209	1388.7521	1387.7448	1387.7459	-0.0011	0	QAYAATVAAAPQVK	(No match)
210 - 219	1112.5931	1111.5858	1111.5913	-0.0055	0	YAVFEAALTK	(No match)
210 - 219	1112.5931	1111.5858	1111.5913	-0.0055	0	YAVFEAALTK	(Ions score 62)
230 - 265	3018.6018	3017.5945	3017.5416	0.0529	1	VSQPATGAATVAAGAATTAAGAASGAATVAAGGYKV	(No match)

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	Accession	Mass	Score	Description
1.	gi|29409364	34277	98	biostress-resistance-related protein [Triticum aestivum]
2.	gi|194696986	27173	61	unknown [Zea mays]
3.	gi|212722182	21467	53	hypothetical protein LOC100192559 [Zea mays]
4.	gi|195618164	27381	52	acyl-protein thioesterase 2 [Zea mays]
5.	gi|157359927	52226	47	unnamed protein product [Vitis vinifera]
6.	gi|195640738	27346	44	acyl-protein thioesterase 2 [Zea mays]
7.	gi|157335961	45659	38	unnamed protein product [Vitis vinifera]
8.	gi|147811676	72512	38	hypothetical protein [Vitis vinifera]
9.	gi|124360402	55330	37	Helicase, C-terminal [Medicago truncatula]
10.	gi|77641065	27470	36	I2 [Capsicum annuum]

Results List

1. gi|29409364 **Mass:** 34277 **Score:** 98 **Expect:** 8.7e-005 **Queries matched:** 6

biostress-resistance-related protein [Triticum aestivum]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
924.4658	923.4585	923.4613	-0.0028	83	-	89	0	39	RPFEYGR
924.4658	923.4585	923.4613	-0.0028	83	-	89	0	---	RPFEYGR
1401.7102	1400.7029	1400.7048	-0.0018	264	-	275	1	---	ADDVVLYKHGER
1741.9683	1740.9610	1740.9535	0.0075	83	-	96	1	---	RPFEYGRTHVVRPK
2661.3264	2660.3191	2660.3168	0.0023	212	-	236	0	28	YGNGNPYPVNLSVAVGLSGWLPCAR
2661.3264	2660.3191	2660.3168	0.0023	212	-	236	0	---	YGNGNPYPVNLSVAVGLSGWLPCAR

No match to: 713.4111, 724.5042, 734.4912, 736.4973, 750.5189, 768.5254, 864.5361, 886.9907, 907.9000, 1019.6756, 1057.5291, 1151.5706, 1279.7651, 1295.7126, 1334.8842, 1448.9182, 1577.7728, 1577.7728, 1618.0734, 1642.8457, 1642.8457, 1660.8840, 1732.0953, 2057.0217, 2057.0217, 2163.0793, 2201.1816, 2678.3877, 2693.3970

2. gi|194696986 **Mass:** 27173 **Score:** 61 **Expect:** 0.53 **Queries matched:** 4

unknown [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
924.4658	923.4585	923.4613	-0.0028	15	-	21	0	39	RPFEYGR
924.4658	923.4585	923.4613	-0.0028	15	-	21	0	---	RPFEYGR
1295.7126	1294.7053	1294.7067	-0.0014	184	-	195	0	---	ASSIPLLLCHGK
1741.9683	1740.9610	1740.9535	0.0075	15	-	28	1	---	RPFEYGRTHVVRPK

No match to: 713.4111, 724.5042, 734.4912, 736.4973, 750.5189, 768.5254, 864.5361, 886.9907, 907.9000, 1019.6756, 1057.5291, 1151.5706, 1279.7651, 1334.8842, 1401.7102, 1448.9182, 1577.7728, 1577.7728, 1618.0734, 1642.8457, 1642.8457, 1660.8840, 1732.0953, 2057.0217, 2057.0217, 2163.0793, 2201.1816, 2661.3264, 2661.3264, 2678.3877, 2693.3970

3. gi|212722182 **Mass:** 21467 **Score:** 53 **Expect:** 2.8 **Queries matched:** 3

hypothetical protein LOC100192559 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
924.4658	923.4585	923.4613	-0.0028	15	-	21	0	39	RPFEYGR
924.4658	923.4585	923.4613	-0.0028	15	-	21	0	---	RPFEYGR
1741.9683	1740.9610	1740.9535	0.0075	15	-	28	1	---	RPFEYGRTHVVRPK

No match to: 713.4111, 724.5042, 734.4912, 736.4973, 750.5189, 768.5254, 864.5361, 886.9907, 907.9000, 1019.6756, 1057.5291, 1151.5706, 1279.7651, 1295.7126, 1334.8842, 1401.7102, 1448.9182, 1577.7728, 1577.7728, 1618.0734, 1642.8457, 1642.8457, 1660.8840, 1732.0953, 2057.0217, 2057.0217, 2163.0793, 2201.1816, 2661.3264, 2661.3264, 2678.3877, 2693.3970

4. gi|195618164 **Mass:** 27381 **Score:** 52 **Expect:** 4.2 **Queries matched:** 3

acyl-protein thioesterase 2 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
924.4658	923.4585	923.4613	-0.0028	15	-	21	0	39	RPFEYGR
924.4658	923.4585	923.4613	-0.0028	15	-	21	0	---	RPFEYGR
1741.9683	1740.9610	1740.9535	0.0075	15	-	28	1	---	RPFEYGRTHVVRPK

No match to: 713.4111, 724.5042, 734.4912, 736.4973, 750.5189, 768.5254, 864.5361, 886.9907, 907.9000, 1019.6756, 1057.5291, 1151.5706, 1279.7651, 1295.7126, 1334.8842, 1401.7102, 1448.9182, 1577.7728, 1577.7728, 1618.0734, 1642.8457, 1642.8457, 1660.8840, 1732.0953, 2057.0217, 2057.0217, 2163.0793, 2201.1816, 2661.3264, 2661.3264, 2678.3877, 2693.3970

5. gi|157359927 **Mass:** 52226 **Score:** 47 **Expect:** 12 **Queries matched:** 8

unnamed protein product [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1577.7728	1576.7655	1576.8348	-0.0693	35	-	48	1	---	TPKDFDIITSAELK
1577.7728	1576.7655	1576.8348	-0.0693	35	-	48	1	---	TPKDFDIITSAELK
1660.8840	1659.8767	1659.8000	0.0767	131	-	144	1	---	IVYDYMGGMQDIKK
1741.9683	1740.9610	1740.8940	0.0670	181	-	195	1	---	DIAHSVRELSCSVLR
2057.0217	2056.0144	2055.9427	0.0717	354	-	371	1	---	SALMKMTDEHFVSQAMSK + Oxidation (M)
2057.0217	2056.0144	2055.9427	0.0717	354	-	371	1	---	SALMKMTDEHFVSQAMSK + Oxidation (M)
2163.0793	2162.0720	2162.0210	0.0511	201	-	219	0	---	ILMEMNYMLAYGSAEASLR
2678.3877	2677.3804	2677.3645	0.0159	291	-	316	0	---	HPMVVAAFSLAVHNGGSLSEAVEIAR + Oxidation (M)

No match to: 713.4111, 724.5042, 734.4912, 736.4973, 750.5189, 768.5254, 864.5361, 886.9907, 907.9000, 924.4658, 924.4658, 1019.6756, 1057.5291, 1151.5706, 1279.7651, 1295.7126, 1334.8842, 1401.7102, 1448.9182, 1618.0734, 1642.8457, 1642.8457, 1732.0953, 2201.1816, 2661.3264, 2661.3264, 2693.3970

6. gi|195640738 **Mass:** 27346 **Score:** 44 **Expect:** 24 **Queries matched:** 2

acyl-protein thioesterase 2 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
924.4658	923.4585	923.4613	-0.0028	15	-	21	0	39	RPFEYGR
924.4658	923.4585	923.4613	-0.0028	15	-	21	0	---	RPFEYGR

No match to: 713.4111, 724.5042, 734.4912, 736.4973, 750.5189, 768.5254, 864.5361, 886.9907, 907.9000, 1019.6756,

1057.5291, 1151.5706, 1279.7651, 1295.7126, 1334.8842, 1401.7102, 1448.9182, 1577.7728, 1577.7728, 1618.0734, 1642.8457, 1642.8457, 1660.8840, 1732.0953, 1741.9683, 2057.0217, 2057.0217, 2163.0793, 2201.1816, 2661.3264, 2661.3264, 2678.3877, 2693.3970

7. gi|157335961 **Mass:** 45659 **Score:** 38 **Expect:** 87 **Queries matched:** 7

unnamed protein product [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1057.5291	1056.5218	1056.4916	0.0302	223	230	0	---	WDAEFYVK
1151.5706	1150.5633	1150.5083	0.0550	273	280	0	---	YHEPEYWK
2057.0217	2056.0144	2056.0007	0.0137	46	62	1	---	RQHEQELQIISEGCTTK
2057.0217	2056.0144	2056.0007	0.0137	46	62	1	---	RQHEQELQIISEGCTTK
2661.3264	2660.3191	2660.3605	-0.0413	231	254	0	---	VDDDVHVNLGMLVATLAHHHSKPR
2661.3264	2660.3191	2660.3605	-0.0413	231	254	0	---	VDDDVHVNLGMLVATLAHHHSKPR
2678.3877	2677.3804	2677.2659	0.1145	317	339	0	---	YANEDVSLGSWFIGLEVEHIDER

No match to: 713.4111, 724.5042, 734.4912, 736.4973, 750.5189, 768.5254, 864.5361, 886.9907, 907.9000, 924.4658, 924.4658, 1019.6756, 1279.7651, 1295.7126, 1334.8842, 1401.7102, 1448.9182, 1577.7728, 1577.7728, 1618.0734, 1642.8457, 1642.8457, 1660.8840, 1732.0953, 1741.9683, 2163.0793, 2201.1816, 2693.3970

8. gi|147811676 **Mass:** 72512 **Score:** 38 **Expect:** 1e+002 **Queries matched:** 5

hypothetical protein [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1295.7126	1294.7053	1294.6768	0.0285	631	642	1	---	DVPSIPPGEEKK
1401.7102	1400.7029	1400.7082	-0.0052	463	476	0	---	QIPSGSTVAMPSAR
1642.8457	1641.8384	1641.8626	-0.0242	140	153	1	---	GHVVEWVEKASFVR
1642.8457	1641.8384	1641.8872	-0.0488	461	476	1	11	LKQIPSGSTVAMPSAR
1660.8840	1659.8767	1659.8038	0.0729	490	503	0	---	GMAQQHDLFTDLLR + Oxidation (M)

No match to: 713.4111, 724.5042, 734.4912, 736.4973, 750.5189, 768.5254, 864.5361, 886.9907, 907.9000, 924.4658, 924.4658, 1019.6756, 1057.5291, 1151.5706, 1279.7651, 1334.8842, 1448.9182, 1577.7728, 1577.7728, 1618.0734, 1732.0953, 1741.9683, 2057.0217, 2057.0217, 2163.0793, 2201.1816, 2661.3264, 2661.3264, 2678.3877, 2693.3970

9. gi|124360402 **Mass:** 55330 **Score:** 37 **Expect:** 1.2e+002 **Queries matched:** 5

Helicase, C-terminal [Medicago truncatula]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1295.7126	1294.7053	1294.6557	0.0496	380	390	1	---	DWVLSEFKSGK
2057.0217	2056.0144	2056.0451	-0.0307	113	131	0	---	AGFVEPTPIQSQGWPMALK
2057.0217	2056.0144	2056.0159	-0.0015	466	486	1	---	VSSELAAMGRGAPPPPSGGFR + Oxidation (M)
2201.1816	2200.1743	2200.1350	0.0393	112	131	1	---	KAGFVEPTPIQSQGWPMALK + Oxidation (M)
2678.3877	2677.3804	2677.4220	-0.0416	218	241	1	---	GVEIIIATPGRLIDMLESNHTNLR + Oxidation (M)

No match to: 713.4111, 724.5042, 734.4912, 736.4973, 750.5189, 768.5254, 864.5361, 886.9907, 907.9000, 924.4658, 924.4658, 1019.6756, 1057.5291, 1151.5706, 1279.7651, 1334.8842, 1401.7102, 1448.9182, 1577.7728, 1577.7728, 1618.0734, 1642.8457, 1642.8457, 1660.8840, 1732.0953, 1741.9683, 2163.0793, 2661.3264, 2661.3264, 2693.3970

10. gi|77641065 **Mass:** 27470 **Score:** 36 **Expect:** 1.4e+002 **Queries matched:** 4

I2 [Capsicum annuum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1577.7728	1576.7655	1576.7733	-0.0077	227 -	239	1	---	SKSEVDEWTDILR
1577.7728	1576.7655	1576.7733	-0.0077	227 -	239	1	---	SKSEVDEWTDILR
1642.8457	1641.8384	1641.8685	-0.0301	3 -	17	1	---	THSTSLVDESKILGR
1642.8457	1641.8384	1641.8685	-0.0301	3 -	17	1	24	THSTSLVDESKILGR

No match to: 713.4111, 724.5042, 734.4912, 736.4973, 750.5189, 768.5254, 864.5361, 886.9907, 907.9000, 924.4658, 924.4658, 1019.6756, 1057.5291, 1151.5706, 1279.7651, 1295.7126, 1334.8842, 1401.7102, 1448.9182, 1618.0734, 1660.8840, 1732.0953, 1741.9683, 2057.0217, 2057.0217, 2163.0793, 2201.1816, 2661.3264, 2661.3264, 2678.3877, 2693.3970

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 35

Protein View

Match to: **gi|29409364** Score: **98** Expect: **8.7e-005**
biostress-resistance-related protein [Triticum aestivum]

Nominal mass (M_r): **34277**; Calculated pI value: **8.93**
NCBI BLAST search of gi|29409364 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Triticum aestivum

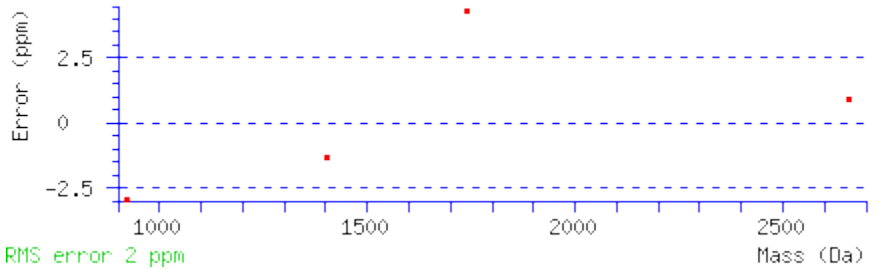
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **15%**

Matched peptides shown in **Bold Red**

```
   1 TRERSGRYEL SSRRIAPHRP ATPARCPPSS PALPNRVAGG REAIGFVALA
  51 SVVARRGGVP AAAATVRGMS FGGASSVAAG GKRPFEYGRT HVVRPKGAHK
 101 ATIVWLHGLG DNGASWSQLL ETLPLPNIKW ICPTAPTRPV AIFGGFPSTA
 151 WFDVADLSED SPDDVEGLDS SAAHVANLLS TEPADIKLGV GGFSMGAATA
 201 LYSGTCFAHG KYGNGNPYPV NLSVAVGLSG WLPCARSLKN KIESSQEAAQ
 251 KASSLPLMLC HGKADDVVLY KHGERSADAL KSTGFANVEF KSYSRLGHYT
 301 VPEEMDEVVK WLTASLELGS SSST
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
83 - 89	924.4658	923.4585	923.4613	-0.0028	0	**RPFEYGR**	(Ions score 39)
83 - 89	924.4658	923.4585	923.4613	-0.0028	0	**RPFEYGR**	(No match)
83 - 96	1741.9683	1740.9610	1740.9535	0.0075	1	**RPFEYGRTHVVRPK**	(No match)
212 - 236	2661.3264	2660.3191	2660.3168	0.0023	0	**YGNGNPYPVNLSVAVGLSGWLPCAR**	(Ions score 28)
212 - 236	2661.3264	2660.3191	2660.3168	0.0023	0	**YGNGNPYPVNLSVAVGLSGWLPCAR**	(No match)
264 - 275	1401.7102	1400.7029	1400.7048	-0.0018	1	**ADDVVLYKHGER**	(No match)



Spot 110

Index

	Accession	Mass	Score	Description
1.	gi|115465581	25365	331	Os05g0574500 [Oryza sativa (japonica cultivar-group)]
2.	gi|16903082	25460	331	small Ras-related GTP-binding protein [Triticum aestivum]
3.	gi|222875504	25474	331	Ran-related GTP-binding protein [Festuca arundinacea]
4.	gi|212722150	25387	328	hypothetical protein LOC100193260 [Zea mays]
5.	gi|157467219	18827	317	Ran3 GTP binding protein [Iberis amara]

Results List

1. gi|115465581 **Mass:** 25365 **Score:** 331 **Expect:** 4.8e-028 **Queries matched:** 20

Os05g0574500 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
751.4608	750.4535	750.4388	0.0147	27	32	1	---	TTFVKR
787.4232	786.4159	786.4136	0.0023	138	143	0	---	QVTFHR
909.4666	908.4593	908.4617	-0.0023	103	109	0	29	NVPTWHR
909.4666	908.4593	908.4617	-0.0023	103	109	0	---	NVPTWHR
960.4713	959.4640	959.4712	-0.0072	33	40	0	---	HLTGEFEK
986.5500	985.5427	985.5457	-0.0030	136	143	1	---	AKQVTFHR
1088.5699	1087.5626	1087.5661	-0.0035	33	41	1	---	HLTGEFEKK
1228.6089	1227.6016	1227.6135	-0.0119	146	155	0	---	NLQYYEISAK
1356.6936	1355.6863	1355.7085	-0.0221	145	155	1	---	KNLQYYEISAK
1404.5765	1403.5692	1403.5816	-0.0123	64	74	0	---	FYCWDTAGQEK
1414.7468	1413.7395	1413.7517	-0.0122	99	109	1	---	LTYKNVPTWHR
1453.6998	1452.6925	1452.7044	-0.0119	103	113	1	---	NVPTWHRDLCR
1515.7472	1514.7399	1514.7585	-0.0185	114	126	0	---	VCENIPIVLCGNK
1673.7617	1672.7544	1672.7667	-0.0123	62	74	1	---	IRFYCWDTAGQEK
1673.7617	1672.7544	1672.7667	-0.0123	62	74	1	37	IRFYCWDTAGQEK
1761.8835	1760.8762	1760.8885	-0.0123	156	169	0	56	SNYNFEKPFLYLAR
1761.8835	1760.8762	1760.8885	-0.0123	156	169	0	---	SNYNFEKPFLYLAR
1889.9771	1888.9698	1888.9835	-0.0137	156	170	1	---	SNYNFEKPFLYLARK
1957.0170	1956.0097	1956.0172	-0.0074	114	130	1	---	VCENIPIVLCGNKVDVK
2405.1904	2404.1831	2404.1732	0.0099	41	61	1	---	KYEPTIGVEVHPLDFTTNCGK

No match to: 713.4155, 724.5088, 768.5280, 770.3993, 838.5317, 886.9846, 925.4635, 941.4553, 1057.4362, 1112.6140, 1114.6326, 1135.5704, 1291.6636, 1484.7964, 1571.8694, 1578.7662, 1578.7662, 1600.7502, 1747.9948, 1747.9948, 1960.0065, 2227.1614, 2236.1770, 2253.1958, 2502.2573, 2538.1960, 2576.3521, 2582.3872, 2674.3650, 2781.5051, 3307.7974, 3347.7061

2. gi|16903082 **Mass:** 25460 **Score:** 331 **Expect:** 4.8e-028 **Queries matched:** 20

small Ras-related GTP-binding protein [Triticum aestivum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
751.4608	750.4535	750.4388	0.0147	27 -	32	1	---	TTFVKR
787.4232	786.4159	786.4136	0.0023	138 -	143	0	---	QVTFHR
909.4666	908.4593	908.4617	-0.0023	103 -	109	0	29	NVPTWHR
909.4666	908.4593	908.4617	-0.0023	103 -	109	0	---	NVPTWHR
960.4713	959.4640	959.4712	-0.0072	33 -	40	0	---	HLTGEFEK
986.5500	985.5427	985.5457	-0.0030	136 -	143	1	---	AKQVTFHR
1088.5699	1087.5626	1087.5661	-0.0035	33 -	41	1	---	HLTGEFEKK
1228.6089	1227.6016	1227.6135	-0.0119	146 -	155	0	---	NLQYYEISAK
1356.6936	1355.6863	1355.7085	-0.0221	145 -	155	1	---	KNLQYYEISAK
1404.5765	1403.5692	1403.5816	-0.0123	64 -	74	0	---	FYCWDTAGQEK
1414.7468	1413.7395	1413.7517	-0.0122	99 -	109	1	---	LTYKNVPTWHR
1453.6998	1452.6925	1452.7044	-0.0119	103 -	113	1	---	NVPTWHRDLCR
1515.7472	1514.7399	1514.7585	-0.0185	114 -	126	0	---	VCENIPIVLCGNK
1673.7617	1672.7544	1672.7667	-0.0123	62 -	74	1	---	IRFYCWDTAGQEK
1673.7617	1672.7544	1672.7667	-0.0123	62 -	74	1	37	IRFYCWDTAGQEK
1761.8835	1760.8762	1760.8885	-0.0123	156 -	169	0	56	SNYNFEKPFLYLAR
1761.8835	1760.8762	1760.8885	-0.0123	156 -	169	0	---	SNYNFEKPFLYLAR
1889.9771	1888.9698	1888.9835	-0.0137	156 -	170	1	---	SNYNFEKPFLYLARK
1957.0170	1956.0097	1956.0172	-0.0074	114 -	130	1	---	VCENIPIVLCGNKVDVK
2405.1904	2404.1831	2404.1732	0.0099	41 -	61	1	---	KYEPTIGVEVHPLDFTTNCGK

No match to: 713.4155, 724.5088, 768.5280, 770.3993, 838.5317, 886.9846, 925.4635, 941.4553, 1057.4362, 1112.6140, 1114.6326, 1135.5704, 1291.6636, 1484.7964, 1571.8694, 1578.7662, 1578.7662, 1600.7502, 1747.9948, 1747.9948, 1960.0065, 2227.1614, 2236.1770, 2253.1958, 2502.2573, 2538.1960, 2576.3521, 2582.3872, 2674.3650, 2781.5051, 3307.7974, 3347.7061

3. gi|222875504 **Mass:** 25474 **Score:** 331 **Expect:** 4.8e-028 **Queries matched:** 20

Ran-related GTP-binding protein [Festuca arundinacea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
751.4608	750.4535	750.4388	0.0147	27 -	32	1	---	TTFVKR
787.4232	786.4159	786.4136	0.0023	138 -	143	0	---	QVTFHR
909.4666	908.4593	908.4617	-0.0023	103 -	109	0	29	NVPTWHR
909.4666	908.4593	908.4617	-0.0023	103 -	109	0	---	NVPTWHR
960.4713	959.4640	959.4712	-0.0072	33 -	40	0	---	HLTGEFEK
986.5500	985.5427	985.5457	-0.0030	136 -	143	1	---	AKQVTFHR
1088.5699	1087.5626	1087.5661	-0.0035	33 -	41	1	---	HLTGEFEKK
1228.6089	1227.6016	1227.6135	-0.0119	146 -	155	0	---	NLQYYEISAK
1356.6936	1355.6863	1355.7085	-0.0221	145 -	155	1	---	KNLQYYEISAK
1404.5765	1403.5692	1403.5816	-0.0123	64 -	74	0	---	FYCWDTAGQEK
1414.7468	1413.7395	1413.7517	-0.0122	99 -	109	1	---	LTYKNVPTWHR
1453.6998	1452.6925	1452.7044	-0.0119	103 -	113	1	---	NVPTWHRDLCR

1515.7472	1514.7399	1514.7585	-0.0185	114 - 126	0	---	VCENIPIVLCGNK
1673.7617	1672.7544	1672.7667	-0.0123	62 - 74	1	---	IRFYCWDTAGQEK
1673.7617	1672.7544	1672.7667	-0.0123	62 - 74	1	37	IRFYCWDTAGQEK
1761.8835	1760.8762	1760.8885	-0.0123	156 - 169	0	56	SNYNFEKPFLYLAR
1761.8835	1760.8762	1760.8885	-0.0123	156 - 169	0	---	SNYNFEKPFLYLAR
1889.9771	1888.9698	1888.9835	-0.0137	156 - 170	1	---	SNYNFEKPFLYLARK
1957.0170	1956.0097	1956.0172	-0.0074	114 - 130	1	---	VCENIPIVLCGNKVDVK
2405.1904	2404.1831	2404.1732	0.0099	41 - 61	1	---	KYEPTIGVEVHPLDFTTNCGK

No match to: 713.4155, 724.5088, 768.5280, 770.3993, 838.5317, 886.9846, 925.4635, 941.4553, 1057.4362, 1112.6140, 1114.6326, 1135.5704, 1291.6636, 1484.7964, 1571.8694, 1578.7662, 1578.7662, 1600.7502, 1747.9948, 1747.9948, 1960.0065, 2227.1614, 2236.1770, 2253.1958, 2502.2573, 2538.1960, 2576.3521, 2582.3872, 2674.3650, 2781.5051, 3307.7974, 3347.7061

4. gi|212722150 **Mass:** 25387 **Score:** 328 **Expect:** 9.6e-028 **Queries matched:** 20

hypothetical protein LOC100193260 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
751.4608	750.4535	750.4388	0.0147	27 -	32	1	---	TTFVKR
787.4232	786.4159	786.4136	0.0023	138 -	143	0	---	QVTFHR
909.4666	908.4593	908.4617	-0.0023	103 -	109	0	29	NVPTWHR
909.4666	908.4593	908.4617	-0.0023	103 -	109	0	---	NVPTWHR
960.4713	959.4640	959.4712	-0.0072	33 -	40	0	---	HLTGEFEK
986.5500	985.5427	985.5457	-0.0030	136 -	143	1	---	AKQVTFHR
1088.5699	1087.5626	1087.5661	-0.0035	33 -	41	1	---	HLTGEFEKK
1228.6089	1227.6016	1227.6135	-0.0119	146 -	155	0	---	NLQYYEISAK
1356.6936	1355.6863	1355.7085	-0.0221	145 -	155	1	---	KNLQYYEISAK
1404.5765	1403.5692	1403.5816	-0.0123	64 -	74	0	---	FYCWDTAGQEK
1414.7468	1413.7395	1413.7517	-0.0122	99 -	109	1	---	LTYKNVPTWHR
1453.6998	1452.6925	1452.7044	-0.0119	103 -	113	1	---	NVPTWHRDLCR
1515.7472	1514.7399	1514.7585	-0.0185	114 -	126	0	---	VCENIPIVLCGNK
1673.7617	1672.7544	1672.7667	-0.0123	62 -	74	1	---	IRFYCWDTAGQEK
1673.7617	1672.7544	1672.7667	-0.0123	62 -	74	1	37	IRFYCWDTAGQEK
1761.8835	1760.8762	1760.8885	-0.0123	156 -	169	0	56	SNYNFEKPFLYLAR
1761.8835	1760.8762	1760.8885	-0.0123	156 -	169	0	---	SNYNFEKPFLYLAR
1889.9771	1888.9698	1888.9835	-0.0137	156 -	170	1	---	SNYNFEKPFLYLARK
1957.0170	1956.0097	1956.0172	-0.0074	114 -	130	1	---	VCENIPIVLCGNKVDVK
2405.1904	2404.1831	2404.1732	0.0099	41 -	61	1	---	KYEPTIGVEVHPLDFTTNCGK

No match to: 713.4155, 724.5088, 768.5280, 770.3993, 838.5317, 886.9846, 925.4635, 941.4553, 1057.4362, 1112.6140, 1114.6326, 1135.5704, 1291.6636, 1484.7964, 1571.8694, 1578.7662, 1578.7662, 1600.7502, 1747.9948, 1747.9948, 1960.0065, 2227.1614, 2236.1770, 2253.1958, 2502.2573, 2538.1960, 2576.3521, 2582.3872, 2674.3650, 2781.5051, 3307.7974, 3347.7061

5. gi|157467219 **Mass:** 18827 **Score:** 317 **Expect:** 1.2e-026 **Queries matched:** 19

Ran3 GTP binding protein [Iberis amara]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
751.4608	750.4535	750.4388	0.0147	14	-	19	1	---	TTFVKR
787.4232	786.4159	786.4136	0.0023	125	-	130	0	---	QVTFHR
909.4666	908.4593	908.4617	-0.0023	90	-	96	0	29	NVPTWHR
909.4666	908.4593	908.4617	-0.0023	90	-	96	0	---	NVPTWHR
960.4713	959.4640	959.4712	-0.0072	20	-	27	0	---	HLTGEFEK
986.5500	985.5427	985.5457	-0.0030	123	-	130	1	---	AKQVTFHR
1088.5699	1087.5626	1087.5661	-0.0035	20	-	28	1	---	HLTGEFEKK
1228.6089	1227.6016	1227.6135	-0.0119	133	-	142	0	---	NLQYYEISAK
1356.6936	1355.6863	1355.7085	-0.0221	132	-	142	1	---	KNLQYYEISAK
1404.5765	1403.5692	1403.5816	-0.0123	51	-	61	0	---	FYCWDTAGQEK
1414.7468	1413.7395	1413.7517	-0.0122	86	-	96	1	---	LTYKNVPTWHR
1453.6998	1452.6925	1452.7044	-0.0119	90	-	100	1	---	NVPTWHRDLCR
1515.7472	1514.7399	1514.7585	-0.0185	101	-	113	0	---	VCENIPIVLCGNK
1673.7617	1672.7544	1672.7667	-0.0123	49	-	61	1	---	IRFYCWDTAGQEK
1673.7617	1672.7544	1672.7667	-0.0123	49	-	61	1	37	IRFYCWDTAGQEK
1761.8835	1760.8762	1760.8885	-0.0123	143	-	156	0	56	SNYNFEKPFLYLAR
1761.8835	1760.8762	1760.8885	-0.0123	143	-	156	0	---	SNYNFEKPFLYLAR
1889.9771	1888.9698	1888.9835	-0.0137	143	-	157	1	---	SNYNFEKPFLYLARK
1957.0170	1956.0097	1956.0172	-0.0074	101	-	117	1	---	VCENIPIVLCGNKVDVK

No match to: 713.4155, 724.5088, 768.5280, 770.3993, 838.5317, 886.9846, 925.4635, 941.4553, 1057.4362, 1112.6140, 1114.6326, 1135.5704, 1291.6636, 1484.7964, 1571.8694, 1578.7662, 1578.7662, 1600.7502, 1747.9948, 1747.9948, 1960.0065, 2227.1614, 2236.1770, 2253.1958, 2405.1904, 2502.2573, 2538.1960, 2576.3521, 2582.3872, 2674.3650, 2781.5051, 3307.7974, 3347.7061

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 52

Protein View

Match to: **gi|16903082** Score: **331** Expect: **4.8e-028**
small Ras-related GTP-binding protein [Triticum aestivum]

Nominal mass (M_r): **25460**; Calculated pI value: **6.66**
NCBI BLAST search of gi|16903082 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Triticum aestivum
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|19919694 from Triticum aestivum

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **51%**

Matched peptides shown in **Bold Red**

```
     1 MALPNQNTVD YPSFKLVIVG DGGTGKTTFV KRHLTGEFEK KYEPTIGVEV
    51 HPLDFTTNCG KIRFYCWDTA GQEKFGGLRD GYYIHGQCAI IMFDVTSRLT
   101 YKNVPTWHRD LCRVCENIPI VLCGNKVDVK NRQVKAKQVT FHRKKNLQYY
   151 EISAKSNYNF EKPFLYLARK LAGDPNIHFV EAVALKPPEV TFDLAMQQQH
   201 EAELAAAAAQ PLPDDDDDLI E
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
27 - 32	751.4608	750.4535	750.4388	0.0147	1	TTFVKR	(No match)
33 - 40	960.4713	959.4640	959.4712	-0.0072	0	HLTGEFEK	(No match)
33 - 41	1088.5699	1087.5626	1087.5661	-0.0035	1	HLTGEFEKK	(No match)
41 - 61	2405.1904	2404.1831	2404.1732	0.0099	1	KYEPTIGVEVHPLDFTTNCGK	(No match)
62 - 74	1673.7617	1672.7544	1672.7667	-0.0123	1	IRFYCWDTAGQEK	(No match)
62 - 74	1673.7617	1672.7544	1672.7667	-0.0123	1	IRFYCWDTAGQEK	(Ions score 37)
64 - 74	1404.5765	1403.5692	1403.5816	-0.0123	0	FYCWDTAGQEK	(No match)
99 - 109	1414.7468	1413.7395	1413.7517	-0.0122	1	LTYKNVPTWHR	(No match)
103 - 109	909.4666	908.4593	908.4617	-0.0023	0	NVPTWHR	(Ions score 29)
103 - 109	909.4666	908.4593	908.4617	-0.0023	0	NVPTWHR	(No match)
103 - 113	1453.6998	1452.6925	1452.7044	-0.0119	1	NVPTWHRDLCR	(No match)
114 - 126	1515.7472	1514.7399	1514.7585	-0.0185	0	VCENIPIVLCGNK	(No match)
114 - 130	1957.0170	1956.0097	1956.0172	-0.0074	1	VCENIPIVLCGNKVDVK	(No match)
136 - 143	986.5500	985.5427	985.5457	-0.0030	1	AKQVTFHR	(No match)
138 - 143	787.4232	786.4159	786.4136	0.0023	0	QVTFHR	(No match)
145 - 155	1356.6936	1355.6863	1355.7085	-0.0221	1	KNLQYYEISAK	(No match)
146 - 155	1228.6089	1227.6016	1227.6135	-0.0119	0	NLQYYEISAK	(No match)
156 - 169	1761.8835	1760.8762	1760.8885	-0.0123	0	SNYNFEKPFLYLAR	(Ions score 56)
156 - 169	1761.8835	1760.8762	1760.8885	-0.0123	0	SNYNFEKPFLYLAR	(No match)
156 - 170	1889.9771	1888.9698	1888.9835	-0.0137	1	SNYNFEKPFLYLARK	(No match)

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	Accession	Mass	Score	Description
1.	gi|1582250	28542	228	allergen PhI p I
2.	gi|3901094	28584	228	pollen allergen Phl pI [Phleum pratense]
3.	gi|125583637	46268	65	hypothetical protein OsJ_08330 [Oryza sativa Japonica Group]
4.	gi|115448599	48315	65	Os02g0741200 [Oryza sativa (japonica cultivar-group)]
5.	gi|218196234	9946	63	hypothetical protein OsI_18774 [Oryza sativa Indica Group]
6.	gi|218198765	39022	55	hypothetical protein OsI_24206 [Oryza sativa Indica Group]
7.	gi|222636099	38991	55	hypothetical protein OsJ_22393 [Oryza sativa Japonica Group]
8.	gi|157327315	125165	54	unnamed protein product [Vitis vinifera]
9.	gi|57899087	14450	54	hypothetical protein [Oryza sativa Japonica Group]
10.	gi|145343374	21734	53	predicted protein [Ostreococcus lucimarinus CCE9901]

Results List

1. gi|1582250 **Mass:** 28542 **Score:** 228 **Expect:** 9.6e-018 **Queries matched:** 8

allergen PhI p I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1057.4436	1056.4363	1056.4368	-0.0005	91	99	0	---	GCGSCFEIK
1135.5762	1134.5689	1134.5669	0.0021	149	158	0	60	SAGEVEIQFR
1135.5762	1134.5689	1134.5669	0.0021	149	158	0	---	SAGEVEIQFR
1291.6766	1290.6693	1290.6680	0.0014	149	159	1	34	SAGEVEIQFRR
1291.6766	1290.6693	1290.6680	0.0014	149	159	1	---	SAGEVEIQFRR
1357.6074	1356.6001	1356.5914	0.0087	88	99	1	---	SGRGCGSCFEIK
1571.8879	1570.8806	1570.8718	0.0088	221	234	1	---	IDTPEVLKGPFTVR
1571.8879	1570.8806	1570.8718	0.0088	221	234	1	73	IDTPEVLKGPFTVR

No match to: 713.4120, 768.5225, 973.5364, 1470.6798, 1470.6798, 1778.8425, 1826.8568, 1826.8568, 1957.1014, 2256.0889

2. gi|3901094 **Mass:** 28584 **Score:** 228 **Expect:** 9.6e-018 **Queries matched:** 8

pollen allergen Phl pI [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1057.4436	1056.4363	1056.4368	-0.0005	91	99	0	---	GCGSCFEIK
1135.5762	1134.5689	1134.5669	0.0021	149	158	0	60	SAGEVEIQFR
1135.5762	1134.5689	1134.5669	0.0021	149	158	0	---	SAGEVEIQFR
1291.6766	1290.6693	1290.6680	0.0014	149	159	1	34	SAGEVEIQFRR
1291.6766	1290.6693	1290.6680	0.0014	149	159	1	---	SAGEVEIQFRR
1357.6074	1356.6001	1356.5914	0.0087	88	99	1	---	SGRGCGSCFEIK
1571.8879	1570.8806	1570.8718	0.0088	222	235	1	---	IDTPEVLKGPFTVR
1571.8879	1570.8806	1570.8718	0.0088	222	235	1	73	IDTPEVLKGPFTVR

No match to: 713.4120, 768.5225, 973.5364, 1470.6798, 1470.6798, 1778.8425, 1826.8568, 1826.8568, 1957.1014, 2256.0889

3. gi|125583637 **Mass:** 46268 **Score:** 65 **Expect:** 0.18 **Queries matched:** 4

hypothetical protein OsJ_08330 [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1470.6798	1469.6725	1469.6609	0.0116	126 -	137	0	---	LSPDYYAQTCPR
1470.6798	1469.6725	1469.6609	0.0116	126 -	137	0	36	LSPDYYAQTCPR
1826.8568	1825.8495	1825.8417	0.0078	126 -	140	1	---	LSPDYYAQTCPRAER
1826.8568	1825.8495	1825.8417	0.0078	126 -	140	1	15	LSPDYYAQTCPRAER

No match to: 713.4120, 768.5225, 973.5364, 1057.4436, 1135.5762, 1135.5762, 1291.6766, 1291.6766, 1357.6074, 1571.8879, 1571.8879, 1778.8425, 1957.1014, 2256.0889

4. gi|115448599 **Mass:** 48315 **Score:** 65 **Expect:** 0.2 **Queries matched:** 4

Os02g0741200 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1470.6798	1469.6725	1469.6609	0.0116	142 -	153	0	---	LSPDYYAQTCPR
1470.6798	1469.6725	1469.6609	0.0116	142 -	153	0	36	LSPDYYAQTCPR
1826.8568	1825.8495	1825.8417	0.0078	142 -	156	1	---	LSPDYYAQTCPRAER
1826.8568	1825.8495	1825.8417	0.0078	142 -	156	1	15	LSPDYYAQTCPRAER

No match to: 713.4120, 768.5225, 973.5364, 1057.4436, 1135.5762, 1135.5762, 1291.6766, 1291.6766, 1357.6074, 1571.8879, 1571.8879, 1778.8425, 1957.1014, 2256.0889

5. gi|218196234 **Mass:** 9946 **Score:** 63 **Expect:** 0.32 **Queries matched:** 5

hypothetical protein OsI_18774 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1135.5762	1134.5689	1134.5516	0.0173	7 -	17	0	---	STVESAVESAR
1135.5762	1134.5689	1134.5516	0.0173	7 -	17	0	---	STVESAVESAR
1291.6766	1290.6693	1290.6527	0.0166	6 -	17	1	21	RSTVESAVESAR
1291.6766	1290.6693	1290.6527	0.0166	6 -	17	1	---	RSTVESAVESAR
2256.0889	2255.0816	2255.0864	-0.0048	56 -	78	1	---	AMAAAAVEVESAHGGGSVGARWR + Oxidation (M)

No match to: 713.4120, 768.5225, 973.5364, 1057.4436, 1357.6074, 1470.6798, 1470.6798, 1571.8879, 1571.8879, 1778.8425, 1826.8568, 1826.8568, 1957.1014

6. gi|218198765 **Mass:** 39022 **Score:** 55 **Expect:** 2 **Queries matched:** 8

hypothetical protein OsI_24206 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
973.5364	972.5291	972.4633	0.0658	3 -	10	1	---	EMMGPPRR
1057.4436	1056.4363	1056.4737	-0.0374	60 -	67	0	---	DHRPDDFR
1135.5762	1134.5689	1134.5516	0.0173	249 -	259	0	---	SVALSTSEEGR
1135.5762	1134.5689	1134.5516	0.0173	249 -	259	0	---	SVALSTSEEGR
1291.6766	1290.6693	1290.6527	0.0166	248 -	259	1	14	RSVALSTSEEGR

1291.6766	1290.6693	1290.6527	0.0166	248 - 259	1	---	RSVALSTSEEGR
1470.6798	1469.6725	1469.6092	0.0633	266 - 277	1	---	ESYDNRDPMSEK
1470.6798	1469.6725	1469.6092	0.0633	266 - 277	1	---	ESYDNRDPMSEK

No match to: 713.4120, 768.5225, 1357.6074, 1571.8879, 1571.8879, 1778.8425, 1826.8568, 1826.8568, 1957.1014, 2256.0889

7. gi|222636099 **Mass:** 38991 **Score:** 55 **Expect:** 2 **Queries matched:** 8

hypothetical protein OsJ_22393 [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
973.5364	972.5291	972.4633	0.0658	3 -	10	1	---	EMMGPPRR
1057.4436	1056.4363	1056.4737	-0.0374	60 -	67	0	---	DHRPDDFR
1135.5762	1134.5689	1134.5516	0.0173	249 -	259	0	---	SVALSTSEEGR
1135.5762	1134.5689	1134.5516	0.0173	249 -	259	0	---	SVALSTSEEGR
1291.6766	1290.6693	1290.6527	0.0166	248 -	259	1	14	RSVALSTSEEGR
1291.6766	1290.6693	1290.6527	0.0166	248 -	259	1	---	RSVALSTSEEGR
1470.6798	1469.6725	1469.6092	0.0633	266 -	277	1	---	ESYDNRDPMSEK
1470.6798	1469.6725	1469.6092	0.0633	266 -	277	1	---	ESYDNRDPMSEK

No match to: 713.4120, 768.5225, 1357.6074, 1571.8879, 1571.8879, 1778.8425, 1826.8568, 1826.8568, 1957.1014, 2256.0889

8. gi|157327315 **Mass:** 125165 **Score:** 54 **Expect:** 2.4 **Queries matched:** 9

unnamed protein product [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1135.5762	1134.5689	1134.5314	0.0375	148 -	156	0	---	CAFISLHCK
1135.5762	1134.5689	1134.5314	0.0375	663 -	671	0	---	CAFISLHCK
1291.6766	1290.6693	1290.6325	0.0368	147 -	156	1	---	RCAFISLHCK
1291.6766	1290.6693	1290.6325	0.0368	662 -	671	1	---	RCAFISLHCK
1571.8879	1570.8806	1570.9082	-0.0276	846 -	858	1	---	LLPKDILFENLTR
1571.8879	1570.8806	1570.9082	-0.0276	846 -	858	1	---	LLPKDILFENLTR
1826.8568	1825.8495	1825.9607	-0.1112	780 -	794	1	---	LLDLNDCEKLEVIPR
1826.8568	1825.8495	1825.9607	-0.1112	780 -	794	1	3	LLDLNDCEKLEVIPR
2256.0889	2255.0816	2255.2300	-0.1484	387 -	405	1	---	EGKILIILDDIWTEIDLEK

No match to: 713.4120, 768.5225, 973.5364, 1057.4436, 1357.6074, 1470.6798, 1470.6798, 1778.8425, 1957.1014

9. gi|57899087 **Mass:** 14450 **Score:** 54 **Expect:** 2.5 **Queries matched:** 4

hypothetical protein [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1135.5762	1134.5689	1134.5273	0.0416	38 -	49	0	---	GGGATAMAALCR
1135.5762	1134.5689	1134.5273	0.0416	66 -	77	0	---	GGGATAMAALCR
1291.6766	1290.6693	1290.6284	0.0409	37 -	49	1	5	RGGGATAMAALCR
1291.6766	1290.6693	1290.6284	0.0409	66 -	78	1	---	GGGATAMAALCRR

No match to: 713.4120, 768.5225, 973.5364, 1057.4436, 1357.6074, 1470.6798, 1470.6798, 1571.8879, 1571.8879,

1778.8425, 1826.8568, 1826.8568, 1957.1014, 2256.0889

10. gi|145343374 **Mass:** 21734 **Score:** 53 **Expect:** 2.8 **Queries matched:** 6
predicted protein [Ostreococcus lucimarinus CCE9901]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1291.6766	1290.6693	1290.6204	0.0490	69	-	80	0	9	TGEPLNEFGATR
1291.6766	1290.6693	1290.6204	0.0490	69	-	80	0	---	TGEPLNEFGATR
1571.8879	1570.8806	1570.8202	0.0604	55	-	68	1	---	DLVLDERGDLIDAK
1571.8879	1570.8806	1570.8202	0.0604	55	-	68	1	10	DLVLDERGDLIDAK
1826.8568	1825.8495	1825.8594	-0.0099	37	-	54	1	---	ARAVPEGGDDAATPDWAK
1826.8568	1825.8495	1825.8594	-0.0099	37	-	54	1	---	ARAVPEGGDDAATPDWAK

No match to: 713.4120, 768.5225, 973.5364, 1057.4436, 1135.5762, 1135.5762, 1357.6074, 1470.6798, 1470.6798, 1778.8425, 1957.1014, 2256.0889

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 18

Protein View

Match to: **gi|3901094** Score: **228** Expect: **9.6e-018**
pollen allergen Phl pI [Phleum pratense]

Nominal mass (M_r): **28584**; Calculated pI value: **7.53**
NCBI BLAST search of gi|3901094 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

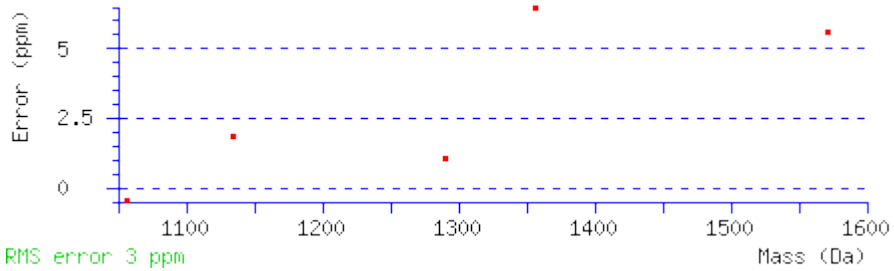
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **14%**

Matched peptides shown in **Bold Red**

```
   1 MASSSSVLLV VALFAVFLGS AHGIPKVPPG PNITATYGDK WLDAKSTWYG
  51 KPTAAGPKDN GGACGYKDVD KPPFSGMTGC GNTPIFKSGR GCGSCFEIKC
 101 TKPEACSGEP VVVHITDDNE EPIAAYHFDL SGIAFGSMAK KGDEQKLRSA
 151 GEVEIQFRRV KCKYPEGTKV TFHVEKGSNP NYLALLVKFV AGDGDVVAVD
 201 IKEKGKDKWI ALKESWGAIW RIDTPEVLKG PFTVRYTTEG GTKGEAKDVI
 251 PEGWKADTAY ESK
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
88 - 99	1357.6074	1356.6001	1356.5914	0.0087	1	SGRGCGSCFEIK	(No match)
91 - 99	1057.4436	1056.4363	1056.4368	-0.0005	0	GCGSCFEIK	(No match)
149 - 158	1135.5762	1134.5689	1134.5669	0.0021	0	SAGEVEIQFR	(Ions score 60)
149 - 158	1135.5762	1134.5689	1134.5669	0.0021	0	SAGEVEIQFR	(No match)
149 - 159	1291.6766	1290.6693	1290.6680	0.0014	1	SAGEVEIQFRR	(Ions score 34)
149 - 159	1291.6766	1290.6693	1290.6680	0.0014	1	SAGEVEIQFRR	(No match)
222 - 235	1571.8879	1570.8806	1570.8718	0.0088	1	IDTPEVLKGPFTVR	(No match)
222 - 235	1571.8879	1570.8806	1570.8718	0.0088	1	IDTPEVLKGPFTVR	(Ions score 73)



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	Accession	Mass	Score	Description
1.	gi|3901094	28584	275	pollen allergen Phl pI [Phleum pratense]
2.	gi|1582250	28542	260	allergen PhI p I
3.	gi|108705735	13020	49	hypothetical protein LOC_Os03g01560 [Oryza sativa (japonica cultivar-group)]
4.	gi|222625176	110501	47	hypothetical protein OsJ_11363 [Oryza sativa Japonica Group]
5.	gi|218193105	110599	47	hypothetical protein OsI_12150 [Oryza sativa Indica Group]

Results List

1. gi|3901094 **Mass:** 28584 **Score:** 275 **Expect:** 1.9e-022 **Queries matched:** 13

pollen allergen Phl pI [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1004.4977	1003.4904	1003.4875	0.0029	214	221	0	---	ESWGAIWR
1057.4410	1056.4337	1056.4368	-0.0031	91	99	0	---	GCGSCFEIK
1135.5773	1134.5700	1134.5669	0.0032	149	158	0	52	SAGEVEIQFR
1135.5773	1134.5700	1134.5669	0.0032	149	158	0	---	SAGEVEIQFR
1288.7156	1287.7083	1287.7186	-0.0103	177	188	0	---	GSNPNYLALLVK
1291.6731	1290.6658	1290.6680	-0.0021	149	159	1	46	SAGEVEIQFRR
1291.6731	1290.6658	1290.6680	-0.0021	149	159	1	---	SAGEVEIQFRR
1357.6017	1356.5944	1356.5914	0.0030	88	99	1	1	SGRGCGSCFEIK
1357.6017	1356.5944	1356.5914	0.0030	88	99	1	---	SGRGCGSCFEIK
1404.7252	1403.7179	1403.7296	-0.0116	189	202	0	---	FVAGDGDVVAVDIK
1571.8796	1570.8723	1570.8718	0.0005	222	235	1	---	IDTPEVLKGPFTVR
1571.8796	1570.8723	1570.8718	0.0005	222	235	1	94	IDTPEVLKGPFTVR
1661.8712	1660.8639	1660.8671	-0.0032	189	204	1	---	FVAGDGDVVAVDIKEK

No match to: 713.4092, 724.4952, 734.4943, 750.5146, 768.5223, 838.5319, 864.5438, 886.9845, 973.5504, 1111.6461, 1275.0961, 1279.7662, 1334.8851, 1345.5874, 1448.9158, 1518.8381, 1560.8591, 1619.0618, 1792.8754, 1805.8756, 1940.9850, 2044.0988, 2050.0757, 2130.1726, 2166.0784, 2230.2034, 2240.1431, 2247.2046, 2537.2002, 2565.1833, 2823.3286, 2923.3540, 3015.4795, 3015.4795, 3031.4668, 3516.6541

2. gi|1582250 **Mass:** 28542 **Score:** 260 **Expect:** 6e-021 **Queries matched:** 12

allergen PhI p I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1004.4977	1003.4904	1003.4875	0.0029	213	220	0	---	ESWGAIWR
1057.4410	1056.4337	1056.4368	-0.0031	91	99	0	---	GCGSCFEIK
1135.5773	1134.5700	1134.5669	0.0032	149	158	0	52	SAGEVEIQFR
1135.5773	1134.5700	1134.5669	0.0032	149	158	0	---	SAGEVEIQFR
1288.7156	1287.7083	1287.7186	-0.0103	177	188	0	---	GSNPNYLALLVK

1291.6731	1290.6658	1290.6680	-0.0021	149 - 159	1	46	SAGEVEIQFRR
1291.6731	1290.6658	1290.6680	-0.0021	149 - 159	1	---	SAGEVEIQFRR
1357.6017	1356.5944	1356.5914	0.0030	88 - 99	1	1	SGRGCGSCFEIK
1357.6017	1356.5944	1356.5914	0.0030	88 - 99	1	---	SGRGCGSCFEIK
1404.7252	1403.7179	1403.7520	-0.0341	147 - 158	1	---	LRSAGEVEIQFR
1571.8796	1570.8723	1570.8718	0.0005	221 - 234	1	---	IDTPEVLKGPFTVR
1571.8796	1570.8723	1570.8718	0.0005	221 - 234	1	94	IDTPEVLKGPFTVR

No match to: 713.4092, 724.4952, 734.4943, 750.5146, 768.5223, 838.5319, 864.5438, 886.9845, 973.5504, 1111.6461, 1275.0961, 1279.7662, 1334.8851, 1345.5874, 1448.9158, 1518.8381, 1560.8591, 1619.0618, 1661.8712, 1792.8754, 1805.8756, 1940.9850, 2044.0988, 2050.0757, 2130.1726, 2166.0784, 2230.2034, 2240.1431, 2247.2046, 2537.2002, 2565.1833, 2823.3286, 2923.3540, 3015.4795, 3015.4795, 3031.4668, 3516.6541

3. gi|108705735 **Mass:** 13020 **Score:** 49 **Expect:** 7.4 **Queries matched:** 6

hypothetical protein LOC_Os03g01560 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1135.5773	1134.5700	1134.6032	-0.0332	3 - 15	0	6	TGGGFGGAALSIK
1135.5773	1134.5700	1134.6032	-0.0332	3 - 15	0	---	TGGGFGGAALSIK
1291.6731	1290.6658	1290.7043	-0.0385	2 - 15	1	2	RTGGGFGGAALSIK
1291.6731	1290.6658	1290.7043	-0.0385	2 - 15	1	---	RTGGGFGGAALSIK
1518.8381	1517.8308	1517.7851	0.0457	91 - 103	1	---	TGPYPLPTRHSHR
2166.0784	2165.0711	2165.0952	-0.0241	81 - 99	1	---	QALHGVWGCRTGPYPLPTR

No match to: 713.4092, 724.4952, 734.4943, 750.5146, 768.5223, 838.5319, 864.5438, 886.9845, 973.5504, 1004.4977, 1057.4410, 1111.6461, 1275.0961, 1279.7662, 1288.7156, 1334.8851, 1345.5874, 1357.6017, 1357.6017, 1404.7252, 1448.9158, 1560.8591, 1571.8796, 1571.8796, 1619.0618, 1661.8712, 1792.8754, 1805.8756, 1940.9850, 2044.0988, 2050.0757, 2130.1726, 2230.2034, 2240.1431, 2247.2046, 2537.2002, 2565.1833, 2823.3286, 2923.3540, 3015.4795, 3015.4795, 3031.4668, 3516.6541

4. gi|222625176 **Mass:** 110501 **Score:** 47 **Expect:** 11 **Queries matched:** 7

hypothetical protein OsJ_11363 [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1004.4977	1003.4904	1003.5021	-0.0117	783 - 790	0	---	HIHCNPVK
1135.5773	1134.5700	1134.5821	-0.0121	754 - 763	0	11	TGGALWDIFR
1135.5773	1134.5700	1134.5821	-0.0121	754 - 763	0	---	TGGALWDIFR
1291.6731	1290.6658	1290.6832	-0.0174	754 - 764	1	19	TGGALWDIFRR
1291.6731	1290.6658	1290.6832	-0.0174	754 - 764	1	---	TGGALWDIFRR
2240.1431	2239.1358	2239.0864	0.0494	47 - 65	1	---	FNELLNDEAIMMKPSKESK + Oxidation (M)
2537.2002	2536.1929	2536.2631	-0.0701	2 - 27	0	---	GLSDYDLMGVAVPGTGVGGPHPEALK

No match to: 713.4092, 724.4952, 734.4943, 750.5146, 768.5223, 838.5319, 864.5438, 886.9845, 973.5504, 1057.4410, 1111.6461, 1275.0961, 1279.7662, 1288.7156, 1334.8851, 1345.5874, 1357.6017, 1357.6017, 1404.7252, 1448.9158, 1518.8381, 1560.8591, 1571.8796, 1571.8796, 1619.0618, 1661.8712, 1792.8754, 1805.8756, 1940.9850, 2044.0988, 2050.0757, 2130.1726, 2166.0784, 2230.2034, 2247.2046, 2565.1833, 2823.3286, 2923.3540, 3015.4795, 3015.4795, 3031.4668, 3516.6541

5. gi|218193105 **Mass:** 110599 **Score:** 47 **Expect:** 11 **Queries matched:** 7

hypothetical protein OsI_12150 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1004.4977	1003.4904	1003.5021	-0.0117	783	790	0	---	HIHCNPVK
1135.5773	1134.5700	1134.5821	-0.0121	754	763	0	11	TGGALWDIFR
1135.5773	1134.5700	1134.5821	-0.0121	754	763	0	---	TGGALWDIFR
1291.6731	1290.6658	1290.6832	-0.0174	754	764	1	19	TGGALWDIFRR
1291.6731	1290.6658	1290.6832	-0.0174	754	764	1	---	TGGALWDIFRR
2240.1431	2239.1358	2239.0864	0.0494	47	65	1	---	FNELLNDEAIMMKPSKESK + Oxidation (M)
2537.2002	2536.1929	2536.2631	-0.0701	2	27	0	---	GLSDYDLMGVAVPGTGVGGPHPEALK

No match to: 713.4092, 724.4952, 734.4943, 750.5146, 768.5223, 838.5319, 864.5438, 886.9845, 973.5504, 1057.4410, 1111.6461, 1275.0961, 1279.7662, 1288.7156, 1334.8851, 1345.5874, 1357.6017, 1357.6017, 1404.7252, 1448.9158, 1518.8381, 1560.8591, 1571.8796, 1571.8796, 1619.0618, 1661.8712, 1792.8754, 1805.8756, 1940.9850, 2044.0988, 2050.0757, 2130.1726, 2166.0784, 2230.2034, 2247.2046, 2565.1833, 2823.3286, 2923.3540, 3015.4795, 3015.4795, 3031.4668, 3516.6541

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 49

Protein View

Match to: **gi|3901094** Score: **275** Expect: **1.9e-022**
pollen allergen Phl pI [Phleum pratense]

Nominal mass (M_r): **28584**; Calculated pI value: **7.53**
NCBI BLAST search of gi|3901094 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **27%**

Matched peptides shown in **Bold Red**

```
    1 MASSSSVLLV VALFAVFLGS AHGIPKVPPG PNITATYGDK WLDAKSTWYG
   51 KPTAAGPKDN GGACGYKDVD KPPFSGMTGC GNTPIFKSGR GCGSCFEIKC
  101 TKPEACSGEP VVVHITDDNE EPIAAYHFDL SGIAFGSMAK KGDEQKLRSA
  151 GEVEIQFRRV KCKYPEGTKV TFHVEKGSNP NYLALLVKFV AGDGDVVAVD
  201 IKEKGKDKWI ALKESWGAIW RIDTPEVLKG PFTVRYTTEG GTKGEAKDVI
  251 PEGWKADTAY ESK
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
88 - 99	1357.6017	1356.5944	1356.5914	0.0030	1	SGRGCGSCFEIK	(Ions score 1)
88 - 99	1357.6017	1356.5944	1356.5914	0.0030	1	SGRGCGSCFEIK	(No match)
91 - 99	1057.4410	1056.4337	1056.4368	-0.0031	0	GCGSCFEIK	(No match)
149 - 158	1135.5773	1134.5700	1134.5669	0.0032	0	SAGEVEIQFR	(Ions score 52)
149 - 158	1135.5773	1134.5700	1134.5669	0.0032	0	SAGEVEIQFR	(No match)
149 - 159	1291.6731	1290.6658	1290.6680	-0.0021	1	SAGEVEIQFRR	(Ions score 46)
149 - 159	1291.6731	1290.6658	1290.6680	-0.0021	1	SAGEVEIQFRR	(No match)
177 - 188	1288.7156	1287.7083	1287.7186	-0.0103	0	GSNPNYLALLVK	(No match)
189 - 202	1404.7252	1403.7179	1403.7296	-0.0116	0	FVAGDGDVVAVDIK	(No match)
189 - 204	1661.8712	1660.8639	1660.8671	-0.0032	1	FVAGDGDVVAVDIKEK	(No match)
214 - 221	1004.4977	1003.4904	1003.4875	0.0029	0	ESWGAIWR	(No match)
222 - 235	1571.8796	1570.8723	1570.8718	0.0005	1	IDTPEVLKGPFTVR	(No match)
222 - 235	1571.8796	1570.8723	1570.8718	0.0005	1	IDTPEVLKGPFTVR	(Ions score 94)

Spot 113

Index

	Accession	Mass	Score	Description
1.	gi|1582250	28542	265	allergen PhI p I
2.	gi|3901094	28584	265	pollen allergen Phl pI [Phleum pratense]
3.	gi|57899087	14450	53	hypothetical protein [Oryza sativa Japonica Group]
4.	gi|222844420	69729	48	predicted protein [Populus trichocarpa]
5.	gi|125583469	50632	47	hypothetical protein OsJ_08155 [Oryza sativa Japonica Group]
6.	gi|195654073	11983	47	hypothetical protein [Zea mays]
7.	gi|115453645	52978	46	Os03g0430400 [Oryza sativa (japonica cultivar-group)]
8.	gi|45735863	62457	46	hypothetical protein [Oryza sativa Japonica Group]
9.	gi|115448309	62516	46	Os02g0717600 [Oryza sativa (japonica cultivar-group)]
10.	gi|108705735	13020	45	hypothetical protein LOC_Os03g01560 [Oryza sativa (japonica cultivar-group)]

Results List

1. gi|1582250 **Mass:** 28542 **Score:** 265 **Expect:** 1.9e-021 **Queries matched:** 9

allergen PhI p I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1057.4406	1056.4333	1056.4368	-0.0035	91	99	0	---	GCGSCFEIK
1135.5850	1134.5777	1134.5669	0.0109	149	158	0	---	SAGEVEIQFR
1135.5850	1134.5777	1134.5669	0.0109	149	158	0	59	SAGEVEIQFR
1291.6805	1290.6732	1290.6680	0.0053	149	159	1	59	SAGEVEIQFRR
1291.6805	1290.6732	1290.6680	0.0053	149	159	1	---	SAGEVEIQFRR
1357.6044	1356.5971	1356.5914	0.0057	88	99	1	2	SGRGCGSCFEIK
1357.6044	1356.5971	1356.5914	0.0057	88	99	1	---	SGRGCGSCFEIK
1571.8843	1570.8770	1570.8718	0.0052	221	234	1	---	IDTPEVLKGPFTVR
1571.8843	1570.8770	1570.8718	0.0052	221	234	1	88	IDTPEVLKGPFTVR

No match to: 713.4052, 724.4925, 768.5173, 881.2715, 973.5442, 1275.1039, 1518.8414, 2239.1553, 2246.2056, 2524.2290, 2524.2290, 2540.2144, 2824.3171

2. gi|3901094 **Mass:** 28584 **Score:** 265 **Expect:** 1.9e-021 **Queries matched:** 9

pollen allergen Phl pI [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1057.4406	1056.4333	1056.4368	-0.0035	91	99	0	---	GCGSCFEIK
1135.5850	1134.5777	1134.5669	0.0109	149	158	0	---	SAGEVEIQFR
1135.5850	1134.5777	1134.5669	0.0109	149	158	0	59	SAGEVEIQFR
1291.6805	1290.6732	1290.6680	0.0053	149	159	1	59	SAGEVEIQFRR
1291.6805	1290.6732	1290.6680	0.0053	149	159	1	---	SAGEVEIQFRR
1357.6044	1356.5971	1356.5914	0.0057	88	99	1	2	SGRGCGSCFEIK
1357.6044	1356.5971	1356.5914	0.0057	88	99	1	---	SGRGCGSCFEIK

1571.8843	1570.8770	1570.8718	0.0052	222 - 235	1	---	IDTPEVLKGPFTVR
1571.8843	1570.8770	1570.8718	0.0052	222 - 235	1	88	IDTPEVLKGPFTVR

No match to: 713.4052, 724.4925, 768.5173, 881.2715, 973.5442, 1275.1039, 1518.8414, 2239.1553, 2246.2056, 2524.2290, 2524.2290, 2540.2144, 2824.3171

3. gi|57899087 **Mass:** 14450 **Score:** 53 **Expect:** 2.9 **Queries matched:** 4

hypothetical protein [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1135.5850	1134.5777	1134.5273	0.0504	66 -	77	0	---	GGGATAMAALCR
1135.5850	1134.5777	1134.5273	0.0504	38 -	49	0	---	GGGATAMAALCR
1291.6805	1290.6732	1290.6284	0.0448	37 -	49	1	8	RGGGATAMAALCR
1291.6805	1290.6732	1290.6284	0.0448	66 -	78	1	---	GGGATAMAALCRR

No match to: 713.4052, 724.4925, 768.5173, 881.2715, 973.5442, 1057.4406, 1275.1039, 1357.6044, 1357.6044, 1518.8414, 1571.8843, 1571.8843, 2239.1553, 2246.2056, 2524.2290, 2524.2290, 2540.2144, 2824.3171

4. gi|222844420 **Mass:** 69729 **Score:** 48 **Expect:** 10 **Queries matched:** 7

predicted protein [Populus trichocarpa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
973.5442	972.5369	972.5141	0.0229	326 -	333	1	---	THGIRDFK
1135.5850	1134.5777	1134.5889	-0.0112	167 -	175	0	---	MIQTLINMR + Oxidation (M)
1135.5850	1134.5777	1134.5889	-0.0112	167 -	175	0	1	MIQTLINMR + Oxidation (M)
1291.6805	1290.6732	1290.6853	-0.0120	228 -	239	1	19	VMKLVETEGSAK
1291.6805	1290.6732	1290.6853	-0.0120	228 -	239	1	---	VMKLVETEGSAK
1518.8414	1517.8341	1517.7772	0.0569	240 -	251	1	---	ERPPFLCTNRTK
2246.2056	2245.1983	2245.1306	0.0677	112 -	130	1	---	ELFDGTELYFGNPLDKFLK

No match to: 713.4052, 724.4925, 768.5173, 881.2715, 1057.4406, 1275.1039, 1357.6044, 1357.6044, 1571.8843, 1571.8843, 2239.1553, 2524.2290, 2524.2290, 2540.2144, 2824.3171

5. gi|125583469 **Mass:** 50632 **Score:** 47 **Expect:** 11 **Queries matched:** 4

hypothetical protein OsJ_08155 [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1135.5850	1134.5777	1134.5669	0.0108	392 -	401	0	---	QDSFAIGELR
1135.5850	1134.5777	1134.5669	0.0108	392 -	401	0	13	QDSFAIGELR
1291.6805	1290.6732	1290.6680	0.0052	392 -	402	1	23	QDSFAIGELRR
1291.6805	1290.6732	1290.6680	0.0052	392 -	402	1	---	QDSFAIGELRR

No match to: 713.4052, 724.4925, 768.5173, 881.2715, 973.5442, 1057.4406, 1275.1039, 1357.6044, 1357.6044, 1518.8414, 1571.8843, 1571.8843, 2239.1553, 2246.2056, 2524.2290, 2524.2290, 2540.2144, 2824.3171

6. gi|195654073 **Mass:** 11983 **Score:** 47 **Expect:** 14 **Queries matched:** 4

hypothetical protein [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1135.5850	1134.5777	1134.6032	-0.0255	49 -	59	0	---	GVASLYGAELR

1135.5850	1134.5777	1134.6032	-0.0255	49 - 59	0	---	GVASLYGAELR
1291.6805	1290.6732	1290.7043	-0.0311	49 - 60	1	24	GVASLYGAELRR
1291.6805	1290.6732	1290.7043	-0.0311	49 - 60	1	---	GVASLYGAELRR

No match to: 713.4052, 724.4925, 768.5173, 881.2715, 973.5442, 1057.4406, 1275.1039, 1357.6044, 1357.6044, 1518.8414, 1571.8843, 1571.8843, 2239.1553, 2246.2056, 2524.2290, 2524.2290, 2540.2144, 2824.3171

7. gi|115453645 **Mass:** 52978 **Score:** 46 **Expect:** 15 **Queries matched:** 4

Os03g0430400 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start - End	Miss	Ions	Peptide
1135.5850	1134.5777	1134.5821	-0.0044	259 - 268	0	---	TGGALWDIFR
1135.5850	1134.5777	1134.5821	-0.0044	259 - 268	0	16	TGGALWDIFR
1291.6805	1290.6732	1290.6832	-0.0100	259 - 269	1	21	TGGALWDIFRR
1291.6805	1290.6732	1290.6832	-0.0100	259 - 269	1	---	TGGALWDIFRR

No match to: 713.4052, 724.4925, 768.5173, 881.2715, 973.5442, 1057.4406, 1275.1039, 1357.6044, 1357.6044, 1518.8414, 1571.8843, 1571.8843, 2239.1553, 2246.2056, 2524.2290, 2524.2290, 2540.2144, 2824.3171

8. gi|45735863 **Mass:** 62457 **Score:** 46 **Expect:** 16 **Queries matched:** 4

hypothetical protein [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start - End	Miss	Ions	Peptide
1135.5850	1134.5777	1134.5669	0.0108	507 - 516	0	---	QDSFAIGELR
1135.5850	1134.5777	1134.5669	0.0108	507 - 516	0	13	QDSFAIGELR
1291.6805	1290.6732	1290.6680	0.0052	507 - 517	1	23	QDSFAIGELRR
1291.6805	1290.6732	1290.6680	0.0052	507 - 517	1	---	QDSFAIGELRR

No match to: 713.4052, 724.4925, 768.5173, 881.2715, 973.5442, 1057.4406, 1275.1039, 1357.6044, 1357.6044, 1518.8414, 1571.8843, 1571.8843, 2239.1553, 2246.2056, 2524.2290, 2524.2290, 2540.2144, 2824.3171

9. gi|115448309 **Mass:** 62516 **Score:** 46 **Expect:** 16 **Queries matched:** 4

Os02g0717600 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start - End	Miss	Ions	Peptide
1135.5850	1134.5777	1134.5669	0.0108	505 - 514	0	---	QDSFAIGELR
1135.5850	1134.5777	1134.5669	0.0108	505 - 514	0	13	QDSFAIGELR
1291.6805	1290.6732	1290.6680	0.0052	505 - 515	1	23	QDSFAIGELRR
1291.6805	1290.6732	1290.6680	0.0052	505 - 515	1	---	QDSFAIGELRR

No match to: 713.4052, 724.4925, 768.5173, 881.2715, 973.5442, 1057.4406, 1275.1039, 1357.6044, 1357.6044, 1518.8414, 1571.8843, 1571.8843, 2239.1553, 2246.2056, 2524.2290, 2524.2290, 2540.2144, 2824.3171

10. gi|108705735 **Mass:** 13020 **Score:** 45 **Expect:** 20 **Queries matched:** 5

hypothetical protein LOC_Os03g01560 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start - End	Miss	Ions	Peptide
1135.5850	1134.5777	1134.6032	-0.0255	3 - 15	0	---	TGGGFGGAALSIK
1135.5850	1134.5777	1134.6032	-0.0255	3 - 15	0	7	TGGGFGGAALSIK
1291.6805	1290.6732	1290.7043	-0.0311	2 - 15	1	---	RTGGGFGGAALSIK

1291.6805 1290.6732 1290.7043 -0.0311   2 - 15   1 --- RTGGGFGGAALSIK
1518.8414 1517.8341 1517.7851   0.0490   91 - 103   1 --- TGPYPLPTRHSHR
No match to: 713.4052, 724.4925, 768.5173, 881.2715, 973.5442, 1057.4406, 1275.1039, 1357.6044, 1357.6044, 1571.8843, 1571.8843, 2239.1553, 2246.2056, 2524.2290, 2524.2290, 2540.2144, 2824.3171

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 22

Protein View

Match to: **gi|3901094** Score: **265** Expect: **1.9e-021**
pollen allergen Phl pI [Phleum pratense]

Nominal mass (M_r): **28584**; Calculated pI value: **7.53**
NCBI BLAST search of gi|3901094 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

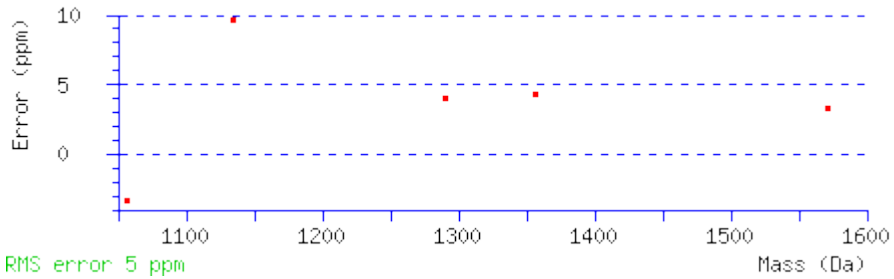
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **14%**

Matched peptides shown in **Bold Red**

```
   1 MASSSSVLLV VALFAVFLGS AHGIPKVPPG PNITATYGDK WLDAKSTWYG
  51 KPTAAGPKDN GGACGYKDVD KPPFSGMTGC GNTPIFKSGR GCGSCFEIKC
 101 TKPEACSGEP VVVHITDDNE EPIAAYHFDL SGIAFGSMAK KGDEQKLRSA
 151 GEVEIQFRRV KCKYPEGTKV TFHVEKGSNP NYLALLVKFV AGDGDVVAVD
 201 IKEKGKDKWI ALKESWGAIW RIDTPEVLKG PFTVRYTTEG GTKGEAKDVI
 251 PEGWKADTAY ESK
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
88 - 99	1357.6044	1356.5971	1356.5914	0.0057	1	SGRGCGSCFEIK	(Ions score 2)
88 - 99	1357.6044	1356.5971	1356.5914	0.0057	1	SGRGCGSCFEIK	(No match)
91 - 99	1057.4406	1056.4333	1056.4368	-0.0035	0	GCGSCFEIK	(No match)
149 - 158	1135.5850	1134.5777	1134.5669	0.0109	0	SAGEVEIQFR	(No match)
149 - 158	1135.5850	1134.5777	1134.5669	0.0109	0	SAGEVEIQFR	(Ions score 59)
149 - 159	1291.6805	1290.6732	1290.6680	0.0053	1	SAGEVEIQFRR	(Ions score 59)
149 - 159	1291.6805	1290.6732	1290.6680	0.0053	1	SAGEVEIQFRR	(No match)
222 - 235	1571.8843	1570.8770	1570.8718	0.0052	1	IDTPEVLKGPFTVR	(No match)
222 - 235	1571.8843	1570.8770	1570.8718	0.0052	1	IDTPEVLKGPFTVR	(Ions score 88)



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Index

	Accession	Mass	Score	Description
1.	gi|3901094	28584	92	pollen allergen Phl pI [Phleum pratense]
2.	gi|1582250	28542	92	allergen PhI p I
3.	gi|79322231	12069	84	unknown protein [Arabidopsis thaliana]
4.	gi|46390015	24106	61	fructose-bisphosphate aldolase-like protein [Oryza sativa Japonica Group]
5.	gi|94312898	26621	59	CheW protein [Ralstonia metallidurans CH34]
6.	gi|108864609	43147	59	expressed protein [Oryza sativa (japonica cultivar-group)]
7.	gi|30685538	10608	58	unknown protein [Arabidopsis thaliana]
8.	gi|19338630	51110	55	48-kDa glycoprotein precursor [Corylus avellana]
9.	gi|145360628	17394	53	unknown protein [Arabidopsis thaliana]
10.	gi|62361173	19379	53	resistance protein PLTR [Arachis hypogaea]

Results List

1. gi|3901094 **Mass:** 28584 **Score:** 92 **Expect:** 0.00041 **Queries matched:** 3

pollen allergen Phl pI [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1291.6726	1290.6653	1290.6680	-0.0026	149	159	1	---	SAGEVEIQFRR
1571.8851	1570.8778	1570.8718	0.0060	222	235	1	---	IDTPEVLKGPFTVR
1571.8851	1570.8778	1570.8718	0.0060	222	235	1	71	IDTPEVLKGPFTVR

No match to: 713.4065, 768.5207, 864.5054, 881.2744, 1077.5911, 1077.5911, 1233.6743, 1233.6743

2. gi|1582250 **Mass:** 28542 **Score:** 92 **Expect:** 0.00042 **Queries matched:** 3

allergen PhI p I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1291.6726	1290.6653	1290.6680	-0.0026	149	159	1	---	SAGEVEIQFRR
1571.8851	1570.8778	1570.8718	0.0060	221	234	1	---	IDTPEVLKGPFTVR
1571.8851	1570.8778	1570.8718	0.0060	221	234	1	71	IDTPEVLKGPFTVR

No match to: 713.4065, 768.5207, 864.5054, 881.2744, 1077.5911, 1077.5911, 1233.6743, 1233.6743

3. gi|79322231 **Mass:** 12069 **Score:** 84 **Expect:** 0.0024 **Queries matched:** 6

unknown protein [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1077.5911	1076.5838	1076.5535	0.0303	92	101	0	---	SLAELSCVAK
1077.5911	1076.5838	1076.5535	0.0303	92	101	0	---	SLAELSCVAK
1233.6743	1232.6670	1232.6546	0.0124	91	101	1	17	RSLAELSCVAK
1233.6743	1232.6670	1232.6546	0.0124	91	101	1	---	RSLAELSCVAK
1571.8851	1570.8778	1570.7781	0.0997	14	26	1	---	VFLLLGGMCMSRR + 2 Oxidation (M)
1571.8851	1570.8778	1570.7781	0.0997	13	25	1	---	RVFLLLGGMCMSR + 2 Oxidation (M)

No match to: 713.4065, 768.5207, 864.5054, 881.2744, 1291.6726

4. gi|46390015 **Mass:** 24106 **Score:** 61 **Expect:** 0.5 **Queries matched:** 4

fructose-bisphosphate aldolase-like protein [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1077.5911	1076.5838	1076.5098	0.0740	78	88	0	11	TASTSDAATPR
1077.5911	1076.5838	1076.5098	0.0740	78	88	0	---	TASTSDAATPR
1233.6743	1232.6670	1232.6109	0.0561	77	88	1	28	RTASTSDAATPR
1233.6743	1232.6670	1232.6109	0.0561	77	88	1	---	RTASTSDAATPR

No match to: 713.4065, 768.5207, 864.5054, 881.2744, 1291.6726, 1571.8851, 1571.8851

5. gi|94312898 **Mass:** 26621 **Score:** 59 **Expect:** 0.76 **Queries matched:** 4

CheW protein [Ralstonia metallidurans CH34]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1077.5911	1076.5838	1076.6454	-0.0616	121	131	0	13	HAALIGVAAVR
1077.5911	1076.5838	1076.6454	-0.0616	121	131	0	---	HAALIGVAAVR
1233.6743	1232.6670	1232.7465	-0.0795	120	131	1	23	RHAALIGVAAVR
1233.6743	1232.6670	1232.7465	-0.0795	120	131	1	---	RHAALIGVAAVR

No match to: 713.4065, 768.5207, 864.5054, 881.2744, 1291.6726, 1571.8851, 1571.8851

6. gi|108864609 **Mass:** 43147 **Score:** 59 **Expect:** 0.82 **Queries matched:** 6

expressed protein [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
864.5054	863.4981	863.4613	0.0368	234	240	0	---	QDVLHPR
1077.5911	1076.5838	1076.5839	-0.0001	232	240	1	---	GRQDVLHPR
1077.5911	1076.5838	1076.5839	-0.0001	232	240	1	---	GRQDVLHPR
1233.6743	1232.6670	1232.6010	0.0660	334	343	1	12	RDEHDVHLGR
1233.6743	1232.6670	1232.6010	0.0660	335	344	1	---	DEHDVHLGRR
1291.6726	1290.6653	1290.6581	0.0072	25	35	1	---	SAPPTPHSWRR

No match to: 713.4065, 768.5207, 881.2744, 1571.8851, 1571.8851

7. gi|30685538 **Mass:** 10608 **Score:** 58 **Expect:** 1.1 **Queries matched:** 5

unknown protein [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
864.5054	863.4981	863.4534	0.0447	57	64	1	---	CKGTGTIK
1077.5911	1076.5838	1076.5614	0.0224	28	37	0	---	VDAFIAASQR
1077.5911	1076.5838	1076.5614	0.0224	28	37	0	---	VDAFIAASQR
1233.6743	1232.6670	1232.6625	0.0045	28	38	1	10	VDAFIAASQRR
1233.6743	1232.6670	1232.6625	0.0045	28	38	1	---	VDAFIAASQRR

No match to: 713.4065, 768.5207, 881.2744, 1291.6726, 1571.8851, 1571.8851

8. gi|19338630 **Mass:** 51110 **Score:** 55 **Expect:** 2 **Queries matched:** 7

48-kDa glycoprotein precursor [Corylus avellana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1077.5911	1076.5838	1076.5250	0.0588	395 -	403	0	0	GNIVNEFER
1077.5911	1076.5838	1076.5865	-0.0027	80 -	88	0	---	VQVLENFTK
1233.6743	1232.6670	1232.6877	-0.0206	80 -	89	1	---	VQVLENFTKR
1233.6743	1232.6670	1232.6877	-0.0206	80 -	89	1	---	VQVLENFTKR
1291.6726	1290.6653	1290.7044	-0.0390	90 -	100	1	---	SRLLSGIENFR
1571.8851	1570.8778	1570.7851	0.0927	140 -	152	1	---	RESFNVEHGDIIR
1571.8851	1570.8778	1570.7851	0.0927	140 -	152	1	---	RESFNVEHGDIIR

No match to: 713.4065, 768.5207, 864.5054, 881.2744

9. gi|145360628 **Mass:** 17394 **Score:** 53 **Expect:** 3 **Queries matched:** 6

unknown protein [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1077.5911	1076.5838	1076.5172	0.0666	96 -	105	0	2	ADIATMQAEK
1077.5911	1076.5838	1076.5172	0.0666	96 -	105	0	---	ADIATMQAEK
1233.6743	1232.6670	1232.6183	0.0487	96 -	106	1	12	ADIATMQAEKR
1233.6743	1232.6670	1232.6183	0.0487	96 -	106	1	---	ADIATMQAEKR
1571.8851	1570.8778	1570.8137	0.0642	21 -	35	1	---	SLSSGNHVDKLGMVK
1571.8851	1570.8778	1570.8137	0.0642	21 -	35	1	---	SLSSGNHVDKLGMVK

No match to: 713.4065, 768.5207, 864.5054, 881.2744, 1291.6726

10. gi|62361173 **Mass:** 19379 **Score:** 53 **Expect:** 3.2 **Queries matched:** 5

resistance protein PLTR [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
713.4065	712.3992	712.3802	0.0190	74 -	78	1	---	LCHKR
1077.5911	1076.5838	1076.5648	0.0191	1 -	12	1	---	GMGGGGKTTIAK
1077.5911	1076.5838	1076.5648	0.0191	1 -	12	1	---	GMGGGGKTTIAK
1233.6743	1232.6670	1232.6699	-0.0029	120 -	129	1	14	MRGVEPIIYR
1233.6743	1232.6670	1232.6699	-0.0029	120 -	129	1	---	MRGVEPIIYR

No match to: 768.5207, 864.5054, 881.2744, 1291.6726, 1571.8851, 1571.8851

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 11

Protein View

Match to: **gi|3901094** Score: **92** Expect: **0.00041**
pollen allergen Phl pI [Phleum pratense]

Nominal mass (M_r): **28584**; Calculated pI value: **7.53**
NCBI BLAST search of gi|3901094 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

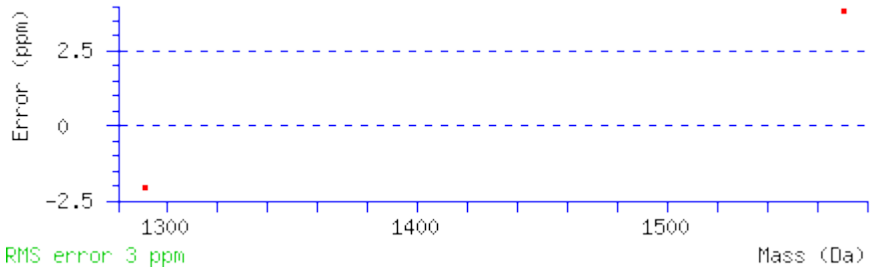
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **9%**

Matched peptides shown in **Bold Red**

```
     1 MASSSSVLLV VALFAVFLGS AHGIPKVPPG PNITATYGDK WLDAKSTWYG
    51 KPTAAGPKDN GGACGYKDVD KPPFSGMTGC GNTPIFKSGR GCGSCFEIKC
   101 TKPEACSGEP VVVHITDDNE EPIAAYHFDL SGIAFGSMAK KGDEQKLRSA
   151 GEVEIQFRRV KCKYPEGTKV TFHVEKGSNP NYLALLVKFV AGDGDVVAVD
   201 IKEKGKDKWI ALKESWGAIW RIDTPEVLKG PFTVRYTTEG GTKGEAKDVI
   251 PEGWKADTAY ESK
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
149 - 159	1291.6726	1290.6653	1290.6680	-0.0026	1	SAGEVEIQFRR	(No match)
222 - 235	1571.8851	1570.8778	1570.8718	0.0060	1	IDTPEVLKGPFTVR	(No match)
222 - 235	1571.8851	1570.8778	1570.8718	0.0060	1	IDTPEVLKGPFTVR	(Ions score 71)



Peptide View

MS/MS Fragmentation of **IDTPEVLKGPFTVR**
Found in **gi|3901094**, pollen allergen Phl pI [Phleum pratense]

Match to Query 11: 1570.877824 from(1571.885100,1+)
MaldiWellID: 71010, SpectrumID: 163032,

Click mouse within plot area to zoom in by factor of two about that point
Or, to Da
MONOISOTOPIC mass of neutral peptide Mr(calc): 1570.8718
Fixed modifications: Carbamidomethyl (C)
Ions Score: 71 **Expect:** 4.1e-005
Matches (Bold Red): 25/217 fragment ions using 22 most intense peaks

#	Immon.	a	a*	a^0	b	b*	b^0	Seq.	v	y	y*	y^0	#
1	**86.0964**	**86.0964**			114.0913			I					14
2	88.0393	201.1234		183.1128	**229.1183**		211.1077	D	1398.7739	1458.7951	1441.7685	1440.7845	13
3	74.0600	302.1710		284.1605	**330.1660**		312.1554	T	1297.7263	**1343.7681**	1326.7416	1325.7576	12
4	**70.0651**	399.2238		381.2132	427.2187		409.2082	P	1200.6735	**1242.7204**	1225.6939	1224.7099	11
5	102.0550	528.2664		510.2558	**556.2613**		538.2507	E	1071.6309	1145.6677	1128.6411	1127.6571	10
6	72.0808	627.3348		609.3242	655.3297		637.3192	V	972.5625	**1016.6251**	999.5986	998.6145	9
7	**86.0964**	740.4189		722.4083	768.4138		750.4032	L	859.4784	917.5567	900.5301	899.5461	8

8	101.1073	868.5138	851.4873	850.5033	896.5087	879.4822	878.4982	K	731.3835	804.4726	787.4461	786.4621	7
9	30.0338	925.5353	908.5087	907.5247	953.5302	936.5037	935.5196	G		676.3777	659.3511	658.3671	6
10	70.0651	1022.5880	1005.5615	1004.5775	1050.5830	1033.5564	1032.5724	P	577.3093	619.3562	602.3297	601.3456	5
11	120.0808	1169.6565	1152.6299	1151.6459	1197.6514	1180.6248	1179.6408	F	430.2408	522.3034	505.2769	504.2929	4
12	74.0600	1270.7041	1253.6776	1252.6936	1298.6990	1281.6725	1280.6885	T	329.1932	375.2350	358.2085	357.2245	3
13	72.0808	1369.7725	1352.7460	1351.7620	1397.7675	1380.7409	1379.7569	V	230.1248	274.1874	257.1608		2
14	129.1135							R	74.0236	175.1189	158.0924		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
DT	189.0870	217.0819	DTP	286.1397	314.1347	DTPE	415.1823	443.1772
DTPEV	514.2507	542.2457	DTPEVL	627.3348	655.3297	TP	171.1128	199.1077
TPE	300.1554	328.1503	TPEV	399.2238	427.2187	TPEVL	512.3079	540.3028
TPEVLK	640.4028	668.3977	TPEVLKG	697.4243	725.4192	PE	199.1077	227.1026
PEV	298.1761	326.1710	PEVL	411.2602	439.2551	PEVLK	539.3551	567.3501
PEVLKG	596.3766	624.3715	PEVLKGP	693.4294	721.4243	EV	201.1234	229.1183
EVL	314.2074	342.2023	EVLK	442.3024	470.2973	EVLKG	499.3238	527.3188
EVLKGP	596.3766	624.3715	VL	185.1648	213.1597	VLK	313.2598	341.2547
VLKG	370.2813	398.2762	VLKGP	467.3340	495.3289	VLKGPF	614.4024	642.3973
LK	214.1914	242.1863	LKG	271.2128	299.2078	LKGP	368.2656	396.2605
LKGPF	515.3340	543.3289	LKGPFT	616.3817	644.3766	KG	158.1288	186.1237
KGP	255.1815	283.1765	KGPF	402.2500	430.2449	KGPFT	503.2976	531.2925
KGPFTV	602.3660	630.3610	GP	127.0866	155.0815	GPF	274.1550	302.1499
GPFT	375.2027	403.1976	GPFTV	474.2711	502.2660	PF	217.1335	245.1284
PFT	318.1812	346.1761	PFTV	417.2496	445.2445	FT	221.1285	249.1234
FTV	320.1969	348.1918	TV	173.1285	201.1234			

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Index

	Accession	Mass	Score	Description
1.	gi|3901094	28584	101	pollen allergen Phl pI [Phleum pratense]
2.	gi|1582250	28542	88	allergen PhI p I
3.	gi|125531990	40337	52	hypothetical protein OsI_33653 [Oryza sativa Indica Group]
4.	gi|255564126	19229	50	pentatricopeptide repeat-containing protein, putative [Ricinus communis]
5.	gi|168060349	17471	47	predicted protein [Physcomitrella patens subsp. patens]
6.	gi|145341238	12212	46	predicted protein [Ostreococcus lucimarinus CCE9901]
7.	gi|52077370	5874	44	hypothetical protein [Oryza sativa Japonica Group]
8.	gi|16517019	29228	44	beta-expansin OsEXPB13 [Oryza sativa]
9.	gi|116054789	67850	42	DNA replication licensing factor, putative (ISS) [Ostreococcus tauri]
10.	gi|3024020	17731	42	RecName: Full=Eukaryotic translation initiation factor 5A-3; Short=eIF-5A-3; AltName: Full=eIF

Results List

1. gi|3901094 **Mass:** 28584 **Score:** 101 **Expect:** 4.8e-005 **Queries matched:** 14

pollen allergen Phl pI [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1004.4994	1003.4921	1003.4875	0.0046	214	221	0	---	ESWGAIWR
1057.4429	1056.4356	1056.4368	-0.0012	91	99	0	---	GCGSCFEIK
1057.4429	1056.4356	1056.4368	-0.0012	91	99	0	---	GCGSCFEIK
1135.5831	1134.5758	1134.5669	0.0090	149	158	0	---	SAGEVEIQFR
1135.5831	1134.5758	1134.5669	0.0090	149	158	0	---	SAGEVEIQFR
1291.6770	1290.6697	1290.6680	0.0018	149	159	1	8	SAGEVEIQFRR
1291.6770	1290.6697	1290.6680	0.0018	149	159	1	---	SAGEVEIQFRR
1357.6090	1356.6017	1356.5914	0.0103	88	99	1	---	SGRGCGSCFEIK
1357.6090	1356.6017	1356.5914	0.0103	88	99	1	---	SGRGCGSCFEIK
1404.7385	1403.7312	1403.7296	0.0017	189	202	0	---	FVAGDGDVVAVDIK
1571.8834	1570.8761	1570.8718	0.0043	222	235	1	---	IDTPEVLKGPFTVR
1661.8845	1660.8772	1660.8671	0.0101	189	204	1	---	FVAGDGDVVAVDIKEK
2129.1895	2128.1822	2128.1680	0.0143	170	188	1	---	VTFHVEKGSNPNYLALLVK
3090.3774	3089.3701	3089.3680	0.0021	59	87	1	---	DNGGACGYKDVDKPPFSGMTGCGNTPIFK

No match to: 713.4033, 724.4960, 734.4932, 736.4900, 750.5147, 768.5157, 782.4718, 838.5277, 848.5242, 864.5429, 973.5500, 1133.7042, 1215.6549, 1275.1162, 1279.7664, 1315.7185, 1315.7185, 1334.8818, 1448.9176, 1518.8439, 1560.8657, 1562.9249, 1618.0773, 1732.1088, 1805.8971, 1940.9431, 2044.1256, 2050.0930, 2051.0679, 2061.1184, 2230.2222, 2239.1448, 2246.2126, 2302.2534, 2409.0627, 2564.1907, 2663.3904, 2779.9524, 2780.4636, 2823.3259, 2922.3547, 3107.3955, 3241.7551, 3332.5764, 3349.6138

2. gi|1582250 **Mass:** 28542 **Score:** 88 **Expect:** 0.001 **Queries matched:** 13

allergen PhI p I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1004.4994	1003.4921	1003.4875	0.0046	213	220	0	---	ESWGAIWR
1057.4429	1056.4356	1056.4368	-0.0012	91	99	0	---	GCGSCFEIK
1057.4429	1056.4356	1056.4368	-0.0012	91	99	0	---	GCGSCFEIK
1135.5831	1134.5758	1134.5669	0.0090	149	158	0	---	SAGEVEIQFR
1135.5831	1134.5758	1134.5669	0.0090	149	158	0	---	SAGEVEIQFR
1291.6770	1290.6697	1290.6680	0.0018	149	159	1	8	SAGEVEIQFRR
1291.6770	1290.6697	1290.6680	0.0018	149	159	1	---	SAGEVEIQFRR
1357.6090	1356.6017	1356.5914	0.0103	88	99	1	---	SGRGCGSCFEIK
1357.6090	1356.6017	1356.5914	0.0103	88	99	1	---	SGRGCGSCFEIK
1404.7385	1403.7312	1403.7520	-0.0208	147	158	1	---	LRSAGEVEIQFR
1571.8834	1570.8761	1570.8718	0.0043	221	234	1	---	IDTPEVLKGPFTVR
2129.1895	2128.1822	2128.1680	0.0143	170	188	1	---	VTFHVEKGSNPNYLALLVK
3090.3774	3089.3701	3089.3680	0.0021	59	87	1	---	DNGGACGYKDVDKPPFSGMTGCGNTPIFK

No match to: 713.4033, 724.4960, 734.4932, 736.4900, 750.5147, 768.5157, 782.4718, 838.5277, 848.5242, 864.5429, 973.5500, 1133.7042, 1215.6549, 1275.1162, 1279.7664, 1315.7185, 1315.7185, 1334.8818, 1448.9176, 1518.8439, 1560.8657, 1562.9249, 1618.0773, 1661.8845, 1732.1088, 1805.8971, 1940.9431, 2044.1256, 2050.0930, 2051.0679, 2061.1184, 2230.2222, 2239.1448, 2246.2126, 2302.2534, 2409.0627, 2564.1907, 2663.3904, 2779.9524, 2780.4636, 2823.3259, 2922.3547, 3107.3955, 3241.7551, 3332.5764, 3349.6138

3. gi|125531990 **Mass:** 40337 **Score:** 52 **Expect:** 3.9 **Queries matched:** 7

hypothetical protein OsI_33653 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1560.8657	1559.8584	1559.8419	0.0165	35	48	1	---	TKNVVPNGQFITSR
1805.8971	1804.8898	1804.8379	0.0519	185	201	0	---	HFGDLLASGDGADVEFR
2051.0679	2050.0606	2049.9571	0.1035	271	289	1	---	GTTREEAAMAQNMIVAADR + Oxidation (M)
2061.1184	2060.1111	2060.0074	0.1037	185	203	1	---	HFGDLLASGDGADVEFRVR
2409.0627	2408.0554	2408.2079	-0.1525	343	365	1	---	AATATDGFGQLSCPTVLKELMAK
2823.3259	2822.3186	2822.4054	-0.0868	2	28	1	---	PMTMTADEPTTASAIVAGVKTGHHVLR + 2 Oxidation (M)
2922.3547	2921.3474	2921.4561	-0.1087	1	28	1	---	MPMTMTADEPTTASAIVAGVKTGHHVLR

No match to: 713.4033, 724.4960, 734.4932, 736.4900, 750.5147, 768.5157, 782.4718, 838.5277, 848.5242, 864.5429, 973.5500, 1004.4994, 1057.4429, 1057.4429, 1133.7042, 1135.5831, 1135.5831, 1215.6549, 1275.1162, 1279.7664, 1291.6770, 1291.6770, 1315.7185, 1315.7185, 1334.8818, 1357.6090, 1357.6090, 1404.7385, 1448.9176, 1518.8439, 1562.9249, 1571.8834, 1618.0773, 1661.8845, 1732.1088, 1940.9431, 2044.1256, 2050.0930, 2129.1895, 2230.2222, 2239.1448, 2246.2126, 2302.2534, 2564.1907, 2663.3904, 2779.9524, 2780.4636, 3090.3774, 3107.3955, 3241.7551, 3332.5764, 3349.6138

4. gi|255564126 **Mass:** 19229 **Score:** 50 **Expect:** 6.8 **Queries matched:** 5

pentatricopeptide repeat-containing protein, putative [Ricinus communis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
2246.2126	2245.2053	2245.0758	0.1295	9	28	1	---	SKGIEPNVFTYSSLMDGLCK
2823.3259	2822.3186	2822.4245	-0.1059	95	119	1	---	LTWSLHVRTNNIVVQGLCSSGDPNR
2922.3547	2921.3474	2921.4817	-0.1343	103	128	1	---	TNNIVVQGLCSSGDPNRAFQLYLSLR

3107.3955	3106.3882	3106.5388	-0.1506	139 - 165	0	---	LVDEMVLDGCVPDQLTLTIVLCGFLDR + Oxidation (M)
3332.5764	3331.5691	3331.5774	-0.0082	11 - 40	1	---	GIEPNVFTYSSLMDGLCKDGCSSQALELLK

No match to: 713.4033, 724.4960, 734.4932, 736.4900, 750.5147, 768.5157, 782.4718, 838.5277, 848.5242, 864.5429, 973.5500, 1004.4994, 1057.4429, 1057.4429, 1133.7042, 1135.5831, 1135.5831, 1215.6549, 1275.1162, 1279.7664, 1291.6770, 1291.6770, 1315.7185, 1315.7185, 1334.8818, 1357.6090, 1357.6090, 1404.7385, 1448.9176, 1518.8439, 1560.8657, 1562.9249, 1571.8834, 1618.0773, 1661.8845, 1732.1088, 1805.8971, 1940.9431, 2044.1256, 2050.0930, 2051.0679, 2061.1184, 2129.1895, 2230.2222, 2239.1448, 2302.2534, 2409.0627, 2564.1907, 2663.3904, 2779.9524, 2780.4636, 3090.3774, 3241.7551, 3349.6138

5. gi|168060349 **Mass:** 17471 **Score:** 47 **Expect:** 12 **Queries matched:** 6

predicted protein [Physcomitrella patens subsp. patens]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1135.5831	1134.5758	1134.6140	-0.0382	1 -	10	1	---	MPMKLVTVGK + 2 Oxidation (M)
1135.5831	1134.5758	1134.6140	-0.0382	1 -	10	1	---	MPMKLVTVGK + 2 Oxidation (M)
1518.8439	1517.8366	1517.8452	-0.0086	13 -	26	1	---	GAALENVALEYIKK
1661.8845	1660.8772	1660.8783	-0.0011	11 -	25	1	---	DRGAALENVALEYIK
3241.7551	3240.7478	3240.8208	-0.0730	123 -	149	1	---	LSTMVLNHQIAFLVLLEQIYRAWTILR
3349.6138	3348.6065	3348.5680	0.0385	30 -	58	1	---	YCPFEEVQLRPNPKNSSDVPTQVSSEGER

No match to: 713.4033, 724.4960, 734.4932, 736.4900, 750.5147, 768.5157, 782.4718, 838.5277, 848.5242, 864.5429, 973.5500, 1004.4994, 1057.4429, 1057.4429, 1133.7042, 1215.6549, 1275.1162, 1279.7664, 1291.6770, 1291.6770, 1315.7185, 1315.7185, 1334.8818, 1357.6090, 1357.6090, 1404.7385, 1448.9176, 1560.8657, 1562.9249, 1571.8834, 1618.0773, 1732.1088, 1805.8971, 1940.9431, 2044.1256, 2050.0930, 2051.0679, 2061.1184, 2129.1895, 2230.2222, 2239.1448, 2246.2126, 2302.2534, 2409.0627, 2564.1907, 2663.3904, 2779.9524, 2780.4636, 2823.3259, 2922.3547, 3090.3774, 3107.3955, 3332.5764

6. gi|145341238 **Mass:** 12212 **Score:** 46 **Expect:** 16 **Queries matched:** 7

predicted protein [Ostreococcus lucimarinus CCE9901]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1057.4429	1056.4356	1056.5096	-0.0739	38 -	46	1	---	SACFLKMGK + Oxidation (M)
1057.4429	1056.4356	1056.5096	-0.0739	38 -	46	1	---	SACFLKMGK + Oxidation (M)
1315.7185	1314.7112	1314.6680	0.0432	57 -	68	1	---	AVDIDGHYAKAR
1315.7185	1314.7112	1314.6680	0.0432	57 -	68	1	---	AVDIDGHYAKAR
1404.7385	1403.7312	1403.7078	0.0234	71 -	85	0	---	VGAAALAMGNTDVAK + Oxidation (M)
1560.8657	1559.8584	1559.8089	0.0495	71 -	86	1	---	VGAAALAMGNTDVAKR + Oxidation (M)
1661.8845	1660.8772	1660.8566	0.0207	69 -	85	1	---	TRVGAAALAMGNTDVAK + Oxidation (M)

No match to: 713.4033, 724.4960, 734.4932, 736.4900, 750.5147, 768.5157, 782.4718, 838.5277, 848.5242, 864.5429, 973.5500, 1004.4994, 1133.7042, 1135.5831, 1135.5831, 1215.6549, 1275.1162, 1279.7664, 1291.6770, 1291.6770, 1334.8818, 1357.6090, 1357.6090, 1448.9176, 1518.8439, 1562.9249, 1571.8834, 1618.0773, 1732.1088, 1805.8971, 1940.9431, 2044.1256, 2050.0930, 2051.0679, 2061.1184, 2129.1895, 2230.2222, 2239.1448, 2246.2126, 2302.2534, 2409.0627, 2564.1907, 2663.3904, 2779.9524, 2780.4636, 2823.3259, 2922.3547, 3090.3774, 3107.3955, 3241.7551, 3332.5764, 3349.6138

7. gi|52077370 **Mass:** 5874 **Score:** 44 **Expect:** 24 **Queries matched:** 6

hypothetical protein [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1004.4994	1003.4921	1003.5120	-0.0199	1	9	1	---	MAPSDAKLR + Oxidation (M)
1135.5831	1134.5758	1134.5517	0.0242	30	39	0	---	DDTTVQTLSR
1135.5831	1134.5758	1134.5517	0.0242	30	39	0	---	DDTTVQTLSR
1291.6770	1290.6697	1290.6528	0.0170	29	39	1	1	RDDTTVQTLSR
1291.6770	1290.6697	1290.6528	0.0170	29	39	1	---	RDDTTVQTLSR
1805.8971	1804.8898	1804.9835	-0.0937	40	57	1	---	EWRAAPDPAGGGAIIVIL

No match to: 713.4033, 724.4960, 734.4932, 736.4900, 750.5147, 768.5157, 782.4718, 838.5277, 848.5242, 864.5429, 973.5500, 1057.4429, 1057.4429, 1133.7042, 1215.6549, 1275.1162, 1279.7664, 1315.7185, 1315.7185, 1334.8818, 1357.6090, 1357.6090, 1404.7385, 1448.9176, 1518.8439, 1560.8657, 1562.9249, 1571.8834, 1618.0773, 1661.8845, 1732.1088, 1940.9431, 2044.1256, 2050.0930, 2051.0679, 2061.1184, 2129.1895, 2230.2222, 2239.1448, 2246.2126, 2302.2534, 2409.0627, 2564.1907, 2663.3904, 2779.9524, 2780.4636, 2823.3259, 2922.3547, 3090.3774, 3107.3955, 3241.7551, 3332.5764, 3349.6138

8. gi|16517019 **Mass:** 29228 **Score:** 44 **Expect:** 26 **Queries matched:** 8

beta-expansin OsEXPB13 [Oryza sativa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1004.4994	1003.4921	1003.4875	0.0046	214	221	0	---	ESWGAIWR
1057.4429	1056.4356	1056.4368	-0.0012	91	99	0	---	GCGSCFEIK
1057.4429	1056.4356	1056.4368	-0.0012	91	99	0	---	GCGSCFEIK
1357.6090	1356.6017	1356.5802	0.0216	88	99	1	---	DGKGCGSCFEIK
1357.6090	1356.6017	1356.5802	0.0216	88	99	1	---	DGKGCGSCFEIK
1562.9249	1561.9176	1561.8140	0.1036	164	176	1	---	YPADTKITFHIEK
2129.1895	2128.1822	2128.0687	0.1135	236	255	1	---	VTTEGGEKIIAEDAIPDGWK
2564.1907	2563.1834	2563.3059	-0.1224	1	26	0	---	MASSSLLLASVVVAAMVSAVSCGPPK + 2 Oxidation (M)

No match to: 713.4033, 724.4960, 734.4932, 736.4900, 750.5147, 768.5157, 782.4718, 838.5277, 848.5242, 864.5429, 973.5500, 1133.7042, 1135.5831, 1135.5831, 1215.6549, 1275.1162, 1279.7664, 1291.6770, 1291.6770, 1315.7185, 1315.7185, 1334.8818, 1404.7385, 1448.9176, 1518.8439, 1560.8657, 1571.8834, 1618.0773, 1661.8845, 1732.1088, 1805.8971, 1940.9431, 2044.1256, 2050.0930, 2051.0679, 2061.1184, 2230.2222, 2239.1448, 2246.2126, 2302.2534, 2409.0627, 2663.3904, 2779.9524, 2780.4636, 2823.3259, 2922.3547, 3090.3774, 3107.3955, 3241.7551, 3332.5764, 3349.6138

9. gi|116054789 **Mass:** 67850 **Score:** 42 **Expect:** 37 **Queries matched:** 9

DNA replication licensing factor, putative (ISS) [Ostreococcus tauri]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
838.5277	837.5204	837.4960	0.0245	128	134	1	---	TLKSVYK
1291.6770	1290.6697	1290.7084	-0.0387	135	144	1	---	TYLDVFHIRK
1291.6770	1290.6697	1290.6462	0.0235	552	563	1	---	ACLNTSGSGRLR
1560.8657	1559.8584	1559.8572	0.0012	410	422	1	---	HLVSLHYKNPPQK
2050.0930	2049.0857	2048.9948	0.0909	275	294	1	---	GMYTSGRGSSAVGLTAYVTR + Oxidation (M)
2061.1184	2060.1111	2060.0095	0.1016	295	313	1	---	DPESKDMVLESGALVLSDR
2246.2126	2245.2053	2245.1855	0.0199	389	406	1	---	FDLLYLLLDRPNPETDRR
2564.1907	2563.1834	2563.2111	-0.0277	441	463	0	---	ANVQPVLSDEASEELVEGYVEMR

2663.3904	2662.3831	2662.2115	0.1717	177 - 199	1	---	NQGPGQQMEFTPERMAEIEELGR + Oxidation (M)

No match to: 713.4033, 724.4960, 734.4932, 736.4900, 750.5147, 768.5157, 782.4718, 848.5242, 864.5429, 973.5500, 1004.4994, 1057.4429, 1057.4429, 1133.7042, 1135.5831, 1135.5831, 1215.6549, 1275.1162, 1279.7664, 1315.7185, 1315.7185, 1334.8818, 1357.6090, 1357.6090, 1404.7385, 1448.9176, 1518.8439, 1562.9249, 1571.8834, 1618.0773, 1661.8845, 1732.1088, 1805.8971, 1940.9431, 2044.1256, 2051.0679, 2129.1895, 2230.2222, 2239.1448, 2302.2534, 2409.0627, 2779.9524, 2780.4636, 2823.3259, 2922.3547, 3090.3774, 3107.3955, 3241.7551, 3332.5764, 3349.6138

10. gi|3024020 **Mass:** 17731 **Score:** 42 **Expect:** 37 **Queries matched:** 6

RecName: Full=Eukaryotic translation initiation factor 5A-3; Short=eIF-5A-3; AltName: Full=eIF-4D

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
848.5242	847.5169	847.4650	0.0519	42 -	49	0	---	VVEVSTSK
1135.5831	1134.5758	1134.5669	0.0090	126 -	135	1	---	QVKDGFQEGK
1135.5831	1134.5758	1134.5669	0.0090	126 -	135	1	---	QVKDGFQEGK
1404.7385	1403.7312	1403.7707	-0.0394	30 -	41	1	---	NGYIVIKGRPCK
2050.0930	2049.0857	2049.0121	0.0736	136 -	154	0	---	DLVVSVMSAMGEEQINAIK + Oxidation (M)
2564.1907	2563.1834	2563.2872	-0.1038	136 -	159	1	---	DLVVSVMSAMGEEQINAIKDIGTK + Oxidation (M)

No match to: 713.4033, 724.4960, 734.4932, 736.4900, 750.5147, 768.5157, 782.4718, 838.5277, 864.5429, 973.5500, 1004.4994, 1057.4429, 1057.4429, 1133.7042, 1215.6549, 1275.1162, 1279.7664, 1291.6770, 1291.6770, 1315.7185, 1315.7185, 1334.8818, 1357.6090, 1357.6090, 1448.9176, 1518.8439, 1560.8657, 1562.9249, 1571.8834, 1618.0773, 1661.8845, 1732.1088, 1805.8971, 1940.9431, 2044.1256, 2051.0679, 2061.1184, 2129.1895, 2230.2222, 2239.1448, 2246.2126, 2302.2534, 2409.0627, 2663.3904, 2779.9524, 2780.4636, 2823.3259, 2922.3547, 3090.3774, 3107.3955, 3241.7551, 3332.5764, 3349.6138

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 59

Protein View

Match to: **gi|3901094** Score: **101** Expect: **4.8e-005**
pollen allergen Phl pI [Phleum pratense]

Nominal mass (M_r): **28584**; Calculated pI value: **7.53**
NCBI BLAST search of gi|3901094 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **41%**

Matched peptides shown in **Bold Red**

```
    1 MASSSSVLLV VALFAVFLGS AHGIPKVPPG PNITATYGDK WLDAKSTWYG
   51 KPTAAGPKDN GGACGYKDVD KPPFSGMTGC GNTPIFKSGR GCGSCFEIKC
  101 TKPEACSGEP VVVHITDDNE EPIAAYHFDL SGIAFGSMAK KGDEQKLRSA
  151 GEVEIQFRRV KCKYPEGTKV TFHVEKGSNP NYLALLVKFV AGDGDVVAVD
  201 IKEKGKDKWI ALKESWGAIW RIDTPEVLKG PFTVRYTTEG GTKGEAKDVI
  251 PEGWKADTAY ESK
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
59 - 87	3090.3774	3089.3701	3089.3680	0.0021	1	DNGGACGYKDVDKPPFSGMTGCGNTPIFK	(No match)
88 - 99	1357.6090	1356.6017	1356.5914	0.0103	1	SGRGCGSCFEIK	(No match)
88 - 99	1357.6090	1356.6017	1356.5914	0.0103	1	SGRGCGSCFEIK	(No match)
91 - 99	1057.4429	1056.4356	1056.4368	-0.0012	0	GCGSCFEIK	(No match)
91 - 99	1057.4429	1056.4356	1056.4368	-0.0012	0	GCGSCFEIK	(No match)
149 - 158	1135.5831	1134.5758	1134.5669	0.0090	0	SAGEVEIQFR	(No match)
149 - 158	1135.5831	1134.5758	1134.5669	0.0090	0	SAGEVEIQFR	(No match)
149 - 159	1291.6770	1290.6697	1290.6680	0.0018	1	SAGEVEIQFRR	(Ions score 8)
149 - 159	1291.6770	1290.6697	1290.6680	0.0018	1	SAGEVEIQFRR	(No match)
170 - 188	2129.1895	2128.1822	2128.1680	0.0143	1	VTFHVEKGSNPNYLALLVK	(No match)
189 - 202	1404.7385	1403.7312	1403.7296	0.0017	0	FVAGDGDVVAVDIK	(No match)
189 - 204	1661.8845	1660.8772	1660.8671	0.0101	1	FVAGDGDVVAVDIKEK	(No match)
214 - 221	1004.4994	1003.4921	1003.4875	0.0046	0	ESWGAIWR	(No match)
222 - 235	1571.8834	1570.8761	1570.8718	0.0043	1	IDTPEVLKGPFTVR	(No match)

Spot 116

Index

	Accession	Mass	Score	Description
1.	gi|1582250	28542	123	allergen PhI p I
2.	gi|3901094	28584	123	pollen allergen Phl pI [Phleum pratense]
3.	gi|168037743	110199	48	predicted protein [Physcomitrella patens subsp. patens]
4.	gi|125595970	16578	43	hypothetical protein OsJ_20040 [Oryza sativa Japonica Group]
5.	gi|186397273	118471	41	sucrose phosphate synthase [Pyrus pyrifolia]
6.	gi|224127156	20452	39	predicted protein [Populus trichocarpa]
7.	gi|222616985	53884	39	hypothetical protein OsJ_35899 [Oryza sativa Japonica Group]
8.	gi|27125518	40835	39	putative vacuolar ATPase subunit d [Mesembryanthemum crystallinum]
9.	gi|25986843	125895	38	phytochrome [Physcomitrella patens]
10.	gi|6007781	23935	38	NADH ubiquinone oxidoreductase PSST subunit [Lupinus luteus]

Results List

1. gi|1582250 **Mass:** 28542 **Score:** 123 **Expect:** 3e-007 **Queries matched:** 10

allergen PhI p I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1057.4441	1056.4368	1056.4368	0.0000	91	99	0	---	GCGSCFEIK
1057.4441	1056.4368	1056.4368	0.0000	91	99	0	---	GCGSCFEIK
1135.5826	1134.5753	1134.5669	0.0085	149	158	0	---	SAGEVEIQFR
1135.5826	1134.5753	1134.5669	0.0085	149	158	0	15	SAGEVEIQFR
1291.6781	1290.6708	1290.6680	0.0029	149	159	1	31	SAGEVEIQFRR
1291.6781	1290.6708	1290.6680	0.0029	149	159	1	---	SAGEVEIQFRR
1357.6125	1356.6052	1356.5914	0.0138	88	99	1	---	SGRGCGSCFEIK
1357.6125	1356.6052	1356.5914	0.0138	88	99	1	---	SGRGCGSCFEIK
1571.8868	1570.8795	1570.8718	0.0077	221	234	1	36	IDTPEVLKGPFTVR
1571.8868	1570.8795	1570.8718	0.0077	221	234	1	---	IDTPEVLKGPFTVR

No match to: 713.4024, 716.3567, 734.4904, 746.3582, 750.5112, 768.5145, 782.4667, 788.3723, 848.5196, 864.5249, 881.2829, 886.9791, 973.5495, 1098.0032, 1275.1194, 1279.7649, 1334.8788, 1448.9106, 1560.8683, 1734.9553, 2044.1248, 2051.0876, 2231.2241, 2564.2034, 2663.3596, 2780.9712, 2826.3203, 2922.3704, 3332.5647, 3349.6096

2. gi|3901094 **Mass:** 28584 **Score:** 123 **Expect:** 3e-007 **Queries matched:** 10

pollen allergen Phl pI [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1057.4441	1056.4368	1056.4368	0.0000	91	99	0	---	GCGSCFEIK
1057.4441	1056.4368	1056.4368	0.0000	91	99	0	---	GCGSCFEIK
1135.5826	1134.5753	1134.5669	0.0085	149	158	0	---	SAGEVEIQFR
1135.5826	1134.5753	1134.5669	0.0085	149	158	0	15	SAGEVEIQFR
1291.6781	1290.6708	1290.6680	0.0029	149	159	1	31	SAGEVEIQFRR

1291.6781	1290.6708	1290.6680	0.0029	149 - 159	1	---	SAGEVEIQFRR
1357.6125	1356.6052	1356.5914	0.0138	88 - 99	1	---	SGRGCGSCFEIK
1357.6125	1356.6052	1356.5914	0.0138	88 - 99	1	---	SGRGCGSCFEIK
1571.8868	1570.8795	1570.8718	0.0077	222 - 235	1	36	IDTPEVLKGPFTVR
1571.8868	1570.8795	1570.8718	0.0077	222 - 235	1	---	IDTPEVLKGPFTVR

No match to: 713.4024, 716.3567, 734.4904, 746.3582, 750.5112, 768.5145, 782.4667, 788.3723, 848.5196, 864.5249, 881.2829, 886.9791, 973.5495, 1098.0032, 1275.1194, 1279.7649, 1334.8788, 1448.9106, 1560.8683, 1734.9553, 2044.1248, 2051.0876, 2231.2241, 2564.2034, 2663.3596, 2780.9712, 2826.3203, 2922.3704, 3332.5647, 3349.6096

3. gi|168037743 **Mass:** 110199 **Score:** 48 **Expect:** 8.8 **Queries matched:** 10

predicted protein [Physcomitrella patens subsp. patens]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
746.3582	745.3509	745.3606	-0.0097	322 - 327		0	---	VEDDLR
973.5495	972.5422	972.5352	0.0070	624 - 632		1	---	AKASIAEQR
1135.5826	1134.5753	1134.5556	0.0197	154 - 163		0	---	FDDANALLEK
1135.5826	1134.5753	1134.5556	0.0197	154 - 163		0	---	FDDANALLEK
1560.8683	1559.8610	1559.7799	0.0811	242 - 254		1	---	IVQLEKCMEPASR
1734.9553	1733.9480	1733.8505	0.0975	50 - 63		1	---	IRMLEDQVEDLTEK + Oxidation (M)
2044.1248	2043.1175	2043.1186	-0.0011	379 - 396		1	---	FLGENVIAHVTQSKLLMK + Oxidation (M)
2663.3596	2662.3523	2662.2609	0.0914	87 - 109		1	---	TQSDDEYIVVEQEGPNDLENKLK
2826.3203	2825.3130	2825.3979	-0.0848	393 - 416		1	---	LLMKEFTELQSAHILYACESEVSK
2922.3704	2921.3631	2921.4267	-0.0635	581 - 606		1	---	NNVIHEQFASKLEEEASSLAADHNIR

No match to: 713.4024, 716.3567, 734.4904, 750.5112, 768.5145, 782.4667, 788.3723, 848.5196, 864.5249, 881.2829, 886.9791, 1057.4441, 1057.4441, 1098.0032, 1275.1194, 1279.7649, 1291.6781, 1291.6781, 1334.8788, 1357.6125, 1357.6125, 1448.9106, 1571.8868, 1571.8868, 2051.0876, 2231.2241, 2564.2034, 2780.9712, 3332.5647, 3349.6096

4. gi|125595970 **Mass:** 16578 **Score:** 43 **Expect:** 28 **Queries matched:** 6

hypothetical protein OsJ_20040 [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
746.3582	745.3509	745.3718	-0.0209	79 - 86		0	---	TGGVAEGR
1135.5826	1134.5753	1134.4975	0.0779	1 - 11		0	---	MDGVDAIGEGR + Oxidation (M)
1135.5826	1134.5753	1134.4975	0.0779	1 - 11		0	---	MDGVDAIGEGR + Oxidation (M)
1571.8868	1570.8795	1570.8653	0.0142	100 - 112		1	2	LDVLPPQFLMRSR
1571.8868	1570.8795	1570.8653	0.0142	100 - 112		1	---	LDVLPPQFLMRSR
2922.3704	2921.3631	2921.3974	-0.0343	22 - 53		1	---	QAGDAVDEGGGGPAALAAGDGSGTVGEARPRR

No match to: 713.4024, 716.3567, 734.4904, 750.5112, 768.5145, 782.4667, 788.3723, 848.5196, 864.5249, 881.2829, 886.9791, 973.5495, 1057.4441, 1057.4441, 1098.0032, 1275.1194, 1279.7649, 1291.6781, 1291.6781, 1334.8788, 1357.6125, 1357.6125, 1448.9106, 1560.8683, 1734.9553, 2044.1248, 2051.0876, 2231.2241, 2564.2034, 2663.3596, 2780.9712, 2826.3203, 3332.5647, 3349.6096

5. gi|186397273 **Mass:** 118471 **Score:** 41 **Expect:** 44 **Queries matched:** 9

sucrose phosphate synthase [Pyrus pyrifolia]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide

713.4024	712.3951	712.3908	0.0044	968 - 972	0	---	YLYVR
788.3723	787.3650	787.3976	-0.0326	878 - 884	0	---	WGAEGLR
973.5495	972.5422	972.5716	-0.0294	26 - 33	1	---	SSLLLRER
1135.5826	1134.5753	1134.5821	-0.0068	890 - 898	1	---	WVANFNEKK
1135.5826	1134.5753	1134.5821	-0.0068	890 - 898	1	---	WVANFNEKK
2051.0876	2050.0803	2050.0140	0.0664	520 - 538	0	---	DDIDEMSSTNASVLLSILK
2564.2034	2563.1961	2563.3050	-0.1089	520 - 542	1	---	DDIDEMSSTNASVLLSILKLIDR + Oxidation (M)
2663.3596	2662.3523	2662.2584	0.0939	1 - 25	0	---	MAGNDWVNSYLEAILDVGPGLDDAK
3332.5647	3331.5574	3331.6757	-0.1183	1 - 31	1	---	MAGNDWVNSYLEAILDVGPGLDDAKSSLLLR

No match to: 716.3567, 734.4904, 746.3582, 750.5112, 768.5145, 782.4667, 848.5196, 864.5249, 881.2829, 886.9791, 1057.4441, 1057.4441, 1098.0032, 1275.1194, 1279.7649, 1291.6781, 1291.6781, 1334.8788, 1357.6125, 1357.6125, 1448.9106, 1560.8683, 1571.8868, 1571.8868, 1734.9553, 2044.1248, 2231.2241, 2780.9712, 2826.3203, 2922.3704, 3349.6096

6. gi|224127156 **Mass:** 20452 **Score:** 39 **Expect:** 75 **Queries matched:** 5

predicted protein [Populus trichocarpa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1357.6125	1356.6052	1356.6067	-0.0014	160 - 170	0	---	IGNFPPCQHCK
1357.6125	1356.6052	1356.6067	-0.0014	160 - 170	0	---	IGNFPPCQHCK
2663.3596	2662.3523	2662.2155	0.1368	2 - 25	0	---	ASNMYSLASPPEFTGGNYQMQVVR + Oxidation (M)
2826.3203	2825.3130	2825.2458	0.0672	1 - 25	0	---	MASNMYSLASPPEFTGGNYQMQVVR + 3 Oxidation (M)
2922.3704	2921.3631	2921.3509	0.0122	2 - 27	1	---	ASNMYSLASPPEFTGGNYQMQVVRMK + Oxidation (M)

No match to: 713.4024, 716.3567, 734.4904, 746.3582, 750.5112, 768.5145, 782.4667, 788.3723, 848.5196, 864.5249, 881.2829, 886.9791, 973.5495, 1057.4441, 1057.4441, 1098.0032, 1135.5826, 1135.5826, 1275.1194, 1279.7649, 1291.6781, 1291.6781, 1334.8788, 1448.9106, 1560.8683, 1571.8868, 1571.8868, 1734.9553, 2044.1248, 2051.0876, 2231.2241, 2564.2034, 2780.9712, 3332.5647, 3349.6096

7. gi|222616985 **Mass:** 53884 **Score:** 39 **Expect:** 80 **Queries matched:** 7

hypothetical protein OsJ_35899 [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
746.3582	745.3509	745.3831	-0.0321	441 - 446	1	---	ANERTR
1135.5826	1134.5753	1134.6033	-0.0279	129 - 137	1	---	EKGEQILYR
1135.5826	1134.5753	1134.6033	-0.0279	129 - 137	1	---	EKGEQILYR
1291.6781	1290.6708	1290.6608	0.0101	110 - 120	0	11	WDALFNVLGEK
1291.6781	1290.6708	1290.6608	0.0101	110 - 120	0	---	WDALFNVLGEK
1448.9106	1447.9033	1447.8147	0.0887	30 - 42	0	---	DSRPISLLHSVPK
1560.8683	1559.8610	1559.8459	0.0151	110 - 122	1	---	WDALFNVLGEKLR

No match to: 713.4024, 716.3567, 734.4904, 750.5112, 768.5145, 782.4667, 788.3723, 848.5196, 864.5249, 881.2829, 886.9791, 973.5495, 1057.4441, 1057.4441, 1098.0032, 1275.1194, 1279.7649, 1334.8788, 1357.6125, 1357.6125, 1571.8868, 1571.8868, 1734.9553, 2044.1248, 2051.0876, 2231.2241, 2564.2034, 2663.3596, 2780.9712, 2826.3203, 2922.3704, 3332.5647, 3349.6096

8. gi|27125518 **Mass:** 40835 **Score:** 39 **Expect:** 82 **Queries matched:** 6

putative vacuolar ATPase subunit d [Mesembryanthemum crystallinum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
973.5495	972.5422	972.5127	0.0295	121	128	0	---	DVQELLEK
1357.6125	1356.6052	1356.6761	-0.0708	343	353	1	---	HRLHDGVVFMF
1357.6125	1356.6052	1356.6761	-0.0708	343	353	1	---	HRLHDGVVFMF
2231.2241	2230.2168	2230.0865	0.1303	220	240	1	---	ADNITINSFGPDLAPEGDRTK
2663.3596	2662.3523	2662.2749	0.0774	2	24	1	---	YGFEAMNFNVHGGYLEAIVRGYR
2826.3203	2825.3130	2825.3052	0.0078	1	24	1	---	MYGFEAMNFNVHGGYLEAIVRGYR + 2 Oxidation (M)

No match to: 713.4024, 716.3567, 734.4904, 746.3582, 750.5112, 768.5145, 782.4667, 788.3723, 848.5196, 864.5249, 881.2829, 886.9791, 1057.4441, 1057.4441, 1098.0032, 1135.5826, 1135.5826, 1275.1194, 1279.7649, 1291.6781, 1291.6781, 1334.8788, 1448.9106, 1560.8683, 1571.8868, 1571.8868, 1734.9553, 2044.1248, 2051.0876, 2564.2034, 2780.9712, 2922.3704, 3332.5647, 3349.6096

9. gi|25986843 **Mass:** 125895 **Score:** 38 **Expect:** 90 **Queries matched:** 11

phytochrome [Physcomitrella patens]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
713.4024	712.3951	712.3980	-0.0029	16	21	1	---	SKHSVR
1135.5826	1134.5753	1134.6284	-0.0531	844	853	0	---	YVDALLTVNK
1135.5826	1134.5753	1134.6284	-0.0531	844	853	0	---	YVDALLTVNK
1291.6781	1290.6708	1290.7295	-0.0587	844	854	1	---	YVDALLTVNKR
1291.6781	1290.6708	1290.7295	-0.0587	844	854	1	---	YVDALLTVNKR
1448.9106	1447.9033	1447.8034	0.0999	841	853	1	---	QGKYVDALLTVNK
1571.8868	1570.8795	1570.9082	-0.0287	1008	1021	0	---	LQQVLADFLLNAVK
1571.8868	1570.8795	1570.9082	-0.0287	1008	1021	0	---	LQQVLADFLLNAVK
2564.2034	2563.1961	2563.0988	0.0973	810	832	1	---	GQDAMTKFMIALNSAMDGQDTDR + 3 Oxidation (M)
3332.5647	3331.5574	3331.6362	-0.0788	130	160	1	---	TLFTPSSAAALEKCAGAVDVTMLNPISVHCR + Oxidation (M)
3349.6096	3348.6023	3348.7135	-0.1112	854	883	1	---	RTDAEGSITGVFCFLHTTSVELLQALTVQR

No match to: 716.3567, 734.4904, 746.3582, 750.5112, 768.5145, 782.4667, 788.3723, 848.5196, 864.5249, 881.2829, 886.9791, 973.5495, 1057.4441, 1057.4441, 1098.0032, 1275.1194, 1279.7649, 1334.8788, 1357.6125, 1357.6125, 1560.8683, 1734.9553, 2044.1248, 2051.0876, 2231.2241, 2663.3596, 2780.9712, 2826.3203, 2922.3704

10. gi|6007781 **Mass:** 23935 **Score:** 38 **Expect:** 92 **Queries matched:** 6

NADH ubiquinone oxidoreductase PSST subunit [Lupinus luteus]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1135.5826	1134.5753	1134.5128	0.0626	67	75	0	---	VDDLMNWAR + Oxidation (M)
1135.5826	1134.5753	1134.5128	0.0626	67	75	0	---	VDDLMNWAR + Oxidation (M)
1291.6781	1290.6708	1290.6139	0.0570	67	76	1	---	VDDLMNWARR + Oxidation (M)
1291.6781	1290.6708	1290.6139	0.0570	67	76	1	---	VDDLMNWARR + Oxidation (M)
2826.3203	2825.3130	2825.2692	0.0439	76	100	1	---	RGSIWPMTFGLACCAVEMMHTGAAR + Oxidation (M)
3332.5647	3331.5574	3331.4704	0.0870	77	105	1	---	GSIWPMTFGLACCAVEMMHTGAARYDLDR + Oxidation (M)

No match to: 713.4024, 716.3567, 734.4904, 746.3582, 750.5112, 768.5145, 782.4667, 788.3723, 848.5196, 864.5249, 881.2829, 886.9791, 973.5495, 1057.4441, 1057.4441, 1098.0032, 1275.1194, 1279.7649, 1334.8788, 1357.6125, 1357.6125, 1448.9106, 1560.8683, 1571.8868, 1571.8868, 1734.9553, 2044.1248, 2051.0876, 2231.2241, 2564.2034,

2663.3596, 2780.9712, 2922.3704, 3349.6096

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 40

Protein View

Match to: **gi|3901094** Score: **123** Expect: **3e-007**
pollen allergen Phl pI [Phleum pratense]

Nominal mass (M_r): **28584**; Calculated pI value: **7.53**
NCBI BLAST search of gi|3901094 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

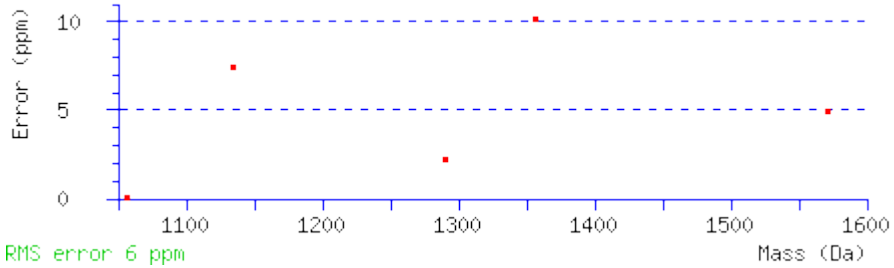
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **14%**

Matched peptides shown in **Bold Red**

```
  1 MASSSSVLLV VALFAVFLGS AHGIPKVPPG PNITATYGDK WLDAKSTWYG
 51 KPTAAGPKDN GGACGYKDVD KPPFSGMTGC GNTPIFKSGR GCGSCFEIKC
101 TKPEACSGEP VVVHITDDNE EPIAAYHFDL SGIAFGSMAK KGDEQKLRSA
151 GEVEIQFRRV KCKYPEGTKV TFHVEKGSNP NYLALLVKFV AGDGDVVAVD
201 IKEKGKDKWI ALKESWGAIW RIDTPEVLKG PFTVRYTTEG GTKGEAKDVI
251 PEGWKADTAY ESK
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
88 - 99	1357.6125	1356.6052	1356.5914	0.0138	1	SGRGCGSCFEIK	(No match)
88 - 99	1357.6125	1356.6052	1356.5914	0.0138	1	SGRGCGSCFEIK	(No match)
91 - 99	1057.4441	1056.4368	1056.4368	0.0000	0	GCGSCFEIK	(No match)
91 - 99	1057.4441	1056.4368	1056.4368	0.0000	0	GCGSCFEIK	(No match)
149 - 158	1135.5826	1134.5753	1134.5669	0.0085	0	SAGEVEIQFR	(No match)
149 - 158	1135.5826	1134.5753	1134.5669	0.0085	0	SAGEVEIQFR	(Ions score 15)
149 - 159	1291.6781	1290.6708	1290.6680	0.0029	1	SAGEVEIQFRR	(Ions score 31)
149 - 159	1291.6781	1290.6708	1290.6680	0.0029	1	SAGEVEIQFRR	(No match)
222 - 235	1571.8868	1570.8795	1570.8718	0.0077	1	IDTPEVLKGPFTVR	(Ions score 36)
222 - 235	1571.8868	1570.8795	1570.8718	0.0077	1	IDTPEVLKGPFTVR	(No match)



Spot 117

Index

	Accession	Mass	Score	Description
1.	gi|15808779	27964	276	ascorbate peroxidase [Hordeum vulgare]
2.	gi|226530305	27462	177	APx1 - Cytosolic Ascorbate Peroxidase [Zea mays]
3.	gi|804973	27656	142	L-ascorbate peroxidase [Capsicum annuum]
4.	gi|28627542	27755	141	putative ascorbate peroxidase [Capsicum annuum]
5.	gi|559005	27656	140	ascorbate peroxidase
6.	gi|2586151	19745	128	ripening-associated protein [Musa acuminata]
7.	gi|42558486	27709	127	ascorbate peroxidase [Rehmannia glutinosa]
8.	gi|194707280	27325	127	unknown [Zea mays]
9.	gi|195643366	27299	127	APx2 - Cytosolic Ascorbate Peroxidase [Zea mays]
10.	gi|6066418	27789	125	ascorbate peroxidase [Solanum lycopersicum]

Results List

1. gi|15808779 **Mass:** 27964 **Score:** 276 **Expect:** 1.5e-022 **Queries matched:** 10

ascorbate peroxidase [Hordeum vulgare]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
974.5036	973.4963	973.4837	0.0126	32	39	0	---	NCAPLMLR
990.4990	989.4917	989.4786	0.0131	32	39	0	---	NCAPLMLR + Oxidation (M)
1309.6653	1308.6580	1308.6422	0.0158	132	143	0	---	LPDATQGSDHLR
1503.7776	1502.7703	1502.7517	0.0186	40	53	0	---	LAWHSAGTFDVATK
1585.8788	1584.8715	1584.8479	0.0236	26	39	1	---	GLIAEKNCAPLMLR
1585.8788	1584.8715	1584.8479	0.0236	26	39	1	51	GLIAEKNCAPLMLR
1601.8770	1600.8697	1600.8429	0.0269	26	39	1	---	GLIAEKNCAPLMLR + Oxidation (M)
1686.8203	1685.8130	1685.7970	0.0160	5	19	0	---	CYPTVSDEYLAAVAK
1834.9519	1833.9446	1833.9155	0.0291	63	80	0	---	CPAELAHGANAGLDIAVR
1834.9519	1833.9446	1833.9155	0.0291	63	80	0	146	CPAELAHGANAGLDIAVR

No match to: 768.5389, 923.4504, 923.4504, 936.5009, 939.4462, 1294.6946, 1294.6946, 1817.9304, 1817.9304, 2158.1196

2. gi|226530305 **Mass:** 27462 **Score:** 177 **Expect:** 1.2e-012 **Queries matched:** 4

APx1 - Cytosolic Ascorbate Peroxidase [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1309.6653	1308.6580	1308.6786	-0.0205	131	142	1	---	LPDATKGSDHLR
1686.8203	1685.8130	1685.7784	0.0347	4	18	0	---	NYPTVSAEYSEAVEK
1834.9519	1833.9446	1833.9155	0.0291	62	79	0	---	CPAELAHGANAGLDIAVR
1834.9519	1833.9446	1833.9155	0.0291	62	79	0	146	CPAELAHGANAGLDIAVR

No match to: 768.5389, 923.4504, 923.4504, 936.5009, 939.4462, 974.5036, 990.4990, 1294.6946, 1294.6946, 1503.7776, 1585.8788, 1585.8788, 1601.8770, 1817.9304, 1817.9304, 2158.1196

3. gi|804973 **Mass:** 27656 **Score:** 142 **Expect:** 3.8e-009 **Queries matched:** 10

L-ascorbate peroxidase [Capsicum annuum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
923.4504	922.4431	922.4330	0.0101	53	61	0	---	TGGPFGTMR
923.4504	922.4431	922.4330	0.0101	53	61	0	30	TGGPFGTMR
936.5009	935.4936	935.4599	0.0337	242	250	0	---	LSELGFAEA
939.4462	938.4389	938.4279	0.0110	53	61	0	---	TGGPFGTMR + Oxidation (M)
974.5036	973.4963	973.4837	0.0126	31	38	0	---	NCAPLMLR
990.4990	989.4917	989.4786	0.0131	31	38	0	---	NCAPLMLR + Oxidation (M)
1309.6653	1308.6580	1308.6786	-0.0205	131	142	1	---	LPDATKGSDHLR
1585.8788	1584.8715	1584.8479	0.0236	25	38	1	---	GLIAEKNCAPLMLR
1585.8788	1584.8715	1584.8479	0.0236	25	38	1	51	GLIAEKNCAPLMLR
1601.8770	1600.8697	1600.8429	0.0269	25	38	1	---	GLIAEKNCAPLMLR + Oxidation (M)

No match to: 768.5389, 1294.6946, 1294.6946, 1503.7776, 1686.8203, 1817.9304, 1817.9304, 1834.9519, 1834.9519, 2158.1196

4. gi|28627542 **Mass:** 27755 **Score:** 141 **Expect:** 4.8e-009 **Queries matched:** 10

putative ascorbate peroxidase [Capsicum annuum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
923.4504	922.4431	922.4330	0.0101	53	61	0	---	TGGPFGTMR
923.4504	922.4431	922.4330	0.0101	53	61	0	30	TGGPFGTMR
936.5009	935.4936	935.4599	0.0337	242	250	0	---	LSELGFAEA
939.4462	938.4389	938.4279	0.0110	53	61	0	---	TGGPFGTMR + Oxidation (M)
974.5036	973.4963	973.4837	0.0126	31	38	0	---	NCAPLMLR
990.4990	989.4917	989.4786	0.0131	31	38	0	---	NCAPLMLR + Oxidation (M)
1309.6653	1308.6580	1308.6786	-0.0205	131	142	1	---	LPDATKGSDHLR
1585.8788	1584.8715	1584.8479	0.0236	25	38	1	---	GLIAEKNCAPLMLR
1585.8788	1584.8715	1584.8479	0.0236	25	38	1	51	GLIAEKNCAPLMLR
1601.8770	1600.8697	1600.8429	0.0269	25	38	1	---	GLIAEKNCAPLMLR + Oxidation (M)

No match to: 768.5389, 1294.6946, 1294.6946, 1503.7776, 1686.8203, 1817.9304, 1817.9304, 1834.9519, 1834.9519, 2158.1196

5. gi|559005 **Mass:** 27656 **Score:** 140 **Expect:** 6.1e-009 **Queries matched:** 10

ascorbate peroxidase

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
923.4504	922.4431	922.4330	0.0101	53	61	0	---	TGGPFGTMR
923.4504	922.4431	922.4330	0.0101	53	61	0	30	TGGPFGTMR
936.5009	935.4936	935.4599	0.0337	242	250	0	---	LSELGFAEA
939.4462	938.4389	938.4279	0.0110	53	61	0	---	TGGPFGTMR + Oxidation (M)
974.5036	973.4963	973.4837	0.0126	31	38	0	---	NCAPLMLR
990.4990	989.4917	989.4786	0.0131	31	38	0	---	NCAPLMLR + Oxidation (M)

1309.6653	1308.6580	1308.6786	-0.0205	131 - 142	1	---	LPDATKGSDHLR
1585.8788	1584.8715	1584.8479	0.0236	25 - 38	1	---	GLIAEKNCAPLMLR
1585.8788	1584.8715	1584.8479	0.0236	25 - 38	1	51	GLIAEKNCAPLMLR
1601.8770	1600.8697	1600.8429	0.0269	25 - 38	1	---	GLIAEKNCAPLMLR + Oxidation (M)

No match to: 768.5389, 1294.6946, 1294.6946, 1503.7776, 1686.8203, 1817.9304, 1817.9304, 1834.9519, 1834.9519, 2158.1196

6. gi|2586151 **Mass:** 19745 **Score:** 128 **Expect:** 9.6e-008 **Queries matched:** 7

ripening-associated protein [Musa acuminata]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
923.4504	922.4431	922.4330	0.0101	53 - 61		0	---	TGGPFGTMR
923.4504	922.4431	922.4330	0.0101	53 - 61		0	30	TGGPFGTMR
939.4462	938.4389	938.4279	0.0110	53 - 61		0	---	TGGPFGTMR + Oxidation (M)
974.5036	973.4963	973.4837	0.0126	31 - 38		0	---	NCAPLMLR
990.4990	989.4917	989.4786	0.0131	31 - 38		0	---	NCAPLMLR + Oxidation (M)
1309.6653	1308.6580	1308.6786	-0.0205	131 - 142		1	---	LPDATKGSDHLR
1585.8788	1584.8715	1584.8479	0.0236	25 - 38		1	51	GLIAEKNCAPLMLR

No match to: 768.5389, 936.5009, 1294.6946, 1294.6946, 1503.7776, 1585.8788, 1601.8770, 1686.8203, 1817.9304, 1817.9304, 1834.9519, 1834.9519, 2158.1196

7. gi|42558486 **Mass:** 27709 **Score:** 127 **Expect:** 1.2e-007 **Queries matched:** 9

ascorbate peroxidase [Rehmannia glutinosa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
923.4504	922.4431	922.4330	0.0101	53 - 61		0	---	TGGPFGTMR
923.4504	922.4431	922.4330	0.0101	53 - 61		0	30	TGGPFGTMR
939.4462	938.4389	938.4279	0.0110	53 - 61		0	---	TGGPFGTMR + Oxidation (M)
974.5036	973.4963	973.4837	0.0126	31 - 38		0	---	NCAPIMLR
990.4990	989.4917	989.4786	0.0131	31 - 38		0	---	NCAPIMLR + Oxidation (M)
1309.6653	1308.6580	1308.6786	-0.0205	131 - 142		1	---	LPDATKGSDHLR
1585.8788	1584.8715	1584.8479	0.0236	25 - 38		1	---	GLIAEKNCAPIMLR
1585.8788	1584.8715	1584.8479	0.0236	25 - 38		1	51	GLIAEKNCAPIMLR
1601.8770	1600.8697	1600.8429	0.0269	25 - 38		1	---	GLIAEKNCAPIMLR + Oxidation (M)

No match to: 768.5389, 936.5009, 1294.6946, 1294.6946, 1503.7776, 1686.8203, 1817.9304, 1817.9304, 1834.9519, 1834.9519, 2158.1196

8. gi|194707280 **Mass:** 27325 **Score:** 127 **Expect:** 1.2e-007 **Queries matched:** 9

unknown [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
936.5009	935.4936	935.4599	0.0337	242 - 250		0	---	LSELGFAEA
974.5036	973.4963	973.4837	0.0126	31 - 38		0	---	NCAPLMLR
990.4990	989.4917	989.4786	0.0131	31 - 38		0	---	NCAPLMLR + Oxidation (M)
1309.6653	1308.6580	1308.6422	0.0158	131 - 142		0	---	LPDATQGSDHLR

1503.7776	1502.7703	1502.7517	0.0186	39 - 52	0	---	LAWHSAGTFDVATK
1585.8788	1584.8715	1584.8479	0.0236	25 - 38	1	---	GLIAEKNCAPLMLR
1585.8788	1584.8715	1584.8479	0.0236	25 - 38	1	51	GLIAEKNCAPLMLR
1601.8770	1600.8697	1600.8429	0.0269	25 - 38	1	---	GLIAEKNCAPLMLR + Oxidation (M)
1686.8203	1685.8130	1685.8334	-0.0204	1 - 14	1	---	MVKAYPTVNEDYLK + Oxidation (M)

No match to: 768.5389, 923.4504, 923.4504, 939.4462, 1294.6946, 1294.6946, 1817.9304, 1817.9304, 1834.9519, 1834.9519, 2158.1196

9. gi|195643366 **Mass:** 27299 **Score:** 127 **Expect:** 1.2e-007 **Queries matched:** 9

APx2 - Cytosolic Ascorbate Peroxidase [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
936.5009	935.4936	935.4599	0.0337	242 - 250		0	---	LSELGFAEA
974.5036	973.4963	973.4837	0.0126	31 - 38		0	---	NCAPLMLR
990.4990	989.4917	989.4786	0.0131	31 - 38		0	---	NCAPLMLR + Oxidation (M)
1309.6653	1308.6580	1308.6422	0.0158	131 - 142		0	---	LPDATQGSDHLR
1503.7776	1502.7703	1502.7517	0.0186	39 - 52		0	---	LAWHSAGTFDVATK
1585.8788	1584.8715	1584.8479	0.0236	25 - 38		1	---	GLIAEKNCAPLMLR
1585.8788	1584.8715	1584.8479	0.0236	25 - 38		1	51	GLIAEKNCAPLMLR
1601.8770	1600.8697	1600.8429	0.0269	25 - 38		1	---	GLIAEKNCAPLMLR + Oxidation (M)
1686.8203	1685.8130	1685.8334	-0.0204	1 - 14		1	---	MVKAYPTVNEDYLK + Oxidation (M)

No match to: 768.5389, 923.4504, 923.4504, 939.4462, 1294.6946, 1294.6946, 1817.9304, 1817.9304, 1834.9519, 1834.9519, 2158.1196

10. gi|6066418 **Mass:** 27789 **Score:** 125 **Expect:** 1.9e-007 **Queries matched:** 9

ascorbate peroxidase [Solanum lycopersicum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
923.4504	922.4431	922.4330	0.0101	53 - 61		0	---	TGGPFGTMR
923.4504	922.4431	922.4330	0.0101	53 - 61		0	30	TGGPFGTMR
936.5009	935.4936	935.4599	0.0337	242 - 250		0	---	LSELGFAEA
939.4462	938.4389	938.4279	0.0110	53 - 61		0	---	TGGPFGTMR + Oxidation (M)
974.5036	973.4963	973.4837	0.0126	31 - 38		0	---	NCAPIMLR
990.4990	989.4917	989.4786	0.0131	31 - 38		0	---	NCAPIMLR + Oxidation (M)
1585.8788	1584.8715	1584.8479	0.0236	25 - 38		1	---	GLIAEKNCAPIMLR
1585.8788	1584.8715	1584.8479	0.0236	25 - 38		1	51	GLIAEKNCAPIMLR
1601.8770	1600.8697	1600.8429	0.0269	25 - 38		1	---	GLIAEKNCAPIMLR + Oxidation (M)

No match to: 768.5389, 1294.6946, 1294.6946, 1309.6653, 1503.7776, 1686.8203, 1817.9304, 1817.9304, 1834.9519, 1834.9519, 2158.1196

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 20

Protein View

Match to: **gi|15808779** Score: **276** Expect: **1.5e-022**
ascorbate peroxidase [Hordeum vulgare]

Nominal mass (M_r): **27964**; Calculated pI value: **5.10**
NCBI BLAST search of gi|15808779 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Hordeum vulgare subsp. vulgare

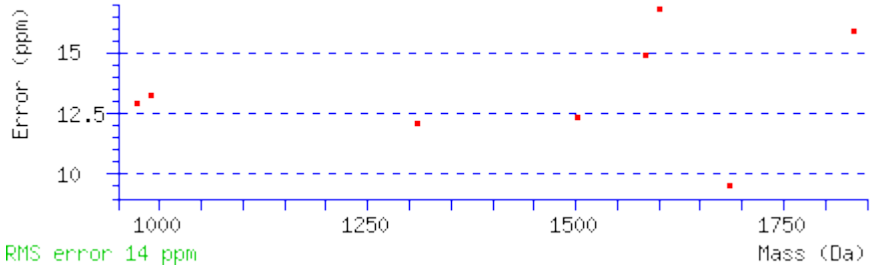
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **28%**

Matched peptides shown in **Bold Red**

```
     1 MAAKCYPTVS DEYLAAVAKA RRKLRGLIAE KNCAPLMLRL AWHSAGTFDV
    51 ATKTGGPFGT MKCPAELAHG ANAGLDIAVR LLEPIKEQFP ILSYADFYQL
   101 AGVVAVEVTG GPEVPFHPGR QDKPEPPPEG RLPDATQGSD HLRQVFSTQM
   151 GLSDQDIVAL SGGHTLGRCH KERSGFEGAW TANPLIFDNS YFTELLSGEK
   201 EGLLQLPTDK VLLTDPAFRP LVDKYAADED AFFADYAEAH LKLSELGFGE
   251 ASEGCC
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
5 - 19	1686.8203	1685.8130	1685.7970	0.0160	0	**CYPTVSDEYLAAVAK** (No match)
26 - 39	1585.8788	1584.8715	1584.8479	0.0236	1	**GLIAEKNCAPLMLR** (No match)
26 - 39	1585.8788	1584.8715	1584.8479	0.0236	1	**GLIAEKNCAPLMLR** (Ions score 51)
26 - 39	1601.8770	1600.8697	1600.8429	0.0269	1	**GLIAEKNCAPLMLR** Oxidation (M) (No match)
32 - 39	974.5036	973.4963	973.4837	0.0126	0	**NCAPLMLR** (No match)
32 - 39	990.4990	989.4917	989.4786	0.0131	0	**NCAPLMLR** Oxidation (M) (No match)
40 - 53	1503.7776	1502.7703	1502.7517	0.0186	0	**LAWHSAGTFDVATK** (No match)
63 - 80	1834.9519	1833.9446	1833.9155	0.0291	0	**CPAELAHGANAGLDIAVR** (No match)
63 - 80	1834.9519	1833.9446	1833.9155	0.0291	0	**CPAELAHGANAGLDIAVR** (Ions score 146)
132 - 143	1309.6653	1308.6580	1308.6422	0.0158	0	**LPDATQGSDHLR** (No match)



Spot 118

Index

	Accession	Mass	Score	Description
1.	gi|2507469	26948	120	RecName: Full=Triosephosphate isomerase, cytosolic; Short=TIM; Short=Triose-phosphate isomeras
2.	gi|147772560	27129	103	hypothetical protein [Vitis vinifera]
3.	gi|115434516	27274	103	Os01g0147900 [Oryza sativa (japonica cultivar-group)]
4.	gi|136057	27244	103	RecName: Full=Triosephosphate isomerase, cytosolic; Short=TIM; Short=Triose-phosphate isomeras
5.	gi|1174749	27138	103	RecName: Full=Triosephosphate isomerase, cytosolic; Short=TIM; Short=Triose-phosphate isomeras
6.	gi|226495391	27236	103	triosephosphate isomerase, cytosolic [Zea mays]
7.	gi|11124572	27014	103	triosephosphat-isomerase [Triticum aestivum]
8.	gi|165973012	27308	103	triosephosphate isomerase [Oryza coarctata]
9.	gi|195605636	27278	103	triosephosphate isomerase, cytosolic [Zea mays]
10.	gi|553107	27816	103	triosephosphate isomerase [Oryza sativa]

Results List

1. gi|2507469 **Mass:** 26948 **Score:** 120 **Expect:** 6.1e-007 **Queries matched:** 6

RecName: Full=Triosephosphate isomerase, cytosolic; Short=TIM; Short=Triose-phosphate isomerase

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
954.4944	953.4871	953.4759	0.0113	5 -	12	0	45	FFVGGNWK
954.4944	953.4871	953.4759	0.0113	5 -	12	0	---	FFVGGNWK
1374.7251	1373.7178	1373.6972	0.0206	124 -	135	0	---	VIACVGETLEQR
1374.7251	1373.7178	1373.6972	0.0206	124 -	135	0	37	VIACVGETLEQR
2147.1506	2146.1433	2146.1283	0.0151	176 -	194	1	---	VATPAQAQEVHANLRDWLK
2147.1506	2146.1433	2146.1283	0.0151	176 -	194	1	---	VATPAQAQEVHANLRDWLK

No match to: 768.5283, 1199.5742, 1295.7174, 1295.7174, 1303.6664, 1303.6664, 1327.6556

2. gi|147772560 **Mass:** 27129 **Score:** 103 **Expect:** 3e-005 **Queries matched:** 4

hypothetical protein [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
954.4944	953.4871	953.4759	0.0113	5 -	12	0	45	FFVGGNWK
954.4944	953.4871	953.4759	0.0113	5 -	12	0	---	FFVGGNWK
1374.7251	1373.7178	1373.6972	0.0206	124 -	135	0	---	VIACVGETLEQR
1374.7251	1373.7178	1373.6972	0.0206	124 -	135	0	37	VIACVGETLEQR

No match to: 768.5283, 1199.5742, 1295.7174, 1295.7174, 1303.6664, 1303.6664, 1327.6556, 2147.1506, 2147.1506

3. gi|115434516 **Mass:** 27274 **Score:** 103 **Expect:** 3e-005 **Queries matched:** 4

Os01g0147900 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
954.4944	953.4871	953.4759	0.0113	5 -	12	0	45	FFVGGNWK
954.4944	953.4871	953.4759	0.0113	5 -	12	0	---	FFVGGNWK

1374.7251 1373.7178 1373.6972 0.0206 124 - 135 0 --- VIACVGETLEQR
1374.7251 1373.7178 1373.6972 0.0206 124 - 135 0 37 VIACVGETLEQR
No match to: 768.5283, 1199.5742, 1295.7174, 1295.7174, 1303.6664, 1303.6664, 1327.6556, 2147.1506, 2147.1506

4. gi|136057 **Mass:** 27244 **Score:** 103 **Expect:** 3e-005 **Queries matched:** 4
RecName: Full=Triosephosphate isomerase, cytosolic; Short=TIM; Short=Triose-phosphate isomerase

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
954.4944	953.4871	953.4759	0.0113	5 -	12	0	45	FFVGGNWK
954.4944	953.4871	953.4759	0.0113	5 -	12	0	---	FFVGGNWK
1374.7251	1373.7178	1373.6972	0.0206	124 -	135	0	---	VIACVGETLEQR
1374.7251	1373.7178	1373.6972	0.0206	124 -	135	0	37	VIACVGETLEQR

No match to: 768.5283, 1199.5742, 1295.7174, 1295.7174, 1303.6664, 1303.6664, 1327.6556, 2147.1506, 2147.1506

5. gi|1174749 **Mass:** 27138 **Score:** 103 **Expect:** 3e-005 **Queries matched:** 4
RecName: Full=Triosephosphate isomerase, cytosolic; Short=TIM; Short=Triose-phosphate isomerase

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
954.4944	953.4871	953.4759	0.0113	5 -	12	0	45	FFVGGNWK
954.4944	953.4871	953.4759	0.0113	5 -	12	0	---	FFVGGNWK
1374.7251	1373.7178	1373.6972	0.0206	124 -	135	0	---	VIACVGETLEQR
1374.7251	1373.7178	1373.6972	0.0206	124 -	135	0	37	VIACVGETLEQR

No match to: 768.5283, 1199.5742, 1295.7174, 1295.7174, 1303.6664, 1303.6664, 1327.6556, 2147.1506, 2147.1506

6. gi|226495391 **Mass:** 27236 **Score:** 103 **Expect:** 3e-005 **Queries matched:** 4
triosephosphate isomerase, cytosolic [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
954.4944	953.4871	953.4759	0.0113	5 -	12	0	45	FFVGGNWK
954.4944	953.4871	953.4759	0.0113	5 -	12	0	---	FFVGGNWK
1374.7251	1373.7178	1373.6972	0.0206	124 -	135	0	---	VIACVGETLEQR
1374.7251	1373.7178	1373.6972	0.0206	124 -	135	0	37	VIACVGETLEQR

No match to: 768.5283, 1199.5742, 1295.7174, 1295.7174, 1303.6664, 1303.6664, 1327.6556, 2147.1506, 2147.1506

7. gi|11124572 **Mass:** 27014 **Score:** 103 **Expect:** 3e-005 **Queries matched:** 4
triosephosphat-isomerase [Triticum aestivum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
954.4944	953.4871	953.4759	0.0113	5 -	12	0	45	FFVGGNWK
954.4944	953.4871	953.4759	0.0113	5 -	12	0	---	FFVGGNWK
1374.7251	1373.7178	1373.6972	0.0206	124 -	135	0	---	VIACVGETLEQR
1374.7251	1373.7178	1373.6972	0.0206	124 -	135	0	37	VIACVGETLEQR

No match to: 768.5283, 1199.5742, 1295.7174, 1295.7174, 1303.6664, 1303.6664, 1327.6556, 2147.1506, 2147.1506

8. gi|165973012 **Mass:** 27308 **Score:** 103 **Expect:** 3e-005 **Queries matched:** 4
triosephosphate isomerase [Oryza coarctata]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
954.4944	953.4871	953.4759	0.0113	5 -	12	0	45	FFVGGNWK
954.4944	953.4871	953.4759	0.0113	5 -	12	0	---	FFVGGNWK
1374.7251	1373.7178	1373.6972	0.0206	124 -	135	0	---	VIACVGETLEQR
1374.7251	1373.7178	1373.6972	0.0206	124 -	135	0	37	VIACVGETLEQR

No match to: 768.5283, 1199.5742, 1295.7174, 1295.7174, 1303.6664, 1303.6664, 1327.6556, 2147.1506, 2147.1506

9. gi|195605636 **Mass:** 27278 **Score:** 103 **Expect:** 3e-005 **Queries matched:** 4

triosephosphate isomerase, cytosolic [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
954.4944	953.4871	953.4759	0.0113	5 -	12	0	45	FFVGGNWK
954.4944	953.4871	953.4759	0.0113	5 -	12	0	---	FFVGGNWK
1374.7251	1373.7178	1373.6972	0.0206	124 -	135	0	---	VIACVGETLEQR
1374.7251	1373.7178	1373.6972	0.0206	124 -	135	0	37	VIACVGETLEQR

No match to: 768.5283, 1199.5742, 1295.7174, 1295.7174, 1303.6664, 1303.6664, 1327.6556, 2147.1506, 2147.1506

10. gi|553107 **Mass:** 27816 **Score:** 103 **Expect:** 3e-005 **Queries matched:** 4

triosephosphate isomerase [Oryza sativa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
954.4944	953.4871	953.4759	0.0113	5 -	12	0	45	FFVGGNWK
954.4944	953.4871	953.4759	0.0113	5 -	12	0	---	FFVGGNWK
1374.7251	1373.7178	1373.6972	0.0206	124 -	135	0	---	VIACVGETLEQR
1374.7251	1373.7178	1373.6972	0.0206	124 -	135	0	37	VIACVGETLEQR

No match to: 768.5283, 1199.5742, 1295.7174, 1295.7174, 1303.6664, 1303.6664, 1327.6556, 2147.1506, 2147.1506

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 13

Protein View

Match to: **gi|2507469** Score: **120** Expect: **6.1e-007**
RecName: Full=Triosephosphate isomerase, cytosolic; Short=TIM; Short=Triose-phosphate isomerase

Nominal mass (M_r): **26948**; Calculated pI value: **5.39**
NCBI BLAST search of gi|2507469 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Hordeum vulgare
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|1785948 from Hordeum vulgare

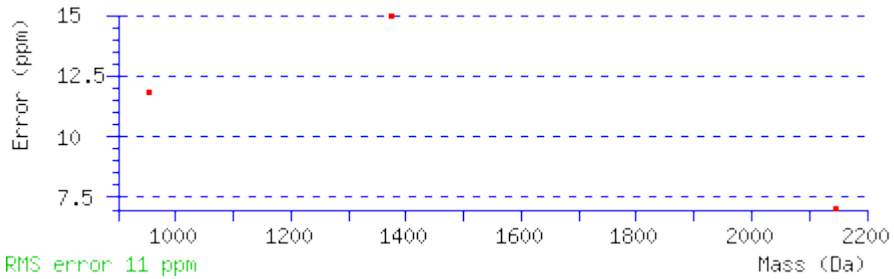
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **15%**

Matched peptides shown in **Bold Red**

```
   1 MGRKFFVGGN WKCNGTVEQV EAIVQTLNAG QIVSPDVVEV VVSPPYVFLP
  51 IVKAKLRPEI QVAAQNCWVK KGGAFTGEVS AEMLANLGVP WVILGHSERR
 101 SLLGESSEFV GEKVAYALAQ GLKVIACVGE TLEQREAGST MEVVAEQTKA
 151 IAGKIKDWSN GVVAYEPVWA IGTGKVATPA QAQEVHANLR DWLKTNVSPE
 201 VAESTRIIYG GSVTGASCKE LAAQADVDGF LVGGASLKPE FIDIINAAAV
 251 KSA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
5 - 12	954.4944	953.4871	953.4759	0.0113	0	FFVGGNWK	(Ions score 45)
5 - 12	954.4944	953.4871	953.4759	0.0113	0	FFVGGNWK	(No match)
124 - 135	1374.7251	1373.7178	1373.6972	0.0206	0	VIACVGETLEQR	(No match)
124 - 135	1374.7251	1373.7178	1373.6972	0.0206	0	VIACVGETLEQR	(Ions score 37)
176 - 194	2147.1506	2146.1433	2146.1283	0.0151	1	VATPAQAQEVHANLRDWLK	(No match)
176 - 194	2147.1506	2146.1433	2146.1283	0.0151	1	VATPAQAQEVHANLRDWLK	(No match)



Spot 119

Index

	Accession	Mass	Score	Description
1.	gi|2507469	26948	312	RecName: Full=Triosephosphate isomerase, cytosolic; Short=TIM; Short=Triose-phosphate isomeras
2.	gi|1174749	27138	230	RecName: Full=Triosephosphate isomerase, cytosolic; Short=TIM; Short=Triose-phosphate isomeras
3.	gi|11124572	27014	189	triosephosphat-isomerase [Triticum aestivum]
4.	gi|147772560	27129	128	hypothetical protein [Vitis vinifera]
5.	gi|115434516	27274	128	Os01g0147900 [Oryza sativa (japonica cultivar-group)]
6.	gi|136057	27244	128	RecName: Full=Triosephosphate isomerase, cytosolic; Short=TIM; Short=Triose-phosphate isomeras
7.	gi|226495391	27236	128	triosephosphate isomerase, cytosolic [Zea mays]
8.	gi|165973012	27308	128	triosephosphate isomerase [Oryza coarctata]
9.	gi|195605636	27278	128	triosephosphate isomerase, cytosolic [Zea mays]
10.	gi|553107	27816	127	triosephosphate isomerase [Oryza sativa]

Results List

1. gi|2507469 **Mass:** 26948 **Score:** 312 **Expect:** 3.8e-026 **Queries matched:** 10

RecName: Full=Triosephosphate isomerase, cytosolic; Short=TIM; Short=Triose-phosphate isomerase

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
954.4726	953.4653	953.4759	-0.0105	5	12	0	43	FFVGGNWK
954.4726	953.4653	953.4759	-0.0105	5	12	0	---	FFVGGNWK
1082.5521	1081.5448	1081.5708	-0.0260	4	12	1	---	KFFVGGNWK
1374.6858	1373.6785	1373.6972	-0.0187	124	135	0	60	VIACVGETLEQR
1374.6858	1373.6785	1373.6972	-0.0187	124	135	0	---	VIACVGETLEQR
1604.8236	1603.8163	1603.8430	-0.0267	176	190	0	---	VATPAQAQEVHANLR
1811.9297	1810.9224	1810.9512	-0.0287	56	70	0	---	LRPEIQVAAQNCWVK
1811.9297	1810.9224	1810.9512	-0.0287	56	70	0	48	LRPEIQVAAQNCWVK
2147.0935	2146.0862	2146.1283	-0.0420	176	194	1	93	VATPAQAQEVHANLRDWLK
2147.0935	2146.0862	2146.1283	-0.0420	176	194	1	---	VATPAQAQEVHANLRDWLK

No match to: 1295.6831, 1303.6271, 1321.6628, 1559.7057, 1684.8610, 1716.8110, 1843.8727, 2055.0442, 2055.0442, 2145.0769, 2163.0818, 2179.0779, 2366.2126, 2522.3105, 3039.4983, 3181.4207, 3196.5969

2. gi|1174749 **Mass:** 27138 **Score:** 230 **Expect:** 6.1e-018 **Queries matched:** 9

RecName: Full=Triosephosphate isomerase, cytosolic; Short=TIM; Short=Triose-phosphate isomerase

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
954.4726	953.4653	953.4759	-0.0105	5	12	0	43	FFVGGNWK
954.4726	953.4653	953.4759	-0.0105	5	12	0	---	FFVGGNWK
1082.5521	1081.5448	1081.5708	-0.0260	4	12	1	---	KFFVGGNWK
1374.6858	1373.6785	1373.6972	-0.0187	124	135	0	60	VIACVGETLEQR
1374.6858	1373.6785	1373.6972	-0.0187	124	135	0	---	VIACVGETLEQR
1811.9297	1810.9224	1810.9512	-0.0287	56	70	0	---	LRPEIQVAAQNCWVK

1811.9297	1810.9224	1810.9512	-0.0287	56 - 70	0	48	LRPEIQVAAQNCWVK
2055.0442	2054.0369	2054.0731	-0.0361	54 - 70	1	---	DKLRPEIQVAAQNCWVK
2055.0442	2054.0369	2054.0731	-0.0361	54 - 70	1	26	DKLRPEIQVAAQNCWVK

No match to: 1295.6831, 1303.6271, 1321.6628, 1559.7057, 1604.8236, 1684.8610, 1716.8110, 1843.8727, 2145.0769, 2147.0935, 2147.0935, 2163.0818, 2179.0779, 2366.2126, 2522.3105, 3039.4983, 3181.4207, 3196.5969

3. gi|11124572 **Mass:** 27014 **Score:** 189 **Expect:** 7.6e-014 **Queries matched:** 7

triosephosphat-isomerase [Triticum aestivum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
954.4726	953.4653	953.4759	-0.0105	5 -	12	0	43	FFVGGNWK
954.4726	953.4653	953.4759	-0.0105	5 -	12	0	---	FFVGGNWK
1082.5521	1081.5448	1081.5708	-0.0260	4 -	12	1	---	KFFVGGNWK
1374.6858	1373.6785	1373.6972	-0.0187	124 -	135	0	60	VIACVGETLEQR
1374.6858	1373.6785	1373.6972	-0.0187	124 -	135	0	---	VIACVGETLEQR
1811.9297	1810.9224	1810.9512	-0.0287	56 -	70	0	---	LRPEIQVAAQNCWVK
1811.9297	1810.9224	1810.9512	-0.0287	56 -	70	0	48	LRPEIQVAAQNCWVK

No match to: 1295.6831, 1303.6271, 1321.6628, 1559.7057, 1604.8236, 1684.8610, 1716.8110, 1843.8727, 2055.0442, 2055.0442, 2145.0769, 2147.0935, 2147.0935, 2163.0818, 2179.0779, 2366.2126, 2522.3105, 3039.4983, 3181.4207, 3196.5969

4. gi|147772560 **Mass:** 27129 **Score:** 128 **Expect:** 9.6e-008 **Queries matched:** 5

hypothetical protein [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
954.4726	953.4653	953.4759	-0.0105	5 -	12	0	43	FFVGGNWK
954.4726	953.4653	953.4759	-0.0105	5 -	12	0	---	FFVGGNWK
1082.5521	1081.5448	1081.5708	-0.0260	4 -	12	1	---	KFFVGGNWK
1374.6858	1373.6785	1373.6972	-0.0187	124 -	135	0	60	VIACVGETLEQR
1374.6858	1373.6785	1373.6972	-0.0187	124 -	135	0	---	VIACVGETLEQR

No match to: 1295.6831, 1303.6271, 1321.6628, 1559.7057, 1604.8236, 1684.8610, 1716.8110, 1811.9297, 1811.9297, 1843.8727, 2055.0442, 2055.0442, 2145.0769, 2147.0935, 2147.0935, 2163.0818, 2179.0779, 2366.2126, 2522.3105, 3039.4983, 3181.4207, 3196.5969

5. gi|115434516 **Mass:** 27274 **Score:** 128 **Expect:** 9.6e-008 **Queries matched:** 5

Os01g0147900 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
954.4726	953.4653	953.4759	-0.0105	5 -	12	0	43	FFVGGNWK
954.4726	953.4653	953.4759	-0.0105	5 -	12	0	---	FFVGGNWK
1082.5521	1081.5448	1081.5708	-0.0260	4 -	12	1	---	KFFVGGNWK
1374.6858	1373.6785	1373.6972	-0.0187	124 -	135	0	60	VIACVGETLEQR
1374.6858	1373.6785	1373.6972	-0.0187	124 -	135	0	---	VIACVGETLEQR

No match to: 1295.6831, 1303.6271, 1321.6628, 1559.7057, 1604.8236, 1684.8610, 1716.8110, 1811.9297, 1811.9297, 1843.8727, 2055.0442, 2055.0442, 2145.0769, 2147.0935, 2147.0935, 2163.0818, 2179.0779, 2366.2126, 2522.3105, 3039.4983, 3181.4207, 3196.5969

6. gi|136057 **Mass:** 27244 **Score:** 128 **Expect:** 9.6e-008 **Queries matched:** 5

RecName: Full=Triosephosphate isomerase, cytosolic; Short=TIM; Short=Triose-phosphate isomerase

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
954.4726	953.4653	953.4759	-0.0105	5	12	0	43	FFVGGNWK
954.4726	953.4653	953.4759	-0.0105	5	12	0	---	FFVGGNWK
1082.5521	1081.5448	1081.5708	-0.0260	4	12	1	---	KFFVGGNWK
1374.6858	1373.6785	1373.6972	-0.0187	124	135	0	60	VIACVGETLEQR
1374.6858	1373.6785	1373.6972	-0.0187	124	135	0	---	VIACVGETLEQR

No match to: 1295.6831, 1303.6271, 1321.6628, 1559.7057, 1604.8236, 1684.8610, 1716.8110, 1811.9297, 1811.9297, 1843.8727, 2055.0442, 2055.0442, 2145.0769, 2147.0935, 2147.0935, 2163.0818, 2179.0779, 2366.2126, 2522.3105, 3039.4983, 3181.4207, 3196.5969

7. gi|226495391 **Mass:** 27236 **Score:** 128 **Expect:** 9.6e-008 **Queries matched:** 5

triosephosphate isomerase, cytosolic [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
954.4726	953.4653	953.4759	-0.0105	5	12	0	43	FFVGGNWK
954.4726	953.4653	953.4759	-0.0105	5	12	0	---	FFVGGNWK
1082.5521	1081.5448	1081.5708	-0.0260	4	12	1	---	KFFVGGNWK
1374.6858	1373.6785	1373.6972	-0.0187	124	135	0	60	VIACVGETLEQR
1374.6858	1373.6785	1373.6972	-0.0187	124	135	0	---	VIACVGETLEQR

No match to: 1295.6831, 1303.6271, 1321.6628, 1559.7057, 1604.8236, 1684.8610, 1716.8110, 1811.9297, 1811.9297, 1843.8727, 2055.0442, 2055.0442, 2145.0769, 2147.0935, 2147.0935, 2163.0818, 2179.0779, 2366.2126, 2522.3105, 3039.4983, 3181.4207, 3196.5969

8. gi|165973012 **Mass:** 27308 **Score:** 128 **Expect:** 9.6e-008 **Queries matched:** 5

triosephosphate isomerase [Oryza coarctata]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
954.4726	953.4653	953.4759	-0.0105	5	12	0	43	FFVGGNWK
954.4726	953.4653	953.4759	-0.0105	5	12	0	---	FFVGGNWK
1082.5521	1081.5448	1081.5708	-0.0260	4	12	1	---	KFFVGGNWK
1374.6858	1373.6785	1373.6972	-0.0187	124	135	0	60	VIACVGETLEQR
1374.6858	1373.6785	1373.6972	-0.0187	124	135	0	---	VIACVGETLEQR

No match to: 1295.6831, 1303.6271, 1321.6628, 1559.7057, 1604.8236, 1684.8610, 1716.8110, 1811.9297, 1811.9297, 1843.8727, 2055.0442, 2055.0442, 2145.0769, 2147.0935, 2147.0935, 2163.0818, 2179.0779, 2366.2126, 2522.3105, 3039.4983, 3181.4207, 3196.5969

9. gi|195605636 **Mass:** 27278 **Score:** 128 **Expect:** 9.6e-008 **Queries matched:** 5

triosephosphate isomerase, cytosolic [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
954.4726	953.4653	953.4759	-0.0105	5	12	0	43	FFVGGNWK
954.4726	953.4653	953.4759	-0.0105	5	12	0	---	FFVGGNWK
1082.5521	1081.5448	1081.5708	-0.0260	4	12	1	---	KFFVGGNWK

1374.6858	1373.6785	1373.6972	-0.0187	124 - 135	0	60	VIACVGETLEQR
1374.6858	1373.6785	1373.6972	-0.0187	124 - 135	0	---	VIACVGETLEQR

No match to: 1295.6831, 1303.6271, 1321.6628, 1559.7057, 1604.8236, 1684.8610, 1716.8110, 1811.9297, 1811.9297, 1843.8727, 2055.0442, 2055.0442, 2145.0769, 2147.0935, 2147.0935, 2163.0818, 2179.0779, 2366.2126, 2522.3105, 3039.4983, 3181.4207, 3196.5969

10. gi|553107 **Mass:** 27816 **Score:** 127 **Expect:** 1.2e-007 **Queries matched:** 5

triosephosphate isomerase [Oryza sativa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
954.4726	953.4653	953.4759	-0.0105	5 -	12	0	43	FFVGGNWK
954.4726	953.4653	953.4759	-0.0105	5 -	12	0	---	FFVGGNWK
1082.5521	1081.5448	1081.5708	-0.0260	4 -	12	1	---	KFFVGGNWK
1374.6858	1373.6785	1373.6972	-0.0187	124 -	135	0	60	VIACVGETLEQR
1374.6858	1373.6785	1373.6972	-0.0187	124 -	135	0	---	VIACVGETLEQR

No match to: 1295.6831, 1303.6271, 1321.6628, 1559.7057, 1604.8236, 1684.8610, 1716.8110, 1811.9297, 1811.9297, 1843.8727, 2055.0442, 2055.0442, 2145.0769, 2147.0935, 2147.0935, 2163.0818, 2179.0779, 2366.2126, 2522.3105, 3039.4983, 3181.4207, 3196.5969

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 27

Protein View

Match to: **gi|2507469** Score: **312** Expect: **3.8e-026**
RecName: Full=Triosephosphate isomerase, cytosolic; Short=TIM; Short=Triose-phosphate isomerase

Nominal mass (M_r): **26948**; Calculated pI value: **5.39**
NCBI BLAST search of gi|2507469 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Hordeum vulgare
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|1785948 from Hordeum vulgare

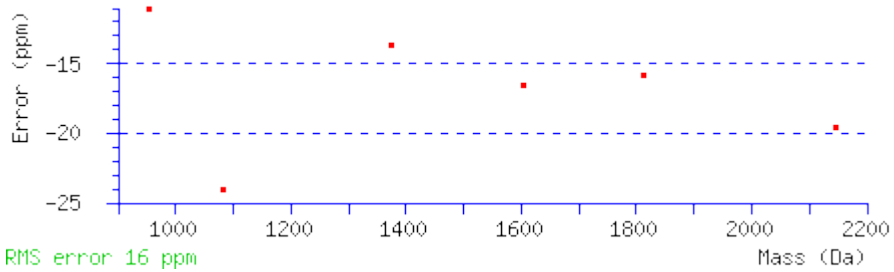
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **21%**

Matched peptides shown in **Bold Red**

```
    1 MGRKFFVGGN WKCNGTVEQV EAIVQTLNAG QIVSPDVVEV VVSPPYVFLP
   51 IVKAKLRPEI QVAAQNCWVK KGGAFTGEVS AEMLANLGVP WVILGHSERR
  101 SLLGESSEFV GEKVAYALAQ GLKVIACVGE TLEQREAGST MEVVAEQTKA
  151 IAGKIKDWSN GVVAYEPVWA IGTGKVATPA QAQEVHANLR DWLKTNVSPE
  201 VAESTRIIYG GSVTGASCKE LAAQADVDGF LVGGASLKPE FIDIINAAAV
  251 KSA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
4 - 12	1082.5521	1081.5448	1081.5708	-0.0260	1	KFFVGGNWK	(No match)
5 - 12	954.4726	953.4653	953.4759	-0.0105	0	FFVGGNWK	(Ions score 43)
5 - 12	954.4726	953.4653	953.4759	-0.0105	0	FFVGGNWK	(No match)
56 - 70	1811.9297	1810.9224	1810.9512	-0.0287	0	LRPEIQVAAQNCWVK	(No match)
56 - 70	1811.9297	1810.9224	1810.9512	-0.0287	0	LRPEIQVAAQNCWVK	(Ions score 48)
124 - 135	1374.6858	1373.6785	1373.6972	-0.0187	0	VIACVGETLEQR	(Ions score 60)
124 - 135	1374.6858	1373.6785	1373.6972	-0.0187	0	VIACVGETLEQR	(No match)
176 - 190	1604.8236	1603.8163	1603.8430	-0.0267	0	VATPAQAQEVHANLR	(No match)
176 - 194	2147.0935	2146.0862	2146.1283	-0.0420	1	VATPAQAQEVHANLRDWLK	(Ions score 93)
176 - 194	2147.0935	2146.0862	2146.1283	-0.0420	1	VATPAQAQEVHANLRDWLK	(No match)


Error (ppm)
-15
-20
-25
1000
1200
1400
1600
1800
2000
2200
Mass (Da)
RMS error 16 ppm

Spot 120

Index

	Accession	Mass	Score	Description
1.	gi|729003	35736	133	RecName: Full=Carbonic anhydrase, chloroplastic; AltName: Full=Carbonate dehydratase; Flags: P
2.	gi|224085099	36204	55	predicted protein [Populus trichocarpa]
3.	gi|157340699	40522	46	unnamed protein product [Vitis vinifera]
4.	gi|125589731	20100	45	hypothetical protein OsJ_14143 [Oryza sativa Japonica Group]
5.	gi|116783767	27860	45	unknown [Picea sitchensis]
6.	gi|116059714	37555	42	unnamed protein product [Ostreococcus tauri]
7.	gi|49388064	20395	39	hypothetical protein [Oryza sativa Japonica Group]
8.	gi|147775403	38132	38	hypothetical protein [Vitis vinifera]
9.	gi|116786328	57351	38	unknown [Picea sitchensis]
10.	gi|84514181	45265	38	cytochrome P450 monooxygenase CYP72A66 [Medicago truncatula]

Results List

1. gi|729003 **Mass:** 35736 **Score:** 133 **Expect:** 3e-008 **Queries matched:** 10

RecName: Full=Carbonic anhydrase, chloroplastic; AltName: Full=Carbonate dehydratase; Flags: Precur

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1219.5287	1218.5214	1218.5161	0.0053	160	169	0	43	YMVFACADSR
1219.5287	1218.5214	1218.5161	0.0053	160	169	0	---	YMVFACADSR
1235.5109	1234.5036	1234.5110	-0.0074	160	169	0	(16)	YMVFACADSR + Oxidation (M)
1235.5109	1234.5036	1234.5110	-0.0074	160	169	0	---	YMVFACADSR + Oxidation (M)
1296.6012	1295.5939	1295.6002	-0.0063	188	198	0	---	NIANMVPAYCK + Oxidation (M)
1672.9178	1671.9105	1671.8984	0.0122	145	159	1	---	KPDFFEPLKAGQAPK
1794.7917	1793.7844	1793.7645	0.0200	239	253	0	---	DGADDSFHFVEDWVR
2023.9443	2022.9370	2023.0408	-0.1037	110	129	0	---	TTPVQAAPVAPALMDAAVER + Oxidation (M)
2420.1953	2419.1880	2419.1807	0.0073	233	253	1	---	ALLSLKDGADDSFHFVEDWVR
2420.1953	2419.1880	2419.1807	0.0073	233	253	1	44	ALLSLKDGADDSFHFVEDWVR

No match to: 713.4023, 734.4883, 746.3673, 750.5075, 768.5144, 782.4719, 833.3879, 855.0323, 864.5243, 886.9821, 908.9750, 930.9597, 1090.5162, 1097.9995, 1098.5942, 1106.4879, 1171.5496, 1279.7605, 1312.6029, 1334.8767, 1448.9105, 1470.6846, 1609.8042, 1932.0006, 1932.0006, 1946.9951, 2070.0024, 2092.0566, 2235.1628, 2565.1921, 2653.3762, 2653.3762, 2669.3633, 2825.3228, 2922.3650, 3333.5723, 3350.5940

2. gi|224085099 **Mass:** 36204 **Score:** 55 **Expect:** 2.1 **Queries matched:** 7

predicted protein [Populus trichocarpa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1090.5162	1089.5089	1089.5302	-0.0212	215	224	0	---	DTNGLTVENK
1098.5942	1097.5869	1097.6332	-0.0463	156	165	0	---	LAELSLIDPK
1609.8042	1608.7969	1608.8518	-0.0549	228	240	1	---	LRLQAMEQQAHLR + Oxidation (M)
1672.9178	1671.9105	1671.8692	0.0413	256	271	0	---	IATGQITAVNGNPFNR

2235.1628	2234.1555	2234.1576	-0.0021	195 - 214	0	---	VQTLQTEATTLSAQVTMLQR + Oxidation (M)
2922.3650	2921.3577	2921.2708	0.0870	123 - 148	1	---	AADHHRHSYSMDGSFEAESLMIDGVK + 2 Oxidation (M)
3333.5723	3332.5650	3332.7979	-0.2328	299 - 330	1	---	LLTGSPALASQTLARGSNVTGELYLLEFNVAK

No match to: 713.4023, 734.4883, 746.3673, 750.5075, 768.5144, 782.4719, 833.3879, 855.0323, 864.5243, 886.9821, 908.9750, 930.9597, 1097.9995, 1106.4879, 1171.5496, 1219.5287, 1219.5287, 1235.5109, 1235.5109, 1279.7605, 1296.6012, 1312.6029, 1334.8767, 1448.9105, 1470.6846, 1794.7917, 1932.0006, 1932.0006, 1946.9951, 2023.9443, 2070.0024, 2092.0566, 2420.1953, 2420.1953, 2565.1921, 2653.3762, 2653.3762, 2669.3633, 2825.3228, 3350.5940

3. gi|157340699 **Mass:** 40522 **Score:** 46 **Expect:** 17 **Queries matched:** 8

unnamed protein product [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
833.3879	832.3806	832.3827	-0.0021	331 -	337	0	---	GETGQWR
1090.5162	1089.5089	1089.5059	0.0030	288 -	296	0	---	LCLMHSSSR
1106.4879	1105.4806	1105.5008	-0.0202	288 -	296	0	---	LCLMHSSSR + Oxidation (M)
1171.5496	1170.5423	1170.4863	0.0561	272 -	280	1	---	DDYNKEEMK
1296.6012	1295.5939	1295.6213	-0.0274	277 -	287	1	---	EEMKTMVVAAR + 2 Oxidation (M)
2023.9443	2022.9370	2022.9468	-0.0098	40 -	57	1	---	DFSPEMVIGEGGHSKVYR + Oxidation (M)
2092.0566	2091.0493	2090.9475	0.1019	1 -	16	1	---	MTMQLPDFMEEKLFQR + 3 Oxidation (M)
2825.3228	2824.3155	2824.2908	0.0247	161 -	185	0	---	SSNVLLSENCHPQLSDFGSAMVYNR

No match to: 713.4023, 734.4883, 746.3673, 750.5075, 768.5144, 782.4719, 855.0323, 864.5243, 886.9821, 908.9750, 930.9597, 1097.9995, 1098.5942, 1219.5287, 1219.5287, 1235.5109, 1235.5109, 1279.7605, 1312.6029, 1334.8767, 1448.9105, 1470.6846, 1609.8042, 1672.9178, 1794.7917, 1932.0006, 1932.0006, 1946.9951, 2070.0024, 2235.1628, 2420.1953, 2420.1953, 2565.1921, 2653.3762, 2653.3762, 2669.3633, 2922.3650, 3333.5723, 3350.5940

4. gi|125589731 **Mass:** 20100 **Score:** 45 **Expect:** 18 **Queries matched:** 7

hypothetical protein OsJ_14143 [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
833.3879	832.3806	832.4178	-0.0371	35 -	41	0	---	ILEEDSK
1090.5162	1089.5089	1089.5641	-0.0551	1 -	9	1	---	MEKAHALYK
1219.5287	1218.5214	1218.5954	-0.0740	136 -	144	1	---	MEKYQTYLK + Oxidation (M)
1219.5287	1218.5214	1218.5954	-0.0740	136 -	144	1	---	MEKYQTYLK + Oxidation (M)
2420.1953	2419.1880	2419.0622	0.1258	47 -	68	1	---	ISESGAYTSSSNQETEEETSRK
2420.1953	2419.1880	2419.0622	0.1258	47 -	68	1	---	ISESGAYTSSSNQETEEETSRK
2669.3633	2668.3560	2668.3860	-0.0299	86 -	110	1	---	GKKPAPSPLGDQPSQDFVLFNEAVK

No match to: 713.4023, 734.4883, 746.3673, 750.5075, 768.5144, 782.4719, 855.0323, 864.5243, 886.9821, 908.9750, 930.9597, 1097.9995, 1098.5942, 1106.4879, 1171.5496, 1235.5109, 1235.5109, 1279.7605, 1296.6012, 1312.6029, 1334.8767, 1448.9105, 1470.6846, 1609.8042, 1672.9178, 1794.7917, 1932.0006, 1932.0006, 1946.9951, 2023.9443, 2070.0024, 2092.0566, 2235.1628, 2565.1921, 2653.3762, 2653.3762, 2825.3228, 2922.3650, 3333.5723, 3350.5940

5. gi|116783767 **Mass:** 27860 **Score:** 45 **Expect:** 19 **Queries matched:** 9

unknown [Picea sitchensis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1219.5287	1218.5214	1218.5703	-0.0488	143 -	153	0	---	DVFGHMGLTDK

1219.5287	1218.5214	1218.5703	-0.0488	143 - 153	0	---	DVFGHMGLTDK
1235.5109	1234.5036	1234.5652	-0.0615	143 - 153	0	---	DVFGHMGLTDK + Oxidation (M)
1235.5109	1234.5036	1234.5652	-0.0615	143 - 153	0	---	DVFGHMGLTDK + Oxidation (M)
1672.9178	1671.9105	1671.8177	0.0928	1 - 14	1	---	MGKLYPTVSEEYQK
2565.1921	2564.1848	2564.1971	-0.0123	170 - 191	1	---	ERSGFEGAWTSNPLIFDNSYFK
2653.3762	2652.3689	2652.2019	0.1670	218 - 240	1	---	SYVEKYAADEDAFFADYAEAHLK
2653.3762	2652.3689	2652.2019	0.1670	218 - 240	1	---	SYVEKYAADEDAFFADYAEAHLK
2669.3633	2668.3560	2668.3932	-0.0372	62 - 85	1	---	HSDELSHNANNGLDIAIRLLEPIK

No match to: 713.4023, 734.4883, 746.3673, 750.5075, 768.5144, 782.4719, 833.3879, 855.0323, 864.5243, 886.9821, 908.9750, 930.9597, 1090.5162, 1097.9995, 1098.5942, 1106.4879, 1171.5496, 1279.7605, 1296.6012, 1312.6029, 1334.8767, 1448.9105, 1470.6846, 1609.8042, 1794.7917, 1932.0006, 1932.0006, 1946.9951, 2023.9443, 2070.0024, 2092.0566, 2235.1628, 2420.1953, 2420.1953, 2825.3228, 2922.3650, 3333.5723, 3350.5940

6. gi|116059714 **Mass:** 37555 **Score:** 42 **Expect:** 43 **Queries matched:** 8

unnamed protein product [Ostreococcus tauri]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
746.3673	745.3600	745.3970	-0.0369	2 - 8	0	---	ASELAQK
782.4719	781.4646	781.4558	0.0088	144 - 149	1	---	TQRHLK
864.5243	863.5170	863.4977	0.0193	17 - 23	1	---	SRYALVR
1219.5287	1218.5214	1218.5880	-0.0666	29 - 39	1	---	KEDVFGEPNGK
1219.5287	1218.5214	1218.5880	-0.0666	29 - 39	1	---	KEDVFGEPNGK
2235.1628	2234.1555	2234.0756	0.0799	261 - 281	0	---	GTSDPLASAWGLPNSTTFWAR
2653.3762	2652.3689	2652.3084	0.0605	258 - 281	1	---	VYRGTSDPLASAWGLPNSTTFWAR
2653.3762	2652.3689	2652.3084	0.0605	258 - 281	1	---	VYRGTSDPLASAWGLPNSTTFWAR

No match to: 713.4023, 734.4883, 750.5075, 768.5144, 833.3879, 855.0323, 886.9821, 908.9750, 930.9597, 1090.5162, 1097.9995, 1098.5942, 1106.4879, 1171.5496, 1235.5109, 1235.5109, 1279.7605, 1296.6012, 1312.6029, 1334.8767, 1448.9105, 1470.6846, 1609.8042, 1672.9178, 1794.7917, 1932.0006, 1932.0006, 1946.9951, 2023.9443, 2070.0024, 2092.0566, 2420.1953, 2420.1953, 2565.1921, 2669.3633, 2825.3228, 2922.3650, 3333.5723, 3350.5940

7. gi|49388064 **Mass:** 20395 **Score:** 39 **Expect:** 75 **Queries matched:** 5

hypothetical protein [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
864.5243	863.5170	863.4786	0.0384	176 - 183	1	---	MSVSIKLA + Oxidation (M)
1098.5942	1097.5869	1097.5175	0.0694	136 - 144	0	---	SSNYLMVER
1470.6846	1469.6773	1469.7725	-0.0952	76 - 89	0	---	LVDDAPSVDALLSR
1672.9178	1671.9105	1671.8402	0.0703	131 - 144	1	---	IFAARSSNYLMVER + Oxidation (M)
1946.9951	1945.9878	1945.9277	0.0601	102 - 118	1	---	KASVAADYCCLYLSPTK

No match to: 713.4023, 734.4883, 746.3673, 750.5075, 768.5144, 782.4719, 833.3879, 855.0323, 886.9821, 908.9750, 930.9597, 1090.5162, 1097.9995, 1106.4879, 1171.5496, 1219.5287, 1219.5287, 1235.5109, 1235.5109, 1279.7605, 1296.6012, 1312.6029, 1334.8767, 1448.9105, 1609.8042, 1794.7917, 1932.0006, 1932.0006, 2023.9443, 2070.0024, 2092.0566, 2235.1628, 2420.1953, 2420.1953, 2565.1921, 2653.3762, 2653.3762, 2669.3633, 2825.3228, 2922.3650, 3333.5723, 3350.5940

8. gi|147775403 **Mass:** 38132 **Score:** 38 **Expect:** 88 **Queries matched:** 8

hypothetical protein [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1296.6012	1295.5939	1295.6584	-0.0644	1	10	0	---	MPLDLYYPIR + Oxidation (M)
1312.6029	1311.5956	1311.6063	-0.0107	168	179	1	---	RVVDGGFMSGCK
2420.1953	2419.1880	2419.3297	-0.1416	307	327	1	---	STLPNLPIYFMSLLRLPSSVR + Oxidation (M)
2420.1953	2419.1880	2419.3297	-0.1416	307	327	1	---	STLPNLPIYFMSLLRLPSSVR + Oxidation (M)
2653.3762	2652.3689	2652.2868	0.0821	91	112	1	---	AYNNVNWYFLLTIMQKMGFGDK
2653.3762	2652.3689	2652.2868	0.0821	91	112	1	---	AYNNVNWYFLLTIMQKMGFGDK
2669.3633	2668.3560	2668.2817	0.0743	91	112	1	---	AYNNVNWYFLLTIMQKMGFGDK + Oxidation (M)
2922.3650	2921.3577	2921.3733	-0.0156	52	76	1	---	ASGPDGFTMAFWQFAWDFVKEEVLK + Oxidation (M)

No match to: 713.4023, 734.4883, 746.3673, 750.5075, 768.5144, 782.4719, 833.3879, 855.0323, 864.5243, 886.9821, 908.9750, 930.9597, 1090.5162, 1097.9995, 1098.5942, 1106.4879, 1171.5496, 1219.5287, 1219.5287, 1235.5109, 1235.5109, 1279.7605, 1334.8767, 1448.9105, 1470.6846, 1609.8042, 1672.9178, 1794.7917, 1932.0006, 1932.0006, 1946.9951, 2023.9443, 2070.0024, 2092.0566, 2235.1628, 2565.1921, 2825.3228, 3333.5723, 3350.5940

9. gi|116786328 **Mass:** 57351 **Score:** 38 **Expect:** 96 **Queries matched:** 8

unknown [Picea sitchensis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1235.5109	1234.5036	1234.5499	-0.0463	163	173	0	---	GGLMSEEEDLR
1235.5109	1234.5036	1234.5499	-0.0463	163	173	0	---	GGLMSEEEDLR
1470.6846	1469.6773	1469.7296	-0.0523	417	428	1	---	QLEEHLEGMKTR
1672.9178	1671.9105	1671.9453	-0.0348	211	226	1	---	GIRVSVCSALAGLTLR
2092.0566	2091.0493	2091.0119	0.0374	40	57	1	---	AVDDEYEESIPSLRAELR
2653.3762	2652.3689	2652.3448	0.0241	59	80	1	---	LFKLVHPDLFYSHPDAQEVNQR
2653.3762	2652.3689	2652.3448	0.0241	59	80	1	---	LFKLVHPDLFYSHPDAQEVNQR
2825.3228	2824.3155	2824.3833	-0.0678	94	117	1	---	GNSSPQHHVYHFIFYLHKDAATQK

No match to: 713.4023, 734.4883, 746.3673, 750.5075, 768.5144, 782.4719, 833.3879, 855.0323, 864.5243, 886.9821, 908.9750, 930.9597, 1090.5162, 1097.9995, 1098.5942, 1106.4879, 1171.5496, 1219.5287, 1219.5287, 1279.7605, 1296.6012, 1312.6029, 1334.8767, 1448.9105, 1609.8042, 1794.7917, 1932.0006, 1932.0006, 1946.9951, 2023.9443, 2070.0024, 2235.1628, 2420.1953, 2420.1953, 2565.1921, 2669.3633, 2922.3650, 3333.5723, 3350.5940

10. gi|84514181 **Mass:** 45265 **Score:** 38 **Expect:** 98 **Queries matched:** 6

cytochrome P450 monooxygenase CYP72A66 [Medicago truncatula]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
713.4023	712.3950	712.3769	0.0182	24	28	1	---	WSKHR
1171.5496	1170.5423	1170.6032	-0.0609	231	240	0	---	EEVLHVFGNK
1296.6012	1295.5939	1295.6451	-0.0511	329	339	0	---	VSFFPFGWGPR
2023.9443	2022.9370	2023.0778	-0.1407	8	26	1	---	IFPLLASGLASYGGEKWSK
2565.1921	2564.1848	2564.2830	-0.0981	163	184	1	---	NDLLSILLESNHKEIENNNNNK
2669.3633	2668.3560	2668.4774	-0.1213	280	303	0	---	LGNLTLPAGVEVFLPILLIHHDCK

No match to: 734.4883, 746.3673, 750.5075, 768.5144, 782.4719, 833.3879, 855.0323, 864.5243, 886.9821, 908.9750, 930.9597, 1090.5162, 1097.9995, 1098.5942, 1106.4879, 1219.5287, 1219.5287, 1235.5109, 1235.5109, 1279.7605,

1312.6029, 1334.8767, 1448.9105, 1470.6846, 1609.8042, 1672.9178, 1794.7917, 1932.0006, 1932.0006, 1946.9951, 2070.0024, 2092.0566, 2235.1628, 2420.1953, 2420.1953, 2653.3762, 2653.3762, 2825.3228, 2922.3650, 3333.5723, 3350.5940

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 47

Protein View

Match to: **gi|729003** Score: **133** Expect: **3e-008**
RecName: Full=Carbonic anhydrase, chloroplastic; AltName: Full=Carbonate dehydratase; Flags: Precur

Nominal mass (M_r): **35736**; Calculated pI value: **8.93**
NCBI BLAST search of gi|729003 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Hordeum vulgare
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|558499 from Hordeum vulgare

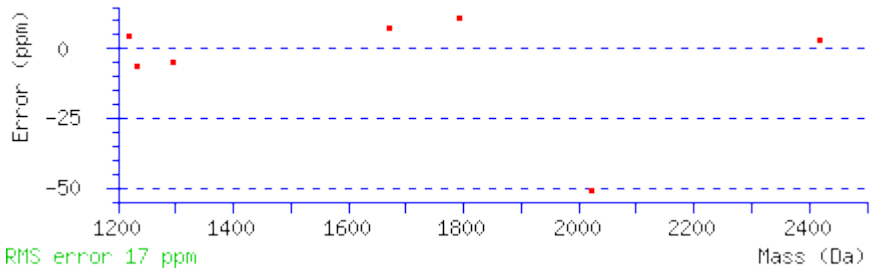
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **23%**

Matched peptides shown in **Bold Red**

```
   1 MSLQIGRTER ARSPVFVFAH KRQLLHGRCS TIDNANCSTC SMKINSTCTL
  51 TALPIAALPG PRTTSHYSTA AANWCYATVA PRARSSTIAA SLGTPAPSSS
 101 ASFRPKLIRT TPVQAAPVAP ALMDAAVERL KTGFEKFKTE VYDKKPDFFE
 151 PLKAGQAPKY MVFACADSRV CPSVTLGLEP GEAFTIRNIA NMVPAYCKNK
 201 YAGVGSAIEY AVCALKVEVI VVIGHSRCGG IKALLSLKDG ADDSFHFVED
 251 WVRIGFPAKK KVQTECASMP FDDQCTVLEK EAVNVSLQNL LTYPFVKEGV
 301 TNGTLKLVGG HYDFVSGKFE TWEQ
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
110 - 129	2023.9443	2022.9370	2023.0408	-0.1037	0	**TTPVQAAPVAPALMDAAVER** Oxidation (M) (No match)
145 - 159	1672.9178	1671.9105	1671.8984	0.0122	1	**KPDFFEPLKAGQAPK** (No match)
160 - 169	1219.5287	1218.5214	1218.5161	0.0053	0	**YMVFACADSR** (Ions score 43)
160 - 169	1219.5287	1218.5214	1218.5161	0.0053	0	**YMVFACADSR** (No match)
160 - 169	1235.5109	1234.5036	1234.5110	-0.0074	0	**YMVFACADSR** Oxidation (M) (Ions score 16)
160 - 169	1235.5109	1234.5036	1234.5110	-0.0074	0	**YMVFACADSR** Oxidation (M) (No match)
188 - 198	1296.6012	1295.5939	1295.6002	-0.0063	0	**NIANMVPAYCK** Oxidation (M) (No match)
233 - 253	2420.1953	2419.1880	2419.1807	0.0073	1	**ALLSLKDGADDSFHFVEDWVR** (No match)
233 - 253	2420.1953	2419.1880	2419.1807	0.0073	1	**ALLSLKDGADDSFHFVEDWVR** (Ions score 44)
239 - 253	1794.7917	1793.7844	1793.7645	0.0200	0	**DGADDSFHFVEDWVR** (No match)



Spot 121

Index

	Accession	Mass	Score	Description
1.	gi|729003	35736	131	RecName: Full=Carbonic anhydrase, chloroplastic; AltName: Full=Carbonate dehydratase; Flags: P
2.	gi|125559457	49390	45	hypothetical protein OsI_27173 [Oryza sativa Indica Group]
3.	gi|197259946	40548	45	leucoanthoxyanidin dioxygenase [Gossypium hirsutum]
4.	gi|108862916	51797	44	amidase, hydantoinase/carbamoylase family protein, expressed [Oryza sativa (japonica cultivar-
5.	gi|145345966	92395	43	predicted protein [Ostreococcus lucimarinus CCE9901]
6.	gi|125589731	20100	42	hypothetical protein OsJ_14143 [Oryza sativa Japonica Group]
7.	gi|159486028	43066	41	hypothetical protein CHLREDRAFT_113105 [Chlamydomonas reinhardtii]
8.	gi|168041003	26749	40	predicted protein [Physcomitrella patens subsp. patens]
9.	gi|125551392	20137	40	hypothetical protein OsI_19024 [Oryza sativa Indica Group]
10.	gi|224082348	57067	40	predicted protein [Populus trichocarpa]

Results List

1. gi|729003 **Mass:** 35736 **Score:** 131 **Expect:** 4.8e-008 **Queries matched:** 10

RecName: Full=Carbonic anhydrase, chloroplastic; AltName: Full=Carbonate dehydratase; Flags: Precur

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1219.5280	1218.5207	1218.5161	0.0046	160	169	0	---	YMVFACADSR
1219.5280	1218.5207	1218.5161	0.0046	160	169	0	32	YMVFACADSR
1235.5168	1234.5095	1234.5110	-0.0015	160	169	0	(11)	YMVFACADSR + Oxidation (M)
1235.5168	1234.5095	1234.5110	-0.0015	160	169	0	---	YMVFACADSR + Oxidation (M)
1296.5996	1295.5923	1295.6002	-0.0078	188	198	0	---	NIANMVPAYCK + Oxidation (M)
1771.8381	1770.8308	1770.8181	0.0127	154	169	1	---	AGQAPKYMVFACADSR
1787.8333	1786.8260	1786.8130	0.0130	154	169	1	---	AGQAPKYMVFACADSR + Oxidation (M)
1794.7860	1793.7787	1793.7645	0.0143	239	253	0	---	DGADDSFHFVEDWVR
2420.1987	2419.1914	2419.1807	0.0107	233	253	1	---	ALLSLKDGADDSFHFVEDWVR
2420.1987	2419.1914	2419.1807	0.0107	233	253	1	66	ALLSLKDGADDSFHFVEDWVR

No match to: 713.4030, 724.4927, 734.4892, 750.5089, 768.5173, 782.4689, 833.3798, 838.5240, 849.3781, 864.5316, 1074.5685, 1090.5322, 1106.4882, 1173.0205, 1279.7622, 1312.5990, 1334.8823, 1448.9089, 1470.6823, 1554.7408, 1636.8518, 1652.8406, 1826.8616, 1857.8073, 1868.9318, 1931.9994, 1931.9994, 1947.9858, 1953.9854, 2070.0044, 2070.0044, 2101.0767, 2118.0708, 2213.0811, 2257.1062, 2437.1990, 2564.1897, 2653.3792, 2669.3757, 2780.4661, 2780.9429, 2825.3113, 2914.4883, 2922.3679

2. gi|125559457 **Mass:** 49390 **Score:** 45 **Expect:** 18 **Queries matched:** 8

hypothetical protein OsI_27173 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
833.3798	832.3725	832.4178	-0.0452	302	308	0	---	ILEEDSK
849.3781	848.3708	848.4248	-0.0540	65	71	0	---	MVALMER
1219.5280	1218.5207	1218.5954	-0.0747	403	411	1	---	MEKYQTYLK + Oxidation (M)

1219.5280	1218.5207	1218.5954	-0.0747	403 - 411	1	---	MEKYQTYLK + Oxidation (M)
2118.0708	2117.0635	2117.0752	-0.0117	187 - 205	1	---	LLSSWLNNSLDSINGNDKK
2420.1987	2419.1914	2419.0622	0.1292	314 - 335	1	---	ISESGAYTSSSNQETEEETSRK
2420.1987	2419.1914	2419.0576	0.1338	206 - 226	1	---	GEYYWRDVAAEFNGNASSNNR
2669.3757	2668.3684	2668.3860	-0.0175	353 - 377	1	---	GKKPAPSPLGDQPSQDFVLFNEAVK

No match to: 713.4030, 724.4927, 734.4892, 750.5089, 768.5173, 782.4689, 838.5240, 864.5316, 1074.5685, 1090.5322, 1106.4882, 1173.0205, 1235.5168, 1235.5168, 1279.7622, 1296.5996, 1312.5990, 1334.8823, 1448.9089, 1470.6823, 1554.7408, 1636.8518, 1652.8406, 1771.8381, 1787.8333, 1794.7860, 1826.8616, 1857.8073, 1868.9318, 1931.9994, 1931.9994, 1947.9858, 1953.9854, 2070.0044, 2070.0044, 2101.0767, 2213.0811, 2257.1062, 2437.1990, 2564.1897, 2653.3792, 2780.4661, 2780.9429, 2825.3113, 2914.4883, 2922.3679

3. gi|197259946 **Mass:** 40548 **Score:** 45 **Expect:** 21 **Queries matched:** 8

leucoanthoxyanidin dioxygenase [Gossypium hirsutum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1090.5322	1089.5249	1089.5237	0.0013	66 -	73	1	---	ERCQQELK
1931.9994	1930.9921	1930.8656	0.1265	113 -	130	1	---	EKYANDQSSGNVQGYGSK
1931.9994	1930.9921	1930.8656	0.1265	113 -	130	1	---	EKYANDQSSGNVQGYGSK
2101.0767	2100.0694	2100.1612	-0.0918	180 -	199	1	---	ALASKILSALSICLGLEEGR
2257.1062	2256.0989	2256.1008	-0.0019	43 -	62	1	---	KEEGPQVPTIDLTEIESEDK
2653.3792	2652.3719	2652.2610	0.1109	74 -	96	1	---	KAAMEWGVMHLVNHGISEELMDR
2669.3757	2668.3684	2668.2559	0.1125	74 -	96	1	---	KAAMEWGVMHLVNHGISEELMDR + Oxidation (M)
2780.4661	2779.4588	2779.3356	0.1233	75 -	98	1	---	AAMEWGVMHLVNHGISEELMDRVR

No match to: 713.4030, 724.4927, 734.4892, 750.5089, 768.5173, 782.4689, 833.3798, 838.5240, 849.3781, 864.5316, 1074.5685, 1106.4882, 1173.0205, 1219.5280, 1219.5280, 1235.5168, 1235.5168, 1279.7622, 1296.5996, 1312.5990, 1334.8823, 1448.9089, 1470.6823, 1554.7408, 1636.8518, 1652.8406, 1771.8381, 1787.8333, 1794.7860, 1826.8616, 1857.8073, 1868.9318, 1947.9858, 1953.9854, 2070.0044, 2070.0044, 2118.0708, 2213.0811, 2420.1987, 2420.1987, 2437.1990, 2564.1897, 2780.9429, 2825.3113, 2914.4883, 2922.3679

4. gi|108862916 **Mass:** 51797 **Score:** 44 **Expect:** 24 **Queries matched:** 8

amidase, hydantoinase/carbamoylase family protein, expressed [Oryza sativa (japonica cultivar-group

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1554.7408	1553.7335	1553.7685	-0.0350	354 -	366	1	---	SHVEIDVRDIDEK
1794.7860	1793.7787	1793.8981	-0.1194	183 -	197	1	---	RSLEVIMFTSEEPTR
1826.8616	1825.8543	1825.8967	-0.0424	425 -	439	1	---	LMISRAYHDSLFMAR + Oxidation (M)
1947.9858	1946.9785	1946.9585	0.0200	79 -	96	0	---	QIDELASFSDSPVPSVTR
2070.0044	2068.9971	2069.0033	-0.0062	198 -	216	1	---	FGISCLGSRLMAGSEELAR + Oxidation (M)
2070.0044	2068.9971	2069.0033	-0.0062	198 -	216	1	---	FGISCLGSRLMAGSEELAR + Oxidation (M)
2653.3792	2652.3719	2652.3282	0.0437	79 -	102	1	---	QIDELASFSDSPVPSVTRVLYSDK
2780.4661	2779.4588	2779.2994	0.1594	430 -	452	1	---	AYHDSLFMARISPMGMIFIPCYK + 2 Oxidation (M)

No match to: 713.4030, 724.4927, 734.4892, 750.5089, 768.5173, 782.4689, 833.3798, 838.5240, 849.3781, 864.5316, 1074.5685, 1090.5322, 1106.4882, 1173.0205, 1219.5280, 1219.5280, 1235.5168, 1235.5168, 1279.7622, 1296.5996, 1312.5990, 1334.8823, 1448.9089, 1470.6823, 1636.8518, 1652.8406, 1771.8381, 1787.8333, 1857.8073, 1868.9318, 1931.9994, 1931.9994, 1953.9854, 2101.0767, 2118.0708, 2213.0811, 2257.1062, 2420.1987, 2420.1987, 2437.1990,

2564.1897, 2669.3757, 2780.9429, 2825.3113, 2914.4883, 2922.3679

5. gi|145345966 **Mass:** 92395 **Score:** 43 **Expect:** 34 **Queries matched:** 10

predicted protein [Ostreococcus lucimarinus CCE9901]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1554.7408	1553.7335	1553.6854	0.0482	227	238	1	---	NLMHEDTFEKMK + 2 Oxidation (M)
1636.8518	1635.8445	1635.8692	-0.0247	359	372	1	---	QPEIVTRDQNPLAR
1931.9994	1930.9921	1930.9537	0.0385	254	270	0	---	ATHIVISEHASAVDYYR
1931.9994	1930.9921	1930.8951	0.0971	542	557	1	0	MMCVLVDAKYSDQLSR + Oxidation (M)
1947.9858	1946.9785	1946.9333	0.0452	402	419	1	---	QDESGQPTSDSIPFVGKR
2420.1987	2419.1914	2419.1590	0.0324	250	270	1	---	DMNKATHIVISEHASAVDYYR
2420.1987	2419.1914	2419.1590	0.0324	250	270	1	---	DMNKATHIVISEHASAVDYYR
2564.1897	2563.1824	2563.0600	0.1225	450	471	1	---	TGREFMNADYMVCPSMPSADER
2825.3113	2824.3040	2824.3862	-0.0822	83	106	1	---	FMVPPFLGCVVSITGFMDLTHRER + Oxidation (M)
2922.3679	2921.3606	2921.3647	-0.0041	702	727	0	---	TLTGRPSAGEQTEALFDQVMQNMEPR + Oxidation (M)

No match to: 713.4030, 724.4927, 734.4892, 750.5089, 768.5173, 782.4689, 833.3798, 838.5240, 849.3781, 864.5316, 1074.5685, 1090.5322, 1106.4882, 1173.0205, 1219.5280, 1219.5280, 1235.5168, 1235.5168, 1279.7622, 1296.5996, 1312.5990, 1334.8823, 1448.9089, 1470.6823, 1652.8406, 1771.8381, 1787.8333, 1794.7860, 1826.8616, 1857.8073, 1868.9318, 1953.9854, 2070.0044, 2070.0044, 2101.0767, 2118.0708, 2213.0811, 2257.1062, 2437.1990, 2653.3792, 2669.3757, 2780.4661, 2780.9429, 2914.4883

6. gi|125589731 **Mass:** 20100 **Score:** 42 **Expect:** 38 **Queries matched:** 7

hypothetical protein OsJ_14143 [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
833.3798	832.3725	832.4178	-0.0452	35	41	0	---	ILEEDSK
1090.5322	1089.5249	1089.5641	-0.0391	1	9	1	---	MEKAHALYK
1219.5280	1218.5207	1218.5954	-0.0747	136	144	1	---	MEKYQTYLK + Oxidation (M)
1219.5280	1218.5207	1218.5954	-0.0747	136	144	1	---	MEKYQTYLK + Oxidation (M)
2420.1987	2419.1914	2419.0622	0.1292	47	68	1	---	ISESGAYTSSSNQETEEETSRK
2420.1987	2419.1914	2419.0622	0.1292	47	68	1	---	ISESGAYTSSSNQETEEETSRK
2669.3757	2668.3684	2668.3860	-0.0175	86	110	1	---	GKKPAPSPLGDQPSQDFVLFNEAVK

No match to: 713.4030, 724.4927, 734.4892, 750.5089, 768.5173, 782.4689, 838.5240, 849.3781, 864.5316, 1074.5685, 1106.4882, 1173.0205, 1235.5168, 1235.5168, 1279.7622, 1296.5996, 1312.5990, 1334.8823, 1448.9089, 1470.6823, 1554.7408, 1636.8518, 1652.8406, 1771.8381, 1787.8333, 1794.7860, 1826.8616, 1857.8073, 1868.9318, 1931.9994, 1931.9994, 1947.9858, 1953.9854, 2070.0044, 2070.0044, 2101.0767, 2118.0708, 2213.0811, 2257.1062, 2437.1990, 2564.1897, 2653.3792, 2780.4661, 2780.9429, 2825.3113, 2914.4883, 2922.3679

7. gi|159486028 **Mass:** 43066 **Score:** 41 **Expect:** 52 **Queries matched:** 6

hypothetical protein CHLREDRAFT_113105 [Chlamydomonas reinhardtii]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1448.9089	1447.9016	1447.8187	0.0830	144	156	0	---	VPFADVNLLHVPK
2101.0767	2100.0694	2100.0826	-0.0131	332	349	1	---	AGQTPVQKYWGHLLEMVK + Oxidation (M)
2118.0708	2117.0635	2117.0073	0.0562	252	270	0	---	LVPGGPDVCIEAVGFHYCK

2420.1987	2419.1914	2419.2093	-0.0179	353 - 373	0	---	LDPTMIITHELPIEDAPHAYK + Oxidation (M)
2420.1987	2419.1914	2419.1624	0.0291	32 - 54	0	---	VTSSAICGSDLHLYLGSAPGMQR
2437.1990	2436.1917	2436.0804	0.1114	121 - 143	0	---	TAGMFGYAHVTGGYEGGQTDYVR

No match to: 713.4030, 724.4927, 734.4892, 750.5089, 768.5173, 782.4689, 833.3798, 838.5240, 849.3781, 864.5316, 1074.5685, 1090.5322, 1106.4882, 1173.0205, 1219.5280, 1219.5280, 1235.5168, 1235.5168, 1279.7622, 1296.5996, 1312.5990, 1334.8823, 1470.6823, 1554.7408, 1636.8518, 1652.8406, 1771.8381, 1787.8333, 1794.7860, 1826.8616, 1857.8073, 1868.9318, 1931.9994, 1931.9994, 1947.9858, 1953.9854, 2070.0044, 2070.0044, 2213.0811, 2257.1062, 2564.1897, 2653.3792, 2669.3757, 2780.4661, 2780.9429, 2825.3113, 2914.4883, 2922.3679

8. gi|168041003 **Mass:** 26749 **Score:** 40 **Expect:** 59 **Queries matched:** 6

predicted protein [Physcomitrella patens subsp. patens]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1219.5280	1218.5207	1218.5815	-0.0608	225 - 234		1	---	LAFHKQTSCQ
1219.5280	1218.5207	1218.5815	-0.0608	225 - 234		1	---	LAFHKQTSCQ
1826.8616	1825.8543	1825.8304	0.0239	99 - 113		1	---	FHESTDFEGMKNLQK + Oxidation (M)
1868.9318	1867.9245	1867.9535	-0.0290	142 - 156		1	---	KLYTLACLECTEIVR
2213.0811	2212.0738	2212.0734	0.0004	42 - 61		0	---	NAWFLSSALGFECAGNSILR
2825.3113	2824.3040	2824.4408	-0.1368	10 - 34		1	---	HGVSETETWSPSQHPPALFLRHLAK

No match to: 713.4030, 724.4927, 734.4892, 750.5089, 768.5173, 782.4689, 833.3798, 838.5240, 849.3781, 864.5316, 1074.5685, 1090.5322, 1106.4882, 1173.0205, 1235.5168, 1235.5168, 1279.7622, 1296.5996, 1312.5990, 1334.8823, 1448.9089, 1470.6823, 1554.7408, 1636.8518, 1652.8406, 1771.8381, 1787.8333, 1794.7860, 1857.8073, 1931.9994, 1931.9994, 1947.9858, 1953.9854, 2070.0044, 2070.0044, 2101.0767, 2118.0708, 2257.1062, 2420.1987, 2420.1987, 2437.1990, 2564.1897, 2653.3792, 2669.3757, 2780.4661, 2780.9429, 2914.4883, 2922.3679

9. gi|125551392 **Mass:** 20137 **Score:** 40 **Expect:** 61 **Queries matched:** 6

hypothetical protein OsI_19024 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
838.5240	837.5167	837.5072	0.0095	170 - 176		0	---	QHISIIK
1219.5280	1218.5207	1218.5491	-0.0284	104 - 112		0	---	CRPAFYYDK
1219.5280	1218.5207	1218.5491	-0.0284	104 - 112		0	---	CRPAFYYDK
1554.7408	1553.7335	1553.7507	-0.0172	91 - 103		1	---	TIGEMAEEFLSRR + Oxidation (M)
1953.9854	1952.9781	1952.8911	0.0870	28 - 44		1	---	ITTSSSARGWSNCQGWR
2257.1062	2256.0989	2256.1895	-0.0906	1 - 23		0	---	MASLLPRPVLPAAAAASTSSSSR + Oxidation (M)

No match to: 713.4030, 724.4927, 734.4892, 750.5089, 768.5173, 782.4689, 833.3798, 849.3781, 864.5316, 1074.5685, 1090.5322, 1106.4882, 1173.0205, 1235.5168, 1235.5168, 1279.7622, 1296.5996, 1312.5990, 1334.8823, 1448.9089, 1470.6823, 1636.8518, 1652.8406, 1771.8381, 1787.8333, 1794.7860, 1826.8616, 1857.8073, 1868.9318, 1931.9994, 1931.9994, 1947.9858, 2070.0044, 2070.0044, 2101.0767, 2118.0708, 2213.0811, 2420.1987, 2420.1987, 2437.1990, 2564.1897, 2653.3792, 2669.3757, 2780.4661, 2780.9429, 2825.3113, 2914.4883, 2922.3679

10. gi|224082348 **Mass:** 57067 **Score:** 40 **Expect:** 62 **Queries matched:** 7

predicted protein [Populus trichocarpa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
734.4892	733.4819	733.4738	0.0082	2 - 7		0	---	TIFIIK

1090.5322	1089.5249	1089.4913	0.0336	283 - 291	0	---	CPFIHDSSK
1868.9318	1867.9245	1867.9474	-0.0229	339 - 354	1	---	HVRVNPNASICEGFLR
2101.0767	2100.0694	2100.0963	-0.0269	66 - 85	0	---	SFLPKPSSISNHSSLSSIGR
2118.0708	2117.0635	2117.0727	-0.0092	412 - 430	1	---	YFGLMHASTTELRNPVPGK
2213.0811	2212.0738	2212.1065	-0.0326	41 - 59	1	---	NDGDSLHYGKVLSHLFPWK
2257.1062	2256.0989	2255.9939	0.1050	366 - 385	1	---	KHSYVCPTYEATGSCPQGSK

No match to: 713.4030, 724.4927, 750.5089, 768.5173, 782.4689, 833.3798, 838.5240, 849.3781, 864.5316, 1074.5685, 1106.4882, 1173.0205, 1219.5280, 1219.5280, 1235.5168, 1235.5168, 1279.7622, 1296.5996, 1312.5990, 1334.8823, 1448.9089, 1470.6823, 1554.7408, 1636.8518, 1652.8406, 1771.8381, 1787.8333, 1794.7860, 1826.8616, 1857.8073, 1931.9994, 1931.9994, 1947.9858, 1953.9854, 2070.0044, 2070.0044, 2420.1987, 2420.1987, 2437.1990, 2564.1897, 2653.3792, 2669.3757, 2780.4661, 2780.9429, 2825.3113, 2914.4883, 2922.3679

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 54

Protein View

Match to: **gi|729003** Score: **131** Expect: **4.8e-008**
RecName: Full=Carbonic anhydrase, chloroplastic; AltName: Full=Carbonate dehydratase; Flags: Precur

Nominal mass (M_r): **35736**; Calculated pI value: **8.93**
NCBI BLAST search of gi|729003 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Hordeum vulgare
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|558499 from Hordeum vulgare

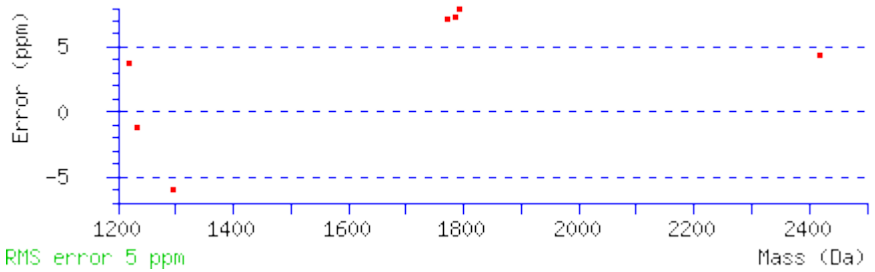
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **14%**

Matched peptides shown in **Bold Red**

```
   1 MSLQIGRTER ARSPVFVFAH KRQLLHGRCS TIDNANCSTC SMKINSTCTL
  51 TALPIAALPG PRTTSHYSTA AANWCYATVA PRARSSTIAA SLGTPAPSSS
 101 ASFRPKLIRT TPVQAAPVAP ALMDAAVERL KTGFEKFKTE VYDKKPDFFE
 151 PLKAGQAPKY MVFACADSRV CPSVTLGLEP GEAFTIRNIA NMVPAYCKNK
 201 YAGVGSAIEY AVCALKVEVI VVIGHSRCGG IKALLSLKDG ADDSFHFVED
 251 WVRIGFPAKK KVQTECASMP FDDQCTVLEK EAVNVSLQNL LTYPFVKEGV
 301 TNGTLKLVGG HYDFVSGKFE TWEQ
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
154 - 169	1771.8381	1770.8308	1770.8181	0.0127	1	**AGQAPKYMVFACADSR** (No match)
154 - 169	1787.8333	1786.8260	1786.8130	0.0130	1	**AGQAPKYMVFACADSR** Oxidation (M) (No match)
160 - 169	1219.5280	1218.5207	1218.5161	0.0046	0	**YMVFACADSR** (No match)
160 - 169	1219.5280	1218.5207	1218.5161	0.0046	0	**YMVFACADSR** (Ions score 32)
160 - 169	1235.5168	1234.5095	1234.5110	-0.0015	0	**YMVFACADSR** Oxidation (M) (Ions score 11)
160 - 169	1235.5168	1234.5095	1234.5110	-0.0015	0	**YMVFACADSR** Oxidation (M) (No match)
188 - 198	1296.5996	1295.5923	1295.6002	-0.0078	0	**NIANMVPAYCK** Oxidation (M) (No match)
233 - 253	2420.1987	2419.1914	2419.1807	0.0107	1	**ALLSLKDGADDSFHFVEDWVR** (No match)
233 - 253	2420.1987	2419.1914	2419.1807	0.0107	1	**ALLSLKDGADDSFHFVEDWVR** (Ions score 66)
239 - 253	1794.7860	1793.7787	1793.7645	0.0143	0	**DGADDSFHFVEDWVR** (No match)



Spot 122

Index

	Accession	Mass	Score	Description
1.	gi|37788308	26062	81	cyclophilin-like protein [Triticum aestivum]
2.	gi|133741925	26084	81	peptidylprolyl isomerase [Triticum aestivum]
3.	gi|37788312	25989	69	cyclophilin-like protein [Triticum aestivum]
4.	gi|83700344	16409	63	chloroplast-localized cyclophilin [Triticum aestivum]
5.	gi|83700338	16527	62	chloroplast-localized cyclophilin [Triticum aestivum]
6.	gi|83700342	16499	62	chloroplast-localized cyclophilin [Triticum aestivum]
7.	gi|108862529	196835	54	retrotransposon protein, putative, unclassified [Oryza sativa (japonica cultivar-group)]
8.	gi|47846294	31522	53	hypothetical protein [Hordeum vulgare subsp. vulgare]
9.	gi|168062783	119719	50	predicted protein [Physcomitrella patens subsp. patens]
10.	gi|222623073	46746	49	hypothetical protein OsJ_07164 [Oryza sativa Japonica Group]

Results List

1. gi|37788308 **Mass:** 26062 **Score:** 81 **Expect:** 0.0053 **Queries matched:** 10

cyclophilin-like protein [Triticum aestivum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1242.5968	1241.5895	1241.5941	-0.0045	122	132	1	---	GFGYKGSSFHR
1242.5968	1241.5895	1241.5941	-0.0045	122	132	1	---	GFGYKGSSFHR
1556.8491	1555.8418	1555.8430	-0.0012	44	58	1	---	VASPALSVSQQSRAR
1698.8995	1697.8922	1697.8922	-0.0000	203	217	0	13	HVVFGQVLEGMDIVR
1698.8995	1697.8922	1697.8922	-0.0000	203	217	0	---	HVVFGQVLEGMDIVR
1714.8849	1713.8776	1713.8871	-0.0095	203	217	0	(1)	HVVFGQVLEGMDIVR + Oxidation (M)
1714.8849	1713.8776	1713.8871	-0.0095	203	217	0	---	HVVFGQVLEGMDIVR + Oxidation (M)
1850.9985	1849.9912	1849.9937	-0.0025	76	92	1	---	VTNKVYFDISIGNPVGK
2035.0466	2034.0393	2034.0421	-0.0028	97	114	0	21	IVIGLYGDDVPQTVENFR
2035.0466	2034.0393	2034.0421	-0.0028	97	114	0	---	IVIGLYGDDVPQTVENFR

No match to: 713.4033, 734.4868, 750.5184, 768.5142, 782.4771, 864.5305, 886.9829, 1279.7448, 1333.7170, 1334.8057, 1376.6588, 1436.7476, 1448.8995, 1588.7866, 1652.5116, 1845.9839, 2001.9570, 2001.9570, 2184.0742, 2200.0632, 2277.2354, 2462.2896, 2564.1892, 2662.3862, 2780.4480, 2780.9680, 2922.3689, 3332.5874, 3349.6301

2. gi|133741925 **Mass:** 26084 **Score:** 81 **Expect:** 0.0053 **Queries matched:** 10

peptidylprolyl isomerase [Triticum aestivum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1242.5968	1241.5895	1241.5941	-0.0045	122	132	1	---	GFGYKGSSFHR
1242.5968	1241.5895	1241.5941	-0.0045	122	132	1	---	GFGYKGSSFHR
1556.8491	1555.8418	1555.8430	-0.0012	44	58	1	---	VASPALSVSQQSRAR
1698.8995	1697.8922	1697.8922	-0.0000	203	217	0	13	HVVFGQVLEGMDIVR
1698.8995	1697.8922	1697.8922	-0.0000	203	217	0	---	HVVFGQVLEGMDIVR

1714.8849	1713.8776	1713.8871	-0.0095	203 - 217	0	(1)	HVVFGQVLEGMDIVR + Oxidation (M)
1714.8849	1713.8776	1713.8871	-0.0095	203 - 217	0	---	HVVFGQVLEGMDIVR + Oxidation (M)
1850.9985	1849.9912	1849.9937	-0.0025	76 - 92	1	---	VTNKVYFDISIGNPVGK
2035.0466	2034.0393	2034.0421	-0.0028	97 - 114	0	21	IVIGLYGDDVPQTVENFR
2035.0466	2034.0393	2034.0421	-0.0028	97 - 114	0	---	IVIGLYGDDVPQTVENFR

No match to: 713.4033, 734.4868, 750.5184, 768.5142, 782.4771, 864.5305, 886.9829, 1279.7448, 1333.7170, 1334.8057, 1376.6588, 1436.7476, 1448.8995, 1588.7866, 1652.5116, 1845.9839, 2001.9570, 2001.9570, 2184.0742, 2200.0632, 2277.2354, 2462.2896, 2564.1892, 2662.3862, 2780.4480, 2780.9680, 2922.3689, 3332.5874, 3349.6301

3. gi|37788312 **Mass:** 25989 **Score:** 69 **Expect:** 0.086 **Queries matched:** 9

cyclophilin-like protein [Triticum aestivum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1242.5968	1241.5895	1241.5941	-0.0045	122 - 132		1	---	GFGYKGSSFHR
1242.5968	1241.5895	1241.5941	-0.0045	122 - 132		1	---	GFGYKGSSFHR
1698.8995	1697.8922	1697.8922	-0.0000	203 - 217		0	13	HVVFGQVLEGMDIVR
1698.8995	1697.8922	1697.8922	-0.0000	203 - 217		0	---	HVVFGQVLEGMDIVR
1714.8849	1713.8776	1713.8871	-0.0095	203 - 217		0	(1)	HVVFGQVLEGMDIVR + Oxidation (M)
1714.8849	1713.8776	1713.8871	-0.0095	203 - 217		0	---	HVVFGQVLEGMDIVR + Oxidation (M)
1850.9985	1849.9912	1849.9937	-0.0025	76 - 92		1	---	VTNKVYFDISIGNPVGK
2035.0466	2034.0393	2034.0421	-0.0028	97 - 114		0	21	IVIGLYGDDVPQTVENFR
2035.0466	2034.0393	2034.0421	-0.0028	97 - 114		0	---	IVIGLYGDDVPQTVENFR

No match to: 713.4033, 734.4868, 750.5184, 768.5142, 782.4771, 864.5305, 886.9829, 1279.7448, 1333.7170, 1334.8057, 1376.6588, 1436.7476, 1448.8995, 1556.8491, 1588.7866, 1652.5116, 1845.9839, 2001.9570, 2001.9570, 2184.0742, 2200.0632, 2277.2354, 2462.2896, 2564.1892, 2662.3862, 2780.4480, 2780.9680, 2922.3689, 3332.5874, 3349.6301

4. gi|83700344 **Mass:** 16409 **Score:** 63 **Expect:** 0.32 **Queries matched:** 8

chloroplast-localized cyclophilin [Triticum aestivum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1242.5968	1241.5895	1241.5941	-0.0045	33 - 43		1	---	GFGYKGSSFHR
1242.5968	1241.5895	1241.5941	-0.0045	33 - 43		1	---	GFGYKGSSFHR
1698.8995	1697.8922	1697.8922	-0.0000	114 - 128		0	13	HVVFGQVLEGMDIVR
1698.8995	1697.8922	1697.8922	-0.0000	114 - 128		0	---	HVVFGQVLEGMDIVR
1714.8849	1713.8776	1713.8871	-0.0095	114 - 128		0	(1)	HVVFGQVLEGMDIVR + Oxidation (M)
1714.8849	1713.8776	1713.8871	-0.0095	114 - 128		0	---	HVVFGQVLEGMDIVR + Oxidation (M)
2035.0466	2034.0393	2034.0421	-0.0028	8 - 25		0	21	IVIGLYGDDVPQTVENFR
2035.0466	2034.0393	2034.0421	-0.0028	8 - 25		0	---	IVIGLYGDDVPQTVENFR

No match to: 713.4033, 734.4868, 750.5184, 768.5142, 782.4771, 864.5305, 886.9829, 1279.7448, 1333.7170, 1334.8057, 1376.6588, 1436.7476, 1448.8995, 1556.8491, 1588.7866, 1652.5116, 1845.9839, 1850.9985, 2001.9570, 2001.9570, 2184.0742, 2200.0632, 2277.2354, 2462.2896, 2564.1892, 2662.3862, 2780.4480, 2780.9680, 2922.3689, 3332.5874, 3349.6301

5. gi|83700338 **Mass:** 16527 **Score:** 62 **Expect:** 0.39 **Queries matched:** 8

chloroplast-localized cyclophilin [Triticum aestivum]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1242.5968	1241.5895	1241.5941	-0.0045	33	-	43	1	---	GFGYKGSSFHR
1242.5968	1241.5895	1241.5941	-0.0045	33	-	43	1	---	GFGYKGSSFHR
1698.8995	1697.8922	1697.8922	-0.0000	114	-	128	0	13	HVVFGQVLEGMDIVR
1698.8995	1697.8922	1697.8922	-0.0000	114	-	128	0	---	HVVFGQVLEGMDIVR
1714.8849	1713.8776	1713.8871	-0.0095	114	-	128	0	(1)	HVVFGQVLEGMDIVR + Oxidation (M)
1714.8849	1713.8776	1713.8871	-0.0095	114	-	128	0	---	HVVFGQVLEGMDIVR + Oxidation (M)
2035.0466	2034.0393	2034.0421	-0.0028	8	-	25	0	21	IVIGLYGDDVPQTVENFR
2035.0466	2034.0393	2034.0421	-0.0028	8	-	25	0	---	IVIGLYGDDVPQTVENFR

No match to: 713.4033, 734.4868, 750.5184, 768.5142, 782.4771, 864.5305, 886.9829, 1279.7448, 1333.7170, 1334.8057, 1376.6588, 1436.7476, 1448.8995, 1556.8491, 1588.7866, 1652.5116, 1845.9839, 1850.9985, 2001.9570, 2001.9570, 2184.0742, 2200.0632, 2277.2354, 2462.2896, 2564.1892, 2662.3862, 2780.4480, 2780.9680, 2922.3689, 3332.5874, 3349.6301

6. gi|83700342 **Mass:** 16499 **Score:** 62 **Expect:** 0.39 **Queries matched:** 8

chloroplast-localized cyclophilin [Triticum aestivum]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1242.5968	1241.5895	1241.5941	-0.0045	33	-	43	1	---	GFGYKGSSFHR
1242.5968	1241.5895	1241.5941	-0.0045	33	-	43	1	---	GFGYKGSSFHR
1698.8995	1697.8922	1697.8922	-0.0000	114	-	128	0	13	HVVFGQVLEGMDIVR
1698.8995	1697.8922	1697.8922	-0.0000	114	-	128	0	---	HVVFGQVLEGMDIVR
1714.8849	1713.8776	1713.8871	-0.0095	114	-	128	0	(1)	HVVFGQVLEGMDIVR + Oxidation (M)
1714.8849	1713.8776	1713.8871	-0.0095	114	-	128	0	---	HVVFGQVLEGMDIVR + Oxidation (M)
2035.0466	2034.0393	2034.0421	-0.0028	8	-	25	0	21	IVIGLYGDDVPQTVENFR
2035.0466	2034.0393	2034.0421	-0.0028	8	-	25	0	---	IVIGLYGDDVPQTVENFR

No match to: 713.4033, 734.4868, 750.5184, 768.5142, 782.4771, 864.5305, 886.9829, 1279.7448, 1333.7170, 1334.8057, 1376.6588, 1436.7476, 1448.8995, 1556.8491, 1588.7866, 1652.5116, 1845.9839, 1850.9985, 2001.9570, 2001.9570, 2184.0742, 2200.0632, 2277.2354, 2462.2896, 2564.1892, 2662.3862, 2780.4480, 2780.9680, 2922.3689, 3332.5874, 3349.6301

7. gi|108862529 **Mass:** 196835 **Score:** 54 **Expect:** 2.5 **Queries matched:** 15

retrotransposon protein, putative, unclassified [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1242.5968	1241.5895	1241.5598	0.0298	1324	-	1333	0	---	NDTLMVYNEK + Oxidation (M)
1242.5968	1241.5895	1241.5598	0.0298	1324	-	1333	0	---	NDTLMVYNEK + Oxidation (M)
1333.7170	1332.7097	1332.6646	0.0451	608	-	618	1	---	SYNRGNRPNQK
1376.6588	1375.6515	1375.6103	0.0413	708	-	720	0	---	QADVDDVEEASAK
1436.7476	1435.7403	1435.8221	-0.0817	1	-	14	0	---	MAIPIVGGHVLTTK
1698.8995	1697.8922	1697.7865	0.1058	1133	-	1147	1	---	MNPTKCAFGISAETR + Oxidation (M)
1698.8995	1697.8922	1697.7865	0.1058	1133	-	1147	1	---	MNPTKCAFGISAETR + Oxidation (M)
1714.8849	1713.8776	1713.9049	-0.0273	39	-	54	1	---	SEPKGNLFGPALELSR

1714.8849	1713.8776	1713.9049	-0.0273	39 - 54	1	---	SEPKGNLFGPALELSR
2001.9570	2000.9497	2000.9486	0.0011	1439 - 1457	0	---	AAIGEVHEGICGTHQSAHK
2001.9570	2000.9497	2000.9486	0.0011	1439 - 1457	0	---	AAIGEVHEGICGTHQSAHK
2277.2354	2276.2281	2276.0789	0.1492	1439 - 1459	1	---	AAIGEVHEGICGTHQSAHKMK + Oxidation (M)
2564.1892	2563.1819	2563.0930	0.0890	135 - 155	0	---	DQYQGPNCTIASTFAMCWEIR + Oxidation (M)
2922.3689	2921.3616	2921.3904	-0.0288	1265 - 1290	0	---	GASFEFACTIKPYATNNQAEYEAVLK
3349.6301	3348.6228	3348.4404	0.1824	391 - 419	1	---	INHVYPYMYGSDDEDDDSEVAAAEWVKSK + Oxidation (M)

No match to: 713.4033, 734.4868, 750.5184, 768.5142, 782.4771, 864.5305, 886.9829, 1279.7448, 1334.8057, 1448.8995, 1556.8491, 1588.7866, 1652.5116, 1845.9839, 1850.9985, 2035.0466, 2035.0466, 2184.0742, 2200.0632, 2462.2896, 2662.3862, 2780.4480, 2780.9680, 3332.5874

8. gi|47846294 **Mass:** 31522 **Score:** 53 **Expect:** 2.8 **Queries matched:** 7

hypothetical protein [Hordeum vulgare subsp. vulgare]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1242.5968	1241.5895	1241.6476	-0.0581	82 - 92		1	---	IDAGQEQLGRR
1242.5968	1241.5895	1241.6476	-0.0581	82 - 92		1	---	IDAGQEQLGRR
1279.7448	1278.7375	1278.7295	0.0080	274 - 285		1	---	QIAEIGASLIKH
1376.6588	1375.6515	1375.6442	0.0073	203 - 213		0	---	QQLIDWMEADK
2277.2354	2276.2281	2276.0969	0.1312	54 - 71		1	---	ILESFRPEERFPMMSTFK + 2 Oxidation (M)
2564.1892	2563.1819	2563.3281	-0.1462	42 - 63		1	---	VGYIELDLNSGKILESFRPEER
2662.3862	2661.3789	2661.3353	0.0436	119 - 144		0	---	ELCSAAITMSDNTAANLLLTTIGGPK

No match to: 713.4033, 734.4868, 750.5184, 768.5142, 782.4771, 864.5305, 886.9829, 1333.7170, 1334.8057, 1436.7476, 1448.8995, 1556.8491, 1588.7866, 1652.5116, 1698.8995, 1698.8995, 1714.8849, 1714.8849, 1845.9839, 1850.9985, 2001.9570, 2001.9570, 2035.0466, 2035.0466, 2184.0742, 2200.0632, 2462.2896, 2780.4480, 2780.9680, 2922.3689, 3332.5874, 3349.6301

9. gi|168062783 **Mass:** 119719 **Score:** 50 **Expect:** 5.5 **Queries matched:** 9

predicted protein [Physcomitrella patens subsp. patens]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1436.7476	1435.7403	1435.7095	0.0308	982 - 993		1	---	DGWGIEKFLSER
1556.8491	1555.8418	1555.8140	0.0278	910 - 924		1	---	AGPIGIGCKEQGLTR
1845.9839	1844.9766	1844.9203	0.0564	721 - 736		1	---	SSWNCLPRVQLESAAK
2001.9570	2000.9497	2001.0200	-0.0703	700 - 718		0	---	ASLIGIGCQEQVQLESAAK
2001.9570	2000.9497	2000.9836	-0.0339	852 - 870		0	---	ASPVGIGCQEQVQLESTAK
2200.0632	2199.0559	2199.0854	-0.0295	620 - 641		1	---	VTWNVAMDATASGASLGARGHK
2277.2354	2276.2281	2276.2238	0.0043	282 - 302		0	---	IQLGMPATLWITTFTTLGGQK
2462.2896	2461.2823	2461.1523	0.1301	163 - 182		1	---	WRDGTTGQHVEYDQRPDVFR
2564.1892	2563.1819	2563.1658	0.0162	103 - 124		0	---	VTTTSWSWICSCQVFGMSGTLR

No match to: 713.4033, 734.4868, 750.5184, 768.5142, 782.4771, 864.5305, 886.9829, 1242.5968, 1242.5968, 1279.7448, 1333.7170, 1334.8057, 1376.6588, 1448.8995, 1588.7866, 1652.5116, 1698.8995, 1698.8995, 1714.8849, 1714.8849, 1850.9985, 2035.0466, 2035.0466, 2184.0742, 2662.3862, 2780.4480, 2780.9680, 2922.3689, 3332.5874, 3349.6301

10. gi|222623073 **Mass:** 46746 **Score:** 49 **Expect:** 7.6 **Queries matched:** 6

hypothetical protein OsJ_07164 [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1279.7448	1278.7375	1278.6615	0.0760	319	329	1	---	TGGHLKCHITR
1850.9985	1849.9912	1849.9210	0.0702	27	42	0	---	WLQEASNQGTLFLDTK
2277.2354	2276.2281	2276.1081	0.1200	195	213	1	---	IFEVIPCPSSIAMWDPRSR + Oxidation (M)
2462.2896	2461.2823	2461.2753	0.0071	105	126	0	---	NVGLGFSQVIQDHVVVGIFYDR
2662.3862	2661.3789	2661.1991	0.1798	51	72	0	---	GLNLMSFVEEDYLFNPCTGYHR
3349.6301	3348.6228	3348.7175	-0.0947	257	286	1	---	FWPDYSLATNVVVPMAVDLTDGRILLNTGR + Oxidation (M)

No match to: 713.4033, 734.4868, 750.5184, 768.5142, 782.4771, 864.5305, 886.9829, 1242.5968, 1242.5968, 1333.7170, 1334.8057, 1376.6588, 1436.7476, 1448.8995, 1556.8491, 1588.7866, 1652.5116, 1698.8995, 1698.8995, 1714.8849, 1714.8849, 1845.9839, 2001.9570, 2001.9570, 2035.0466, 2035.0466, 2184.0742, 2200.0632, 2564.1892, 2780.4480, 2780.9680, 2922.3689, 3332.5874

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 39

Protein View

Match to: **gi|133741925** Score: **81** Expect: **0.0053**
peptidylprolyl isomerase [Triticum aestivum]

Nominal mass (M_r): **26084**; Calculated pI value: **9.40**
NCBI BLAST search of gi|133741925 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Triticum aestivum

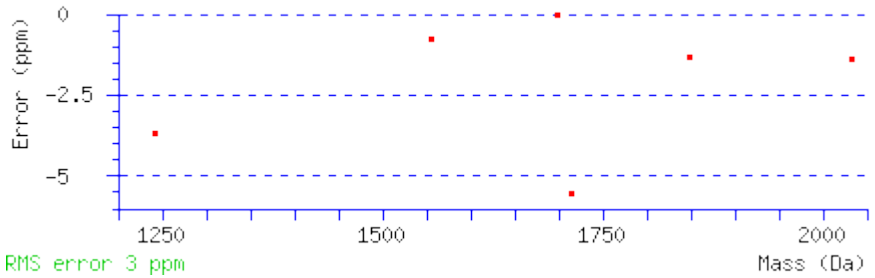
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **31%**

Matched peptides shown in **Bold Red**

```
   1 MAAATSSFAT LAIARPAAAG PAAQRALLAS KAPSSALSLR GVRVASPALS
  51 VSQQSRARFV ASASAEPYAP ELQSKVTNKV YFDISIGNPV GKNVGRIVIG
 101 LYGDDVPQTV ENFRALCTGE KGFGYKGSSF HRVIKDFMIQ GGDFDKGNGT
 151 GGKSIYGRTF KDENFQLVHT GPGVLSMANA GPNTNGSQFF ICTVKTPWLD
 201 GRHVVFGQVL EGMDIVRTIE SSETDRGDRP KKKVVISECG ELPVV
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
44 - 58	1556.8491	1555.8418	1555.8430	-0.0012	1	**VASPALSVSQQSRAR** (No match)
76 - 92	1850.9985	1849.9912	1849.9937	-0.0025	1	**VTNKVYFDISIGNPVGK** (No match)
97 - 114	2035.0466	2034.0393	2034.0421	-0.0028	0	**IVIGLYGDDVPQTVENFR** (Ions score 21)
97 - 114	2035.0466	2034.0393	2034.0421	-0.0028	0	**IVIGLYGDDVPQTVENFR** (No match)
122 - 132	1242.5968	1241.5895	1241.5941	-0.0045	1	**GFGYKGSSFHR** (No match)
122 - 132	1242.5968	1241.5895	1241.5941	-0.0045	1	**GFGYKGSSFHR** (No match)
203 - 217	1698.8995	1697.8922	1697.8922	-0.0000	0	**HVVFGQVLEGMDIVR** (Ions score 13)
203 - 217	1698.8995	1697.8922	1697.8922	-0.0000	0	**HVVFGQVLEGMDIVR** (No match)
203 - 217	1714.8849	1713.8776	1713.8871	-0.0095	0	**HVVFGQVLEGMDIVR** Oxidation (M) (Ions score 1)
203 - 217	1714.8849	1713.8776	1713.8871	-0.0095	0	**HVVFGQVLEGMDIVR** Oxidation (M) (No match)



Spot 123

Index

	Accession	Mass	Score	Description
1.	gi|118103	18184	211	RecName: Full=Peptidyl-prolyl cis-trans isomerase; Short=PPIase; Short=Rotamase; AltName: Full
2.	gi|1563719	18458	159	cyclophylin [Digitalis lanata]
3.	gi|255538956	18370	144	cyclophilin, putative [Ricinus communis]
4.	gi|52788398	18358	141	cyclophilin [Pinus halepensis]
5.	gi|3334157	18501	131	RecName: Full=Peptidyl-prolyl cis-trans isomerase; Short=PPIase; Short=Rotamase; AltName: Full
6.	gi|167599641	18397	129	cyclophilin [Hevea brasiliensis]
7.	gi|119367479	18324	128	putative cyclophilin [Citrus cv. Shiranuhi]
8.	gi|829119	18376	127	cyclophilin [Phaseolus vulgaris]
9.	gi|224105235	18192	126	predicted protein [Populus trichocarpa]
10.	gi|192910744	18387	118	cyclophilin [Elaeis guineensis]

Results List

1. gi|118103 **Mass:** 18184 **Score:** 211 **Expect:** 4.8e-016 **Queries matched:** 7

RecName: Full=Peptidyl-prolyl cis-trans isomerase; Short=PPIase; Short=Rotamase; AltName: Full=Cycl

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
737.3607	736.3534	736.3504	0.0031	32	37	0	---	TAENFR
1420.7521	1419.7448	1419.7510	-0.0061	6	19	0	---	VFFDLTIGGAPAGR
1446.6946	1445.6873	1445.7006	-0.0133	159	171	0	106	CSKPVVIADCGQL
1446.6946	1445.6873	1445.7006	-0.0133	159	171	0	---	CSKPVVIADCGQL
1496.7195	1495.7122	1495.7089	0.0034	32	44	1	59	TAENFRALCTGEK
1496.7195	1495.7122	1495.7089	0.0034	32	44	1	---	TAENFRALCTGEK
2707.2288	2706.2215	2706.2053	0.0163	63	89	0	---	VIPGFMCQGGDFTAGNGTGGESIYGAK + Oxidation (M)

No match to: 713.4017, 768.5120, 969.4769, 986.5150, 1097.5558, 1111.5709, 1117.6079, 1131.6152, 1392.7272, 1405.7461, 1406.7456, 1429.6693, 1429.6693, 1436.7577, 1445.6697, 1451.6726, 1462.6825, 1468.6868, 1537.8118, 1596.8539, 1599.4637, 1600.8365, 1609.8218, 1610.8085, 1610.8085, 1624.8262, 1626.8279, 1627.8309, 1644.8502, 1660.8350, 1837.9299, 1944.0399, 1944.0399, 1958.0278, 1990.0553, 2027.0400, 2095.0964, 2111.0850, 2118.0486, 2212.1062, 2545.2839, 2559.3027, 2692.2368, 3333.5520

2. gi|1563719 **Mass:** 18458 **Score:** 159 **Expect:** 7.6e-011 **Queries matched:** 11

cyclophylin [Digitalis lanata]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
737.3607	736.3534	736.3504	0.0031	32	37	0	---	TAENFR
969.4769	968.4696	968.4603	0.0093	90	97	0	---	FADENFVK
1097.5558	1096.5485	1096.5552	-0.0067	90	98	1	---	FADENFVKK
1392.7272	1391.7199	1391.7370	-0.0170	20	31	0	---	IVMELYADVVPK + Oxidation (M)
1496.7195	1495.7122	1495.7089	0.0034	32	44	1	59	TAENFRALCTGEK
1496.7195	1495.7122	1495.7089	0.0034	32	44	1	---	TAENFRALCTGEK

1600.8365	1599.8292	1599.7173	0.1119	6 - 19	0	---	VFFDMTIGGQPCGR + Oxidation (M)
2027.0400	2026.0327	2025.9400	0.0927	2 - 19	1	---	SNPKVFFDMTIGGQPCGR + Oxidation (M)
2095.0964	2094.0891	2094.0819	0.0072	20 - 37	1	---	IVMELYADVVPKTAENFR
2111.0850	2110.0777	2110.0768	0.0009	20 - 37	1	---	IVMELYADVVPKTAENFR + Oxidation (M)
2707.2288	2706.2215	2706.2053	0.0163	63 - 89	0	---	VIPGFMCQGGDFTAGNGTGGESIYGAK + Oxidation (M)

No match to: 713.4017, 768.5120, 986.5150, 1111.5709, 1117.6079, 1131.6152, 1405.7461, 1406.7456, 1420.7521, 1429.6693, 1429.6693, 1436.7577, 1445.6697, 1446.6946, 1446.6946, 1451.6726, 1462.6825, 1468.6868, 1537.8118, 1596.8539, 1599.4637, 1609.8218, 1610.8085, 1610.8085, 1624.8262, 1626.8279, 1627.8309, 1644.8502, 1660.8350, 1837.9299, 1944.0399, 1944.0399, 1958.0278, 1990.0553, 2118.0486, 2212.1062, 2545.2839, 2559.3027, 2692.2368, 3333.5520

3. gi|255538956 **Mass:** 18370 **Score:** 144 **Expect:** 2.4e-009 **Queries matched:** 10

cyclophilin, putative [Ricinus communis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
737.3607	736.3534	736.3504	0.0031	33 -	38	0	---	TAENFR
1111.5709	1110.5636	1110.5709	-0.0073	91 -	99	1	---	FADENFIKK
1392.7272	1391.7199	1391.7119	0.0081	21 -	32	0	---	IVMELFADTTPR
1446.6946	1445.6873	1445.7799	-0.0926	140 -	152	1	---	VVEGMDIVKAIEK + Oxidation (M)
1446.6946	1445.6873	1445.7799	-0.0926	140 -	152	1	---	VVEGMDIVKAIEK + Oxidation (M)
1496.7195	1495.7122	1495.7089	0.0034	33 -	45	1	59	TAENFRALCTGEK
1496.7195	1495.7122	1495.7089	0.0034	33 -	45	1	---	TAENFRALCTGEK
1600.8365	1599.8292	1599.8269	0.0023	50 -	63	1	---	SGKPLHYKGSSFHR
2111.0850	2110.0777	2110.0517	0.0261	21 -	38	1	---	IVMELFADTTPRTAENFR
2707.2288	2706.2215	2706.2053	0.0163	64 -	90	0	---	VIPGFMCQGGDFTAGNGTGGESIYGAK + Oxidation (M)

No match to: 713.4017, 768.5120, 969.4769, 986.5150, 1097.5558, 1117.6079, 1131.6152, 1405.7461, 1406.7456, 1420.7521, 1429.6693, 1429.6693, 1436.7577, 1445.6697, 1451.6726, 1462.6825, 1468.6868, 1537.8118, 1596.8539, 1599.4637, 1609.8218, 1610.8085, 1610.8085, 1624.8262, 1626.8279, 1627.8309, 1644.8502, 1660.8350, 1837.9299, 1944.0399, 1944.0399, 1958.0278, 1990.0553, 2027.0400, 2095.0964, 2118.0486, 2212.1062, 2545.2839, 2559.3027, 2692.2368, 3333.5520

4. gi|52788398 **Mass:** 18358 **Score:** 141 **Expect:** 4.8e-009 **Queries matched:** 10

cyclophilin [Pinus halepensis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
737.3607	736.3534	736.3504	0.0031	32 -	37	0	---	TAENFR
969.4769	968.4696	968.4603	0.0093	90 -	97	0	---	FADENFVK
1097.5558	1096.5485	1096.5552	-0.0067	90 -	98	1	---	FADENFVKK
1392.7272	1391.7199	1391.7370	-0.0170	20 -	31	0	---	IVMELYADVVPK + Oxidation (M)
1451.6726	1450.6653	1450.7026	-0.0373	6 -	19	0	---	VFFDMQVGGAPAGR
1496.7195	1495.7122	1495.7089	0.0034	32 -	44	1	59	TAENFRALCTGEK
1496.7195	1495.7122	1495.7089	0.0034	32 -	44	1	---	TAENFRALCTGEK
1600.8365	1599.8292	1599.7173	0.1119	63 -	76	0	---	VIPGFMCQGGDFTR + Oxidation (M)
2095.0964	2094.0891	2094.0819	0.0072	20 -	37	1	---	IVMELYADVVPKTAENFR
2111.0850	2110.0777	2110.0768	0.0009	20 -	37	1	---	IVMELYADVVPKTAENFR + Oxidation (M)

No match to: 713.4017, 768.5120, 986.5150, 1111.5709, 1117.6079, 1131.6152, 1405.7461, 1406.7456, 1420.7521, 1429.6693, 1429.6693, 1436.7577, 1445.6697, 1446.6946, 1446.6946, 1462.6825, 1468.6868, 1537.8118, 1596.8539, 1599.4637, 1609.8218, 1610.8085, 1610.8085, 1624.8262, 1626.8279, 1627.8309, 1644.8502, 1660.8350, 1837.9299, 1944.0399, 1944.0399, 1958.0278, 1990.0553, 2027.0400, 2118.0486, 2212.1062, 2545.2839, 2559.3027, 2692.2368, 2707.2288, 3333.5520

5. gi|3334157 **Mass:** 18501 **Score:** 131 **Expect:** 4.8e-008 **Queries matched:** 8

RecName: Full=Peptidyl-prolyl cis-trans isomerase; Short=PPIase; Short=Rotamase; AltName: Full=Cycl

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
737.3607	736.3534	736.3504	0.0031	32	37	0	---	TAENFR
1111.5709	1110.5636	1110.5709	-0.0073	90	98	1	---	FADENFIKK
1392.7272	1391.7199	1391.7119	0.0081	20	31	0	---	IVMELFADTTPR
1496.7195	1495.7122	1495.7089	0.0034	32	44	1	59	TAENFRALCTGEK
1496.7195	1495.7122	1495.7089	0.0034	32	44	1	---	TAENFRALCTGEK
2095.0964	2094.0891	2093.9774	0.1117	1	19	1	---	MPNPRVFFDMSVGGQPAGR + 2 Oxidation (M)
2111.0850	2110.0777	2110.0517	0.0261	20	37	1	---	IVMELFADTTPRTAENFR
2707.2288	2706.2215	2706.2053	0.0163	63	89	0	---	VIPGFMCQGGDFTAGNGTGGESIYGAK + Oxidation (M)

No match to: 713.4017, 768.5120, 969.4769, 986.5150, 1097.5558, 1117.6079, 1131.6152, 1405.7461, 1406.7456, 1420.7521, 1429.6693, 1429.6693, 1436.7577, 1445.6697, 1446.6946, 1446.6946, 1451.6726, 1462.6825, 1468.6868, 1537.8118, 1596.8539, 1599.4637, 1600.8365, 1609.8218, 1610.8085, 1610.8085, 1624.8262, 1626.8279, 1627.8309, 1644.8502, 1660.8350, 1837.9299, 1944.0399, 1944.0399, 1958.0278, 1990.0553, 2027.0400, 2118.0486, 2212.1062, 2545.2839, 2559.3027, 2692.2368, 3333.5520

6. gi|167599641 **Mass:** 18397 **Score:** 129 **Expect:** 7.6e-008 **Queries matched:** 10

cyclophilin [Hevea brasiliensis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
737.3607	736.3534	736.3504	0.0031	32	37	0	---	TAENFR
1111.5709	1110.5636	1110.5709	-0.0073	90	98	1	---	FADENFIKK
1392.7272	1391.7199	1391.7119	0.0081	20	31	0	---	IVMELFADTTPR
1446.6946	1445.6873	1445.7799	-0.0926	139	151	1	---	VVEGMDVVKTIEK
1446.6946	1445.6873	1445.7799	-0.0926	139	151	1	---	VVEGMDVVKTIEK
1462.6825	1461.6752	1461.7748	-0.0996	139	151	1	---	VVEGMDVVKTIEK + Oxidation (M)
1496.7195	1495.7122	1495.7089	0.0034	32	44	1	59	TAENFRALCTGEK
1496.7195	1495.7122	1495.7089	0.0034	32	44	1	---	TAENFRALCTGEK
2111.0850	2110.0777	2110.0517	0.0261	20	37	1	---	IVMELFADTTPRTAENFR
2707.2288	2706.2215	2706.2053	0.0163	63	89	0	---	VIPGFMCQGGDFTAGNGTGGESIYGAK + Oxidation (M)

No match to: 713.4017, 768.5120, 969.4769, 986.5150, 1097.5558, 1117.6079, 1131.6152, 1405.7461, 1406.7456, 1420.7521, 1429.6693, 1429.6693, 1436.7577, 1445.6697, 1451.6726, 1468.6868, 1537.8118, 1596.8539, 1599.4637, 1600.8365, 1609.8218, 1610.8085, 1610.8085, 1624.8262, 1626.8279, 1627.8309, 1644.8502, 1660.8350, 1837.9299, 1944.0399, 1944.0399, 1958.0278, 1990.0553, 2027.0400, 2095.0964, 2118.0486, 2212.1062, 2545.2839, 2559.3027, 2692.2368, 3333.5520

7. gi|119367479 **Mass:** 18324 **Score:** 128 **Expect:** 9.6e-008 **Queries matched:** 8

putative cyclophilin [Citrus cv. Shiranuhi]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
737.3607	736.3534	736.3504	0.0031	32 -	37	0	---	TAENFR
969.4769	968.4696	968.4603	0.0093	90 -	97	0	---	FADENFVK
1097.5558	1096.5485	1096.5552	-0.0067	90 -	98	1	---	FADENFVKK
1420.7521	1419.7448	1419.7431	0.0017	20 -	31	0	---	IVMELFAEVTPR + Oxidation (M)
1496.7195	1495.7122	1495.7089	0.0034	32 -	44	1	59	TAENFRALCTGEK
1496.7195	1495.7122	1495.7089	0.0034	32 -	44	1	---	TAENFRALCTGEK
1600.8365	1599.8292	1599.8269	0.0023	49 -	62	1	---	SGKPLHYKGSSFHR
2707.2288	2706.2215	2706.2053	0.0162	63 -	89	0	---	VIPGFMCQGGDFTAGNGTGGESIYGSK

No match to: 713.4017, 768.5120, 986.5150, 1111.5709, 1117.6079, 1131.6152, 1392.7272, 1405.7461, 1406.7456, 1429.6693, 1429.6693, 1436.7577, 1445.6697, 1446.6946, 1446.6946, 1451.6726, 1462.6825, 1468.6868, 1537.8118, 1596.8539, 1599.4637, 1609.8218, 1610.8085, 1610.8085, 1624.8262, 1626.8279, 1627.8309, 1644.8502, 1660.8350, 1837.9299, 1944.0399, 1944.0399, 1958.0278, 1990.0553, 2027.0400, 2095.0964, 2111.0850, 2118.0486, 2212.1062, 2545.2839, 2559.3027, 2692.2368, 3333.5520

8. gi|829119 **Mass:** 18376 **Score:** 127 **Expect:** 1.2e-007 **Queries matched:** 8

cyclophilin [Phaseolus vulgaris]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
737.3607	736.3534	736.3504	0.0031	32 -	37	0	---	TAENFR
969.4769	968.4696	968.4603	0.0093	90 -	97	0	---	FADENFVK
1097.5558	1096.5485	1096.5552	-0.0067	90 -	98	1	---	FADENFVKK
1496.7195	1495.7122	1495.7089	0.0034	32 -	44	1	59	TAENFRALCTGEK
1496.7195	1495.7122	1495.7089	0.0034	32 -	44	1	---	TAENFRALCTGEK
1596.8539	1595.8466	1595.8684	-0.0218	49 -	62	1	---	SGKPVHFKGSIFHR
1624.8262	1623.8189	1623.8983	-0.0794	133 -	147	0	---	HVVFGQVVEGLDVVK
2095.0964	2094.0891	2094.0026	0.0865	1 -	19	1	---	MPNPKVFFDMTIGGQPAGR + 2 Oxidation (M)

No match to: 713.4017, 768.5120, 986.5150, 1111.5709, 1117.6079, 1131.6152, 1392.7272, 1405.7461, 1406.7456, 1420.7521, 1429.6693, 1429.6693, 1436.7577, 1445.6697, 1446.6946, 1446.6946, 1451.6726, 1462.6825, 1468.6868, 1537.8118, 1599.4637, 1600.8365, 1609.8218, 1610.8085, 1610.8085, 1626.8279, 1627.8309, 1644.8502, 1660.8350, 1837.9299, 1944.0399, 1944.0399, 1958.0278, 1990.0553, 2027.0400, 2111.0850, 2118.0486, 2212.1062, 2545.2839, 2559.3027, 2692.2368, 2707.2288, 3333.5520

9. gi|224105235 **Mass:** 18192 **Score:** 126 **Expect:** 1.5e-007 **Queries matched:** 9

predicted protein [Populus trichocarpa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
737.3607	736.3534	736.3504	0.0031	32 -	37	0	---	TAENFR
969.4769	968.4696	968.4603	0.0093	90 -	97	0	---	FADENFVK
1097.5558	1096.5485	1096.5552	-0.0067	90 -	98	1	---	FADENFVKK
1446.6946	1445.6873	1445.7184	-0.0311	159 -	172	0	---	TSKPVAIADCGQLS
1446.6946	1445.6873	1445.7184	-0.0311	159 -	172	0	---	TSKPVAIADCGQLS
1496.7195	1495.7122	1495.7089	0.0034	32 -	44	1	59	TAENFRALCTGEK
1496.7195	1495.7122	1495.7089	0.0034	32 -	44	1	---	TAENFRALCTGEK

1600.8365	1599.8292	1599.8269	0.0023	49 - 62	1	---	SGKPLHYKGSSFHR
1624.8262	1623.8189	1623.8983	-0.0794	133 - 147	0	---	HVVFGQVVEGLDVVK

No match to: 713.4017, 768.5120, 986.5150, 1111.5709, 1117.6079, 1131.6152, 1392.7272, 1405.7461, 1406.7456, 1420.7521, 1429.6693, 1429.6693, 1436.7577, 1445.6697, 1451.6726, 1462.6825, 1468.6868, 1537.8118, 1596.8539, 1599.4637, 1609.8218, 1610.8085, 1610.8085, 1626.8279, 1627.8309, 1644.8502, 1660.8350, 1837.9299, 1944.0399, 1944.0399, 1958.0278, 1990.0553, 2027.0400, 2095.0964, 2111.0850, 2118.0486, 2212.1062, 2545.2839, 2559.3027, 2692.2368, 2707.2288, 3333.5520

10. gi|192910744 **Mass:** 18387 **Score:** 118 **Expect:** 9.6e-007 **Queries matched:** 8

cyclophilin [Elaeis guineensis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
737.3607	736.3534	736.3504	0.0031	33 -	38	0	---	TAENFR
1420.7521	1419.7448	1419.7431	0.0017	21 -	32	0	---	IVMELYADVVPR + Oxidation (M)
1446.6946	1445.6873	1445.7184	-0.0311	160 -	173	0	---	TSKPVTVADCGQLA
1446.6946	1445.6873	1445.7184	-0.0311	160 -	173	0	---	TSKPVTVADCGQLA
1496.7195	1495.7122	1495.7089	0.0034	33 -	45	1	59	TAENFRALCTGEK
1496.7195	1495.7122	1495.7089	0.0034	33 -	45	1	---	TAENFRALCTGEK
2118.0486	2117.0413	2117.0534	-0.0121	153 -	173	1	---	VGSQSGRTSKPVTVADCGQLA
2707.2288	2706.2215	2706.2053	0.0163	64 -	90	0	---	VIPGFMCQGGDFTAGNGTGGESIYGAK + Oxidation (M)

No match to: 713.4017, 768.5120, 969.4769, 986.5150, 1097.5558, 1111.5709, 1117.6079, 1131.6152, 1392.7272, 1405.7461, 1406.7456, 1429.6693, 1429.6693, 1436.7577, 1445.6697, 1451.6726, 1462.6825, 1468.6868, 1537.8118, 1596.8539, 1599.4637, 1600.8365, 1609.8218, 1610.8085, 1610.8085, 1624.8262, 1626.8279, 1627.8309, 1644.8502, 1660.8350, 1837.9299, 1944.0399, 1944.0399, 1958.0278, 1990.0553, 2027.0400, 2095.0964, 2111.0850, 2212.1062, 2545.2839, 2559.3027, 2692.2368, 3333.5520

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 51

Protein View

Match to: **gi|1563719** Score: **159** Expect: **7.6e-011**
cyclophylin [Digitalis lanata]

Nominal mass (M_r): **18458**; Calculated pI value: **8.52**
NCBI BLAST search of gi|1563719 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Digitalis lanata

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **45%**

Matched peptides shown in **Bold Red**

```
    1 MSNPKVFFDM TIGGQPCGRI VMELYADVVP KTAENFRALC TGEKGVGKTG
   51 KPLHYKGSAF HRVIPGFMCQ GGDFTAGNGT GGESIYGAKF ADENFVKKHT
  101 GPGILSMANA GPGTNGSQFF ICTEKTSWLD GKHVVFGQVV EGMDVVRAIE
  151 KVGSQSGKTA KPVVIADCGQ IC
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
2 - 19	2027.0400	2026.0327	2025.9400	0.0927	1	**SNPKVFFDMTIGGQPCGR** Oxidation (M) (No match)
6 - 19	1600.8365	1599.8292	1599.7173	0.1119	0	**VFFDMTIGGQPCGR** Oxidation (M) (No match)
20 - 31	1392.7272	1391.7199	1391.7370	-0.0170	0	**IVMELYADVVPK** Oxidation (M) (No match)
20 - 37	2095.0964	2094.0891	2094.0819	0.0072	1	**IVMELYADVVPKTAENFR** (No match)
20 - 37	2111.0850	2110.0777	2110.0768	0.0009	1	**IVMELYADVVPKTAENFR** Oxidation (M) (No match)
32 - 37	737.3607	736.3534	736.3504	0.0031	0	**TAENFR** (No match)
32 - 44	1496.7195	1495.7122	1495.7089	0.0034	1	**TAENFRALCTGEK** (Ions score 59)
32 - 44	1496.7195	1495.7122	1495.7089	0.0034	1	**TAENFRALCTGEK** (No match)
63 - 89	2707.2288	2706.2215	2706.2053	0.0163	0	**VIPGFMCQGGDFTAGNGTGGESIYGAK** Oxidation (M) (No match)
90 - 97	969.4769	968.4696	968.4603	0.0093	0	**FADENFVK** (No match)
90 - 98	1097.5558	1096.5485	1096.5552	-0.0067	1	**FADENFVKK** (No match)

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	Accession	Mass	Score	Description
1.	gi|47606039	16111	618	RecName: Full=Pollen allergen Phl p 11; AltName: Allergen=Phl p 11
2.	gi|47605808	15201	424	RecName: Full=Major pollen allergen Lol p 11; AltName: Full=Allergen Lol p XI; AltName: Allerge
3.	gi|195619302	19317	176	pollen allergen Phl p 11 [Zea mays]
4.	gi|115468516	19191	117	Os06g0556600 [Oryza sativa (japonica cultivar-group)]
5.	gi|195638400	18615	90	pollen allergen Phl p 11 [Zea mays]

Results List

1. gi|47606039 **Mass:** 16111 **Score:** 618 **Expect:** 9.6e-057 **Queries matched:** 20

RecName: Full=Pollen allergen Phl p 11; AltName: Allergen=Phl p 11

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
969.3920	968.3847	968.3844	0.0003	12	18	0	---	VYCDPCR
1042.5829	1041.5756	1041.5818	-0.0062	97	106	0	---	VPLTSNNGIK
1098.5732	1097.5659	1097.5658	0.0002	112	120	0	79	YANPIAFFR
1098.5732	1097.5659	1097.5658	0.0002	112	120	0	---	YANPIAFFR
1132.6110	1131.6037	1131.6036	0.0001	1	11	1	93	DKGPGFVVTGR
1132.6110	1131.6037	1131.6036	0.0001	1	11	1	---	DKGPGFVVTGR
1226.6680	1225.6607	1225.6607	0.0000	112	121	1	---	YANPIAFFRK
1269.7296	1268.7223	1268.7200	0.0023	95	106	1	---	ARVPLTSNNGIK
1269.7296	1268.7223	1268.7200	0.0023	95	106	1	48	ARVPLTSNNGIK
1394.6743	1393.6670	1393.6659	0.0011	126	137	0	---	ECGGILQAYDLR
1552.7947	1551.7874	1551.7932	-0.0058	48	61	1	---	LKAEATTDGLGWYK
1570.6661	1569.6588	1569.6617	-0.0028	80	92	0	---	SPDTTCSEIEEFR
1624.9126	1623.9053	1623.9056	-0.0003	97	111	1	---	VPLTSNNGIKQQGIR
1624.9126	1623.9053	1623.9056	-0.0003	97	111	1	119	VPLTSNNGIKQQGIR
1680.8950	1679.8877	1679.8895	-0.0018	107	120	1	---	QQGIRYANPIAFFR
1841.7963	1840.7890	1840.7897	-0.0007	80	94	1	78	SPDTTCSEIEEFRDR
1841.7963	1840.7890	1840.7897	-0.0007	80	94	1	---	SPDTTCSEIEEFRDR
1861.9480	1860.9407	1860.9403	0.0004	122	137	1	---	EPLKECGGILQAYDLR
2004.9377	2003.9304	2003.9258	0.0046	126	143	1	---	ECGGILQAYDLRDAPETP
2168.0542	2167.0469	2167.0466	0.0003	62	79	0	---	IEIDQDHQEEICEVVLAK

No match to: 713.4089, 722.3620, 724.4930, 750.5038, 768.5231, 921.3925, 921.8999, 927.0182, 927.5192, 990.5141, 1087.5913, 1116.0488, 1154.5878, 1252.7017, 1448.9021, 1476.7465, 1535.7998, 1536.3097, 1607.8975, 1610.8955, 1611.8923, 1625.9084, 1693.9429, 1800.8440, 1807.7897, 1824.2601, 1825.2495, 1835.5055, 1837.8052, 1852.0508, 1853.0433, 1990.0446, 2068.9382, 2472.2112, 2505.6069, 2600.3083, 3069.6135, 3679.8989, 3702.8794

2. gi|47605808 **Mass:** 15201 **Score:** 424 **Expect:** 2.4e-037 **Queries matched:** 10

RecName: Full=Major pollen allergen Lol p 11; AltName: Full=Allergen Lol p XI; AltName: Allergen=Lo

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
969.3920	968.3847	968.3844	0.0003	12	18	0	---	VYCDPCR
1098.5732	1097.5659	1097.5658	0.0002	112	120	0	79	YANPIAFFR
1098.5732	1097.5659	1097.5658	0.0002	112	120	0	---	YANPIAFFR
1132.6110	1131.6037	1131.6036	0.0001	1	11	1	93	DKGPGFVVTGR
1132.6110	1131.6037	1131.6036	0.0001	1	11	1	---	DKGPGFVVTGR
1226.6680	1225.6607	1225.6607	0.0000	112	121	1	---	YANPIAFFRK
1269.7296	1268.7223	1268.7200	0.0023	95	106	1	48	ARVPLTSNNGIK
1624.9126	1623.9053	1623.9056	-0.0003	97	111	1	119	VPLTSNNGIKQQGIR
1680.8950	1679.8877	1679.8895	-0.0018	107	120	1	---	QQGIRYANPIAFFR
2168.0542	2167.0469	2167.0466	0.0003	62	79	0	---	IEIDQDHQEEICEVVLAK

No match to: 713.4089, 722.3620, 724.4930, 750.5038, 768.5231, 921.3925, 921.8999, 927.0182, 927.5192, 990.5141, 1042.5829, 1087.5913, 1116.0488, 1154.5878, 1252.7017, 1269.7296, 1394.6743, 1448.9021, 1476.7465, 1535.7998, 1536.3097, 1552.7947, 1570.6661, 1607.8975, 1610.8955, 1611.8923, 1624.9126, 1625.9084, 1693.9429, 1800.8440, 1807.7897, 1824.2601, 1825.2495, 1835.5055, 1837.8052, 1841.7963, 1841.7963, 1852.0508, 1853.0433, 1861.9480, 1990.0446, 2004.9377, 2068.9382, 2472.2112, 2505.6069, 2600.3083, 3069.6135, 3679.8989, 3702.8794

3. gi|195619302 **Mass:** 19317 **Score:** 176 **Expect:** 1.5e-012 **Queries matched:** 8

pollen allergen Phl p 11 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
969.3920	968.3847	968.3844	0.0003	47	53	0	---	VYCDPCR
1042.5829	1041.5756	1041.5818	-0.0062	132	141	0	---	VPLTSNNGIK
1098.5732	1097.5659	1097.5658	0.0002	147	155	0	79	YANPIAFFR
1098.5732	1097.5659	1097.5658	0.0002	147	155	0	---	YANPIAFFR
1226.6680	1225.6607	1225.6607	0.0000	147	156	1	---	YANPIAFFRK
1269.7296	1268.7223	1268.7200	0.0023	130	141	1	---	ARVPLTSNNGIK
1269.7296	1268.7223	1268.7200	0.0023	130	141	1	48	ARVPLTSNNGIK
1610.8955	1609.8882	1609.8899	-0.0017	132	146	1	---	VPLTSNNGIKQQGVR

No match to: 713.4089, 722.3620, 724.4930, 750.5038, 768.5231, 921.3925, 921.8999, 927.0182, 927.5192, 990.5141, 1087.5913, 1116.0488, 1132.6110, 1132.6110, 1154.5878, 1252.7017, 1394.6743, 1448.9021, 1476.7465, 1535.7998, 1536.3097, 1552.7947, 1570.6661, 1607.8975, 1611.8923, 1624.9126, 1624.9126, 1625.9084, 1680.8950, 1693.9429, 1800.8440, 1807.7897, 1824.2601, 1825.2495, 1835.5055, 1837.8052, 1841.7963, 1841.7963, 1852.0508, 1853.0433, 1861.9480, 1990.0446, 2004.9377, 2068.9382, 2168.0542, 2472.2112, 2505.6069, 2600.3083, 3069.6135, 3679.8989, 3702.8794

4. gi|115468516 **Mass:** 19191 **Score:** 117 **Expect:** 1.2e-006 **Queries matched:** 6

Os06g0556600 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
969.3920	968.3847	968.3844	0.0003	44	50	0	---	VYCDPCR
1042.5829	1041.5756	1041.5818	-0.0062	129	138	0	---	VPLTSNNGLK
1098.5732	1097.5659	1097.5658	0.0002	144	152	0	79	YANPIAFFR

1098.5732	1097.5659	1097.5658	0.0002	144 - 152	0	---	YANPIAFFR
1226.6680	1225.6607	1225.6607	0.0000	144 - 153	1	---	YANPIAFFRK
1610.8955	1609.8882	1609.8899	-0.0017	129 - 143	1	---	VPLTSNNGLKQNGIR

No match to: 713.4089, 722.3620, 724.4930, 750.5038, 768.5231, 921.3925, 921.8999, 927.0182, 927.5192, 990.5141, 1087.5913, 1116.0488, 1132.6110, 1132.6110, 1154.5878, 1252.7017, 1269.7296, 1269.7296, 1394.6743, 1448.9021, 1476.7465, 1535.7998, 1536.3097, 1552.7947, 1570.6661, 1607.8975, 1611.8923, 1624.9126, 1624.9126, 1625.9084, 1680.8950, 1693.9429, 1800.8440, 1807.7897, 1824.2601, 1825.2495, 1835.5055, 1837.8052, 1841.7963, 1841.7963, 1852.0508, 1853.0433, 1861.9480, 1990.0446, 2004.9377, 2068.9382, 2168.0542, 2472.2112, 2505.6069, 2600.3083, 3069.6135, 3679.8989, 3702.8794

5. gi|195638400 **Mass:** 18615 **Score:** 90 **Expect:** 0.00065 **Queries matched:** 3

pollen allergen Phl p 11 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1098.5732	1097.5659	1097.5658	0.0002	133 - 141		0	79	YANPIAFFR
1098.5732	1097.5659	1097.5658	0.0002	133 - 141		0	---	YANPIAFFR
1226.6680	1225.6607	1225.6607	0.0000	133 - 142		1	---	YANPIAFFRK

No match to: 713.4089, 722.3620, 724.4930, 750.5038, 768.5231, 921.3925, 921.8999, 927.0182, 927.5192, 969.3920, 990.5141, 1042.5829, 1087.5913, 1116.0488, 1132.6110, 1132.6110, 1154.5878, 1252.7017, 1269.7296, 1269.7296, 1394.6743, 1448.9021, 1476.7465, 1535.7998, 1536.3097, 1552.7947, 1570.6661, 1607.8975, 1610.8955, 1611.8923, 1624.9126, 1624.9126, 1625.9084, 1680.8950, 1693.9429, 1800.8440, 1807.7897, 1824.2601, 1825.2495, 1835.5055, 1837.8052, 1841.7963, 1841.7963, 1852.0508, 1853.0433, 1861.9480, 1990.0446, 2004.9377, 2068.9382, 2168.0542, 2472.2112, 2505.6069, 2600.3083, 3069.6135, 3679.8989, 3702.8794

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 59

Protein View

Match to: **gi|47606039** Score: **618** Expect: **9.6e-057**
RecName: Full=Pollen allergen Phl p 11; AltName: Allergen=Phl p 11

Nominal mass (M_r): **16111**; Calculated pI value: **4.96**
NCBI BLAST search of gi|47606039 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|23452313 from Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **79%**

Matched peptides shown in **Bold Red**

```
    1 DKGPGFVVTG RVYCDPCRAG FETNVSHNVQ GATVAVDCRP FNGGESKLKA
   51 EATTDGLGWY KIEIDQDHQE EICEVVLAKS PDTTCSEIEE FRDRARVPLT
  101 SNNGIKQQGI RYANPIAFFR KEPLKECGGI LQAYDLRDAP ETP
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
1 - 11	1132.6110	1131.6037	1131.6036	0.0001	1	DKGPGFVVTGR	(Ions score 93)
1 - 11	1132.6110	1131.6037	1131.6036	0.0001	1	DKGPGFVVTGR	(No match)
12 - 18	969.3920	968.3847	968.3844	0.0003	0	VYCDPCR	(No match)
48 - 61	1552.7947	1551.7874	1551.7932	-0.0058	1	LKAEATTDGLGWYK	(No match)
62 - 79	2168.0542	2167.0469	2167.0466	0.0003	0	IEIDQDHQEEICEVVLAK	(No match)
80 - 92	1570.6661	1569.6588	1569.6617	-0.0028	0	SPDTTCSEIEEFR	(No match)
80 - 94	1841.7963	1840.7890	1840.7897	-0.0007	1	SPDTTCSEIEEFRDR	(Ions score 78)
80 - 94	1841.7963	1840.7890	1840.7897	-0.0007	1	SPDTTCSEIEEFRDR	(No match)
95 - 106	1269.7296	1268.7223	1268.7200	0.0023	1	ARVPLTSNNGIK	(No match)
95 - 106	1269.7296	1268.7223	1268.7200	0.0023	1	ARVPLTSNNGIK	(Ions score 48)
97 - 106	1042.5829	1041.5756	1041.5818	-0.0062	0	VPLTSNNGIK	(No match)
97 - 111	1624.9126	1623.9053	1623.9056	-0.0003	1	VPLTSNNGIKQQGIR	(No match)
97 - 111	1624.9126	1623.9053	1623.9056	-0.0003	1	VPLTSNNGIKQQGIR	(Ions score 119)
107 - 120	1680.8950	1679.8877	1679.8895	-0.0018	1	QQGIRYANPIAFFR	(No match)
112 - 120	1098.5732	1097.5659	1097.5658	0.0002	0	YANPIAFFR	(Ions score 79)
112 - 120	1098.5732	1097.5659	1097.5658	0.0002	0	YANPIAFFR	(No match)
112 - 121	1226.6680	1225.6607	1225.6607	0.0000	1	YANPIAFFRK	(No match)
122 - 137	1861.9480	1860.9407	1860.9403	0.0004	1	EPLKECGGILQAYDLR	(No match)
126 - 137	1394.6743	1393.6670	1393.6659	0.0011	0	ECGGILQAYDLR	(No match)
126 - 143	2004.9377	2003.9304	2003.9258	0.0046	1	ECGGILQAYDLRDAPETP	(No match)

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	Accession	Mass	Score	Description
1.	gi|47606039	16111	369	RecName: Full=Pollen allergen Phl p 11; AltName: Allergen=Phl p 11
2.	gi|47605808	15201	294	RecName: Full=Major pollen allergen Lol p 11; AltName: Full=Allergen Lol p XI; AltName: Aller
3.	gi|195619302	19317	107	pollen allergen Phl p 11 [Zea mays]
4.	gi|115468516	19191	93	Os06g0556600 [Oryza sativa (japonica cultivar-group)]
5.	gi|195638400	18615	82	pollen allergen Phl p 11 [Zea mays]
6.	gi|167997177	14850	50	predicted protein [Physcomitrella patens subsp. patens]
7.	gi|52077422	9125	47	hypothetical protein [Oryza sativa Japonica Group]
8.	gi|147859354	155442	43	hypothetical protein [Vitis vinifera]
9.	gi|110739146	11165	41	cellulase like protein [Arabidopsis thaliana]
10.	gi|156141101	17589	40	putative NBS domain resistance protein [Coffea spp. mixed genomic library]

Results List

1. gi|47606039 **Mass:** 16111 **Score:** 369 **Expect:** 7.6e-032 **Queries matched:** 11

RecName: Full=Pollen allergen Phl p 11; AltName: Allergen=Phl p 11

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
969.3948	968.3875	968.3844	0.0031	12	18	0	---	VYCDPCR
1098.5804	1097.5731	1097.5658	0.0074	112	120	0	65	YANPIAFFR
1098.5804	1097.5731	1097.5658	0.0074	112	120	0	---	YANPIAFFR
1132.6174	1131.6101	1131.6036	0.0065	1	11	1	85	DKGPGFVVTGR
1132.6174	1131.6101	1131.6036	0.0065	1	11	1	---	DKGPGFVVTGR
1226.6790	1225.6717	1225.6607	0.0110	112	121	1	---	YANPIAFFRK
1269.7378	1268.7305	1268.7200	0.0105	95	106	1	---	ARVPLTSNNGIK
1624.9224	1623.9151	1623.9056	0.0095	97	111	1	82	VPLTSNNGIKQQGIR
1624.9224	1623.9151	1623.9056	0.0095	97	111	1	---	VPLTSNNGIKQQGIR
1841.8070	1840.7997	1840.7897	0.0100	80	94	1	37	SPDTTCSEIEEFRDR
1841.8070	1840.7997	1840.7897	0.0100	80	94	1	---	SPDTTCSEIEEFRDR

No match to: 713.4045, 768.5170, 864.5176, 1154.5941, 1807.8033, 1825.2393, 1835.5189, 1852.0640, 1852.0640, 1990.0741, 2069.9463, 2212.1372, 2472.2043, 2600.3235

2. gi|47605808 **Mass:** 15201 **Score:** 294 **Expect:** 2.4e-024 **Queries matched:** 7

RecName: Full=Major pollen allergen Lol p 11; AltName: Full=Allergen Lol p XI; AltName: Allergen=Lo

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
969.3948	968.3875	968.3844	0.0031	12	18	0	---	VYCDPCR
1098.5804	1097.5731	1097.5658	0.0074	112	120	0	65	YANPIAFFR
1098.5804	1097.5731	1097.5658	0.0074	112	120	0	---	YANPIAFFR
1132.6174	1131.6101	1131.6036	0.0065	1	11	1	85	DKGPGFVVTGR
1132.6174	1131.6101	1131.6036	0.0065	1	11	1	---	DKGPGFVVTGR

1226.6790	1225.6717	1225.6607	0.0110	112 - 121	1	---	YANPIAFFRK
1624.9224	1623.9151	1623.9056	0.0095	97 - 111	1	82	VPLTSNNGIKQQGIR

No match to: 713.4045, 768.5170, 864.5176, 1154.5941, 1269.7378, 1624.9224, 1807.8033, 1825.2393, 1835.5189, 1841.8070, 1841.8070, 1852.0640, 1852.0640, 1990.0741, 2069.9463, 2212.1372, 2472.2043, 2600.3235

3. gi|195619302 **Mass:** 19317 **Score:** 107 **Expect:** 1.2e-005 **Queries matched:** 5

pollen allergen Phl p 11 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
969.3948	968.3875	968.3844	0.0031	47 -	53	0	---	VYCDPCR
1098.5804	1097.5731	1097.5658	0.0074	147 -	155	0	65	YANPIAFFR
1098.5804	1097.5731	1097.5658	0.0074	147 -	155	0	---	YANPIAFFR
1226.6790	1225.6717	1225.6607	0.0110	147 -	156	1	---	YANPIAFFRK
1269.7378	1268.7305	1268.7200	0.0105	130 -	141	1	---	ARVPLTSNNGIK

No match to: 713.4045, 768.5170, 864.5176, 1132.6174, 1132.6174, 1154.5941, 1624.9224, 1624.9224, 1807.8033, 1825.2393, 1835.5189, 1841.8070, 1841.8070, 1852.0640, 1852.0640, 1990.0741, 2069.9463, 2212.1372, 2472.2043, 2600.3235

4. gi|115468516 **Mass:** 19191 **Score:** 93 **Expect:** 0.00034 **Queries matched:** 4

Os06g0556600 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
969.3948	968.3875	968.3844	0.0031	44 -	50	0	---	VYCDPCR
1098.5804	1097.5731	1097.5658	0.0074	144 -	152	0	65	YANPIAFFR
1098.5804	1097.5731	1097.5658	0.0074	144 -	152	0	---	YANPIAFFR
1226.6790	1225.6717	1225.6607	0.0110	144 -	153	1	---	YANPIAFFRK

No match to: 713.4045, 768.5170, 864.5176, 1132.6174, 1132.6174, 1154.5941, 1269.7378, 1624.9224, 1624.9224, 1807.8033, 1825.2393, 1835.5189, 1841.8070, 1841.8070, 1852.0640, 1852.0640, 1990.0741, 2069.9463, 2212.1372, 2472.2043, 2600.3235

5. gi|195638400 **Mass:** 18615 **Score:** 82 **Expect:** 0.0036 **Queries matched:** 3

pollen allergen Phl p 11 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1098.5804	1097.5731	1097.5658	0.0074	133 -	141	0	65	YANPIAFFR
1098.5804	1097.5731	1097.5658	0.0074	133 -	141	0	---	YANPIAFFR
1226.6790	1225.6717	1225.6607	0.0110	133 -	142	1	---	YANPIAFFRK

No match to: 713.4045, 768.5170, 864.5176, 969.3948, 1132.6174, 1132.6174, 1154.5941, 1269.7378, 1624.9224, 1624.9224, 1807.8033, 1825.2393, 1835.5189, 1841.8070, 1841.8070, 1852.0640, 1852.0640, 1990.0741, 2069.9463, 2212.1372, 2472.2043, 2600.3235

6. gi|167997177 **Mass:** 14850 **Score:** 50 **Expect:** 6.6 **Queries matched:** 5

predicted protein [Physcomitrella patens subsp. patens]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1154.5941	1153.5868	1153.5628	0.0240	64 -	74	0	---	QGPPASQAWGR
1624.9224	1623.9151	1623.8296	0.0855	30 -	44	0	---	AGYPDYSAWALLGIK

1624.9224	1623.9151	1623.8296	0.0855	30 - 44	0	---	AGYPDYSAWALLGIK
1807.8033	1806.7960	1806.7995	-0.0035	9 - 23	0	---	SFQSEYHCALPDPTR
2069.9463	2068.9390	2069.0388	-0.0998	112 - 131	1	---	DQTALDVAQSDLSGTKGHVK

No match to: 713.4045, 768.5170, 864.5176, 969.3948, 1098.5804, 1098.5804, 1132.6174, 1132.6174, 1226.6790, 1269.7378, 1825.2393, 1835.5189, 1841.8070, 1841.8070, 1852.0640, 1852.0640, 1990.0741, 2212.1372, 2472.2043, 2600.3235

7. gi|52077422 **Mass:** 9125 **Score:** 47 **Expect:** 11 **Queries matched:** 4

hypothetical protein [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1132.6174	1131.6101	1131.6148	-0.0047	10 -	19	1	10	WLSSARTVGR
1132.6174	1131.6101	1131.6148	-0.0047	10 -	19	1	---	WLSSARTVGR
1807.8033	1806.7960	1806.7982	-0.0021	26 -	40	1	---	DSDDDMLFSKSLQYK + Oxidation (M)
2212.1372	2211.1299	2211.1643	-0.0343	42 -	60	1	---	ELNYTDLMAALISIRMTIK + Oxidation (M)

No match to: 713.4045, 768.5170, 864.5176, 969.3948, 1098.5804, 1098.5804, 1154.5941, 1226.6790, 1269.7378, 1624.9224, 1624.9224, 1825.2393, 1835.5189, 1841.8070, 1841.8070, 1852.0640, 1852.0640, 1990.0741, 2069.9463, 2472.2043, 2600.3235

8. gi|147859354 **Mass:** 155442 **Score:** 43 **Expect:** 33 **Queries matched:** 2

hypothetical protein [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1132.6174	1131.6101	1131.5342	0.0759	1046 -	1055	1	36	DKSEAIPCGR
2472.2043	2471.1970	2471.1103	0.0867	1269 -	1289	0	---	EPFGMFTTGPPYIENWNNDVK + Oxidation (M)

No match to: 713.4045, 768.5170, 864.5176, 969.3948, 1098.5804, 1098.5804, 1132.6174, 1154.5941, 1226.6790, 1269.7378, 1624.9224, 1624.9224, 1807.8033, 1825.2393, 1835.5189, 1841.8070, 1841.8070, 1852.0640, 1852.0640, 1990.0741, 2069.9463, 2212.1372, 2600.3235

9. gi|110739146 **Mass:** 11165 **Score:** 41 **Expect:** 46 **Queries matched:** 3

cellulase like protein [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1807.8033	1806.7960	1806.9223	-0.1263	51 -	68	0	---	NVPNANELTGAILGGPDR
2212.1372	2211.1299	2211.0816	0.0484	26 -	46	0	---	GASVPMHEANAPLSCPLSFVK
2472.2043	2471.1970	2471.2406	-0.0435	77 -	98	0	---	WTSVYTEPCTYINSIAVGVLAK

No match to: 713.4045, 768.5170, 864.5176, 969.3948, 1098.5804, 1098.5804, 1132.6174, 1132.6174, 1154.5941, 1226.6790, 1269.7378, 1624.9224, 1624.9224, 1825.2393, 1835.5189, 1841.8070, 1841.8070, 1852.0640, 1852.0640, 1990.0741, 2069.9463, 2600.3235

10. gi|156141101 **Mass:** 17589 **Score:** 40 **Expect:** 58 **Queries matched:** 5

putative NBS domain resistance protein [Coffea spp. mixed genomic library]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1098.5804	1097.5731	1097.5903	-0.0171	12 -	20	1	---	VYSSLKVMR + Oxidation (M)
1098.5804	1097.5731	1097.5903	-0.0171	12 -	20	1	---	VYSSLKVMR + Oxidation (M)
1132.6174	1131.6101	1131.5407	0.0694	59 -	67	1	10	DEDLEDKLR

1132.6174	1131.6101	1131.5407	0.0694	59 - 67	1	---	DEDLEDKLR
2472.2043	2471.1970	2471.3682	-0.1712	38 - 58	1	---	RLLLEILTGIHGLTEEIHQMR

No match to: 713.4045, 768.5170, 864.5176, 969.3948, 1154.5941, 1226.6790, 1269.7378, 1624.9224, 1624.9224, 1807.8033, 1825.2393, 1835.5189, 1841.8070, 1841.8070, 1852.0640, 1852.0640, 1990.0741, 2069.9463, 2212.1372, 2600.3235

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 25

Protein View

Match to: **gi|47606039** Score: **369** Expect: **7.6e-032**
RecName: Full=Pollen allergen Phl p 11; AltName: Allergen=Phl p 11

Nominal mass (M_r): **16111**; Calculated pI value: **4.96**
NCBI BLAST search of gi|47606039 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|23452313 from Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **41%**

Matched peptides shown in **Bold Red**

```
    1 DKGPGFVVTG RVYCDPCRAG FETNVSHNVQ GATVAVDCRP FNGGESKLKA
   51 EATTDGLGWY KIEIDQDHQE EICEVVLAKS PDTTCSEIEE FRDRARVPLT
  101 SNNGIKQQGI RYANPIAFFR KEPLKECGGI LQAYDLRDAP ETP
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
1 - 11	1132.6174	1131.6101	1131.6036	0.0065	1	DKGPGFVVTGR	(Ions score 85)
1 - 11	1132.6174	1131.6101	1131.6036	0.0065	1	DKGPGFVVTGR	(No match)
12 - 18	969.3948	968.3875	968.3844	0.0031	0	VYCDPCR	(No match)
80 - 94	1841.8070	1840.7997	1840.7897	0.0100	1	SPDTTCSEIEEFRDR	(Ions score 37)
80 - 94	1841.8070	1840.7997	1840.7897	0.0100	1	SPDTTCSEIEEFRDR	(No match)
95 - 106	1269.7378	1268.7305	1268.7200	0.0105	1	ARVPLTSNNGIK	(No match)
97 - 111	1624.9224	1623.9151	1623.9056	0.0095	1	VPLTSNNGIKQQGIR	(Ions score 82)
97 - 111	1624.9224	1623.9151	1623.9056	0.0095	1	VPLTSNNGIKQQGIR	(No match)
112 - 120	1098.5804	1097.5731	1097.5658	0.0074	0	YANPIAFFR	(Ions score 65)
112 - 120	1098.5804	1097.5731	1097.5658	0.0074	0	YANPIAFFR	(No match)
112 - 121	1226.6790	1225.6717	1225.6607	0.0110	1	YANPIAFFRK	(No match)

Spot 126

Index

	Accession	Mass	Score	Description
1.	gi|47606039	16111	348	RecName: Full=Pollen allergen Phl p 11; AltName: Allergen=Phl p 11
2.	gi|47605808	15201	220	RecName: Full=Major pollen allergen Lol p 11; AltName: Full=Allergen Lol p XI; AltName: Allerg
3.	gi|226505364	19317	86	pollen allergen Phl p 11 [Zea mays]
4.	gi|115468516	19191	75	Os06g0556600 [Oryza sativa (japonica cultivar-group)]
5.	gi|226501190	18615	67	pollen allergen Phl p 11 [Zea mays]
6.	gi|155965998	58336	54	tryptophan decarboxylase [Ophiorrhiza prostrata]
7.	gi|226492441	21908	52	electron transporter [Zea mays]
8.	gi|18411352	38317	46	NADP-dependent oxidoreductase, putative [Arabidopsis thaliana]
9.	gi|21555641	38331	46	allyl alcohol dehydrogenase-like protein [Arabidopsis thaliana]
10.	gi|37991857	14748	43	hypothetical protein [Oryza sativa (japonica cultivar-group)]

Results List

1. gi|47606039 **Mass:** 16111 **Score:** 348 **Expect:** 9.6e-030 **Queries matched:** 16

RecName: Full=Pollen allergen Phl p 11; AltName: Allergen=Phl p 11

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
969.3927	968.3854	968.3844	0.0010	12	18	0	---	VYCDPCR
1098.5762	1097.5689	1097.5658	0.0032	112	120	0	---	YANPIAFFR
1098.5762	1097.5689	1097.5658	0.0032	112	120	0	54	YANPIAFFR
1132.6115	1131.6042	1131.6036	0.0006	1	11	1	---	DKGPGFVVTGR
1132.6115	1131.6042	1131.6036	0.0006	1	11	1	53	DKGPGFVVTGR
1226.6727	1225.6654	1225.6607	0.0047	112	121	1	---	YANPIAFFRK
1269.7351	1268.7278	1268.7200	0.0078	95	106	1	---	ARVPLTSNNGIK
1394.6818	1393.6745	1393.6659	0.0086	126	137	0	---	ECGGILQAYDLR
1570.6788	1569.6715	1569.6617	0.0099	80	92	0	---	SPDTTCSEIEEFR
1624.9215	1623.9142	1623.9056	0.0086	97	111	1	---	VPLTSNNGIKQQGIR
1624.9215	1623.9142	1623.9056	0.0086	97	111	1	48	VPLTSNNGIKQQGIR
1841.8000	1840.7927	1840.7897	0.0030	80	94	1	24	SPDTTCSEIEEFRDR
1841.8000	1840.7927	1840.7897	0.0030	80	94	1	---	SPDTTCSEIEEFRDR
1861.9562	1860.9489	1860.9403	0.0086	122	137	1	---	EPLKECGGILQAYDLR
2168.0627	2167.0554	2167.0466	0.0088	62	79	0	---	IEIDQDHQEEICEVVLAK
3048.4309	3047.4236	3047.4154	0.0082	19	47	0	---	AGFETNVSHNVQGATVAVDCRPFNGGESK

No match to: 713.3981, 734.4800, 750.5067, 768.5120, 782.4769, 864.5298, 886.9810, 1279.7653, 1294.6757, 1334.8738, 1388.5916, 1448.9089, 1584.7885, 1625.9182, 1693.9507, 1807.7954, 1808.7955, 1824.2646, 1825.2598, 1835.5110, 1837.8099, 1852.0553, 1852.0553, 1990.0532, 2472.2129, 2600.3132, 3069.6060

2. gi|47605808 **Mass:** 15201 **Score:** 220 **Expect:** 6.1e-017 **Queries matched:** 8

RecName: Full=Major pollen allergen Lol p 11; AltName: Full=Allergen Lol p XI; AltName: Allergen=Lo

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
969.3927	968.3854	968.3844	0.0010	12 -	18	0	---	VYCDPCR
1098.5762	1097.5689	1097.5658	0.0032	112 -	120	0	---	YANPIAFFR
1098.5762	1097.5689	1097.5658	0.0032	112 -	120	0	54	YANPIAFFR
1132.6115	1131.6042	1131.6036	0.0006	1 -	11	1	---	DKGPGFVVTGR
1132.6115	1131.6042	1131.6036	0.0006	1 -	11	1	53	DKGPGFVVTGR
1226.6727	1225.6654	1225.6607	0.0047	112 -	121	1	---	YANPIAFFRK
1624.9215	1623.9142	1623.9056	0.0086	97 -	111	1	48	VPLTSNNGIKQQGIR
2168.0627	2167.0554	2167.0466	0.0088	62 -	79	0	---	IEIDQDHQEEICEVVLAK

No match to: 713.3981, 734.4800, 750.5067, 768.5120, 782.4769, 864.5298, 886.9810, 1269.7351, 1279.7653, 1294.6757, 1334.8738, 1388.5916, 1394.6818, 1448.9089, 1570.6788, 1584.7885, 1624.9215, 1625.9182, 1693.9507, 1807.7954, 1808.7955, 1824.2646, 1825.2598, 1835.5110, 1837.8099, 1841.8000, 1841.8000, 1852.0553, 1852.0553, 1861.9562, 1990.0532, 2472.2129, 2600.3132, 3048.4309, 3069.6060

3. gi|226505364 **Mass:** 19317 **Score:** 86 **Expect:** 0.0014 **Queries matched:** 5

pollen allergen Phl p 11 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
969.3927	968.3854	968.3844	0.0010	47 -	53	0	---	VYCDPCR
1098.5762	1097.5689	1097.5658	0.0032	147 -	155	0	---	YANPIAFFR
1098.5762	1097.5689	1097.5658	0.0032	147 -	155	0	54	YANPIAFFR
1226.6727	1225.6654	1225.6607	0.0047	147 -	156	1	---	YANPIAFFRK
1269.7351	1268.7278	1268.7200	0.0078	130 -	141	1	---	ARVPLTSNNGIK

No match to: 713.3981, 734.4800, 750.5067, 768.5120, 782.4769, 864.5298, 886.9810, 1132.6115, 1132.6115, 1279.7653, 1294.6757, 1334.8738, 1388.5916, 1394.6818, 1448.9089, 1570.6788, 1584.7885, 1624.9215, 1624.9215, 1625.9182, 1693.9507, 1807.7954, 1808.7955, 1824.2646, 1825.2598, 1835.5110, 1837.8099, 1841.8000, 1841.8000, 1852.0553, 1852.0553, 1861.9562, 1990.0532, 2168.0627, 2472.2129, 2600.3132, 3048.4309, 3069.6060

4. gi|115468516 **Mass:** 19191 **Score:** 75 **Expect:** 0.019 **Queries matched:** 4

Os06g0556600 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
969.3927	968.3854	968.3844	0.0010	44 -	50	0	---	VYCDPCR
1098.5762	1097.5689	1097.5658	0.0032	144 -	152	0	---	YANPIAFFR
1098.5762	1097.5689	1097.5658	0.0032	144 -	152	0	54	YANPIAFFR
1226.6727	1225.6654	1225.6607	0.0047	144 -	153	1	---	YANPIAFFRK

No match to: 713.3981, 734.4800, 750.5067, 768.5120, 782.4769, 864.5298, 886.9810, 1132.6115, 1132.6115, 1269.7351, 1279.7653, 1294.6757, 1334.8738, 1388.5916, 1394.6818, 1448.9089, 1570.6788, 1584.7885, 1624.9215, 1624.9215, 1625.9182, 1693.9507, 1807.7954, 1808.7955, 1824.2646, 1825.2598, 1835.5110, 1837.8099, 1841.8000, 1841.8000, 1852.0553, 1852.0553, 1861.9562, 1990.0532, 2168.0627, 2472.2129, 2600.3132, 3048.4309, 3069.6060

5. gi|226501190 **Mass:** 18615 **Score:** 67 **Expect:** 0.11 **Queries matched:** 3

pollen allergen Phl p 11 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1098.5762	1097.5689	1097.5658	0.0032	133 -	141	0	---	YANPIAFFR

1098.5762	1097.5689	1097.5658	0.0032	133 - 141	0	54	YANPIAFFR
1226.6727	1225.6654	1225.6607	0.0047	133 - 142	1	---	YANPIAFFRK

No match to: 713.3981, 734.4800, 750.5067, 768.5120, 782.4769, 864.5298, 886.9810, 969.3927, 1132.6115, 1132.6115, 1269.7351, 1279.7653, 1294.6757, 1334.8738, 1388.5916, 1394.6818, 1448.9089, 1570.6788, 1584.7885, 1624.9215, 1624.9215, 1625.9182, 1693.9507, 1807.7954, 1808.7955, 1824.2646, 1825.2598, 1835.5110, 1837.8099, 1841.8000, 1841.8000, 1852.0553, 1852.0553, 1861.9562, 1990.0532, 2168.0627, 2472.2129, 2600.3132, 3048.4309, 3069.6060

6. gi|155965998 **Mass:** 58336 **Score:** 54 **Expect:** 2.3 **Queries matched:** 6

tryptophan decarboxylase [Ophiorrhiza prostrata]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1132.6115	1131.6042	1131.5785	0.0257	364 -	372	1	25	DWQIGTTRR
1294.6757	1293.6684	1293.6387	0.0298	403 -	413	1	---	MFEGLVKSDPR + Oxidation (M)
1837.8099	1836.8026	1836.8887	-0.0861	494 -	509	1	---	ECTDASLTKTNIIESR
1841.8000	1840.7927	1840.9181	-0.1254	29 -	43	1	1	KQAHIMVDFIADYYK
1841.8000	1840.7927	1840.9181	-0.1254	29 -	43	1	---	KQAHIMVDFIADYYK
2600.3132	2599.3059	2599.2740	0.0320	186 -	208	1	---	IGMENVGKLVVYGSDQTHSFFQK + Oxidation (M)

No match to: 713.3981, 734.4800, 750.5067, 768.5120, 782.4769, 864.5298, 886.9810, 969.3927, 1098.5762, 1098.5762, 1132.6115, 1226.6727, 1269.7351, 1279.7653, 1334.8738, 1388.5916, 1394.6818, 1448.9089, 1570.6788, 1584.7885, 1624.9215, 1624.9215, 1625.9182, 1693.9507, 1807.7954, 1808.7955, 1824.2646, 1825.2598, 1835.5110, 1852.0553, 1852.0553, 1861.9562, 1990.0532, 2168.0627, 2472.2129, 3048.4309, 3069.6060

7. gi|226492441 **Mass:** 21908 **Score:** 52 **Expect:** 4.1 **Queries matched:** 5

electron transporter [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
969.3927	968.3854	968.3327	0.0527	1 -	10	0	---	MDDCGGGGGK + Oxidation (M)
1132.6115	1131.6042	1131.6261	-0.0219	137 -	146	1	17	DRPAPAPPRR
1294.6757	1293.6684	1293.7516	-0.0832	101 -	112	0	---	EVQALLAAARPR
1334.8738	1333.8665	1333.8207	0.0458	159 -	168	1	---	LWRRPVRPVR
1837.8099	1836.8026	1836.8358	-0.0332	1 -	17	1	---	MDDCGGGGGKRPFQLAR + Oxidation (M)

No match to: 713.3981, 734.4800, 750.5067, 768.5120, 782.4769, 864.5298, 886.9810, 1098.5762, 1098.5762, 1132.6115, 1226.6727, 1269.7351, 1279.7653, 1388.5916, 1394.6818, 1448.9089, 1570.6788, 1584.7885, 1624.9215, 1624.9215, 1625.9182, 1693.9507, 1807.7954, 1808.7955, 1824.2646, 1825.2598, 1835.5110, 1841.8000, 1841.8000, 1852.0553, 1852.0553, 1861.9562, 1990.0532, 2168.0627, 2472.2129, 2600.3132, 3048.4309, 3069.6060

8. gi|18411352 **Mass:** 38317 **Score:** 46 **Expect:** 14 **Queries matched:** 8

NADP-dependent oxidoreductase, putative [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1132.6115	1131.6042	1131.6764	-0.0721	9 -	17	1	---	QVILRNYVK
1132.6115	1131.6042	1131.6764	-0.0721	9 -	17	1	---	QVILRNYVK
1584.7885	1583.7812	1583.7799	0.0013	181 -	195	1	---	LMGCYVVGSAGSKQK
1624.9215	1623.9142	1623.8476	0.0666	240 -	253	1	---	MLDAVLLNMKTYGR
1624.9215	1623.9142	1623.8476	0.0666	240 -	253	1	---	MLDAVLLNMKTYGR

1837.8099	1836.8026	1836.8504	-0.0478	284 - 298	1	---	MQGFASYDFIDRFPK + Oxidation (M)
1861.9562	1860.9489	1860.8572	0.0917	49 - 63	0	---	NLYLSCDPYMGILMR + Oxidation (M)
2472.2129	2471.2056	2471.2439	-0.0383	228 - 249	1	---	GIDIYFENVGGKMLDAVLLNMK + 2 Oxidation (M)

No match to: 713.3981, 734.4800, 750.5067, 768.5120, 782.4769, 864.5298, 886.9810, 969.3927, 1098.5762, 1098.5762, 1226.6727, 1269.7351, 1279.7653, 1294.6757, 1334.8738, 1388.5916, 1394.6818, 1448.9089, 1570.6788, 1625.9182, 1693.9507, 1807.7954, 1808.7955, 1824.2646, 1825.2598, 1835.5110, 1841.8000, 1841.8000, 1852.0553, 1852.0553, 1990.0532, 2168.0627, 2600.3132, 3048.4309, 3069.6060

9. gi|21555641 **Mass:** 38331 **Score:** 46 **Expect:** 14 **Queries matched:** 8

allyl alcohol dehydrogenase-like protein [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1132.6115	1131.6042	1131.6764	-0.0721	9 - 17		1	---	QVILRNYVK
1132.6115	1131.6042	1131.6764	-0.0721	9 - 17		1	---	QVILRNYVK
1584.7885	1583.7812	1583.7799	0.0013	181 - 195		1	---	LMGCYVVGSAGSKQK
1624.9215	1623.9142	1623.8476	0.0666	240 - 253		1	---	MLDAVLLNMKTYGR
1624.9215	1623.9142	1623.8476	0.0666	240 - 253		1	---	MLDAVLLNMKTYGR
1837.8099	1836.8026	1836.8504	-0.0478	284 - 298		1	---	MQGFASYDFIDRFPK + Oxidation (M)
1861.9562	1860.9489	1860.8572	0.0917	49 - 63		0	---	NLYLSCDPYMGILMR + Oxidation (M)
2472.2129	2471.2056	2471.2439	-0.0383	228 - 249		1	---	GIDIYFENVGGKMLDAVLLNMK + 2 Oxidation (M)

No match to: 713.3981, 734.4800, 750.5067, 768.5120, 782.4769, 864.5298, 886.9810, 969.3927, 1098.5762, 1098.5762, 1226.6727, 1269.7351, 1279.7653, 1294.6757, 1334.8738, 1388.5916, 1394.6818, 1448.9089, 1570.6788, 1625.9182, 1693.9507, 1807.7954, 1808.7955, 1824.2646, 1825.2598, 1835.5110, 1841.8000, 1841.8000, 1852.0553, 1852.0553, 1990.0532, 2168.0627, 2600.3132, 3048.4309, 3069.6060

10. gi|37991857 **Mass:** 14748 **Score:** 43 **Expect:** 30 **Queries matched:** 6

hypothetical protein [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1098.5762	1097.5689	1097.5801	-0.0112	63 - 74		1	---	GGTGGGGRPARR
1098.5762	1097.5689	1097.5801	-0.0112	63 - 74		1	---	GGTGGGGRPARR
1132.6115	1131.6042	1131.5268	0.0775	112 - 125		0	---	DGGAASGSAVGAGR
1132.6115	1131.6042	1131.5268	0.0775	112 - 125		0	10	DGGAASGSAVGAGR
1226.6727	1225.6654	1225.6387	0.0267	61 - 73		1	---	QRGGTGGGGRPAR
1269.7351	1268.7278	1268.7128	0.0150	11 - 20		1	---	TEILLKYFSR

No match to: 713.3981, 734.4800, 750.5067, 768.5120, 782.4769, 864.5298, 886.9810, 969.3927, 1279.7653, 1294.6757, 1334.8738, 1388.5916, 1394.6818, 1448.9089, 1570.6788, 1584.7885, 1624.9215, 1624.9215, 1625.9182, 1693.9507, 1807.7954, 1808.7955, 1824.2646, 1825.2598, 1835.5110, 1837.8099, 1841.8000, 1841.8000, 1852.0553, 1852.0553, 1861.9562, 1990.0532, 2168.0627, 2472.2129, 2600.3132, 3048.4309, 3069.6060

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 43

Protein View

Match to: **gi|47606039** Score: **348** Expect: **9.6e-030**
RecName: Full=Pollen allergen Phl p 11; AltName: Allergen=Phl p 11

Nominal mass (M_r): **16111**; Calculated pI value: **4.96**
NCBI BLAST search of gi|47606039 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|23452313 from Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **86%**

Matched peptides shown in **Bold Red**

```
     1 DKGPGFVVTG RVYCDPCRAG FETNVSHNVQ GATVAVDCRP FNGGESKLKA
    51 EATTDGLGWY KIEIDQDHQE EICEVVLAKS PDTTCSEIEE FRDRARVPLT
   101 SNNGIKQQGI RYANPIAFFR KEPLKECGGI LQAYDLRDAP ETP
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
1 - 11	1132.6115	1131.6042	1131.6036	0.0006	1	DKGPGFVVTGR (No match)
1 - 11	1132.6115	1131.6042	1131.6036	0.0006	1	DKGPGFVVTGR (Ions score 53)
12 - 18	969.3927	968.3854	968.3844	0.0010	0	VYCDPCR (No match)
19 - 47	3048.4309	3047.4236	3047.4154	0.0082	0	AGFETNVSHNVQGATVAVDCRPFNGGESK (No match)
62 - 79	2168.0627	2167.0554	2167.0466	0.0088	0	IEIDQDHQEEICEVVLAK (No match)
80 - 92	1570.6788	1569.6715	1569.6617	0.0099	0	SPDTTCSEIEEFR (No match)
80 - 94	1841.8000	1840.7927	1840.7897	0.0030	1	SPDTTCSEIEEFRDR (Ions score 24)
80 - 94	1841.8000	1840.7927	1840.7897	0.0030	1	SPDTTCSEIEEFRDR (No match)
95 - 106	1269.7351	1268.7278	1268.7200	0.0078	1	ARVPLTSNNGIK (No match)
97 - 111	1624.9215	1623.9142	1623.9056	0.0086	1	VPLTSNNGIKQQGIR (No match)
97 - 111	1624.9215	1623.9142	1623.9056	0.0086	1	VPLTSNNGIKQQGIR (Ions score 48)
112 - 120	1098.5762	1097.5689	1097.5658	0.0032	0	YANPIAFFR (No match)
112 - 120	1098.5762	1097.5689	1097.5658	0.0032	0	YANPIAFFR (Ions score 54)
112 - 121	1226.6727	1225.6654	1225.6607	0.0047	1	YANPIAFFRK (No match)
122 - 137	1861.9562	1860.9489	1860.9403	0.0086	1	EPLKECGGILQAYDLR (No match)
126 - 137	1394.6818	1393.6745	1393.6659	0.0086	0	ECGGILQAYDLR (No match)

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	Accession	Mass	Score	Description
1.	gi|47606039	16111	438	RecName: Full=Pollen allergen Phl p 11; AltName: Allergen=Phl p 11
2.	gi|47605808	15201	276	RecName: Full=Major pollen allergen Lol p 11; AltName: Full=Allergen Lol p XI; AltName: Aller
3.	gi|226505364	19317	99	pollen allergen Phl p 11 [Zea mays]
4.	gi|115468516	19191	85	Os06g0556600 [Oryza sativa (japonica cultivar-group)]
5.	gi|226501190	18615	75	pollen allergen Phl p 11 [Zea mays]
6.	gi|77554215	57166	53	retrotransposon protein, putative, unclassified [Oryza sativa (japonica cultivar-group)]
7.	gi|222631463	115895	45	hypothetical protein OsJ_18412 [Oryza sativa Japonica Group]
8.	gi|82569933	61731	45	maturase K [Ecdeiocolea monostachya]
9.	gi|115463675	119175	44	Os05g0389800 [Oryza sativa (japonica cultivar-group)]
10.	gi|82569935	61964	44	maturase K [Ecdeiocolea monostachya]

Results List

1. gi|47606039 **Mass:** 16111 **Score:** 438 **Expect:** 9.6e-039 **Queries matched:** 13

RecName: Full=Pollen allergen Phl p 11; AltName: Allergen=Phl p 11

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
969.4172	968.4099	968.3844	0.0255	12	18	0	---	VYCDPCR
1098.5948	1097.5875	1097.5658	0.0218	112	120	0	---	YANPIAFFR
1098.5948	1097.5875	1097.5658	0.0218	112	120	0	57	YANPIAFFR
1132.6355	1131.6282	1131.6036	0.0246	1	11	1	---	DKGPGFVVTGR
1132.6355	1131.6282	1131.6036	0.0246	1	11	1	73	DKGPGFVVTGR
1226.6925	1225.6852	1225.6607	0.0245	112	121	1	---	YANPIAFFRK
1269.7539	1268.7466	1268.7200	0.0266	95	106	1	---	ARVPLTSNNGIK
1394.6936	1393.6863	1393.6659	0.0204	126	137	0	---	ECGGILQAYDLR
1624.9464	1623.9391	1623.9056	0.0335	97	111	1	84	VPLTSNNGIKQQGIR
1624.9464	1623.9391	1623.9056	0.0335	97	111	1	---	VPLTSNNGIKQQGIR
1841.8329	1840.8256	1840.7897	0.0359	80	94	1	85	SPDTTCSEIEEFRDR
1841.8329	1840.8256	1840.7897	0.0359	80	94	1	---	SPDTTCSEIEEFRDR
1861.9734	1860.9661	1860.9403	0.0258	122	137	1	---	EPLKECGGILQAYDLR

No match to: 768.5378, 921.4191, 921.9230, 926.5457, 1693.9648, 1807.8218, 1825.3074, 1837.8442, 1852.0900, 1852.0900, 1855.8372, 1990.0792, 3069.6555

2. gi|47605808 **Mass:** 15201 **Score:** 276 **Expect:** 1.5e-022 **Queries matched:** 7

RecName: Full=Major pollen allergen Lol p 11; AltName: Full=Allergen Lol p XI; AltName: Allergen=Lo

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
969.4172	968.4099	968.3844	0.0255	12	18	0	---	VYCDPCR
1098.5948	1097.5875	1097.5658	0.0218	112	120	0	---	YANPIAFFR
1098.5948	1097.5875	1097.5658	0.0218	112	120	0	57	YANPIAFFR

1132.6355	1131.6282	1131.6036	0.0246	1 - 11	1	---	DKGPGFVVTGR
1132.6355	1131.6282	1131.6036	0.0246	1 - 11	1	73	DKGPGFVVTGR
1226.6925	1225.6852	1225.6607	0.0245	112 - 121	1	---	YANPIAFFRK
1624.9464	1623.9391	1623.9056	0.0335	97 - 111	1	84	VPLTSNNGIKQQGIR

No match to: 768.5378, 921.4191, 921.9230, 926.5457, 1269.7539, 1394.6936, 1624.9464, 1693.9648, 1807.8218, 1825.3074, 1837.8442, 1841.8329, 1841.8329, 1852.0900, 1852.0900, 1855.8372, 1861.9734, 1990.0792, 3069.6555

3. gi|226505364 **Mass:** 19317 **Score:** 99 **Expect:** 8.6e-005 **Queries matched:** 5

pollen allergen Phl p 11 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
969.4172	968.4099	968.3844	0.0255	47 -	53	0	---	VYCDPCR
1098.5948	1097.5875	1097.5658	0.0218	147 -	155	0	---	YANPIAFFR
1098.5948	1097.5875	1097.5658	0.0218	147 -	155	0	57	YANPIAFFR
1226.6925	1225.6852	1225.6607	0.0245	147 -	156	1	---	YANPIAFFRK
1269.7539	1268.7466	1268.7200	0.0266	130 -	141	1	---	ARVPLTSNNGIK

No match to: 768.5378, 921.4191, 921.9230, 926.5457, 1132.6355, 1132.6355, 1394.6936, 1624.9464, 1624.9464, 1693.9648, 1807.8218, 1825.3074, 1837.8442, 1841.8329, 1841.8329, 1852.0900, 1852.0900, 1855.8372, 1861.9734, 1990.0792, 3069.6555

4. gi|115468516 **Mass:** 19191 **Score:** 85 **Expect:** 0.0021 **Queries matched:** 4

Os06g0556600 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
969.4172	968.4099	968.3844	0.0255	44 -	50	0	---	VYCDPCR
1098.5948	1097.5875	1097.5658	0.0218	144 -	152	0	---	YANPIAFFR
1098.5948	1097.5875	1097.5658	0.0218	144 -	152	0	57	YANPIAFFR
1226.6925	1225.6852	1225.6607	0.0245	144 -	153	1	---	YANPIAFFRK

No match to: 768.5378, 921.4191, 921.9230, 926.5457, 1132.6355, 1132.6355, 1269.7539, 1394.6936, 1624.9464, 1624.9464, 1693.9648, 1807.8218, 1825.3074, 1837.8442, 1841.8329, 1841.8329, 1852.0900, 1852.0900, 1855.8372, 1861.9734, 1990.0792, 3069.6555

5. gi|226501190 **Mass:** 18615 **Score:** 75 **Expect:** 0.021 **Queries matched:** 3

pollen allergen Phl p 11 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1098.5948	1097.5875	1097.5658	0.0218	133 -	141	0	---	YANPIAFFR
1098.5948	1097.5875	1097.5658	0.0218	133 -	141	0	57	YANPIAFFR
1226.6925	1225.6852	1225.6607	0.0245	133 -	142	1	---	YANPIAFFRK

No match to: 768.5378, 921.4191, 921.9230, 926.5457, 969.4172, 1132.6355, 1132.6355, 1269.7539, 1394.6936, 1624.9464, 1624.9464, 1693.9648, 1807.8218, 1825.3074, 1837.8442, 1841.8329, 1841.8329, 1852.0900, 1852.0900, 1855.8372, 1861.9734, 1990.0792, 3069.6555

6. gi|77554215 **Mass:** 57166 **Score:** 53 **Expect:** 3.4 **Queries matched:** 8

retrotransposon protein, putative, unclassified [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide

926.5457	925.5384	925.5457	-0.0073	469 - 477	0	---	RPSGLAGLR
969.4172	968.4099	968.4536	-0.0436	312 - 321	1	---	GHDGAGGSRR
1693.9648	1692.9575	1692.8947	0.0628	174 - 188	0	---	LQLPSQPPAQVSSWR
1807.8218	1806.8145	1806.7631	0.0514	233 - 247	1	---	ARGAWEYTGSEDYMR + Oxidation (M)
1841.8329	1840.8256	1840.9543	-0.1287	397 - 414	1	2	VGGTEPFRGNLISPQGGR
1841.8329	1840.8256	1840.9543	-0.1287	397 - 414	1	---	VGGTEPFRGNLISPQGGR
1852.0900	1851.0827	1851.0326	0.0502	405 - 422	1	---	GNLISPQGGRLTDLLAAR
1852.0900	1851.0827	1851.0326	0.0502	405 - 422	1	---	GNLISPQGGRLTDLLAAR

No match to: 768.5378, 921.4191, 921.9230, 1098.5948, 1098.5948, 1132.6355, 1132.6355, 1226.6925, 1269.7539, 1394.6936, 1624.9464, 1624.9464, 1825.3074, 1837.8442, 1855.8372, 1861.9734, 1990.0792, 3069.6555

7. gi|222631463 **Mass:** 115895 **Score:** 45 **Expect:** 20 **Queries matched:** 9

hypothetical protein OsJ_18412 [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
969.4172	968.4099	968.4385	-0.0286	336 -	343	0	---	LQFGSMDR + Oxidation (M)
1394.6936	1393.6863	1393.6621	0.0242	823 -	834	0	---	MAEFPLDPMLSK + Oxidation (M)
1807.8218	1806.8145	1806.8319	-0.0173	1 -	16	1	---	MAASDDGQLRTWVSDR
1841.8329	1840.8256	1840.9260	-0.1003	566 -	581	1	---	FSDFFDAAPVFRIPGR
1841.8329	1840.8256	1840.9260	-0.1003	566 -	581	1	---	FSDFFDAAPVFRIPGR
1852.0900	1851.0827	1851.0101	0.0727	416 -	433	1	---	AIDEHKVLIVVGETGSGK
1852.0900	1851.0827	1851.0101	0.0727	416 -	433	1	---	AIDEHKVLIVVGETGSGK
1861.9734	1860.9661	1860.9065	0.0596	1014 -	1032	0	---	TAAATTPQEQTTAGSTPTK
1990.0792	1989.0719	1989.0014	0.0705	1013 -	1032	1	---	KTAAATTPQEQTTAGSTPTK

No match to: 768.5378, 921.4191, 921.9230, 926.5457, 1098.5948, 1098.5948, 1132.6355, 1132.6355, 1226.6925, 1269.7539, 1624.9464, 1624.9464, 1693.9648, 1825.3074, 1837.8442, 1855.8372, 3069.6555

8. gi|82569933 **Mass:** 61731 **Score:** 45 **Expect:** 21 **Queries matched:** 8

maturase K [Ecdeiocolea monostachya]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1132.6355	1131.6282	1131.6434	-0.0151	441 -	450	1	---	LSCARTLALK
1132.6355	1131.6282	1131.6434	-0.0151	441 -	450	1	---	LSCARTLALK
1226.6925	1225.6852	1225.6641	0.0211	65 -	73	1	---	LIFRMYQQK
1624.9464	1623.9391	1623.9810	-0.0419	369 -	384	0	---	LDTIVPGVLLIGSLSK
1624.9464	1623.9391	1623.9810	-0.0419	369 -	384	0	---	LDTIVPGVLLIGSLSK
1837.8442	1836.8369	1836.9403	-0.1034	353 -	367	1	---	NQMLENSFLIDTRIK + Oxidation (M)
1841.8329	1840.8256	1840.9101	-0.0845	236 -	251	1	7	QSSCLRLTSSGTFLER
1841.8329	1840.8256	1840.9101	-0.0845	236 -	251	1	---	QSSCLRLTSSGTFLER

No match to: 768.5378, 921.4191, 921.9230, 926.5457, 969.4172, 1098.5948, 1098.5948, 1269.7539, 1394.6936, 1693.9648, 1807.8218, 1825.3074, 1852.0900, 1852.0900, 1855.8372, 1861.9734, 1990.0792, 3069.6555

9. gi|115463675 **Mass:** 119175 **Score:** 44 **Expect:** 24 **Queries matched:** 9

Os05g0389800 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
969.4172	968.4099	968.4385	-0.0286	336	-	343	0	---	LQFGSMDR + Oxidation (M)
1394.6936	1393.6863	1393.6621	0.0242	823	-	834	0	---	MAEFPLDPMLSK + Oxidation (M)
1807.8218	1806.8145	1806.8319	-0.0173	1	-	16	1	---	MAASDDGQLRTWVSDR
1841.8329	1840.8256	1840.9260	-0.1003	566	-	581	1	---	FSDFFDAAPVFRIPGR
1841.8329	1840.8256	1840.9260	-0.1003	566	-	581	1	---	FSDFFDAAPVFRIPGR
1852.0900	1851.0827	1851.0101	0.0727	416	-	433	1	---	AIDEHKVLIVVGETGSGK
1852.0900	1851.0827	1851.0101	0.0727	416	-	433	1	---	AIDEHKVLIVVGETGSGK
1861.9734	1860.9661	1860.9065	0.0596	1041	-	1059	0	---	TAAATTPQEQTTAGSTPTK
1990.0792	1989.0719	1989.0014	0.0705	1040	-	1059	1	---	KTAAATTPQEQTTAGSTPTK

No match to: 768.5378, 921.4191, 921.9230, 926.5457, 1098.5948, 1098.5948, 1132.6355, 1132.6355, 1226.6925, 1269.7539, 1624.9464, 1624.9464, 1693.9648, 1825.3074, 1837.8442, 1855.8372, 3069.6555

10. gi|82569935 **Mass:** 61964 **Score:** 44 **Expect:** 24 **Queries matched:** 8

maturase K [Ecdeiocolea monostachya]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1132.6355	1131.6282	1131.6434	-0.0151	443	-	452	1	---	LSCARTLALK
1132.6355	1131.6282	1131.6434	-0.0151	443	-	452	1	---	LSCARTLALK
1226.6925	1225.6852	1225.6641	0.0211	66	-	74	1	---	LIFRMYQQK
1624.9464	1623.9391	1623.9810	-0.0419	371	-	386	0	---	LDTIVPGVLLIGSLSK
1624.9464	1623.9391	1623.9810	-0.0419	371	-	386	0	---	LDTIVPGVLLIGSLSK
1837.8442	1836.8369	1836.9403	-0.1034	355	-	369	1	---	NQMLENSFLIDTRIK + Oxidation (M)
1841.8329	1840.8256	1840.9101	-0.0845	238	-	253	1	7	QSSCLRLTSSGTFLER
1841.8329	1840.8256	1840.9101	-0.0845	238	-	253	1	---	QSSCLRLTSSGTFLER

No match to: 768.5378, 921.4191, 921.9230, 926.5457, 969.4172, 1098.5948, 1098.5948, 1269.7539, 1394.6936, 1693.9648, 1807.8218, 1825.3074, 1852.0900, 1852.0900, 1855.8372, 1861.9734, 1990.0792, 3069.6555

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 26

Protein View

Match to: **gi|47606039** Score: **438** Expect: **9.6e-039**
RecName: Full=Pollen allergen Phl p 11; AltName: Allergen=Phl p 11

Nominal mass (M_r): **16111**; Calculated pI value: **4.96**
NCBI BLAST search of gi|47606039 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|23452313 from Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **53%**

Matched peptides shown in **Bold Red**

```
    1 DKGPGFVVTG RVYCDPCRAG FETNVSHNVQ GATVAVDCRP FNGGESKLKA
   51 EATTDGLGWY KIEIDQDHQE EICEVVLAKS PDTTCSEIEE FRDRARVPLT
  101 SNNGIKQQGI RYANPIAFFR KEPLKECGGI LQAYDLRDAP ETP
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
1 - 11	1132.6355	1131.6282	1131.6036	0.0246	1	DKGPGFVVTGR	(No match)
1 - 11	1132.6355	1131.6282	1131.6036	0.0246	1	DKGPGFVVTGR	(Ions score 73)
12 - 18	969.4172	968.4099	968.3844	0.0255	0	VYCDPCR	(No match)
80 - 94	1841.8329	1840.8256	1840.7897	0.0359	1	SPDTTCSEIEEFRDR	(Ions score 85)
80 - 94	1841.8329	1840.8256	1840.7897	0.0359	1	SPDTTCSEIEEFRDR	(No match)
95 - 106	1269.7539	1268.7466	1268.7200	0.0266	1	ARVPLTSNNGIK	(No match)
97 - 111	1624.9464	1623.9391	1623.9056	0.0335	1	VPLTSNNGIKQQGIR	(Ions score 84)
97 - 111	1624.9464	1623.9391	1623.9056	0.0335	1	VPLTSNNGIKQQGIR	(No match)
112 - 120	1098.5948	1097.5875	1097.5658	0.0218	0	YANPIAFFR	(No match)
112 - 120	1098.5948	1097.5875	1097.5658	0.0218	0	YANPIAFFR	(Ions score 57)
112 - 121	1226.6925	1225.6852	1225.6607	0.0245	1	YANPIAFFRK	(No match)
122 - 137	1861.9734	1860.9661	1860.9403	0.0258	1	EPLKECGGILQAYDLR	(No match)
126 - 137	1394.6936	1393.6863	1393.6659	0.0204	0	ECGGILQAYDLR	(No match)

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	Accession	Mass	Score	Description
1.	gi|125540584	15577	143	hypothetical protein OsI_08373 [Oryza sativa Indica Group]
2.	gi|226503551	16202	142	actin-depolymerizing factor [Zea mays]
3.	gi|115447755	16211	142	Os02g0663800 [Oryza sativa (japonica cultivar-group)]
4.	gi|125550580	14631	92	hypothetical protein OsI_18188 [Oryza sativa Indica Group]
5.	gi|224120004	15954	92	predicted protein [Populus trichocarpa]
6.	gi|157337360	15585	91	unnamed protein product [Vitis vinifera]
7.	gi|116783021	16295	91	unknown [Picea sitchensis]
8.	gi|116792074	16294	91	unknown [Picea sitchensis]
9.	gi|115461713	15995	91	Os05g0113400 [Oryza sativa (japonica cultivar-group)]
10.	gi|3047107	15860	91	Similar to actin binding protein; F6N23.12 [Arabidopsis thaliana]

Results List

1. gi|125540584 **Mass:** 15577 **Score:** 143 **Expect:** 3e-009 **Queries matched:** 7

hypothetical protein OsI_08373 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1070.5205	1069.5132	1069.5226	-0.0094	94	102	1	---	MLYASSKDR
1086.5109	1085.5036	1085.5175	-0.0139	94	102	1	---	MLYASSKDR + Oxidation (M)
1439.7000	1438.6927	1438.7245	-0.0317	78	89	0	36	IFFISWAPDTSR
1439.7000	1438.6927	1438.7245	-0.0317	78	89	0	---	IFFISWAPDTSR
1654.8098	1653.8025	1653.8514	-0.0489	76	89	1	59	SKIFFISWAPDTSR
1654.8098	1653.8025	1653.8514	-0.0489	76	89	1	---	SKIFFISWAPDTSR
1997.8029	1996.7956	1996.8512	-0.0556	60	75	0	---	YAVFDFDFVTDENCQK

No match to: 768.5307, 891.5151, 904.4628, 904.4628, 1021.5618, 1296.6552, 1471.6855, 1709.7306, 1709.7306, 1725.7233, 1725.7233, 2317.8892, 2808.2234

2. gi|226503551 **Mass:** 16202 **Score:** 142 **Expect:** 3.8e-009 **Queries matched:** 7

actin-depolymerizing factor [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1070.5205	1069.5132	1069.5226	-0.0094	101	109	1	---	MLYASSKDR
1086.5109	1085.5036	1085.5175	-0.0139	101	109	1	---	MLYASSKDR + Oxidation (M)
1439.7000	1438.6927	1438.7245	-0.0317	85	96	0	36	IFFISWAPDTSR
1439.7000	1438.6927	1438.7245	-0.0317	85	96	0	---	IFFISWAPDTSR
1654.8098	1653.8025	1653.8514	-0.0489	83	96	1	59	SKIFFISWAPDTSR
1654.8098	1653.8025	1653.8514	-0.0489	83	96	1	---	SKIFFISWAPDTSR
1997.8029	1996.7956	1996.8512	-0.0556	67	82	0	---	YAVFDFDFVTDENCQK

No match to: 768.5307, 891.5151, 904.4628, 904.4628, 1021.5618, 1296.6552, 1471.6855, 1709.7306, 1709.7306, 1725.7233, 1725.7233, 2317.8892, 2808.2234

3. gi|115447755 **Mass:** 16211 **Score:** 142 **Expect:** 3.8e-009 **Queries matched:** 7

Os02g0663800 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1070.5205	1069.5132	1069.5226	-0.0094	101	109	1	---	MLYASSKDR
1086.5109	1085.5036	1085.5175	-0.0139	101	109	1	---	MLYASSKDR + Oxidation (M)
1439.7000	1438.6927	1438.7245	-0.0317	85	96	0	36	IFFISWAPDTSR
1439.7000	1438.6927	1438.7245	-0.0317	85	96	0	---	IFFISWAPDTSR
1654.8098	1653.8025	1653.8514	-0.0489	83	96	1	59	SKIFFISWAPDTSR
1654.8098	1653.8025	1653.8514	-0.0489	83	96	1	---	SKIFFISWAPDTSR
1997.8029	1996.7956	1996.8512	-0.0556	67	82	0	---	YAVFDFDFVTDENCQK

No match to: 768.5307, 891.5151, 904.4628, 904.4628, 1021.5618, 1296.6552, 1471.6855, 1709.7306, 1709.7306, 1725.7233, 1725.7233, 2317.8892, 2808.2234

4. gi|125550580 **Mass:** 14631 **Score:** 92 **Expect:** 0.00038 **Queries matched:** 6

hypothetical protein OsI_18188 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1070.5205	1069.5132	1069.5226	-0.0094	89	97	1	---	MIYASSKDR
1086.5109	1085.5036	1085.5175	-0.0139	89	97	1	---	MIYASSKDR + Oxidation (M)
1439.7000	1438.6927	1438.7245	-0.0317	73	84	0	18	IFFIAWSPDTSR
1439.7000	1438.6927	1438.7245	-0.0317	73	84	0	---	IFFIAWSPDTSR
1654.8098	1653.8025	1653.8514	-0.0489	71	84	1	41	SKIFFIAWSPDTSR
1654.8098	1653.8025	1653.8514	-0.0489	71	84	1	---	SKIFFIAWSPDTSR

No match to: 768.5307, 891.5151, 904.4628, 904.4628, 1021.5618, 1296.6552, 1471.6855, 1709.7306, 1709.7306, 1725.7233, 1725.7233, 1997.8029, 2317.8892, 2808.2234

5. gi|224120004 **Mass:** 15954 **Score:** 92 **Expect:** 0.00042 **Queries matched:** 6

predicted protein [Populus trichocarpa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1070.5205	1069.5132	1069.5226	-0.0094	99	107	1	---	MVYASTKDR
1086.5109	1085.5036	1085.5175	-0.0139	99	107	1	---	MVYASTKDR + Oxidation (M)
1439.7000	1438.6927	1438.7245	-0.0317	83	94	0	18	IFFIAWSPDTSR
1439.7000	1438.6927	1438.7245	-0.0317	83	94	0	---	IFFIAWSPDTSR
1654.8098	1653.8025	1653.8514	-0.0489	81	94	1	41	SKIFFIAWSPDTSR
1654.8098	1653.8025	1653.8514	-0.0489	81	94	1	---	SKIFFIAWSPDTSR

No match to: 768.5307, 891.5151, 904.4628, 904.4628, 1021.5618, 1296.6552, 1471.6855, 1709.7306, 1709.7306, 1725.7233, 1725.7233, 1997.8029, 2317.8892, 2808.2234

6. gi|157337360 **Mass:** 15585 **Score:** 91 **Expect:** 0.00045 **Queries matched:** 6

unnamed protein product [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1070.5205	1069.5132	1069.5226	-0.0094	94	102	1	---	MIYASSKDR

1086.5109	1085.5036	1085.5175	-0.0139	94 - 102	1	---	MIYASSKDR + Oxidation (M)
1439.7000	1438.6927	1438.7245	-0.0317	78 - 89	0	18	IFFIAWSPDTSR
1439.7000	1438.6927	1438.7245	-0.0317	78 - 89	0	---	IFFIAWSPDTSR
1654.8098	1653.8025	1653.8514	-0.0489	76 - 89	1	41	SKIFFIAWSPDTSR
1654.8098	1653.8025	1653.8514	-0.0489	76 - 89	1	---	SKIFFIAWSPDTSR

No match to: 768.5307, 891.5151, 904.4628, 904.4628, 1021.5618, 1296.6552, 1471.6855, 1709.7306, 1709.7306, 1725.7233, 1725.7233, 1997.8029, 2317.8892, 2808.2234

7. gi|116783021 **Mass:** 16295 **Score:** 91 **Expect:** 0.00046 **Queries matched:** 6

unknown [Picea sitchensis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1070.5205	1069.5132	1069.5226	-0.0094	101 - 109	1	---	MLYASSKDR
1086.5109	1085.5036	1085.5175	-0.0139	101 - 109	1	---	MLYASSKDR + Oxidation (M)
1439.7000	1438.6927	1438.7245	-0.0317	85 - 96	0	18	IFFIAWSPDTSR
1439.7000	1438.6927	1438.7245	-0.0317	85 - 96	0	---	IFFIAWSPDTSR
1654.8098	1653.8025	1653.8514	-0.0489	83 - 96	1	41	SKIFFIAWSPDTSR
1654.8098	1653.8025	1653.8514	-0.0489	83 - 96	1	---	SKIFFIAWSPDTSR

No match to: 768.5307, 891.5151, 904.4628, 904.4628, 1021.5618, 1296.6552, 1471.6855, 1709.7306, 1709.7306, 1725.7233, 1725.7233, 1997.8029, 2317.8892, 2808.2234

8. gi|116792074 **Mass:** 16294 **Score:** 91 **Expect:** 0.00046 **Queries matched:** 6

unknown [Picea sitchensis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1070.5205	1069.5132	1069.5226	-0.0094	101 - 109	1	---	MLYASSKDR
1086.5109	1085.5036	1085.5175	-0.0139	101 - 109	1	---	MLYASSKDR + Oxidation (M)
1439.7000	1438.6927	1438.7245	-0.0317	85 - 96	0	18	IFFIAWSPDTSR
1439.7000	1438.6927	1438.7245	-0.0317	85 - 96	0	---	IFFIAWSPDTSR
1654.8098	1653.8025	1653.8514	-0.0489	83 - 96	1	41	SKIFFIAWSPDTSR
1654.8098	1653.8025	1653.8514	-0.0489	83 - 96	1	---	SKIFFIAWSPDTSR

No match to: 768.5307, 891.5151, 904.4628, 904.4628, 1021.5618, 1296.6552, 1471.6855, 1709.7306, 1709.7306, 1725.7233, 1725.7233, 1997.8029, 2317.8892, 2808.2234

9. gi|115461713 **Mass:** 15995 **Score:** 91 **Expect:** 0.00049 **Queries matched:** 6

Os05g0113400 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1070.5205	1069.5132	1069.5226	-0.0094	100 - 108	1	---	MIYASSKDR
1086.5109	1085.5036	1085.5175	-0.0139	100 - 108	1	---	MIYASSKDR + Oxidation (M)
1439.7000	1438.6927	1438.7245	-0.0317	84 - 95	0	18	IFFIAWSPDTSR
1439.7000	1438.6927	1438.7245	-0.0317	84 - 95	0	---	IFFIAWSPDTSR
1654.8098	1653.8025	1653.8514	-0.0489	82 - 95	1	41	SKIFFIAWSPDTSR
1654.8098	1653.8025	1653.8514	-0.0489	82 - 95	1	---	SKIFFIAWSPDTSR

No match to: 768.5307, 891.5151, 904.4628, 904.4628, 1021.5618, 1296.6552, 1471.6855, 1709.7306, 1709.7306,

1725.7233, 1725.7233, 1997.8029, 2317.8892, 2808.2234

10. gi|3047107 **Mass:** 15860 **Score:** 91 **Expect:** 0.0005 **Queries matched:** 6

Similar to actin binding protein; F6N23.12 [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1070.5205	1069.5132	1069.5226	-0.0094	94	102	1	---	MLYASSKDR
1086.5109	1085.5036	1085.5175	-0.0139	94	102	1	---	MLYASSKDR + Oxidation (M)
1439.7000	1438.6927	1438.7245	-0.0317	78	89	0	18	IFFIAWSPDTSR
1439.7000	1438.6927	1438.7245	-0.0317	78	89	0	---	IFFIAWSPDTSR
1654.8098	1653.8025	1653.8514	-0.0489	76	89	1	41	SKIFFIAWSPDTSR
1654.8098	1653.8025	1653.8514	-0.0489	76	89	1	---	SKIFFIAWSPDTSR

No match to: 768.5307, 891.5151, 904.4628, 904.4628, 1021.5618, 1296.6552, 1471.6855, 1709.7306, 1709.7306, 1725.7233, 1725.7233, 1997.8029, 2317.8892, 2808.2234

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 20

Protein View

Match to: **gi|125540584** Score: **143** Expect: **3e-009**
hypothetical protein OsI_08373 [Oryza sativa Indica Group]

Nominal mass (M_r): **15577**; Calculated pI value: **5.56**
NCBI BLAST search of gi|125540584 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Oryza sativa Indica Group
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|125583166 from Oryza sativa Japonica Group

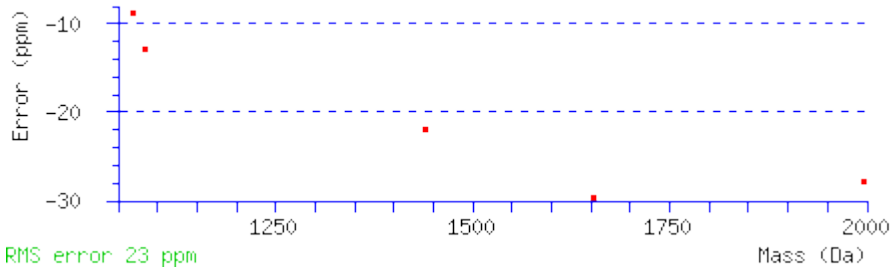
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **29%**

Matched peptides shown in **Bold Red**

```
     1 MAVCDECKLK FLELKAKRSF RFIVFKINEK VQQVVVDRLG QPGESYDDFT
    51 ACLPADECRY AVFDFDFVTD ENCQKSKIFF ISWAPDTSRV RSKMLYASSK
   101 DRFKRELDGI QVELQATDPS EMSMDIVKSR AL
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
60 - 75	1997.8029	1996.7956	1996.8512	-0.0556	0	YAVFDFDFVTDENCQK (No match)
76 - 89	1654.8098	1653.8025	1653.8514	-0.0489	1	SKIFFISWAPDTSR (Ions score 59)
76 - 89	1654.8098	1653.8025	1653.8514	-0.0489	1	SKIFFISWAPDTSR (No match)
78 - 89	1439.7000	1438.6927	1438.7245	-0.0317	0	IFFISWAPDTSR (Ions score 36)
78 - 89	1439.7000	1438.6927	1438.7245	-0.0317	0	IFFISWAPDTSR (No match)
94 - 102	1070.5205	1069.5132	1069.5226	-0.0094	1	MLYASSKDR (No match)
94 - 102	1086.5109	1085.5036	1085.5175	-0.0139	1	MLYASSKDR Oxidation (M) (No match)



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	Accession	Mass	Score	Description
1.	gi|125540584	15577	162	hypothetical protein OsI_08373 [Oryza sativa Indica Group]
2.	gi|115447755	16211	160	Os02g0663800 [Oryza sativa (japonica cultivar-group)]
3.	gi|226503551	16202	138	actin-depolymerizing factor [Zea mays]
4.	gi|89276293	16316	120	actin depolymerizing factor 7 [Gossypium hirsutum]
5.	gi|3047107	15860	119	Similar to actin binding protein; F6N23.12 [Arabidopsis thaliana]
6.	gi|125550580	14631	118	hypothetical protein OsI_18188 [Oryza sativa Indica Group]
7.	gi|18411410	16478	117	ADF8 (ACTIN DEPOLYMERIZING FACTOR 8); actin binding [Arabidopsis thaliana]
8.	gi|157349709	15633	116	unnamed protein product [Vitis vinifera]
9.	gi|225454162	16251	115	PREDICTED: hypothetical protein [Vitis vinifera]
10.	gi|116783021	16295	114	unknown [Picea sitchensis]

Results List

1. gi|125540584 **Mass:** 15577 **Score:** 162 **Expect:** 3.8e-011 **Queries matched:** 10

hypothetical protein OsI_08373 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
942.5424	941.5351	941.5294	0.0058	31	38	0	---	VQQVVVDR
1070.5343	1069.5270	1069.5226	0.0044	94	102	1	---	MLYASSKDR
1137.6541	1136.6468	1136.6593	-0.0125	22	30	1	---	FIVFKINEK
1426.8060	1425.7987	1425.7939	0.0048	27	38	1	---	INEKVQQVVVDR
1439.7397	1438.7324	1438.7245	0.0080	78	89	0	---	IFFISWAPDTSR
1439.7397	1438.7324	1438.7245	0.0080	78	89	0	24	IFFISWAPDTSR
1654.8682	1653.8609	1653.8514	0.0095	76	89	1	---	SKIFFISWAPDTSR
1654.8682	1653.8609	1653.8514	0.0095	76	89	1	65	SKIFFISWAPDTSR
1694.9058	1693.8985	1693.8940	0.0046	78	91	1	---	IFFISWAPDTSRVR
1997.8624	1996.8551	1996.8512	0.0039	60	75	0	---	YAVFDFDFVTDENCQK

No match to: 713.3998, 724.4915, 734.4922, 750.5140, 768.5120, 782.4836, 838.5288, 864.5275, 905.5298, 1009.6190, 1019.6183, 1260.7815, 1279.7595, 1285.6605, 1301.6436, 1334.8807, 1448.9143, 1455.7355, 1471.7377, 1493.8914, 1510.7781, 1588.8717, 1588.8717, 1670.8622, 1686.8585, 1798.7778, 1814.7716, 1814.7716, 1859.9996, 2061.1990, 2214.0376, 2214.9993, 2231.2324, 2240.1555, 2411.0222, 2417.4102, 2428.0264, 2428.0264, 2444.0977, 2460.1150, 2566.1885, 2824.3081, 2922.3640, 3349.6006

2. gi|115447755 **Mass:** 16211 **Score:** 160 **Expect:** 6.1e-011 **Queries matched:** 10

Os02g0663800 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
942.5424	941.5351	941.5294	0.0058	38	45	0	---	VQQVVVDR
1070.5343	1069.5270	1069.5226	0.0044	101	109	1	---	MLYASSKDR
1137.6541	1136.6468	1136.6593	-0.0125	29	37	1	---	FIVFKINEK

1426.8060	1425.7987	1425.7939	0.0048	34 - 45	1	---	INEKVQQVVVDR
1439.7397	1438.7324	1438.7245	0.0080	85 - 96	0	---	IFFISWAPDTSR
1439.7397	1438.7324	1438.7245	0.0080	85 - 96	0	24	IFFISWAPDTSR
1654.8682	1653.8609	1653.8514	0.0095	83 - 96	1	---	SKIFFISWAPDTSR
1654.8682	1653.8609	1653.8514	0.0095	83 - 96	1	65	SKIFFISWAPDTSR
1694.9058	1693.8985	1693.8940	0.0046	85 - 98	1	---	IFFISWAPDTSRVR
1997.8624	1996.8551	1996.8512	0.0039	67 - 82	0	---	YAVFDFDFVTDENCQK

No match to: 713.3998, 724.4915, 734.4922, 750.5140, 768.5120, 782.4836, 838.5288, 864.5275, 905.5298, 1009.6190, 1019.6183, 1260.7815, 1279.7595, 1285.6605, 1301.6436, 1334.8807, 1448.9143, 1455.7355, 1471.7377, 1493.8914, 1510.7781, 1588.8717, 1588.8717, 1670.8622, 1686.8585, 1798.7778, 1814.7716, 1814.7716, 1859.9996, 2061.1990, 2214.0376, 2214.9993, 2231.2324, 2240.1555, 2411.0222, 2417.4102, 2428.0264, 2428.0264, 2444.0977, 2460.1150, 2566.1885, 2824.3081, 2922.3640, 3349.6006

3. gi|226503551 **Mass:** 16202 **Score:** 138 **Expect:** 9.6e-009 **Queries matched:** 8

actin-depolymerizing factor [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
905.5298	904.5225	904.5381	-0.0156	16 -	22	1	---	LKFQELK
1070.5343	1069.5270	1069.5226	0.0044	101 -	109	1	---	MLYASSKDR
1439.7397	1438.7324	1438.7245	0.0080	85 -	96	0	---	IFFISWAPDTSR
1439.7397	1438.7324	1438.7245	0.0080	85 -	96	0	24	IFFISWAPDTSR
1654.8682	1653.8609	1653.8514	0.0095	83 -	96	1	---	SKIFFISWAPDTSR
1654.8682	1653.8609	1653.8514	0.0095	83 -	96	1	65	SKIFFISWAPDTSR
1694.9058	1693.8985	1693.8940	0.0046	85 -	98	1	---	IFFISWAPDTSRVR
1997.8624	1996.8551	1996.8512	0.0039	67 -	82	0	---	YAVFDFDFVTDENCQK

No match to: 713.3998, 724.4915, 734.4922, 750.5140, 768.5120, 782.4836, 838.5288, 864.5275, 942.5424, 1009.6190, 1019.6183, 1137.6541, 1260.7815, 1279.7595, 1285.6605, 1301.6436, 1334.8807, 1426.8060, 1448.9143, 1455.7355, 1471.7377, 1493.8914, 1510.7781, 1588.8717, 1588.8717, 1670.8622, 1686.8585, 1798.7778, 1814.7716, 1814.7716, 1859.9996, 2061.1990, 2214.0376, 2214.9993, 2231.2324, 2240.1555, 2411.0222, 2417.4102, 2428.0264, 2428.0264, 2444.0977, 2460.1150, 2566.1885, 2824.3081, 2922.3640, 3349.6006

4. gi|89276293 **Mass:** 16316 **Score:** 120 **Expect:** 6.1e-007 **Queries matched:** 7

actin depolymerizing factor 7 [Gossypium hirsutum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1070.5343	1069.5270	1069.5226	0.0044	101 -	109	1	---	MLYASSKDR
1439.7397	1438.7324	1438.7245	0.0080	85 -	96	0	---	IFFIAWSPDTSR
1439.7397	1438.7324	1438.7245	0.0080	85 -	96	0	21	IFFIAWSPDTSR
1654.8682	1653.8609	1653.8514	0.0095	83 -	96	1	---	SKIFFIAWSPDTSR
1654.8682	1653.8609	1653.8514	0.0095	83 -	96	1	56	SKIFFIAWSPDTSR
1694.9058	1693.8985	1693.8940	0.0046	85 -	98	1	---	IFFIAWSPDTSRVR
2566.1885	2565.1812	2565.2155	-0.0343	113 -	135	0	---	ELDGVQVELQATDPSEMSFDIVK + Oxidation (M)

No match to: 713.3998, 724.4915, 734.4922, 750.5140, 768.5120, 782.4836, 838.5288, 864.5275, 905.5298, 942.5424, 1009.6190, 1019.6183, 1137.6541, 1260.7815, 1279.7595, 1285.6605, 1301.6436, 1334.8807, 1426.8060, 1448.9143, 1455.7355, 1471.7377, 1493.8914, 1510.7781, 1588.8717, 1588.8717, 1670.8622, 1686.8585, 1798.7778, 1814.7716,

1814.7716, 1859.9996, 1997.8624, 2061.1990, 2214.0376, 2214.9993, 2231.2324, 2240.1555, 2411.0222, 2417.4102, 2428.0264, 2428.0264, 2444.0977, 2460.1150, 2824.3081, 2922.3640, 3349.6006

5. gi|3047107 **Mass:** 15860 **Score:** 119 **Expect:** 7.6e-007 **Queries matched:** 7

Similar to actin binding protein; F6N23.12 [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1070.5343	1069.5270	1069.5226	0.0044	94 -	102	1	---	MLYASSKDR
1439.7397	1438.7324	1438.7245	0.0080	78 -	89	0	---	IFFIAWSPDTSR
1439.7397	1438.7324	1438.7245	0.0080	78 -	89	0	21	IFFIAWSPDTSR
1654.8682	1653.8609	1653.8514	0.0095	76 -	89	1	---	SKIFFIAWSPDTSR
1654.8682	1653.8609	1653.8514	0.0095	76 -	89	1	56	SKIFFIAWSPDTSR
1694.9058	1693.8985	1693.8940	0.0046	78 -	91	1	---	IFFIAWSPDTSRVR
2460.1150	2459.1077	2459.0070	0.1007	39 -	59	0	---	LGNPEETYDDFTSSIPDDECR

No match to: 713.3998, 724.4915, 734.4922, 750.5140, 768.5120, 782.4836, 838.5288, 864.5275, 905.5298, 942.5424, 1009.6190, 1019.6183, 1137.6541, 1260.7815, 1279.7595, 1285.6605, 1301.6436, 1334.8807, 1426.8060, 1448.9143, 1455.7355, 1471.7377, 1493.8914, 1510.7781, 1588.8717, 1588.8717, 1670.8622, 1686.8585, 1798.7778, 1814.7716, 1814.7716, 1859.9996, 1997.8624, 2061.1990, 2214.0376, 2214.9993, 2231.2324, 2240.1555, 2411.0222, 2417.4102, 2428.0264, 2428.0264, 2444.0977, 2566.1885, 2824.3081, 2922.3640, 3349.6006

6. gi|125550580 **Mass:** 14631 **Score:** 118 **Expect:** 9.6e-007 **Queries matched:** 7

hypothetical protein OsI_18188 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1070.5343	1069.5270	1069.5226	0.0044	89 -	97	1	---	MIYASSKDR
1301.6436	1300.6363	1300.6557	-0.0194	1 -	13	1	---	MSAAQVPGAEGKR
1439.7397	1438.7324	1438.7245	0.0080	73 -	84	0	---	IFFIAWSPDTSR
1439.7397	1438.7324	1438.7245	0.0080	73 -	84	0	21	IFFIAWSPDTSR
1654.8682	1653.8609	1653.8514	0.0095	71 -	84	1	---	SKIFFIAWSPDTSR
1654.8682	1653.8609	1653.8514	0.0095	71 -	84	1	56	SKIFFIAWSPDTSR
1694.9058	1693.8985	1693.8940	0.0046	73 -	86	1	---	IFFIAWSPDTSRVR

No match to: 713.3998, 724.4915, 734.4922, 750.5140, 768.5120, 782.4836, 838.5288, 864.5275, 905.5298, 942.5424, 1009.6190, 1019.6183, 1137.6541, 1260.7815, 1279.7595, 1285.6605, 1334.8807, 1426.8060, 1448.9143, 1455.7355, 1471.7377, 1493.8914, 1510.7781, 1588.8717, 1588.8717, 1670.8622, 1686.8585, 1798.7778, 1814.7716, 1814.7716, 1859.9996, 1997.8624, 2061.1990, 2214.0376, 2214.9993, 2231.2324, 2240.1555, 2411.0222, 2417.4102, 2428.0264, 2428.0264, 2444.0977, 2460.1150, 2566.1885, 2824.3081, 2922.3640, 3349.6006

7. gi|18411410 **Mass:** 16478 **Score:** 117 **Expect:** 1.2e-006 **Queries matched:** 7

ADF8 (ACTIN DEPOLYMERIZING FACTOR 8); actin binding [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1070.5343	1069.5270	1069.5226	0.0044	101 -	109	1	---	MLYASSKDR
1439.7397	1438.7324	1438.7245	0.0080	85 -	96	0	---	IFFIAWSPDTSR
1439.7397	1438.7324	1438.7245	0.0080	85 -	96	0	21	IFFIAWSPDTSR
1654.8682	1653.8609	1653.8514	0.0095	83 -	96	1	---	SKIFFIAWSPDTSR
1654.8682	1653.8609	1653.8514	0.0095	83 -	96	1	56	SKIFFIAWSPDTSR

1694.9058	1693.8985	1693.8940	0.0046	85 - 98	1	---	IFFIAWSPDTSRVR
2460.1150	2459.1077	2459.0070	0.1007	46 - 66	0	---	LGNPEETYDDFTSSIPDDECR

No match to: 713.3998, 724.4915, 734.4922, 750.5140, 768.5120, 782.4836, 838.5288, 864.5275, 905.5298, 942.5424, 1009.6190, 1019.6183, 1137.6541, 1260.7815, 1279.7595, 1285.6605, 1301.6436, 1334.8807, 1426.8060, 1448.9143, 1455.7355, 1471.7377, 1493.8914, 1510.7781, 1588.8717, 1588.8717, 1670.8622, 1686.8585, 1798.7778, 1814.7716, 1814.7716, 1859.9996, 1997.8624, 2061.1990, 2214.0376, 2214.9993, 2231.2324, 2240.1555, 2411.0222, 2417.4102, 2428.0264, 2428.0264, 2444.0977, 2566.1885, 2824.3081, 2922.3640, 3349.6006

8. gi|157349709 **Mass:** 15633 **Score:** 116 **Expect:** 1.5e-006 **Queries matched:** 7

unnamed protein product [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1070.5343	1069.5270	1069.5226	0.0044	94 -	102	1	---	MLYASSKDR
1439.7397	1438.7324	1438.7245	0.0080	78 -	89	0	---	IFFIAWSPDTSR
1439.7397	1438.7324	1438.7245	0.0080	78 -	89	0	21	IFFIAWSPDTSR
1654.8682	1653.8609	1653.8514	0.0095	76 -	89	1	---	SKIFFIAWSPDTSR
1654.8682	1653.8609	1653.8514	0.0095	76 -	89	1	56	SKIFFIAWSPDTSR
1694.9058	1693.8985	1693.8940	0.0046	78 -	91	1	---	IFFIAWSPDTSRVR
2214.9993	2213.9920	2213.9575	0.0345	60 -	77	1	---	YAVFDFDFTTDENCQKSK

No match to: 713.3998, 724.4915, 734.4922, 750.5140, 768.5120, 782.4836, 838.5288, 864.5275, 905.5298, 942.5424, 1009.6190, 1019.6183, 1137.6541, 1260.7815, 1279.7595, 1285.6605, 1301.6436, 1334.8807, 1426.8060, 1448.9143, 1455.7355, 1471.7377, 1493.8914, 1510.7781, 1588.8717, 1588.8717, 1670.8622, 1686.8585, 1798.7778, 1814.7716, 1814.7716, 1859.9996, 1997.8624, 2061.1990, 2214.0376, 2231.2324, 2240.1555, 2411.0222, 2417.4102, 2428.0264, 2428.0264, 2444.0977, 2460.1150, 2566.1885, 2824.3081, 2922.3640, 3349.6006

9. gi|225454162 **Mass:** 16251 **Score:** 115 **Expect:** 1.9e-006 **Queries matched:** 7

PREDICTED: hypothetical protein [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1070.5343	1069.5270	1069.5226	0.0044	101 -	109	1	---	MLYASSKDR
1439.7397	1438.7324	1438.7245	0.0080	85 -	96	0	---	IFFIAWSPDTSR
1439.7397	1438.7324	1438.7245	0.0080	85 -	96	0	21	IFFIAWSPDTSR
1654.8682	1653.8609	1653.8514	0.0095	83 -	96	1	---	SKIFFIAWSPDTSR
1654.8682	1653.8609	1653.8514	0.0095	83 -	96	1	56	SKIFFIAWSPDTSR
1694.9058	1693.8985	1693.8940	0.0046	85 -	98	1	---	IFFIAWSPDTSRVR
2214.9993	2213.9920	2213.9575	0.0345	67 -	84	1	---	YAVFDFDFTTDENCQKSK

No match to: 713.3998, 724.4915, 734.4922, 750.5140, 768.5120, 782.4836, 838.5288, 864.5275, 905.5298, 942.5424, 1009.6190, 1019.6183, 1137.6541, 1260.7815, 1279.7595, 1285.6605, 1301.6436, 1334.8807, 1426.8060, 1448.9143, 1455.7355, 1471.7377, 1493.8914, 1510.7781, 1588.8717, 1588.8717, 1670.8622, 1686.8585, 1798.7778, 1814.7716, 1814.7716, 1859.9996, 1997.8624, 2061.1990, 2214.0376, 2231.2324, 2240.1555, 2411.0222, 2417.4102, 2428.0264, 2428.0264, 2444.0977, 2460.1150, 2566.1885, 2824.3081, 2922.3640, 3349.6006

10. gi|116783021 **Mass:** 16295 **Score:** 114 **Expect:** 2.4e-006 **Queries matched:** 7

unknown [Picea sitchensis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide

864.5275	863.5202	863.5116	0.0086	18 - 24	1	---	FLELKSK
1070.5343	1069.5270	1069.5226	0.0044	101 - 109	1	---	MLYASSKDR
1439.7397	1438.7324	1438.7245	0.0080	85 - 96	0	---	IFFIAWSPDTSR
1439.7397	1438.7324	1438.7245	0.0080	85 - 96	0	21	IFFIAWSPDTSR
1654.8682	1653.8609	1653.8514	0.0095	83 - 96	1	---	SKIFFIAWSPDTSR
1654.8682	1653.8609	1653.8514	0.0095	83 - 96	1	56	SKIFFIAWSPDTSR
1694.9058	1693.8985	1693.8940	0.0046	85 - 98	1	---	IFFIAWSPDTSRVR

No match to: 713.3998, 724.4915, 734.4922, 750.5140, 768.5120, 782.4836, 838.5288, 905.5298, 942.5424, 1009.6190, 1019.6183, 1137.6541, 1260.7815, 1279.7595, 1285.6605, 1301.6436, 1334.8807, 1426.8060, 1448.9143, 1455.7355, 1471.7377, 1493.8914, 1510.7781, 1588.8717, 1588.8717, 1670.8622, 1686.8585, 1798.7778, 1814.7716, 1814.7716, 1859.9996, 1997.8624, 2061.1990, 2214.0376, 2214.9993, 2231.2324, 2240.1555, 2411.0222, 2417.4102, 2428.0264, 2428.0264, 2444.0977, 2460.1150, 2566.1885, 2824.3081, 2922.3640, 3349.6006

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 54

Protein View

Match to: **gi|125540584** Score: **162** Expect: **3.8e-011**
hypothetical protein OsI_08373 [Oryza sativa Indica Group]

Nominal mass (M_r): **15577**; Calculated pI value: **5.56**
NCBI BLAST search of gi|125540584 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Oryza sativa Indica Group
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|125583166 from Oryza sativa Japonica Group

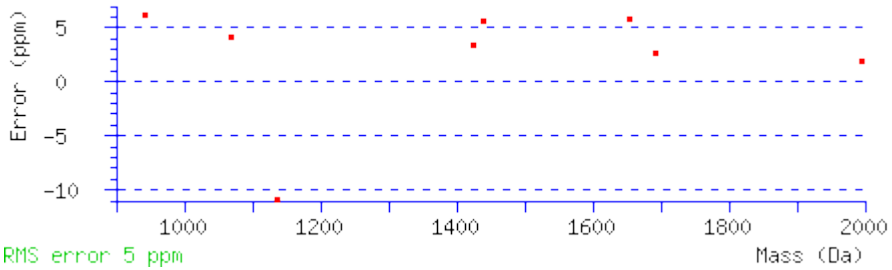
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **43%**

Matched peptides shown in **Bold Red**

```
     1 MAVCDECKLK FLELKAKRSF RFIVFKINEK VQQVVVDRLG QPGESYDDFT
    51 ACLPADECRY AVFDFDFVTD ENCQKSKIFF ISWAPDTSRV RSKMLYASSK
   101 DRFKRELDGI QVELQATDPS EMSMDIVKSR AL
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
22 - 30	1137.6541	1136.6468	1136.6593	-0.0125	1	FIVFKINEK	(No match)
27 - 38	1426.8060	1425.7987	1425.7939	0.0048	1	INEKVQQVVVDR	(No match)
31 - 38	942.5424	941.5351	941.5294	0.0058	0	VQQVVVDR	(No match)
60 - 75	1997.8624	1996.8551	1996.8512	0.0039	0	YAVFDFDFVTDENCQK	(No match)
76 - 89	1654.8682	1653.8609	1653.8514	0.0095	1	SKIFFISWAPDTSR	(No match)
76 - 89	1654.8682	1653.8609	1653.8514	0.0095	1	SKIFFISWAPDTSR	(Ions score 65)
78 - 89	1439.7397	1438.7324	1438.7245	0.0080	0	IFFISWAPDTSR	(No match)
78 - 89	1439.7397	1438.7324	1438.7245	0.0080	0	IFFISWAPDTSR	(Ions score 24)
78 - 91	1694.9058	1693.8985	1693.8940	0.0046	1	IFFISWAPDTSRVR	(No match)
94 - 102	1070.5343	1069.5270	1069.5226	0.0044	1	MLYASSKDR	(No match)



Spot 130

Index

	Accession	Mass	Score	Description
1.	gi|115472099	16280	299	Os07g0484200 [Oryza sativa (japonica cultivar-group)]
2.	gi|218199609	16250	299	hypothetical protein OsI_26009 [Oryza sativa Indica Group]
3.	gi|162462304	16301	184	actin depolymerizing factor [Zea mays]
4.	gi|195635623	16815	156	actin-depolymerizing factor 1 [Zea mays]
5.	gi|164414398	16386	156	actin-depolymerizing factor [Zea mays]
6.	gi|222637040	10840	140	hypothetical protein OsJ_24260 [Oryza sativa Japonica Group]
7.	gi|10122055	17548	74	putative actin depolymerizing factor [Oryza sativa (japonica cultivar-group)]
8.	gi|115482990	17489	74	Os10g0521100 [Oryza sativa (japonica cultivar-group)]
9.	gi|226530639	17559	74	actin-depolymerizing factor [Zea mays]
10.	gi|116061652	48248	57	unnamed protein product [Ostreococcus tauri]

Results List

1. gi|115472099 **Mass:** 16280 **Score:** 299 **Expect:** 7.6e-025 **Queries matched:** 6

Os07g0484200 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1473.7145	1472.7072	1472.7088	-0.0016	85	-	96	0	65	IFFFSWSPDTAR
1473.7145	1472.7072	1472.7088	-0.0016	85	-	96	0	---	IFFFSWSPDTAR
1688.8347	1687.8274	1687.8358	-0.0084	83	-	96	1	71	SKIFFFSWSPDTAR
1688.8347	1687.8274	1687.8358	-0.0084	83	-	96	1	---	SKIFFFSWSPDTAR
1979.8674	1978.8601	1978.8618	-0.0017	67	-	82	0	128	YAVYDLDFVTDENCQK
1979.8674	1978.8601	1978.8618	-0.0017	67	-	82	0	---	YAVYDLDFVTDENCQK

No match to: 768.5190, 862.5120, 1018.6111, 1138.6332, 1489.7133, 1505.7097, 1529.8510, 1727.8308, 1727.8308, 2195.9944, 2382.0281, 2382.0281

2. gi|218199609 **Mass:** 16250 **Score:** 299 **Expect:** 7.6e-025 **Queries matched:** 6

hypothetical protein OsI_26009 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1473.7145	1472.7072	1472.7088	-0.0016	85	-	96	0	65	IFFFSWSPDTAR
1473.7145	1472.7072	1472.7088	-0.0016	85	-	96	0	---	IFFFSWSPDTAR
1688.8347	1687.8274	1687.8358	-0.0084	83	-	96	1	71	SKIFFFSWSPDTAR
1688.8347	1687.8274	1687.8358	-0.0084	83	-	96	1	---	SKIFFFSWSPDTAR
1979.8674	1978.8601	1978.8618	-0.0017	67	-	82	0	128	YAVYDLDFVTDENCQK
1979.8674	1978.8601	1978.8618	-0.0017	67	-	82	0	---	YAVYDLDFVTDENCQK

No match to: 768.5190, 862.5120, 1018.6111, 1138.6332, 1489.7133, 1505.7097, 1529.8510, 1727.8308, 1727.8308, 2195.9944, 2382.0281, 2382.0281

3. gi|162462304 **Mass:** 16301 **Score:** 184 **Expect:** 2.4e-013 **Queries matched:** 6

actin depolymerizing factor [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1473.7145	1472.7072	1472.7088	-0.0016	85	-	96	0	65	IFFFSWSPDTAR
1473.7145	1472.7072	1472.7088	-0.0016	85	-	96	0	---	IFFFSWSPDTAR
1688.8347	1687.8274	1687.8358	-0.0084	83	-	96	1	71	SKIFFFSWSPDTAR
1688.8347	1687.8274	1687.8358	-0.0084	83	-	96	1	---	SKIFFFSWSPDTAR
1979.8674	1978.8601	1978.8982	-0.0381	67	-	82	0	13	YAIYDLDFTTVENCQK
1979.8674	1978.8601	1978.8982	-0.0381	67	-	82	0	---	YAIYDLDFTTVENCQK

No match to: 768.5190, 862.5120, 1018.6111, 1138.6332, 1489.7133, 1505.7097, 1529.8510, 1727.8308, 1727.8308, 2195.9944, 2382.0281, 2382.0281

4. gi|195635623 **Mass:** 16815 **Score:** 156 **Expect:** 1.5e-010 **Queries matched:** 4

actin-depolymerizing factor 1 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1473.7145	1472.7072	1472.7088	-0.0016	90	-	101	0	65	IFFFSWSPDTAR
1473.7145	1472.7072	1472.7088	-0.0016	90	-	101	0	---	IFFFSWSPDTAR
1688.8347	1687.8274	1687.8358	-0.0084	88	-	101	1	71	SKIFFFSWSPDTAR
1688.8347	1687.8274	1687.8358	-0.0084	88	-	101	1	---	SKIFFFSWSPDTAR

No match to: 768.5190, 862.5120, 1018.6111, 1138.6332, 1489.7133, 1505.7097, 1529.8510, 1727.8308, 1727.8308, 1979.8674, 1979.8674, 2195.9944, 2382.0281, 2382.0281

5. gi|164414398 **Mass:** 16386 **Score:** 156 **Expect:** 1.5e-010 **Queries matched:** 4

actin-depolymerizing factor [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1473.7145	1472.7072	1472.7088	-0.0016	85	-	96	0	65	IFFFSWSPDTAR
1473.7145	1472.7072	1472.7088	-0.0016	85	-	96	0	---	IFFFSWSPDTAR
1688.8347	1687.8274	1687.8358	-0.0084	83	-	96	1	71	SKIFFFSWSPDTAR
1688.8347	1687.8274	1687.8358	-0.0084	83	-	96	1	---	SKIFFFSWSPDTAR

No match to: 768.5190, 862.5120, 1018.6111, 1138.6332, 1489.7133, 1505.7097, 1529.8510, 1727.8308, 1727.8308, 1979.8674, 1979.8674, 2195.9944, 2382.0281, 2382.0281

6. gi|222637040 **Mass:** 10840 **Score:** 140 **Expect:** 6.1e-009 **Queries matched:** 2

hypothetical protein OsJ_24260 [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1979.8674	1978.8601	1978.8618	-0.0017	67	-	82	0	128	YAVYDLDFVTDENCQK
1979.8674	1978.8601	1978.8618	-0.0017	67	-	82	0	---	YAVYDLDFVTDENCQK

No match to: 768.5190, 862.5120, 1018.6111, 1138.6332, 1473.7145, 1473.7145, 1489.7133, 1505.7097, 1529.8510, 1688.8347, 1688.8347, 1727.8308, 1727.8308, 2195.9944, 2382.0281, 2382.0281

7. gi|10122055 **Mass:** 17548 **Score:** 74 **Expect:** 0.022 **Queries matched:** 2

putative actin depolymerizing factor [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide

1979.8674	1978.8601	1978.8730	-0.0129	79 - 94	1	64	YAVYDLDFVSDDNCRK
1979.8674	1978.8601	1978.8730	-0.0129	79 - 94	1	---	YAVYDLDFVSDDNCRK

No match to: 768.5190, 862.5120, 1018.6111, 1138.6332, 1473.7145, 1473.7145, 1489.7133, 1505.7097, 1529.8510, 1688.8347, 1688.8347, 1727.8308, 1727.8308, 2195.9944, 2382.0281, 2382.0281

8. gi|115482990 **Mass:** 17489 **Score:** 74 **Expect:** 0.024 **Queries matched:** 2

Os10g0521100 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start End	Miss	Ions	Peptide
1979.8674	1978.8601	1978.8730	-0.0129	77 - 92	1	64	YAVYDLDFVSDDNCRK
1979.8674	1978.8601	1978.8730	-0.0129	77 - 92	1	---	YAVYDLDFVSDDNCRK

No match to: 768.5190, 862.5120, 1018.6111, 1138.6332, 1473.7145, 1473.7145, 1489.7133, 1505.7097, 1529.8510, 1688.8347, 1688.8347, 1727.8308, 1727.8308, 2195.9944, 2382.0281, 2382.0281

9. gi|226530639 **Mass:** 17559 **Score:** 74 **Expect:** 0.026 **Queries matched:** 2

actin-depolymerizing factor [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start End	Miss	Ions	Peptide
1979.8674	1978.8601	1978.8730	-0.0129	79 - 94	1	64	YAVYDLDFVSDDNCRK
1979.8674	1978.8601	1978.8730	-0.0129	79 - 94	1	---	YAVYDLDFVSDDNCRK

No match to: 768.5190, 862.5120, 1018.6111, 1138.6332, 1473.7145, 1473.7145, 1489.7133, 1505.7097, 1529.8510, 1688.8347, 1688.8347, 1727.8308, 1727.8308, 2195.9944, 2382.0281, 2382.0281

10. gi|116061652 **Mass:** 48248 **Score:** 57 **Expect:** 1.2 **Queries matched:** 9

unnamed protein product [Ostreococcus tauri]

Observed	Mr(expt)	Mr(calc)	Delta	Start End	Miss	Ions	Peptide
1473.7145	1472.7072	1472.7769	-0.0697	409 - 421	1	5	AVEISRTSMQVPR
1473.7145	1472.7072	1472.7769	-0.0697	409 - 421	1	---	AVEISRTSMQVPR
1489.7133	1488.7060	1488.7718	-0.0658	409 - 421	1	---	AVEISRTSMQVPR + Oxidation (M)
1688.8347	1687.8274	1687.8562	-0.0288	1 - 16	1	9	MASELKDQGGLAEIAR
1688.8347	1687.8274	1687.8562	-0.0288	1 - 16	1	---	MASELKDQGGLAEIAR
1727.8308	1726.8235	1726.8049	0.0186	315 - 329	0	---	DAFIEAYGDDIETLR
1727.8308	1726.8235	1726.8049	0.0186	315 - 329	0	---	DAFIEAYGDDIETLR
1979.8674	1978.8601	1978.8513	0.0088	252 - 268	0	---	STDPLVDNMDPANFQCR
1979.8674	1978.8601	1978.8513	0.0088	252 - 268	0	---	STDPLVDNMDPANFQCR

No match to: 768.5190, 862.5120, 1018.6111, 1138.6332, 1505.7097, 1529.8510, 2195.9944, 2382.0281, 2382.0281

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 18

Protein View

Match to: **gi|218199609** Score: **299** Expect: **7.6e-025**
hypothetical protein OsI_26009 [Oryza sativa Indica Group]

Nominal mass (M_r): **16250**; Calculated pI value: **5.52**
NCBI BLAST search of gi|218199609 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Oryza sativa Indica Group

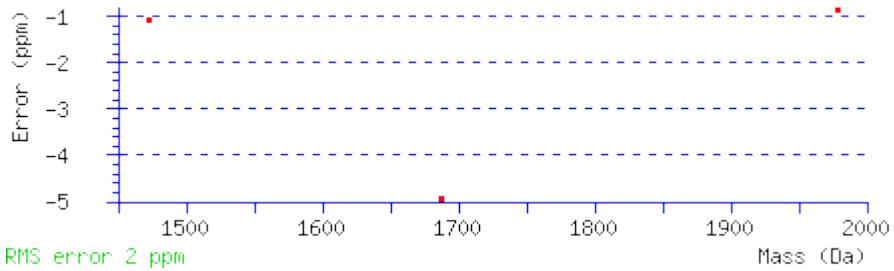
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **21%**

Matched peptides shown in **Bold Red**

```
     1 MANSASGLAV NDECKFKFQE LKARRGFRFI VFKIDDKAME IKVERLGQTA
    51 EGYEDFAATL PADECRYAVY DLDFVTDENC QKSKIFFFSW SPDTARTRSK
   101 MLYASSKDRF RRELDGIQCE IQATDPSEMS LDIIRARAH
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
67 - 82	1979.8674	1978.8601	1978.8618	-0.0017	0	YAVYDLDFVTDENCQK	(Ions score 128)
67 - 82	1979.8674	1978.8601	1978.8618	-0.0017	0	YAVYDLDFVTDENCQK	(No match)
83 - 96	1688.8347	1687.8274	1687.8358	-0.0084	1	SKIFFFSWSPDTAR	(Ions score 71)
83 - 96	1688.8347	1687.8274	1687.8358	-0.0084	1	SKIFFFSWSPDTAR	(No match)
85 - 96	1473.7145	1472.7072	1472.7088	-0.0016	0	IFFFSWSPDTAR	(Ions score 65)
85 - 96	1473.7145	1472.7072	1472.7088	-0.0016	0	IFFFSWSPDTAR	(No match)



Spot 131

Index

	Accession	Mass	Score	Description
1.	gi|3914432	14255	346	RecName: Full=Profilin-2/4; AltName: Full=Pollen allergen Phl p 12; AltName: Full=Allergen Phl
2.	gi|109391821	14199	331	Ole e 2 allergen [Olea europaea]
3.	gi|109391827	14316	331	Ole e 2 allergen [Olea europaea]
4.	gi|110644914	14234	330	pollen profilin variant 6 [Phleum pratense]
5.	gi|110644906	14220	330	pollen profilin variant 2 [Phleum pratense]
6.	gi|110644908	14264	330	pollen profilin variant 3 [Phleum pratense]
7.	gi|3914429	14269	329	RecName: Full=Profilin-3; AltName: Full=Pollen allergen Phl p 12; AltName: Full=Allergen Phl p
8.	gi|115481510	14348	315	Os10g0323600 [Oryza sativa (japonica cultivar-group)]
9.	gi|110644910	14294	314	pollen profilin variant 4 [Phleum pratense]
10.	gi|110644948	14250	314	pollen profilin [Olea europaea]

Results List

1. gi|3914432 **Mass:** 14255 **Score:** 346 **Expect:** 1.5e-029 **Queries matched:** 15

RecName: Full=Profilin-2/4; AltName: Full=Pollen allergen Phl p 12; AltName: Full=Allergen Phl p 11

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1124.5104	1123.5031	1123.5219	-0.0188	122	131	0	---	LGDYLVEQGM
1140.5125	1139.5052	1139.5168	-0.0116	122	131	0	---	LGDYLVEQGM + Oxidation (M)
1432.7703	1431.7630	1431.7543	0.0087	72	84	0	90	YMVIQGEPGAVIR
1432.7703	1431.7630	1431.7543	0.0087	72	84	0	---	YMVIQGEPGAVIR
1448.7581	1447.7508	1447.7493	0.0016	72	84	0	---	YMVIQGEPGAVIR + Oxidation (M)
1617.8820	1616.8747	1616.8708	0.0040	72	86	1	---	YMVIQGEPGAVIRGK
1959.9333	1958.9260	1958.9196	0.0065	53	71	0	---	DFDEPGHLAPTGMFVAGAK
1975.9423	1974.9350	1974.9145	0.0205	53	71	0	---	DFDEPGHLAPTGMFVAGAK + Oxidation (M)
2764.3113	2763.3040	2763.3029	0.0011	97	121	0	---	TGQALVVGIYDEPMTPGQCNMVVER
2764.3113	2763.3040	2763.3029	0.0011	97	121	0	88	TGQALVVGIYDEPMTPGQCNMVVER
2780.3340	2779.3267	2779.2978	0.0289	97	121	0	---	TGQALVVGIYDEPMTPGQCNMVVER + Oxidation (M)
2796.3362	2795.3289	2795.2927	0.0362	97	121	0	---	TGQALVVGIYDEPMTPGQCNMVVER + 2 Oxidation (M)
2892.4175	2891.4102	2891.3979	0.0123	96	121	1	91	KTGQALVVGIYDEPMTPGQCNMVVER
2892.4175	2891.4102	2891.3979	0.0123	96	121	1	---	KTGQALVVGIYDEPMTPGQCNMVVER
2908.4373	2907.4300	2907.3928	0.0372	96	121	1	---	KTGQALVVGIYDEPMTPGQCNMVVER + Oxidation (M)

No match to: 713.4064, 768.5237, 798.4501, 864.4936, 1138.6627, 1146.5154, 1162.4974, 1168.4961, 1324.7083, 1384.7710, 1386.2802, 1386.2802, 1400.7522, 1454.7493, 1470.7361, 1476.7333, 1561.8702, 1619.8840, 1621.8237, 1745.9854, 1973.9518, 1982.9189, 2295.0562, 2407.1331, 2422.1631, 2718.0205, 2778.3386, 2778.3386, 2906.4163, 3592.8142

2. gi|109391821 **Mass:** 14199 **Score:** 331 **Expect:** 4.8e-028 **Queries matched:** 13

Ole e 2 allergen [Olea europaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1432.7703	1431.7630	1431.7543	0.0087	72	-	84	0	90	YMVIQGEPGAVIR
1432.7703	1431.7630	1431.7543	0.0087	72	-	84	0	---	YMVIQGEPGAVIR
1448.7581	1447.7508	1447.7493	0.0016	72	-	84	0	---	YMVIQGEPGAVIR + Oxidation (M)
1617.8820	1616.8747	1616.8708	0.0040	72	-	86	1	---	YMVIQGEPGAVIRGK
1959.9333	1958.9260	1958.9196	0.0065	53	-	71	0	---	DFDEPGHLAPTGMFVAGAK
1975.9423	1974.9350	1974.9145	0.0205	53	-	71	0	---	DFDEPGHLAPTGMFVAGAK + Oxidation (M)
2764.3113	2763.3040	2763.3029	0.0011	97	-	121	0	---	TGQALVVGIYDEPMTPGQCNMVVER
2764.3113	2763.3040	2763.3029	0.0011	97	-	121	0	88	TGQALVVGIYDEPMTPGQCNMVVER
2780.3340	2779.3267	2779.2978	0.0289	97	-	121	0	---	TGQALVVGIYDEPMTPGQCNMVVER + Oxidation (M)
2796.3362	2795.3289	2795.2927	0.0362	97	-	121	0	---	TGQALVVGIYDEPMTPGQCNMVVER + 2 Oxidation (M)
2892.4175	2891.4102	2891.3979	0.0123	96	-	121	1	91	KTGQALVVGIYDEPMTPGQCNMVVER
2892.4175	2891.4102	2891.3979	0.0123	96	-	121	1	---	KTGQALVVGIYDEPMTPGQCNMVVER
2908.4373	2907.4300	2907.3928	0.0372	96	-	121	1	---	KTGQALVVGIYDEPMTPGQCNMVVER + Oxidation (M)

No match to: 713.4064, 768.5237, 798.4501, 864.4936, 1124.5104, 1138.6627, 1140.5125, 1146.5154, 1162.4974, 1168.4961, 1324.7083, 1384.7710, 1386.2802, 1386.2802, 1400.7522, 1454.7493, 1470.7361, 1476.7333, 1561.8702, 1619.8840, 1621.8237, 1745.9854, 1973.9518, 1982.9189, 2295.0562, 2407.1331, 2422.1631, 2718.0205, 2778.3386, 2778.3386, 2906.4163, 3592.8142

3. gi|109391827 **Mass:** 14316 **Score:** 331 **Expect:** 4.8e-028 **Queries matched:** 13

Ole e 2 allergen [Olea europaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1432.7703	1431.7630	1431.7543	0.0087	72	-	84	0	90	YMVIQGEPGAVIR
1432.7703	1431.7630	1431.7543	0.0087	72	-	84	0	---	YMVIQGEPGAVIR
1448.7581	1447.7508	1447.7493	0.0016	72	-	84	0	---	YMVIQGEPGAVIR + Oxidation (M)
1617.8820	1616.8747	1616.8708	0.0040	72	-	86	1	---	YMVIQGEPGAVIRGK
1959.9333	1958.9260	1958.9196	0.0065	53	-	71	0	---	DFDEPGHLAPTGMFVAGAK
1975.9423	1974.9350	1974.9145	0.0205	53	-	71	0	---	DFDEPGHLAPTGMFVAGAK + Oxidation (M)
2764.3113	2763.3040	2763.3029	0.0011	97	-	121	0	---	TGQALVVGIYDEPMTPGQCNMVVER
2764.3113	2763.3040	2763.3029	0.0011	97	-	121	0	88	TGQALVVGIYDEPMTPGQCNMVVER
2780.3340	2779.3267	2779.2978	0.0289	97	-	121	0	---	TGQALVVGIYDEPMTPGQCNMVVER + Oxidation (M)
2796.3362	2795.3289	2795.2927	0.0362	97	-	121	0	---	TGQALVVGIYDEPMTPGQCNMVVER + 2 Oxidation (M)
2892.4175	2891.4102	2891.3979	0.0123	96	-	121	1	91	KTGQALVVGIYDEPMTPGQCNMVVER
2892.4175	2891.4102	2891.3979	0.0123	96	-	121	1	---	KTGQALVVGIYDEPMTPGQCNMVVER
2908.4373	2907.4300	2907.3928	0.0372	96	-	121	1	---	KTGQALVVGIYDEPMTPGQCNMVVER + Oxidation (M)

No match to: 713.4064, 768.5237, 798.4501, 864.4936, 1124.5104, 1138.6627, 1140.5125, 1146.5154, 1162.4974, 1168.4961, 1324.7083, 1384.7710, 1386.2802, 1386.2802, 1400.7522, 1454.7493, 1470.7361, 1476.7333, 1561.8702, 1619.8840, 1621.8237, 1745.9854, 1973.9518, 1982.9189, 2295.0562, 2407.1331, 2422.1631, 2718.0205, 2778.3386, 2778.3386, 2906.4163, 3592.8142

4. gi|110644914 **Mass:** 14234 **Score:** 330 **Expect:** 6e-028 **Queries matched:** 12

pollen profilin variant 6 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1432.7703	1431.7630	1431.7543	0.0087	72	-	84	0	90	YMVIQGEPGAVIR
1432.7703	1431.7630	1431.7543	0.0087	72	-	84	0	---	YMVIQGEPGAVIR
1448.7581	1447.7508	1447.7493	0.0016	72	-	84	0	---	YMVIQGEPGAVIR + Oxidation (M)
1617.8820	1616.8747	1616.8708	0.0040	72	-	86	1	---	YMVIQGEPGAVIRGK
1973.9518	1972.9445	1972.9352	0.0093	53	-	71	0	---	DFDEPGHLAPTGMFVAAAK
2764.3113	2763.3040	2763.3029	0.0011	97	-	121	0	---	TGQALVVGIYDEPMTPGQCNMVVER
2764.3113	2763.3040	2763.3029	0.0011	97	-	121	0	88	TGQALVVGIYDEPMTPGQCNMVVER
2780.3340	2779.3267	2779.2978	0.0289	97	-	121	0	---	TGQALVVGIYDEPMTPGQCNMVVER + Oxidation (M)
2796.3362	2795.3289	2795.2927	0.0362	97	-	121	0	---	TGQALVVGIYDEPMTPGQCNMVVER + 2 Oxidation (M)
2892.4175	2891.4102	2891.3979	0.0123	96	-	121	1	91	KTGQALVVGIYDEPMTPGQCNMVVER
2892.4175	2891.4102	2891.3979	0.0123	96	-	121	1	---	KTGQALVVGIYDEPMTPGQCNMVVER
2908.4373	2907.4300	2907.3928	0.0372	96	-	121	1	---	KTGQALVVGIYDEPMTPGQCNMVVER + Oxidation (M)

No match to: 713.4064, 768.5237, 798.4501, 864.4936, 1124.5104, 1138.6627, 1140.5125, 1146.5154, 1162.4974, 1168.4961, 1324.7083, 1384.7710, 1386.2802, 1386.2802, 1400.7522, 1454.7493, 1470.7361, 1476.7333, 1561.8702, 1619.8840, 1621.8237, 1745.9854, 1959.9333, 1975.9423, 1982.9189, 2295.0562, 2407.1331, 2422.1631, 2718.0205, 2778.3386, 2778.3386, 2906.4163, 3592.8142

5. gi|110644906 **Mass:** 14220 **Score:** 330 **Expect:** 6e-028 **Queries matched:** 12

pollen profilin variant 2 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1432.7703	1431.7630	1431.7543	0.0087	72	-	84	0	90	YMVIQGEPGAVIR
1432.7703	1431.7630	1431.7543	0.0087	72	-	84	0	---	YMVIQGEPGAVIR
1448.7581	1447.7508	1447.7493	0.0016	72	-	84	0	---	YMVIQGEPGAVIR + Oxidation (M)
1617.8820	1616.8747	1616.8708	0.0040	72	-	86	1	---	YMVIQGEPGAVIRGK
1973.9518	1972.9445	1972.9352	0.0093	53	-	71	0	---	DFDEPGHLAPTGMFVAAAK
2764.3113	2763.3040	2763.3029	0.0011	97	-	121	0	---	TGQALVVGIYDEPMTPGQCNMVVER
2764.3113	2763.3040	2763.3029	0.0011	97	-	121	0	88	TGQALVVGIYDEPMTPGQCNMVVER
2780.3340	2779.3267	2779.2978	0.0289	97	-	121	0	---	TGQALVVGIYDEPMTPGQCNMVVER + Oxidation (M)
2796.3362	2795.3289	2795.2927	0.0362	97	-	121	0	---	TGQALVVGIYDEPMTPGQCNMVVER + 2 Oxidation (M)
2892.4175	2891.4102	2891.3979	0.0123	96	-	121	1	91	KTGQALVVGIYDEPMTPGQCNMVVER
2892.4175	2891.4102	2891.3979	0.0123	96	-	121	1	---	KTGQALVVGIYDEPMTPGQCNMVVER
2908.4373	2907.4300	2907.3928	0.0372	96	-	121	1	---	KTGQALVVGIYDEPMTPGQCNMVVER + Oxidation (M)

No match to: 713.4064, 768.5237, 798.4501, 864.4936, 1124.5104, 1138.6627, 1140.5125, 1146.5154, 1162.4974, 1168.4961, 1324.7083, 1384.7710, 1386.2802, 1386.2802, 1400.7522, 1454.7493, 1470.7361, 1476.7333, 1561.8702, 1619.8840, 1621.8237, 1745.9854, 1959.9333, 1975.9423, 1982.9189, 2295.0562, 2407.1331, 2422.1631, 2718.0205, 2778.3386, 2778.3386, 2906.4163, 3592.8142

6. gi|110644908 **Mass:** 14264 **Score:** 330 **Expect:** 6e-028 **Queries matched:** 12

pollen profilin variant 3 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1432.7703	1431.7630	1431.7543	0.0087	72	-	84	0	90	YMVIQGEPGAVIR

1432.7703	1431.7630	1431.7543	0.0087	72 - 84	0	---	YMVIQGEPGAVIR
1448.7581	1447.7508	1447.7493	0.0016	72 - 84	0	---	YMVIQGEPGAVIR + Oxidation (M)
1617.8820	1616.8747	1616.8708	0.0040	72 - 86	1	---	YMVIQGEPGAVIRGK
1973.9518	1972.9445	1972.9352	0.0093	53 - 71	0	---	DFDEPGHLAPTGMFVAAAK
2764.3113	2763.3040	2763.3029	0.0011	97 - 121	0	---	TGQALVVGIYDEPMTPGQCNMVVER
2764.3113	2763.3040	2763.3029	0.0011	97 - 121	0	88	TGQALVVGIYDEPMTPGQCNMVVER
2780.3340	2779.3267	2779.2978	0.0289	97 - 121	0	---	TGQALVVGIYDEPMTPGQCNMVVER + Oxidation (M)
2796.3362	2795.3289	2795.2927	0.0362	97 - 121	0	---	TGQALVVGIYDEPMTPGQCNMVVER + 2 Oxidation (M)
2892.4175	2891.4102	2891.3979	0.0123	96 - 121	1	91	KTGQALVVGIYDEPMTPGQCNMVVER
2892.4175	2891.4102	2891.3979	0.0123	96 - 121	1	---	KTGQALVVGIYDEPMTPGQCNMVVER
2908.4373	2907.4300	2907.3928	0.0372	96 - 121	1	---	KTGQALVVGIYDEPMTPGQCNMVVER + Oxidation (M)

No match to: 713.4064, 768.5237, 798.4501, 864.4936, 1124.5104, 1138.6627, 1140.5125, 1146.5154, 1162.4974, 1168.4961, 1324.7083, 1384.7710, 1386.2802, 1386.2802, 1400.7522, 1454.7493, 1470.7361, 1476.7333, 1561.8702, 1619.8840, 1621.8237, 1745.9854, 1959.9333, 1975.9423, 1982.9189, 2295.0562, 2407.1331, 2422.1631, 2718.0205, 2778.3386, 2778.3386, 2906.4163, 3592.8142

7. gi|3914429 **Mass:** 14269 **Score:** 329 **Expect:** 7.6e-028 **Queries matched:** 13

RecName: Full=Profilin-3; AltName: Full=Pollen allergen Phl p 12; AltName: Full=Allergen Phl p 11;

Observed	Mr(expt)	Mr(calc)	Delta	Start End	Miss	Ions	Peptide
1124.5104	1123.5031	1123.5219	-0.0188	122 - 131	0	---	LGDYLVEQGM
1140.5125	1139.5052	1139.5168	-0.0116	122 - 131	0	---	LGDYLVEQGM + Oxidation (M)
1432.7703	1431.7630	1431.7543	0.0087	72 - 84	0	90	YMVIQGEPGAVIR
1432.7703	1431.7630	1431.7543	0.0087	72 - 84	0	---	YMVIQGEPGAVIR
1448.7581	1447.7508	1447.7493	0.0016	72 - 84	0	---	YMVIQGEPGAVIR + Oxidation (M)
1617.8820	1616.8747	1616.8708	0.0040	72 - 86	1	---	YMVIQGEPGAVIRGK
2764.3113	2763.3040	2763.3029	0.0011	97 - 121	0	---	TGQALVVGIYDEPMTPGQCNMVVER
2764.3113	2763.3040	2763.3029	0.0011	97 - 121	0	88	TGQALVVGIYDEPMTPGQCNMVVER
2780.3340	2779.3267	2779.2978	0.0289	97 - 121	0	---	TGQALVVGIYDEPMTPGQCNMVVER + Oxidation (M)
2796.3362	2795.3289	2795.2927	0.0362	97 - 121	0	---	TGQALVVGIYDEPMTPGQCNMVVER + 2 Oxidation (M)
2892.4175	2891.4102	2891.3979	0.0123	96 - 121	1	91	KTGQALVVGIYDEPMTPGQCNMVVER
2892.4175	2891.4102	2891.3979	0.0123	96 - 121	1	---	KTGQALVVGIYDEPMTPGQCNMVVER
2908.4373	2907.4300	2907.3928	0.0372	96 - 121	1	---	KTGQALVVGIYDEPMTPGQCNMVVER + Oxidation (M)

No match to: 713.4064, 768.5237, 798.4501, 864.4936, 1138.6627, 1146.5154, 1162.4974, 1168.4961, 1324.7083, 1384.7710, 1386.2802, 1386.2802, 1400.7522, 1454.7493, 1470.7361, 1476.7333, 1561.8702, 1619.8840, 1621.8237, 1745.9854, 1959.9333, 1973.9518, 1975.9423, 1982.9189, 2295.0562, 2407.1331, 2422.1631, 2718.0205, 2778.3386, 2778.3386, 2906.4163, 3592.8142

8. gi|115481510 **Mass:** 14348 **Score:** 315 **Expect:** 1.9e-026 **Queries matched:** 11

Os10g0323600 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start End	Miss	Ions	Peptide
1432.7703	1431.7630	1431.7543	0.0087	72 - 84	0	90	YMVIQGEPGAVIR
1432.7703	1431.7630	1431.7543	0.0087	72 - 84	0	---	YMVIQGEPGAVIR

1448.7581	1447.7508	1447.7493	0.0016	72 - 84	0	---	YMVIQGEPGAVIR + Oxidation (M)
1617.8820	1616.8747	1616.8708	0.0040	72 - 86	1	---	YMVIQGEPGAVIRGK
2764.3113	2763.3040	2763.3029	0.0011	97 - 121	0	---	TGQALVVGIYDEPMTPGQCNMVVER
2764.3113	2763.3040	2763.3029	0.0011	97 - 121	0	88	TGQALVVGIYDEPMTPGQCNMVVER
2780.3340	2779.3267	2779.2978	0.0289	97 - 121	0	---	TGQALVVGIYDEPMTPGQCNMVVER + Oxidation (M)
2796.3362	2795.3289	2795.2927	0.0362	97 - 121	0	---	TGQALVVGIYDEPMTPGQCNMVVER + 2 Oxidation (M)
2892.4175	2891.4102	2891.3979	0.0123	96 - 121	1	91	KTGQALVVGIYDEPMTPGQCNMVVER
2892.4175	2891.4102	2891.3979	0.0123	96 - 121	1	---	KTGQALVVGIYDEPMTPGQCNMVVER
2908.4373	2907.4300	2907.3928	0.0372	96 - 121	1	---	KTGQALVVGIYDEPMTPGQCNMVVER + Oxidation (M)

No match to: 713.4064, 768.5237, 798.4501, 864.4936, 1124.5104, 1138.6627, 1140.5125, 1146.5154, 1162.4974, 1168.4961, 1324.7083, 1384.7710, 1386.2802, 1386.2802, 1400.7522, 1454.7493, 1470.7361, 1476.7333, 1561.8702, 1619.8840, 1621.8237, 1745.9854, 1959.9333, 1973.9518, 1975.9423, 1982.9189, 2295.0562, 2407.1331, 2422.1631, 2718.0205, 2778.3386, 2778.3386, 2906.4163, 3592.8142

9. gi|110644910 **Mass:** 14294 **Score:** 314 **Expect:** 2.4e-026 **Queries matched:** 11

pollen profilin variant 4 [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1432.7703	1431.7630	1431.7543	0.0087	72 -	84	0	90	YMVIQGEPGAVIR
1432.7703	1431.7630	1431.7543	0.0087	72 -	84	0	---	YMVIQGEPGAVIR
1448.7581	1447.7508	1447.7493	0.0016	72 -	84	0	---	YMVIQGEPGAVIR + Oxidation (M)
1617.8820	1616.8747	1616.8708	0.0040	72 -	86	1	---	YMVIQGEPGAVIRGK
2764.3113	2763.3040	2763.3029	0.0011	97 -	121	0	---	TGQALVVGIYDEPMTPGQCNMVVER
2764.3113	2763.3040	2763.3029	0.0011	97 -	121	0	88	TGQALVVGIYDEPMTPGQCNMVVER
2780.3340	2779.3267	2779.2978	0.0289	97 -	121	0	---	TGQALVVGIYDEPMTPGQCNMVVER + Oxidation (M)
2796.3362	2795.3289	2795.2927	0.0362	97 -	121	0	---	TGQALVVGIYDEPMTPGQCNMVVER + 2 Oxidation (M)
2892.4175	2891.4102	2891.3979	0.0123	96 -	121	1	91	KTGQALVVGIYDEPMTPGQCNMVVER
2892.4175	2891.4102	2891.3979	0.0123	96 -	121	1	---	KTGQALVVGIYDEPMTPGQCNMVVER
2908.4373	2907.4300	2907.3928	0.0372	96 -	121	1	---	KTGQALVVGIYDEPMTPGQCNMVVER + Oxidation (M)

No match to: 713.4064, 768.5237, 798.4501, 864.4936, 1124.5104, 1138.6627, 1140.5125, 1146.5154, 1162.4974, 1168.4961, 1324.7083, 1384.7710, 1386.2802, 1386.2802, 1400.7522, 1454.7493, 1470.7361, 1476.7333, 1561.8702, 1619.8840, 1621.8237, 1745.9854, 1959.9333, 1973.9518, 1975.9423, 1982.9189, 2295.0562, 2407.1331, 2422.1631, 2718.0205, 2778.3386, 2778.3386, 2906.4163, 3592.8142

10. gi|110644948 **Mass:** 14250 **Score:** 314 **Expect:** 2.4e-026 **Queries matched:** 11

pollen profilin [Olea europaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1432.7703	1431.7630	1431.7543	0.0087	72 -	84	0	90	YMVIQGEPGAVIR
1432.7703	1431.7630	1431.7543	0.0087	72 -	84	0	---	YMVIQGEPGAVIR
1448.7581	1447.7508	1447.7493	0.0016	72 -	84	0	---	YMVIQGEPGAVIR + Oxidation (M)
1617.8820	1616.8747	1616.8708	0.0040	72 -	86	1	---	YMVIQGEPGAVIRGK
2764.3113	2763.3040	2763.3029	0.0011	97 -	121	0	---	TGQALVVGIYDEPMTPGQCNMVVER
2764.3113	2763.3040	2763.3029	0.0011	97 -	121	0	88	TGQALVVGIYDEPMTPGQCNMVVER

2780.3340	2779.3267	2779.2978	0.0289	97 - 121	0	---	TGQALVVGIYDEPMTPGQCNMVVER + Oxidation (M)
2796.3362	2795.3289	2795.2927	0.0362	97 - 121	0	---	TGQALVVGIYDEPMTPGQCNMVVER + 2 Oxidation (M)
2892.4175	2891.4102	2891.3979	0.0123	96 - 121	1	91	KTGQALVVGIYDEPMTPGQCNMVVER
2892.4175	2891.4102	2891.3979	0.0123	96 - 121	1	---	KTGQALVVGIYDEPMTPGQCNMVVER
2908.4373	2907.4300	2907.3928	0.0372	96 - 121	1	---	KTGQALVVGIYDEPMTPGQCNMVVER + Oxidation (M)

No match to: 713.4064, 768.5237, 798.4501, 864.4936, 1124.5104, 1138.6627, 1140.5125, 1146.5154, 1162.4974, 1168.4961, 1324.7083, 1384.7710, 1386.2802, 1386.2802, 1400.7522, 1454.7493, 1470.7361, 1476.7333, 1561.8702, 1619.8840, 1621.8237, 1745.9854, 1959.9333, 1973.9518, 1975.9423, 1982.9189, 2295.0562, 2407.1331, 2422.1631, 2718.0205, 2778.3386, 2778.3386, 2906.4163, 3592.8142

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 45

Protein View

Match to: **gi|3914432** Score: **346** Expect: **1.5e-029**
RecName: Full=Profilin-2/4; AltName: Full=Pollen allergen Phl p 12; AltName: Full=Allergen Phl p 11

Nominal mass (M_r): **14255**; Calculated pI value: **4.92**
NCBI BLAST search of gi|3914432 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|2415698 from Phleum pratense
gi|2415702 from Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **53%**

Matched peptides shown in **Bold Red**

```
   1 MSWQTYVDEH LMCEIEGHHL ASAAILGHDG TVWAQSADFP QFKPEEITGI
  51 MKDFDEPGHL APTGMFVAGA KYMVIQGEPG AVIRGKKGAG GITIKKTGQA
 101 LVVGIYDEPM TPGQCNMVVE RLGDYLVEQG M
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
53 - 71	1959.9333	1958.9260	1958.9196	0.0065	0	**DFDEPGHLAPTGMFVAGAK** (No match)
53 - 71	1975.9423	1974.9350	1974.9145	0.0205	0	**DFDEPGHLAPTGMFVAGAK** Oxidation (M) (No match)
72 - 84	1432.7703	1431.7630	1431.7543	0.0087	0	**YMVIQGEPGAVIR** (Ions score 90)
72 - 84	1432.7703	1431.7630	1431.7543	0.0087	0	**YMVIQGEPGAVIR** (No match)
72 - 84	1448.7581	1447.7508	1447.7493	0.0016	0	**YMVIQGEPGAVIR** Oxidation (M) (No match)
72 - 86	1617.8820	1616.8747	1616.8708	0.0040	1	**YMVIQGEPGAVIRGK** (No match)
96 - 121	2892.4175	2891.4102	2891.3979	0.0123	1	**KTGQALVVGIYDEPMTPGQCNMVVER** (Ions score 91)
96 - 121	2892.4175	2891.4102	2891.3979	0.0123	1	**KTGQALVVGIYDEPMTPGQCNMVVER** (No match)
96 - 121	2908.4373	2907.4300	2907.3928	0.0372	1	**KTGQALVVGIYDEPMTPGQCNMVVER** Oxidation (M) (No match)
97 - 121	2764.3113	2763.3040	2763.3029	0.0011	0	**TGQALVVGIYDEPMTPGQCNMVVER** (No match)
97 - 121	2764.3113	2763.3040	2763.3029	0.0011	0	**TGQALVVGIYDEPMTPGQCNMVVER** (Ions score 88)
97 - 121	2780.3340	2779.3267	2779.2978	0.0289	0	**TGQALVVGIYDEPMTPGQCNMVVER** Oxidation (M) (No match)
97 - 121	2796.3362	2795.3289	2795.2927	0.0362	0	**TGQALVVGIYDEPMTPGQCNMVVER** 2 Oxidation (M) (No match)
122 - 131	1124.5104	1123.5031	1123.5219	-0.0188	0	**LGDYLVEQGM** (No match)
122 - 131	1140.5125	1139.5052	1139.5168	-0.0116	0	**LGDYLVEQGM** Oxidation (M) (No match)

Spot 132

Index

	Accession	Mass	Score	Description
1.	gi|157830392	10809	103	Chain A, A Fibronectin Type Iii Fold In Plant Allergens: The Solution Structure Of Phl Pii Fro
2.	gi|1171009	13410	86	RecName: Full=Pollen allergen Phl p 2; AltName: Full=Allergen Phl p II; AltName: Allergen=Phl
3.	gi|4007040	13380	86	pollen allergen (group II) [Dactylis glomerata]
4.	gi|4006978	13381	86	pollen allergen (group II) [Cynodon dactylon]
5.	gi|21592423	23160	45	zinc finger protein 5, ZFP5 [Arabidopsis thaliana]
6.	gi|15218551	23803	44	ZFP5 (ZINC FINGER PROTEIN 5); nucleic acid binding / transcription factor/ zinc ion binding [A
7.	gi|168009507	14007	43	predicted protein [Physcomitrella patens subsp. patens]
8.	gi|125597873	67916	41	hypothetical protein OsJ_21988 [Oryza sativa Japonica Group]
9.	gi|218197339	45768	41	hypothetical protein OsI_21159 [Oryza sativa Indica Group]
10.	gi|15234987	9932	40	wound-responsive family protein [Arabidopsis thaliana]

Results List

1. gi|157830392 **Mass:** 10809 **Score:** 103 **Expect:** 3e-005 **Queries matched:** 5

Chain A, A Fibronectin Type Iii Fold In Plant Allergens: The Solution Structure Of Phl Pii From Tim

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1147.6656	1146.6583	1146.6648	-0.0065	1	10	1	---	VPKVTFTVEK
2357.1140	2356.1067	2356.1110	-0.0043	76	96	1	---	NVFDDVVPEKYTIGATYAPEE
2357.1140	2356.1067	2356.1110	-0.0043	76	96	1	---	NVFDDVVPEKYTIGATYAPEE
2369.0867	2368.0794	2368.0759	0.0035	47	67	0	---	GEGGVWTFDSEEPLQGPFNFR
2369.0867	2368.0794	2368.0759	0.0035	47	67	0	64	GEGGVWTFDSEEPLQGPFNFR

No match to: 713.3968, 724.4901, 768.5123, 838.5151, 864.5045, 1194.5400, 1320.5876, 1436.5671, 1437.5828, 1494.7247, 1662.9148, 1708.7985, 2136.1013, 2150.1060, 2373.0950, 2385.0754, 2385.0754, 2401.0767, 2401.0767, 2689.2737, 2689.2737

2. gi|1171009 **Mass:** 13410 **Score:** 86 **Expect:** 0.0014 **Queries matched:** 4

RecName: Full=Pollen allergen Phl p 2; AltName: Full=Allergen Phl p II; AltName: Allergen=Phl p 2;

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
2357.1140	2356.1067	2356.1110	-0.0043	102	122	1	---	NVFDDVVPEKYTIGATYAPEE
2357.1140	2356.1067	2356.1110	-0.0043	102	122	1	---	NVFDDVVPEKYTIGATYAPEE
2369.0867	2368.0794	2368.0759	0.0035	73	93	0	---	GEGGVWTFDSEEPLQGPFNFR
2369.0867	2368.0794	2368.0759	0.0035	73	93	0	64	GEGGVWTFDSEEPLQGPFNFR

No match to: 713.3968, 724.4901, 768.5123, 838.5151, 864.5045, 1147.6656, 1194.5400, 1320.5876, 1436.5671, 1437.5828, 1494.7247, 1662.9148, 1708.7985, 2136.1013, 2150.1060, 2373.0950, 2385.0754, 2385.0754, 2401.0767, 2401.0767, 2689.2737, 2689.2737

3. gi|4007040 **Mass:** 13380 **Score:** 86 **Expect:** 0.0014 **Queries matched:** 4

pollen allergen (group II) [Dactylis glomerata]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
2357.1140	2356.1067	2356.1110	-0.0043	102	122	1	---	NVFDDVVPEKYTIGATYAPEE
2357.1140	2356.1067	2356.1110	-0.0043	102	122	1	---	NVFDDVVPEKYTIGATYAPEE
2369.0867	2368.0794	2368.0759	0.0035	73	93	0	---	GEGGVWTFDSEEPLQGPFNFR
2369.0867	2368.0794	2368.0759	0.0035	73	93	0	64	GEGGVWTFDSEEPLQGPFNFR

No match to: 713.3968, 724.4901, 768.5123, 838.5151, 864.5045, 1147.6656, 1194.5400, 1320.5876, 1436.5671, 1437.5828, 1494.7247, 1662.9148, 1708.7985, 2136.1013, 2150.1060, 2373.0950, 2385.0754, 2385.0754, 2401.0767, 2401.0767, 2689.2737, 2689.2737

4. gi|4006978 **Mass:** 13381 **Score:** 86 **Expect:** 0.0016 **Queries matched:** 4

pollen allergen (group II) [Cynodon dactylon]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
2357.1140	2356.1067	2356.1110	-0.0043	102	122	1	---	NVFDDVVPEKYTIGATYAPEE
2357.1140	2356.1067	2356.1110	-0.0043	102	122	1	---	NVFDDVVPEKYTIGATYAPEE
2369.0867	2368.0794	2368.1123	-0.0329	73	93	1	---	GEGGVWTFDSEEPLKGPFNFR
2369.0867	2368.0794	2368.1123	-0.0329	73	93	1	64	GEGGVWTFDSEEPLKGPFNFR

No match to: 713.3968, 724.4901, 768.5123, 838.5151, 864.5045, 1147.6656, 1194.5400, 1320.5876, 1436.5671, 1437.5828, 1494.7247, 1662.9148, 1708.7985, 2136.1013, 2150.1060, 2373.0950, 2385.0754, 2385.0754, 2401.0767, 2401.0767, 2689.2737, 2689.2737

5. gi|21592423 **Mass:** 23160 **Score:** 45 **Expect:** 20 **Queries matched:** 8

zinc finger protein 5, ZFP5 [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1194.5400	1193.5327	1193.5459	-0.0131	180	189	1	---	DLSSRSDQMR
1708.7985	1707.7912	1707.8076	-0.0164	62	77	0	---	EFANSQALGGHQNAHK
2385.0754	2384.0681	2384.1628	-0.0947	30	52	0	---	TPEITTAESVSSSTNTTSLTVMK
2385.0754	2384.0681	2384.1628	-0.0947	30	52	0	---	TPEITTAESVSSSTNTTSLTVMK
2401.0767	2400.0694	2400.1577	-0.0883	30	52	0	---	TPEITTAESVSSSTNTTSLTVMK + Oxidation (M)
2401.0767	2400.0694	2400.1577	-0.0883	30	52	0	---	TPEITTAESVSSSTNTTSLTVMK + Oxidation (M)
2689.2737	2688.2664	2688.1027	0.1637	143	166	0	---	SSQINFGNNDTCQDLNEQSGEMGK + Oxidation (M)
2689.2737	2688.2664	2688.1027	0.1637	143	166	0	---	SSQINFGNNDTCQDLNEQSGEMGK + Oxidation (M)

No match to: 713.3968, 724.4901, 768.5123, 838.5151, 864.5045, 1147.6656, 1320.5876, 1436.5671, 1437.5828, 1494.7247, 1662.9148, 2136.1013, 2150.1060, 2357.1140, 2357.1140, 2369.0867, 2369.0867, 2373.0950

6. gi|15218551 **Mass:** 23803 **Score:** 44 **Expect:** 25 **Queries matched:** 8

ZFP5 (ZINC FINGER PROTEIN 5); nucleic acid binding / transcription factor/ zinc ion binding [Arabid

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1194.5400	1193.5327	1193.5459	-0.0131	186	195	1	---	DLSSRSDQMR
1708.7985	1707.7912	1707.8076	-0.0164	68	83	0	---	EFANSQALGGHQNAHK
2385.0754	2384.0681	2384.1628	-0.0947	36	58	0	---	TPEITTAESVSSSTNTTSLTVMK
2385.0754	2384.0681	2384.1628	-0.0947	36	58	0	---	TPEITTAESVSSSTNTTSLTVMK
2401.0767	2400.0694	2400.1577	-0.0883	36	58	0	---	TPEITTAESVSSSTNTTSLTVMK + Oxidation (M)

2401.0767	2400.0694	2400.1577	-0.0883	36 - 58	0	---	TPEITTAESVSSSTNTTSLTVMK + Oxidation (M)
2689.2737	2688.2664	2688.1027	0.1637	149 - 172	0	---	SSQINFGNNDTCQDLNEQSGEMGK + Oxidation (M)
2689.2737	2688.2664	2688.1027	0.1637	149 - 172	0	---	SSQINFGNNDTCQDLNEQSGEMGK + Oxidation (M)

No match to: 713.3968, 724.4901, 768.5123, 838.5151, 864.5045, 1147.6656, 1320.5876, 1436.5671, 1437.5828, 1494.7247, 1662.9148, 2136.1013, 2150.1060, 2357.1140, 2357.1140, 2369.0867, 2369.0867, 2373.0950

7. gi|168009507 **Mass:** 14007 **Score:** 43 **Expect:** 33 **Queries matched:** 4

predicted protein [Physcomitrella patens subsp. patens]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
838.5151	837.5078	837.4820	0.0258	27 -	33	1	---	ELPAPRR
1437.5828	1436.5755	1436.6275	-0.0520	1 -	12	0	---	MDSQEIDTMPVR + Oxidation (M)
1494.7247	1493.7174	1493.7184	-0.0009	97 -	108	0	---	EQQLEFIADVMR + Oxidation (M)
2136.1013	2135.0940	2134.9987	0.0954	1 -	18	1	---	MDSQEIDTMPVRLSQPTR + 2 Oxidation (M)

No match to: 713.3968, 724.4901, 768.5123, 864.5045, 1147.6656, 1194.5400, 1320.5876, 1436.5671, 1662.9148, 1708.7985, 2150.1060, 2357.1140, 2357.1140, 2369.0867, 2369.0867, 2373.0950, 2385.0754, 2385.0754, 2401.0767, 2401.0767, 2689.2737, 2689.2737

8. gi|125597873 **Mass:** 67916 **Score:** 41 **Expect:** 45 **Queries matched:** 9

hypothetical protein OsJ_21988 [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
864.5045	863.4972	863.4752	0.0220	608 -	615	0	---	ITDFGIAK
1708.7985	1707.7912	1707.8614	-0.0701	457 -	473	1	---	APPLPSSTEPPMGSKGR
2150.1060	2149.0987	2149.1313	-0.0326	166 -	186	1	---	HPTDTLLPGQSMGAGAILRSK
2385.0754	2384.0681	2384.0889	-0.0207	296 -	318	0	---	SSANASWTVADLFPAVGCGMSTR
2385.0754	2384.0681	2384.0889	-0.0207	296 -	318	0	---	SSANASWTVADLFPAVGCGMSTR
2401.0767	2400.0694	2400.0838	-0.0143	296 -	318	0	---	SSANASWTVADLFPAVGCGMSTR + Oxidation (M)
2401.0767	2400.0694	2400.0838	-0.0143	296 -	318	0	---	SSANASWTVADLFPAVGCGMSTR + Oxidation (M)
2689.2737	2688.2664	2688.3005	-0.0341	474 -	498	1	---	WEGGGFGEVYHGMAKSLQPPDIAVK + Oxidation (M)
2689.2737	2688.2664	2688.3005	-0.0341	474 -	498	1	---	WEGGGFGEVYHGMAKSLQPPDIAVK + Oxidation (M)

No match to: 713.3968, 724.4901, 768.5123, 838.5151, 1147.6656, 1194.5400, 1320.5876, 1436.5671, 1437.5828, 1494.7247, 1662.9148, 2136.1013, 2357.1140, 2357.1140, 2369.0867, 2369.0867, 2373.0950

9. gi|218197339 **Mass:** 45768 **Score:** 41 **Expect:** 54 **Queries matched:** 8

hypothetical protein OsI_21159 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1320.5876	1319.5803	1319.6656	-0.0852	127 -	137	1	---	ARSLFDEMPVR
1494.7247	1493.7174	1493.7370	-0.0196	159 -	170	1	---	LWDAAKLLDMMR + 2 Oxidation (M)
2369.0867	2368.0794	2368.0820	-0.0026	28 -	50	1	---	GTKSGDAALDVTACTALVNGCCK
2369.0867	2368.0794	2368.0820	-0.0026	28 -	50	1	---	GTKSGDAALDVTACTALVNGCCK
2401.0767	2400.0694	2400.1830	-0.1136	206 -	227	1	---	AAGFQPSAVTYNMLIAGFCRAR
2401.0767	2400.0694	2400.1830	-0.1136	206 -	227	1	---	AAGFQPSAVTYNMLIAGFCRAR
2689.2737	2688.2664	2688.3944	-0.1280	267 -	291	1	---	AFEILAGMEKAGLEVDAHTYGVLVR

2689.2737	2688.2664	2688.3944	-0.1280	267 - 291	1	---	AFEILAGMEKAGLEVDAHTYGVLVR

No match to: 713.3968, 724.4901, 768.5123, 838.5151, 864.5045, 1147.6656, 1194.5400, 1436.5671, 1437.5828, 1662.9148, 1708.7985, 2136.1013, 2150.1060, 2357.1140, 2357.1140, 2373.0950, 2385.0754, 2385.0754

10. gi|15234987 **Mass:** 9932 **Score:** 40 **Expect:** 65 **Queries matched:** 4

wound-responsive family protein [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
864.5045	863.4972	863.4653	0.0319	29 -	34	0	---	WNYILR
2136.1013	2135.0940	2135.1296	-0.0355	1 -	21	1	---	MSSTSKAWTVAVSIGAVEALK
2357.1140	2356.1067	2356.2572	-0.1505	7 -	28	1	---	AWTVAVSIGAVEALKDQLGLCR
2357.1140	2356.1067	2356.2572	-0.1505	7 -	28	1	---	AWTVAVSIGAVEALKDQLGLCR

No match to: 713.3968, 724.4901, 768.5123, 838.5151, 1147.6656, 1194.5400, 1320.5876, 1436.5671, 1437.5828, 1494.7247, 1662.9148, 1708.7985, 2150.1060, 2369.0867, 2369.0867, 2373.0950, 2385.0754, 2385.0754, 2401.0767, 2401.0767, 2689.2737, 2689.2737

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 26

Protein View

Match to: **gi|157830392** Score: **103** Expect: **3e-005**
Chain A, A Fibronectin Type Iii Fold In Plant Allergens: The Solution Structure Of Phl Pii From Tim

Nominal mass (M_r): **10809**; Calculated pI value: **4.64**
NCBI BLAST search of gi|157830392 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|157834205 from Phleum pratense
gi|157834206 from Phleum pratense
gi|223673813 from Phleum pratense

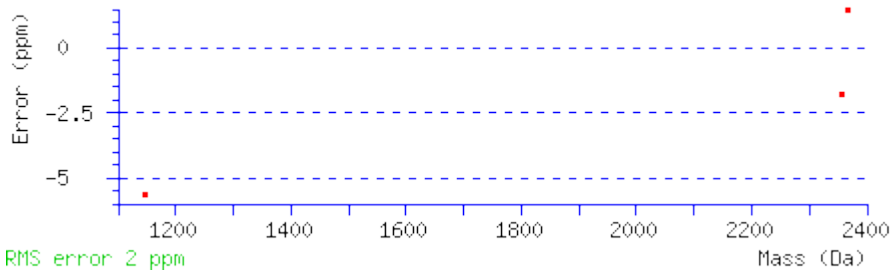
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **54%**

Matched peptides shown in **Bold Red**

```
     1 VPKVTFTVEK GSNEKHLAVL VKYEGDTMAE VELREHGSDE WVAMTKGEGG
    51 VWTFDSEEPL QGPFNFRFLT EKGMKNVFDD VVPEKYTIGA TYAPEE
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
1 - 10	1147.6656	1146.6583	1146.6648	-0.0065	1	VPKVTFTVEK	(No match)
47 - 67	2369.0867	2368.0794	2368.0759	0.0035	0	GEGGVWTFDSEEPLQGPFNFR	(No match)
47 - 67	2369.0867	2368.0794	2368.0759	0.0035	0	GEGGVWTFDSEEPLQGPFNFR	(Ions score 64)
76 - 96	2357.1140	2356.1067	2356.1110	-0.0043	1	NVFDDVVPEKYTIGATYAPEE	(No match)
76 - 96	2357.1140	2356.1067	2356.1110	-0.0043	1	NVFDDVVPEKYTIGATYAPEE	(No match)



Spot 133

Index

	Accession	Mass	Score	Description
1.	gi|126386	10873	139	RecName: Full=Pollen allergen Lol p 2-A; AltName: Full=Allergen Lol p II-A; AltName: Allergen=
2.	gi|939932	9904	65	allergen Lol p II [Lolium perenne]
3.	gi|1093120	22584	64	allergen Dac g II
4.	gi|125601952	34446	55	hypothetical protein OsJ_25784 [Oryza sativa Japonica Group]
5.	gi|8177719	57406	49	fiddlehead protein [Arabidopsis thaliana]
6.	gi|1171011	13912	48	RecName: Full=Pollen allergen Phl p 6; AltName: Full=Allergen Phl p VI; AltName: Allergen=Phl
7.	gi|113205238	51344	47	WD domain containing protein, putative [Solanum demissum]
8.	gi|15225270	62435	47	KCS10 (3-KETOACYL-COA SYNTHASE 10); acyltransferase/ catalytic/ transferase, transferring acyl
9.	gi|8177711	62493	47	fiddlehead protein [Arabidopsis thaliana]
10.	gi|147797628	94104	47	hypothetical protein [Vitis vinifera]

Results List

1. gi|126386 **Mass:** 10873 **Score:** 139 **Expect:** 7.6e-009 **Queries matched:** 7

RecName: Full=Pollen allergen Lol p 2-A; AltName: Full=Allergen Lol p II-A; AltName: Allergen=Lol p

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
737.3999	736.3926	736.3656	0.0270	64	69	0	---	GPFNFR
1163.6118	1162.6045	1162.6709	-0.0664	16	25	1	---	NLALSIKYNK
1365.6533	1364.6460	1364.6612	-0.0151	78	89	0	---	NVFDDVVPADFK
1365.6533	1364.6460	1364.6612	-0.0151	78	89	0	42	NVFDDVVPADFK
1405.7593	1404.7520	1404.7513	0.0007	58	69	1	52	SDKPLKGPFNFR
1405.7593	1404.7520	1404.7513	0.0007	58	69	1	---	SDKPLKGPFNFR
1725.8275	1724.8202	1724.8191	0.0011	75	89	1	---	GMRNVFDDVVPADFK + Oxidation (M)

No match to: 713.3977, 724.4877, 734.4918, 736.4785, 750.5066, 768.5120, 782.4661, 838.5152, 848.5374, 864.5350, 866.5280, 983.4835, 1007.6586, 1049.4784, 1084.5203, 1084.5203, 1177.6132, 1203.7062, 1279.7588, 1334.8743, 1343.6963, 1387.6852, 1427.7457, 1432.7631, 1448.8457, 1458.7144, 1547.7367, 1550.8322, 1619.0604, 1732.0898, 1950.9868, 1964.9956, 2010.0842, 2136.1001, 2150.1226, 2240.1355, 2322.1616, 2370.1550, 2370.1550, 2404.2458, 2408.2378, 2420.2344, 2436.2371, 2436.2371, 2492.2673, 2533.3164, 2565.2500, 2715.3198, 2723.3972, 2730.3013, 2824.3169, 2922.3699, 2974.5173, 2989.5088, 3349.6150

2. gi|939932 **Mass:** 9904 **Score:** 65 **Expect:** 0.22 **Queries matched:** 3

allergen Lol p II [Lolium perenne]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
737.3999	736.3926	736.3656	0.0270	60	65	0	---	GPFNFR
1405.7593	1404.7520	1404.7513	0.0007	54	65	1	52	SDKPLKGPFNFR
1405.7593	1404.7520	1404.7513	0.0007	54	65	1	---	SDKPLKGPFNFR

No match to: 713.3977, 724.4877, 734.4918, 736.4785, 750.5066, 768.5120, 782.4661, 838.5152, 848.5374, 864.5350, 866.5280, 983.4835, 1007.6586, 1049.4784, 1084.5203, 1084.5203, 1163.6118, 1177.6132, 1203.7062, 1279.7588, 1334.8743, 1343.6963, 1365.6533, 1365.6533, 1387.6852, 1427.7457, 1432.7631, 1448.8457, 1458.7144, 1547.7367,

1550.8322, 1619.0604, 1725.8275, 1732.0898, 1950.9868, 1964.9956, 2010.0842, 2136.1001, 2150.1226, 2240.1355, 2322.1616, 2370.1550, 2370.1550, 2404.2458, 2408.2378, 2420.2344, 2436.2371, 2436.2371, 2492.2673, 2533.3164, 2565.2500, 2715.3198, 2723.3972, 2730.3013, 2824.3169, 2922.3699, 2974.5173, 2989.5088, 3349.6150

3. gi|1093120 **Mass:** 22584 **Score:** 64 **Expect:** 0.23 **Queries matched:** 4

allergen Dac g II

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
737.3999	736.3926	736.3656	0.0270	64	-	69	0	---	GPFNFR
1163.6118	1162.6045	1162.6709	-0.0664	16	-	25	1	---	NLALSIKYNK
1405.7593	1404.7520	1404.7513	0.0007	58	-	69	1	52	SDKPLKGPFNFR
1405.7593	1404.7520	1404.7513	0.0007	58	-	69	1	---	SDKPLKGPFNFR

No match to: 713.3977, 724.4877, 734.4918, 736.4785, 750.5066, 768.5120, 782.4661, 838.5152, 848.5374, 864.5350, 866.5280, 983.4835, 1007.6586, 1049.4784, 1084.5203, 1084.5203, 1177.6132, 1203.7062, 1279.7588, 1334.8743, 1343.6963, 1365.6533, 1365.6533, 1387.6852, 1427.7457, 1432.7631, 1448.8457, 1458.7144, 1547.7367, 1550.8322, 1619.0604, 1725.8275, 1732.0898, 1950.9868, 1964.9956, 2010.0842, 2136.1001, 2150.1226, 2240.1355, 2322.1616, 2370.1550, 2370.1550, 2404.2458, 2408.2378, 2420.2344, 2436.2371, 2436.2371, 2492.2673, 2533.3164, 2565.2500, 2715.3198, 2723.3972, 2730.3013, 2824.3169, 2922.3699, 2974.5173, 2989.5088, 3349.6150

4. gi|125601952 **Mass:** 34446 **Score:** 55 **Expect:** 2.2 **Queries matched:** 9

hypothetical protein OsJ_25784 [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1049.4784	1048.4711	1048.4978	-0.0266	2	-	9	0	---	SDPELFWR
1163.6118	1162.6045	1162.5771	0.0274	224	-	232	0	---	TITWVDWSR
2136.1001	2135.0928	2135.1336	-0.0408	276	-	295	1	---	KFAPSALGPLMNLTSTILDF
2240.1355	2239.1282	2239.0981	0.0302	240	-	259	1	---	YGASNISEEFIQAIRNNGTR
2370.1550	2369.1477	2369.1875	-0.0398	233	-	254	1	---	GGPHPARYGASNISEEFIQAIR
2370.1550	2369.1477	2369.1875	-0.0398	233	-	254	1	---	GGPHPARYGASNISEEFIQAIR
2436.2371	2435.2298	2435.2174	0.0124	46	-	65	1	---	FFRGHHGLYSVYVHTLPDYK
2436.2371	2435.2298	2435.2174	0.0124	46	-	65	1	---	FFRGHHGLYSVYVHTLPDYK
2723.3972	2722.3899	2722.3213	0.0686	1	-	23	1	---	MSDPELFWRASLVPVADDFPFQR

No match to: 713.3977, 724.4877, 734.4918, 736.4785, 737.3999, 750.5066, 768.5120, 782.4661, 838.5152, 848.5374, 864.5350, 866.5280, 983.4835, 1007.6586, 1084.5203, 1084.5203, 1177.6132, 1203.7062, 1279.7588, 1334.8743, 1343.6963, 1365.6533, 1365.6533, 1387.6852, 1405.7593, 1405.7593, 1427.7457, 1432.7631, 1448.8457, 1458.7144, 1547.7367, 1550.8322, 1619.0604, 1725.8275, 1732.0898, 1950.9868, 1964.9956, 2010.0842, 2150.1226, 2322.1616, 2404.2458, 2408.2378, 2420.2344, 2492.2673, 2533.3164, 2565.2500, 2715.3198, 2730.3013, 2824.3169, 2922.3699, 2974.5173, 2989.5088, 3349.6150

5. gi|8177719 **Mass:** 57406 **Score:** 49 **Expect:** 8 **Queries matched:** 9

fiddlehead protein [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1177.6132	1176.6059	1176.5696	0.0364	364	-	374	0	---	DLMEVGGEALK + Oxidation (M)
1458.7144	1457.7071	1457.6310	0.0761	346	-	357	0	---	SVYQEEDEQGFK
2240.1355	2239.1282	2239.1007	0.0275	190	-	209	1	---	EGREEASTVIFGALDELFEK

2404.2458	2403.2385	2403.1950	0.0435	455 - 475	1	---	VVLEELQKNLGLSEENMEASR + Oxidation (M)
2436.2371	2435.2298	2435.2300	-0.0002	245 - 268	0	---	GNILSYNLGGMGCSAGIIAIDLAR
2436.2371	2435.2298	2435.2300	-0.0002	245 - 268	0	---	GNILSYNLGGMGCSAGIIAIDLAR
2723.3972	2722.3899	2722.3716	0.0183	243 - 268	1	---	MRGNILSYNLGGMGCSAGIIAIDLAR
2824.3169	2823.3096	2823.2995	0.0101	476 - 499	1	---	MTLHRFGNTSSSGIWYELAYMEAK + 2 Oxidation (M)
2974.5173	2973.5100	2973.5091	0.0009	216 - 242	0	---	DVGVLVVNCSIFNPTPSLSAMVINHYK

No match to: 713.3977, 724.4877, 734.4918, 736.4785, 737.3999, 750.5066, 768.5120, 782.4661, 838.5152, 848.5374, 864.5350, 866.5280, 983.4835, 1007.6586, 1049.4784, 1084.5203, 1084.5203, 1163.6118, 1203.7062, 1279.7588, 1334.8743, 1343.6963, 1365.6533, 1365.6533, 1387.6852, 1405.7593, 1405.7593, 1427.7457, 1432.7631, 1448.8457, 1547.7367, 1550.8322, 1619.0604, 1725.8275, 1732.0898, 1950.9868, 1964.9956, 2010.0842, 2136.1001, 2150.1226, 2322.1616, 2370.1550, 2370.1550, 2408.2378, 2420.2344, 2492.2673, 2533.3164, 2565.2500, 2715.3198, 2730.3013, 2922.3699, 2989.5088, 3349.6150

6. gi|1171011 **Mass:** 13912 **Score:** 48 **Expect:** 8.8 **Queries matched:** 5

RecName: Full=Pollen allergen Phl p 6; AltName: Full=Allergen Phl p VI; AltName: Allergen=Phl p 6;

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1163.6118	1162.6045	1162.5982	0.0063	32 -	41	0	---	LIEDVNASFR
1343.6963	1342.6890	1342.6880	0.0010	58 -	69	1	---	TFEAAFTVSSKR
1550.8322	1549.8249	1549.8827	-0.0578	70 -	84	1	---	NLADAVSKAPQLVPK
1950.9868	1949.9795	1949.9694	0.0102	25 -	41	1	---	ATTEEQKLIEDVNASFR
2989.5088	2988.5015	2988.5840	-0.0825	2 -	31	1	---	VAMFLAVAVVLGLATSPTAEGGKATTEEQK

No match to: 713.3977, 724.4877, 734.4918, 736.4785, 737.3999, 750.5066, 768.5120, 782.4661, 838.5152, 848.5374, 864.5350, 866.5280, 983.4835, 1007.6586, 1049.4784, 1084.5203, 1084.5203, 1177.6132, 1203.7062, 1279.7588, 1334.8743, 1365.6533, 1365.6533, 1387.6852, 1405.7593, 1405.7593, 1427.7457, 1432.7631, 1448.8457, 1458.7144, 1547.7367, 1619.0604, 1725.8275, 1732.0898, 1964.9956, 2010.0842, 2136.1001, 2150.1226, 2240.1355, 2322.1616, 2370.1550, 2370.1550, 2404.2458, 2408.2378, 2420.2344, 2436.2371, 2436.2371, 2492.2673, 2533.3164, 2565.2500, 2715.3198, 2723.3972, 2730.3013, 2824.3169, 2922.3699, 2974.5173, 3349.6150

7. gi|113205238 **Mass:** 51344 **Score:** 47 **Expect:** 11 **Queries matched:** 8

WD domain containing protein, putative [Solanum demissum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
864.5350	863.5277	863.4864	0.0413	4 -	10	1	---	RLDLYGK
1343.6963	1342.6890	1342.7568	-0.0678	74 -	86	1	---	KIITASADGQLAR
1427.7457	1426.7384	1426.8143	-0.0759	102 -	114	1	---	LGLVLENGRVETK
1458.7144	1457.7071	1457.6569	0.0503	205 -	216	1	---	MYQLDARTSSDR + Oxidation (M)
1725.8275	1724.8202	1724.9171	-0.0969	87 -	101	0	---	TLYSVDTLFLPAMVR
2150.1226	2149.1153	2149.0772	0.0381	386 -	403	1	---	EDHSRVTLTPDMIMHVLR
2723.3972	2722.3899	2722.3636	0.0264	359 -	382	1	---	LWAPTSKDVTPLPPDVQEIMEANR + Oxidation (M)
3349.6150	3348.6077	3348.6236	-0.0159	123 -	151	1	---	VHKLAVEPGSPYILYSCGEDGFVQHYDLR

No match to: 713.3977, 724.4877, 734.4918, 736.4785, 737.3999, 750.5066, 768.5120, 782.4661, 838.5152, 848.5374, 866.5280, 983.4835, 1007.6586, 1049.4784, 1084.5203, 1084.5203, 1163.6118, 1177.6132, 1203.7062, 1279.7588, 1334.8743, 1365.6533, 1365.6533, 1387.6852, 1405.7593, 1405.7593, 1432.7631, 1448.8457, 1547.7367, 1550.8322, 1619.0604, 1732.0898, 1950.9868, 1964.9956, 2010.0842, 2136.1001, 2240.1355, 2322.1616, 2370.1550, 2370.1550, 2404.2458, 2408.2378, 2420.2344, 2436.2371, 2436.2371, 2492.2673, 2533.3164, 2565.2500, 2715.3198, 2730.3013,

2824.3169, 2922.3699, 2974.5173, 2989.5088

8. gi|15225270 **Mass:** 62435 **Score:** 47 **Expect:** 12 **Queries matched:** 9

KCS10 (3-KETOACYL-COA SYNTHASE 10); acyltransferase/ catalytic/ transferase, transferring acyl grou

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1177.6132	1176.6059	1176.5696	0.0364	364	374	0	---	DLMEVGGEALK + Oxidation (M)
1458.7144	1457.7071	1457.6310	0.0761	346	357	0	---	SVYQEEDEQGFK
2240.1355	2239.1282	2239.1007	0.0275	190	209	1	---	EGREEASTVIFGALDELFEK
2404.2458	2403.2385	2403.1950	0.0435	455	475	1	---	VVLEELQKNLGLSEENMEASR + Oxidation (M)
2436.2371	2435.2298	2435.2300	-0.0002	245	268	0	---	GNILSYNLGGMGCSAGIIAIDLAR
2436.2371	2435.2298	2435.2300	-0.0002	245	268	0	---	GNILSYNLGGMGCSAGIIAIDLAR
2723.3972	2722.3899	2722.3716	0.0183	243	268	1	---	MRGNILSYNLGGMGCSAGIIAIDLAR
2824.3169	2823.3096	2823.2995	0.0101	476	499	1	---	MTLHRFGNTSSSGIWYELAYMEAK + 2 Oxidation (M)
2974.5173	2973.5100	2973.5091	0.0009	216	242	0	---	DVGVLVVNCSIFNPTPSLSAMVINHYK

No match to: 713.3977, 724.4877, 734.4918, 736.4785, 737.3999, 750.5066, 768.5120, 782.4661, 838.5152, 848.5374, 864.5350, 866.5280, 983.4835, 1007.6586, 1049.4784, 1084.5203, 1084.5203, 1163.6118, 1203.7062, 1279.7588, 1334.8743, 1343.6963, 1365.6533, 1365.6533, 1387.6852, 1405.7593, 1405.7593, 1427.7457, 1432.7631, 1448.8457, 1547.7367, 1550.8322, 1619.0604, 1725.8275, 1732.0898, 1950.9868, 1964.9956, 2010.0842, 2136.1001, 2150.1226, 2322.1616, 2370.1550, 2370.1550, 2408.2378, 2420.2344, 2492.2673, 2533.3164, 2565.2500, 2715.3198, 2730.3013, 2922.3699, 2989.5088, 3349.6150

9. gi|8177711 **Mass:** 62493 **Score:** 47 **Expect:** 12 **Queries matched:** 9

fiddlehead protein [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1177.6132	1176.6059	1176.5696	0.0364	364	374	0	---	DLMEVGGEALK + Oxidation (M)
1458.7144	1457.7071	1457.6310	0.0761	346	357	0	---	SVYQEEDEQGFK
2240.1355	2239.1282	2239.1007	0.0275	190	209	1	---	EGREEASTVIFGALDELFEK
2404.2458	2403.2385	2403.1950	0.0435	455	475	1	---	VVLEELQKNLGLSEENMEASR + Oxidation (M)
2436.2371	2435.2298	2435.2300	-0.0002	245	268	0	---	GNILSYNLGGMGCSAGIIAIDLAR
2436.2371	2435.2298	2435.2300	-0.0002	245	268	0	---	GNILSYNLGGMGCSAGIIAIDLAR
2723.3972	2722.3899	2722.3716	0.0183	243	268	1	---	MRGNILSYNLGGMGCSAGIIAIDLAR
2824.3169	2823.3096	2823.2995	0.0101	476	499	1	---	MTLHRFGNTSSSGIWYELAYMEAK + 2 Oxidation (M)
2974.5173	2973.5100	2973.5091	0.0009	216	242	0	---	DVGVLVVNCSIFNPTPSLSAMVINHYK

No match to: 713.3977, 724.4877, 734.4918, 736.4785, 737.3999, 750.5066, 768.5120, 782.4661, 838.5152, 848.5374, 864.5350, 866.5280, 983.4835, 1007.6586, 1049.4784, 1084.5203, 1084.5203, 1163.6118, 1203.7062, 1279.7588, 1334.8743, 1343.6963, 1365.6533, 1365.6533, 1387.6852, 1405.7593, 1405.7593, 1427.7457, 1432.7631, 1448.8457, 1547.7367, 1550.8322, 1619.0604, 1725.8275, 1732.0898, 1950.9868, 1964.9956, 2010.0842, 2136.1001, 2150.1226, 2322.1616, 2370.1550, 2370.1550, 2408.2378, 2420.2344, 2492.2673, 2533.3164, 2565.2500, 2715.3198, 2730.3013, 2922.3699, 2989.5088, 3349.6150

10. gi|147797628 **Mass:** 94104 **Score:** 47 **Expect:** 13 **Queries matched:** 14

hypothetical protein [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide

737.3999	736.3926	736.3616	0.0310	731 - 735	1	---	RYNER
848.5374	847.5301	847.4738	0.0563	56 - 61	1	---	WIMRVK + Oxidation (M)
1049.4784	1048.4711	1048.4106	0.0605	308 - 315	0	---	DHMMEWGK + Oxidation (M)
1177.6132	1176.6059	1176.6424	-0.0364	298 - 307	1	---	ELALTKDLMK + Oxidation (M)
1365.6533	1364.6460	1364.6459	0.0001	154 - 165	0	---	SEDVNEDLFGLK
1365.6533	1364.6460	1364.6459	0.0001	154 - 165	0	9	SEDVNEDLFGLK
1405.7593	1404.7520	1404.6997	0.0523	64 - 76	0	---	WTLVQVDSSASGR
1405.7593	1404.7520	1404.6997	0.0523	64 - 76	0	---	WTLVQVDSSASGR
1432.7631	1431.7558	1431.6630	0.0928	745 - 756	0	---	DLDDSNEWLIGR
1458.7144	1457.7071	1457.6431	0.0640	543 - 554	0	---	NPMGYIYEAMNR
2136.1001	2135.0928	2135.1374	-0.0446	631 - 649	1	---	QEKVVAEVSLFTNAQGLFR
2436.2371	2435.2298	2435.2095	0.0203	661 - 682	1	---	APAEWWVAYGASAPNLQKFAMK
2436.2371	2435.2298	2435.2095	0.0203	661 - 682	1	---	APAEWWVAYGASAPNLQKFAMK
2922.3699	2921.3626	2921.4159	-0.0533	332 - 357	1	---	TLVNFLVNCSKGTMFMQSIDASSMIK

No match to: 713.3977, 724.4877, 734.4918, 736.4785, 750.5066, 768.5120, 782.4661, 838.5152, 864.5350, 866.5280, 983.4835, 1007.6586, 1084.5203, 1084.5203, 1163.6118, 1203.7062, 1279.7588, 1334.8743, 1343.6963, 1387.6852, 1427.7457, 1448.8457, 1547.7367, 1550.8322, 1619.0604, 1725.8275, 1732.0898, 1950.9868, 1964.9956, 2010.0842, 2150.1226, 2240.1355, 2322.1616, 2370.1550, 2370.1550, 2404.2458, 2408.2378, 2420.2344, 2492.2673, 2533.3164, 2565.2500, 2715.3198, 2723.3972, 2730.3013, 2824.3169, 2974.5173, 2989.5088, 3349.6150

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 62

Protein View

Match to: **gi|126386** Score: **139** Expect: **7.6e-009**
RecName: Full=Pollen allergen Lol p 2-A; AltName: Full=Allergen Lol p II-A; AltName: Allergen=Lol p

Nominal mass (M_r): **10873**; Calculated pI value: **5.25**
NCBI BLAST search of gi|126386 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Lolium perenne

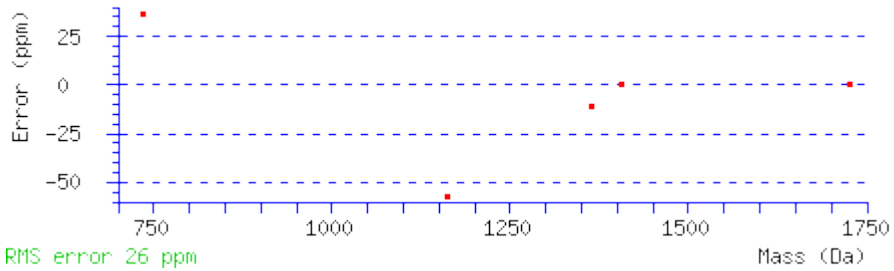
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **38%**

Matched peptides shown in **Bold Red**

```
     1 AAPVEFTVEK GSDEKNLALS IKYNKEGDSM AEVELKEHGS NEWLALKKNG
    51 DGVWEIKSDK PLKGPFNFRF VSEKGMRNVF DDVVPADFKV GTTYKPE
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
16 - 25	1163.6118	1162.6045	1162.6709	-0.0664	1	NLALSIKYNK (No match)
58 - 69	1405.7593	1404.7520	1404.7513	0.0007	1	SDKPLKGPFNFR (Ions score 52)
58 - 69	1405.7593	1404.7520	1404.7513	0.0007	1	SDKPLKGPFNFR (No match)
64 - 69	737.3999	736.3926	736.3656	0.0270	0	GPFNFR (No match)
75 - 89	1725.8275	1724.8202	1724.8191	0.0011	1	GMRNVFDDVVPADFK Oxidation (M) (No match)
78 - 89	1365.6533	1364.6460	1364.6612	-0.0151	0	NVFDDVVPADFK (No match)
78 - 89	1365.6533	1364.6460	1364.6612	-0.0151	0	NVFDDVVPADFK (Ions score 42)



Spot 134

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	Accession	Mass	Score	Description
1.	gi|1171011	13912	278	RecName: Full=Pollen allergen Phl p 6; AltName: Full=Allergen Phl p VI; AltName: Allergen=Phl
2.	gi|3004467	14597	275	Phl p6 allergen [Phleum pratense]
3.	gi|28374059	11914	264	Chain A, Crystal Structure Of Phl P 6, A Major Timothy Grass Pollen Allergen Co-Crystallized W
4.	gi|3004465	14592	108	Phl p6 allergen [Phleum pratense]
5.	gi|3004471	8622	63	Phl p6 IgE binding fragment [Phleum pratense]
6.	gi|18406207	38945	59	unknown protein [Arabidopsis thaliana]
7.	gi|3004469	11392	53	Phl p6 IgE binding fragment [Phleum pratense]
8.	gi|16226903	38911	48	At2g43320/T1O24.6 [Arabidopsis thaliana]
9.	gi|255561576	66762	48	Patellin-5, putative [Ricinus communis]
10.	gi|164652459	50220	46	maturase K [Gymnosporia haberiana]

Results List

1. gi|1171011 **Mass:** 13912 **Score:** 278 **Expect:** 9.6e-023 **Queries matched:** 12

RecName: Full=Pollen allergen Phl p 6; AltName: Full=Allergen Phl p VI; AltName: Allergen=Phl p 6;

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1163.6111	1162.6038	1162.5982	0.0056	32	41	0	---	LIEDVNASFR
1343.7012	1342.6939	1342.6880	0.0059	58	69	1	46	TFEAAFTVSSKR
1343.7012	1342.6939	1342.6880	0.0059	58	69	1	---	TFEAAFTVSSKR
1459.8252	1458.8179	1458.8194	-0.0015	118	132	0	---	IIAGTPEVHAVKPGA
1550.8914	1549.8841	1549.8827	0.0014	70	84	1	---	NLADAVSKAPQLVPK
1648.8354	1647.8281	1647.8290	-0.0009	42	57	1	---	AAMATTANVPPADKYK
1664.8409	1663.8336	1663.8239	0.0097	42	57	1	---	AAMATTANVPPADKYK + Oxidation (M)
1950.9860	1949.9787	1949.9694	0.0094	25	41	1	136	ATTEEQKLIEDVNASFR
1950.9860	1949.9787	1949.9694	0.0094	25	41	1	---	ATTEEQKLIEDVNASFR
2502.2671	2501.2598	2501.2583	0.0015	32	55	1	---	LIEDVNASFRAAMATTANVPPADK
2989.5298	2988.5225	2988.5840	-0.0615	2	31	1	---	VAMFLAVAVVLGLATSPTAEGGKATTEEQK
2989.5298	2988.5225	2988.5840	-0.0615	2	31	1	---	VAMFLAVAVVLGLATSPTAEGGKATTEEQK

No match to: 713.4043, 724.4903, 734.4902, 750.5148, 768.5184, 782.4753, 848.5289, 864.5387, 1177.6243, 1279.7635, 1334.8839, 1387.6929, 1388.7482, 1405.7688, 1432.7742, 1439.7451, 1448.8052, 1634.8640, 1654.8743, 1678.8563, 1707.0027, 1732.1019, 1965.0051, 1972.9658, 2136.1025, 2150.1189, 2231.2253, 2298.1567, 2304.1541, 2305.6213, 2321.1448, 2322.1646, 2322.1646, 2336.1838, 2382.0471, 2384.0222, 2564.1963, 2663.3906, 2790.3083, 2825.3171, 2928.2068, 2973.5183, 2973.5183, 3018.5188, 3033.5247, 3332.6077, 3348.5967

2. gi|3004467 **Mass:** 14597 **Score:** 275 **Expect:** 1.9e-022 **Queries matched:** 11

Phl p6 allergen [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1163.6111	1162.6038	1162.5982	0.0056	38	47	0	---	LIEDVNASFR

1343.7012	1342.6939	1342.6880	0.0059	64 - 75	1	46	TFEAAFTVSSKR
1343.7012	1342.6939	1342.6880	0.0059	64 - 75	1	---	TFEAAFTVSSKR
1459.8252	1458.8179	1458.8194	-0.0015	124 - 138	0	---	IIAGTPEVHAVKPGA
1550.8914	1549.8841	1549.8827	0.0014	76 - 90	1	---	NLADAVSKAPQLVPK
1648.8354	1647.8281	1647.8290	-0.0009	48 - 63	1	---	AAMATTANVPPADKYK
1664.8409	1663.8336	1663.8239	0.0097	48 - 63	1	---	AAMATTANVPPADKYK + Oxidation (M)
1950.9860	1949.9787	1949.9694	0.0094	31 - 47	1	136	ATTEEQKLIEDVNASFR
1950.9860	1949.9787	1949.9694	0.0094	31 - 47	1	---	ATTEEQKLIEDVNASFR
2502.2671	2501.2598	2501.2583	0.0015	38 - 61	1	---	LIEDVNASFRAAMATTANVPPADK
3018.5188	3017.5115	3017.5903	-0.0788	1 - 30	1	---	MAAHKFMVAMFLAVAVVLGLATSPTAEGGK

No match to: 713.4043, 724.4903, 734.4902, 750.5148, 768.5184, 782.4753, 848.5289, 864.5387, 1177.6243, 1279.7635, 1334.8839, 1387.6929, 1388.7482, 1405.7688, 1432.7742, 1439.7451, 1448.8052, 1634.8640, 1654.8743, 1678.8563, 1707.0027, 1732.1019, 1965.0051, 1972.9658, 2136.1025, 2150.1189, 2231.2253, 2298.1567, 2304.1541, 2305.6213, 2321.1448, 2322.1646, 2322.1646, 2336.1838, 2382.0471, 2384.0222, 2564.1963, 2663.3906, 2790.3083, 2825.3171, 2928.2068, 2973.5183, 2973.5183, 2989.5298, 2989.5298, 3033.5247, 3332.6077, 3348.5967

3. gi|28374059 **Mass:** 11914 **Score:** 264 **Expect:** 2.4e-021 **Queries matched:** 10

Chain A, Crystal Structure Of Phl P 6, A Major Timothy Grass Pollen Allergen Co-Crystallized With Z

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1163.6111	1162.6038	1162.5982	0.0056	11 -	20	0	---	LIEDVNASFR
1343.7012	1342.6939	1342.6880	0.0059	37 -	48	1	46	TFEAAFTVSSKR
1343.7012	1342.6939	1342.6880	0.0059	37 -	48	1	---	TFEAAFTVSSKR
1459.8252	1458.8179	1458.8194	-0.0015	97 -	111	0	---	IIAGTPEVHAVKPGA
1550.8914	1549.8841	1549.8827	0.0014	49 -	63	1	---	NLADAVSKAPQLVPK
1648.8354	1647.8281	1647.8290	-0.0009	21 -	36	1	---	AAMATTANVPPADKYK
1664.8409	1663.8336	1663.8239	0.0097	21 -	36	1	---	AAMATTANVPPADKYK + Oxidation (M)
1950.9860	1949.9787	1949.9694	0.0094	4 -	20	1	136	ATTEEQKLIEDVNASFR
1950.9860	1949.9787	1949.9694	0.0094	4 -	20	1	---	ATTEEQKLIEDVNASFR
2502.2671	2501.2598	2501.2583	0.0015	11 -	34	1	---	LIEDVNASFRAAMATTANVPPADK

No match to: 713.4043, 724.4903, 734.4902, 750.5148, 768.5184, 782.4753, 848.5289, 864.5387, 1177.6243, 1279.7635, 1334.8839, 1387.6929, 1388.7482, 1405.7688, 1432.7742, 1439.7451, 1448.8052, 1634.8640, 1654.8743, 1678.8563, 1707.0027, 1732.1019, 1965.0051, 1972.9658, 2136.1025, 2150.1189, 2231.2253, 2298.1567, 2304.1541, 2305.6213, 2321.1448, 2322.1646, 2322.1646, 2336.1838, 2382.0471, 2384.0222, 2564.1963, 2663.3906, 2790.3083, 2825.3171, 2928.2068, 2973.5183, 2973.5183, 2989.5298, 2989.5298, 3018.5188, 3033.5247, 3332.6077, 3348.5967

4. gi|3004465 **Mass:** 14592 **Score:** 108 **Expect:** 9.6e-006 **Queries matched:** 8

Phl p6 allergen [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1177.6243	1176.6170	1176.6138	0.0032	38 -	47	0	---	LIEDINASFR
1343.7012	1342.6939	1342.6880	0.0059	64 -	75	1	46	TFEAAFTVSSKR
1343.7012	1342.6939	1342.6880	0.0059	64 -	75	1	---	TFEAAFTVSSKR
1550.8914	1549.8841	1549.8827	0.0014	76 -	90	1	---	NLADAVSKAPQLVPK
1648.8354	1647.8281	1647.8290	-0.0009	48 -	63	1	---	AAMATTANVPPADKYK

1664.8409	1663.8336	1663.8239	0.0097	48 - 63	1	---	AAMATTANVPPADKYK + Oxidation (M)
1965.0051	1963.9978	1963.9850	0.0128	31 - 47	1	---	ATTEEQKLIEDINASFR
3018.5188	3017.5115	3017.5903	-0.0788	1 - 30	1	---	MAAHKFMVAMFLAVAVVLGLATSPTAEGGK

No match to: 713.4043, 724.4903, 734.4902, 750.5148, 768.5184, 782.4753, 848.5289, 864.5387, 1163.6111, 1279.7635, 1334.8839, 1387.6929, 1388.7482, 1405.7688, 1432.7742, 1439.7451, 1448.8052, 1459.8252, 1634.8640, 1654.8743, 1678.8563, 1707.0027, 1732.1019, 1950.9860, 1950.9860, 1972.9658, 2136.1025, 2150.1189, 2231.2253, 2298.1567, 2304.1541, 2305.6213, 2321.1448, 2322.1646, 2322.1646, 2336.1838, 2382.0471, 2384.0222, 2502.2671, 2564.1963, 2663.3906, 2790.3083, 2825.3171, 2928.2068, 2973.5183, 2973.5183, 2989.5298, 2989.5298, 3033.5247, 3332.6077, 3348.5967

5. gi|3004471 **Mass:** 8622 **Score:** 63 **Expect:** 0.28 **Queries matched:** 3

Phl p6 IgE binding fragment [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1343.7012	1342.6939	1342.6880	0.0059	6 -	17	1	46	TFEAAFTVSSKR
1343.7012	1342.6939	1342.6880	0.0059	6 -	17	1	---	TFEAAFTVSSKR
1550.8914	1549.8841	1549.8827	0.0014	18 -	32	1	---	NLADAVSKAPQLVPK

No match to: 713.4043, 724.4903, 734.4902, 750.5148, 768.5184, 782.4753, 848.5289, 864.5387, 1163.6111, 1177.6243, 1279.7635, 1334.8839, 1387.6929, 1388.7482, 1405.7688, 1432.7742, 1439.7451, 1448.8052, 1459.8252, 1634.8640, 1648.8354, 1654.8743, 1664.8409, 1678.8563, 1707.0027, 1732.1019, 1950.9860, 1950.9860, 1965.0051, 1972.9658, 2136.1025, 2150.1189, 2231.2253, 2298.1567, 2304.1541, 2305.6213, 2321.1448, 2322.1646, 2322.1646, 2336.1838, 2382.0471, 2384.0222, 2502.2671, 2564.1963, 2663.3906, 2790.3083, 2825.3171, 2928.2068, 2973.5183, 2973.5183, 2989.5298, 2989.5298, 3018.5188, 3033.5247, 3332.6077, 3348.5967

6. gi|18406207 **Mass:** 38945 **Score:** 59 **Expect:** 0.78 **Queries matched:** 9

unknown protein [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
864.5387	863.5314	863.5480	-0.0166	289 -	295	1	---	LYSLIKK
1163.6111	1162.6038	1162.5618	0.0420	339 -	347	1	---	ETTDRDIWK
1459.8252	1458.8179	1458.8082	0.0098	91 -	103	0	---	SWESSVVLVNVLK
1654.8743	1653.8670	1653.8370	0.0300	296 -	309	0	---	CLRPPYGVMYLAAK + Oxidation (M)
2136.1025	2135.0952	2135.1343	-0.0391	1 -	19	1	---	MRAPSLLAQCLPGLLPQDR
2150.1189	2149.1116	2149.1175	-0.0059	117 -	135	1	---	RVLELGCNFGVPGIFACLK
2322.1646	2321.1573	2321.2855	-0.1282	29 -	49	1	---	DLQLPTPAVEIIPSKTVAHHR
2322.1646	2321.1573	2321.2855	-0.1282	29 -	49	1	---	DLQLPTPAVEIIPSKTVAHHR
2825.3171	2824.3098	2824.4758	-0.1660	182 -	206	1	---	QAISASVRFYAGEWEELSTVLSIIR

No match to: 713.4043, 724.4903, 734.4902, 750.5148, 768.5184, 782.4753, 848.5289, 1177.6243, 1279.7635, 1334.8839, 1343.7012, 1343.7012, 1387.6929, 1388.7482, 1405.7688, 1432.7742, 1439.7451, 1448.8052, 1550.8914, 1634.8640, 1648.8354, 1664.8409, 1678.8563, 1707.0027, 1732.1019, 1950.9860, 1950.9860, 1965.0051, 1972.9658, 2231.2253, 2298.1567, 2304.1541, 2305.6213, 2321.1448, 2336.1838, 2382.0471, 2384.0222, 2502.2671, 2564.1963, 2663.3906, 2790.3083, 2928.2068, 2973.5183, 2973.5183, 2989.5298, 2989.5298, 3018.5188, 3033.5247, 3332.6077, 3348.5967

7. gi|3004469 **Mass:** 11392 **Score:** 53 **Expect:** 3.1 **Queries matched:** 6

Phl p6 IgE binding fragment [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1163.6111	1162.6038	1162.5982	0.0056	6	15	0	---	LIEDVNASFR
1459.8252	1458.8179	1458.8194	-0.0015	92	106	0	---	IIAGTPEVHAVKPGA
1550.8914	1549.8841	1549.8827	0.0014	44	58	1	---	NLADAVSKAPQLVPK
1648.8354	1647.8281	1647.8290	-0.0009	16	31	1	---	AAMATTANVPPADKYK
1664.8409	1663.8336	1663.8239	0.0097	16	31	1	---	AAMATTANVPPADKYK + Oxidation (M)
2502.2671	2501.2598	2501.2583	0.0015	6	29	1	---	LIEDVNASFRAAMATTANVPPADK

No match to: 713.4043, 724.4903, 734.4902, 750.5148, 768.5184, 782.4753, 848.5289, 864.5387, 1177.6243, 1279.7635, 1334.8839, 1343.7012, 1343.7012, 1387.6929, 1388.7482, 1405.7688, 1432.7742, 1439.7451, 1448.8052, 1634.8640, 1654.8743, 1678.8563, 1707.0027, 1732.1019, 1950.9860, 1950.9860, 1965.0051, 1972.9658, 2136.1025, 2150.1189, 2231.2253, 2298.1567, 2304.1541, 2305.6213, 2321.1448, 2322.1646, 2322.1646, 2336.1838, 2382.0471, 2384.0222, 2564.1963, 2663.3906, 2790.3083, 2825.3171, 2928.2068, 2973.5183, 2973.5183, 2989.5298, 2989.5298, 3018.5188, 3033.5247, 3332.6077, 3348.5967

8. gi|16226903 **Mass:** 38911 **Score:** 48 **Expect:** 9.6 **Queries matched:** 8

At2g43320/T1O24.6 [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
864.5387	863.5314	863.5480	-0.0166	289	295	1	---	LYSLIKK
1163.6111	1162.6038	1162.5618	0.0420	339	347	1	---	ETTDRDIWK
1459.8252	1458.8179	1458.8082	0.0098	91	103	0	---	SWESSVVLVNVLK
1654.8743	1653.8670	1653.8370	0.0300	296	309	0	---	CLRPPYGVMYLAAK + Oxidation (M)
2136.1025	2135.0952	2135.1343	-0.0391	1	19	1	---	MRAPSLLAQCLPGLLPQDR
2322.1646	2321.1573	2321.2855	-0.1282	29	49	1	---	DLQLPTPAVEIIPSKTVAHHR
2322.1646	2321.1573	2321.2855	-0.1282	29	49	1	---	DLQLPTPAVEIIPSKTVAHHR
2825.3171	2824.3098	2824.4758	-0.1660	182	206	1	---	QAISASVRFYAGEWEELSTVLSIIR

No match to: 713.4043, 724.4903, 734.4902, 750.5148, 768.5184, 782.4753, 848.5289, 1177.6243, 1279.7635, 1334.8839, 1343.7012, 1343.7012, 1387.6929, 1388.7482, 1405.7688, 1432.7742, 1439.7451, 1448.8052, 1550.8914, 1634.8640, 1648.8354, 1664.8409, 1678.8563, 1707.0027, 1732.1019, 1950.9860, 1950.9860, 1965.0051, 1972.9658, 2150.1189, 2231.2253, 2298.1567, 2304.1541, 2305.6213, 2321.1448, 2336.1838, 2382.0471, 2384.0222, 2502.2671, 2564.1963, 2663.3906, 2790.3083, 2928.2068, 2973.5183, 2973.5183, 2989.5298, 2989.5298, 3018.5188, 3033.5247, 3332.6077, 3348.5967

9. gi|255561576 **Mass:** 66762 **Score:** 48 **Expect:** 11 **Queries matched:** 9

Patellin-5, putative [Ricinus communis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1387.6929	1386.6856	1386.6877	-0.0021	101	113	0	---	EEVVVDEVDVAGK
1459.8252	1458.8179	1458.7354	0.0825	53	66	0	---	EVSPPPPAPPQESK
1654.8743	1653.8670	1653.8766	-0.0095	439	453	1	---	FVFAGPSKSPETLFK
1950.9860	1949.9787	1950.0098	-0.0310	362	379	0	---	LDFSPGGISTIFQVNDLK
1950.9860	1949.9787	1950.0098	-0.0310	362	379	0	---	LDFSPGGISTIFQVNDLK
2136.1025	2135.0952	2135.0157	0.0795	289	306	1	---	EFKIDELIDEDLGDDLEK
2321.1448	2320.1375	2320.1443	-0.0067	53	74	1	---	EVSPPPPAPPQESKSLAAMMEK
3018.5188	3017.5115	3017.4730	0.0386	155	181	1	---	NLVQEALNTHQFSSSPPPSPPQKEEEK

3033.5247	3032.5174	3032.3809	0.1365	307 - 331	1	---	IVFMHGHDREGHPVCYNVYGEFQNK

No match to: 713.4043, 724.4903, 734.4902, 750.5148, 768.5184, 782.4753, 848.5289, 864.5387, 1163.6111, 1177.6243, 1279.7635, 1334.8839, 1343.7012, 1343.7012, 1388.7482, 1405.7688, 1432.7742, 1439.7451, 1448.8052, 1550.8914, 1634.8640, 1648.8354, 1664.8409, 1678.8563, 1707.0027, 1732.1019, 1965.0051, 1972.9658, 2150.1189, 2231.2253, 2298.1567, 2304.1541, 2305.6213, 2322.1646, 2322.1646, 2336.1838, 2382.0471, 2384.0222, 2502.2671, 2564.1963, 2663.3906, 2790.3083, 2825.3171, 2928.2068, 2973.5183, 2973.5183, 2989.5298, 2989.5298, 3332.6077, 3348.5967

10. gi|164652459 **Mass:** 50220 **Score:** 46 **Expect:** 16 **Queries matched:** 8

maturase K [Gymnosporia haberiana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1432.7742	1431.7669	1431.7398	0.0272	126 -	137	0	---	SIHSIFPFLEDK
1439.7451	1438.7378	1438.7568	-0.0190	193 -	204	1	---	KSIYIFSQSNPR
1448.8052	1447.7979	1447.7612	0.0368	14 -	24	0	---	QHDFLYPLIFR
1654.8743	1653.8670	1653.8622	0.0048	281 -	294	1	---	FILASKDMPFLMNK
2825.3171	2824.3098	2824.4515	-0.1417	205 -	226	1	---	FFLFLYNSYVSEYESIFLFLRK
2973.5183	2972.5110	2972.3908	0.1202	63 -	86	1	---	MDQQNHLIISTNYSNQNLFFKCNK + Oxidation (M)
2973.5183	2972.5110	2972.3908	0.1202	63 -	86	1	---	MDQQNHLIISTNYSNQNLFFKCNK + Oxidation (M)
3332.6077	3331.6004	3331.6270	-0.0265	297 -	323	1	---	FYLVNLCQCHFFAGSQPERIYINQLSK

No match to: 713.4043, 724.4903, 734.4902, 750.5148, 768.5184, 782.4753, 848.5289, 864.5387, 1163.6111, 1177.6243, 1279.7635, 1334.8839, 1343.7012, 1343.7012, 1387.6929, 1388.7482, 1405.7688, 1459.8252, 1550.8914, 1634.8640, 1648.8354, 1664.8409, 1678.8563, 1707.0027, 1732.1019, 1950.9860, 1950.9860, 1965.0051, 1972.9658, 2136.1025, 2150.1189, 2231.2253, 2298.1567, 2304.1541, 2305.6213, 2321.1448, 2322.1646, 2322.1646, 2336.1838, 2382.0471, 2384.0222, 2502.2671, 2564.1963, 2663.3906, 2790.3083, 2928.2068, 2989.5298, 2989.5298, 3018.5188, 3033.5247, 3348.5967

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 59

Protein View

Match to: **gi|1171011** Score: **278** Expect: **9.6e-023**
RecName: Full=Pollen allergen Phl p 6; AltName: Full=Allergen Phl p VI; AltName: Allergen=Phl p 6;

Nominal mass (M_r): **13912**; Calculated pI value: **5.31**
NCBI BLAST search of gi|1171011 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|414712 from Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **74%**

Matched peptides shown in **Bold Red**

```
    1 MVAMFLAVAV VLGLATSPTA EGGKATTEEQ KLIEDVNASF RAAMATTANV
   51 PPADKYKTFE AAFTVSSKRN LADAVSKAPQ LVPKLDEVYN AAYNAADHAA
  101 PEDKYEAFVL HFSEALRIIA GTPEVHAVKP GA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
2 - 31	2989.5298	2988.5225	2988.5840	-0.0615	1	VAMFLAVAVVLGLATSPTAEGGKATTEEQK (No match)
2 - 31	2989.5298	2988.5225	2988.5840	-0.0615	1	VAMFLAVAVVLGLATSPTAEGGKATTEEQK (No match)
25 - 41	1950.9860	1949.9787	1949.9694	0.0094	1	ATTEEQKLIEDVNASFR (Ions score 136)
25 - 41	1950.9860	1949.9787	1949.9694	0.0094	1	ATTEEQKLIEDVNASFR (No match)
32 - 41	1163.6111	1162.6038	1162.5982	0.0056	0	LIEDVNASFR (No match)
32 - 55	2502.2671	2501.2598	2501.2583	0.0015	1	LIEDVNASFRAAMATTANVPPADK (No match)
42 - 57	1648.8354	1647.8281	1647.8290	-0.0009	1	AAMATTANVPPADKYK (No match)
42 - 57	1664.8409	1663.8336	1663.8239	0.0097	1	AAMATTANVPPADKYK Oxidation (M) (No match)
58 - 69	1343.7012	1342.6939	1342.6880	0.0059	1	TFEAAFTVSSKR (Ions score 46)
58 - 69	1343.7012	1342.6939	1342.6880	0.0059	1	TFEAAFTVSSKR (No match)
70 - 84	1550.8914	1549.8841	1549.8827	0.0014	1	NLADAVSKAPQLVPK (No match)
118 - 132	1459.8252	1458.8179	1458.8194	-0.0015	0	IIAGTPEVHAVKPGA (No match)

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	Accession	Mass	Score	Description
1.	gi|1171011	13912	203	RecName: Full=Pollen allergen Phl p 6; AltName: Full=Allergen Phl p VI; AltName: Allergen=Phl p
2.	gi|3004467	14597	201	Phl p6 allergen [Phleum pratense]
3.	gi|28374059	11914	188	Chain A, Crystal Structure Of Phl P 6, A Major Timothy Grass Pollen Allergen Co-Crystallized Wi
4.	gi|3004465	14592	56	Phl p6 allergen [Phleum pratense]
5.	gi|147862150	27700	44	hypothetical protein [Vitis vinifera]

Results List

1. gi|1171011 **Mass:** 13912 **Score:** 203 **Expect:** 3e-015 **Queries matched:** 9

RecName: Full=Pollen allergen Phl p 6; AltName: Full=Allergen Phl p VI; AltName: Allergen=Phl p 6;

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1163.6099	1162.6026	1162.5982	0.0044	32	41	0	---	LIEDVNASFR
1343.6970	1342.6897	1342.6880	0.0017	58	69	1	---	TFEAAFTVSSKR
1343.6970	1342.6897	1342.6880	0.0017	58	69	1	16	TFEAAFTVSSKR
1459.8254	1458.8181	1458.8194	-0.0013	118	132	0	---	IIAGTPEVHAVKPGA
1550.8894	1549.8821	1549.8827	-0.0006	70	84	1	---	NLADAVSKAPQLVPK
1950.9766	1949.9693	1949.9694	-0.0000	25	41	1	120	ATTEEQKLIEDVNASFR
1950.9766	1949.9693	1949.9694	-0.0000	25	41	1	---	ATTEEQKLIEDVNASFR
2989.5269	2988.5196	2988.5840	-0.0644	2	31	1	---	VAMFLAVAVVLGLATSPTAEGGKATTEEQK
2989.5269	2988.5196	2988.5840	-0.0644	2	31	1	---	VAMFLAVAVVLGLATSPTAEGGKATTEEQK

No match to: 713.4088, 724.4957, 734.4910, 750.5148, 768.5228, 782.4743, 838.5289, 848.5228, 864.5468, 886.9863, 1007.6729, 1133.7175, 1161.5786, 1162.0762, 1279.7638, 1334.8838, 1387.6887, 1387.6887, 1388.7415, 1405.7415, 1439.7294, 1446.7434, 1448.9152, 1562.9551, 1618.0667, 1634.8578, 1678.8422, 1706.9818, 1732.1024, 1964.9863, 2136.0920, 2150.1096, 2231.2073, 2239.1594, 2304.1379, 2322.1589, 2322.1589, 2336.1721, 2382.0310, 2564.1943, 2824.3179, 2928.1455, 2973.5139, 3018.5291, 3033.5400

2. gi|3004467 **Mass:** 14597 **Score:** 201 **Expect:** 4.8e-015 **Queries matched:** 8

Phl p6 allergen [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1163.6099	1162.6026	1162.5982	0.0044	38	47	0	---	LIEDVNASFR
1343.6970	1342.6897	1342.6880	0.0017	64	75	1	---	TFEAAFTVSSKR
1343.6970	1342.6897	1342.6880	0.0017	64	75	1	16	TFEAAFTVSSKR
1459.8254	1458.8181	1458.8194	-0.0013	124	138	0	---	IIAGTPEVHAVKPGA
1550.8894	1549.8821	1549.8827	-0.0006	76	90	1	---	NLADAVSKAPQLVPK
1950.9766	1949.9693	1949.9694	-0.0000	31	47	1	120	ATTEEQKLIEDVNASFR
1950.9766	1949.9693	1949.9694	-0.0000	31	47	1	---	ATTEEQKLIEDVNASFR
3018.5291	3017.5218	3017.5903	-0.0685	1	30	1	---	MAAHKFMVAMFLAVAVVLGLATSPTAEGGK

No match to: 713.4088, 724.4957, 734.4910, 750.5148, 768.5228, 782.4743, 838.5289, 848.5228, 864.5468, 886.9863, 1007.6729, 1133.7175, 1161.5786, 1162.0762, 1279.7638, 1334.8838, 1387.6887, 1387.6887, 1388.7415, 1405.7415, 1439.7294, 1446.7434, 1448.9152, 1562.9551, 1618.0667, 1634.8578, 1678.8422, 1706.9818, 1732.1024, 1964.9863, 2136.0920, 2150.1096, 2231.2073, 2239.1594, 2304.1379, 2322.1589, 2322.1589, 2336.1721, 2382.0310, 2564.1943, 2824.3179, 2928.1455, 2973.5139, 2989.5269, 2989.5269, 3033.5400

3. gi|28374059 **Mass:** 11914 **Score:** 188 **Expect:** 9.6e-014 **Queries matched:** 7

Chain A, Crystal Structure Of Phl P 6, A Major Timothy Grass Pollen Allergen Co-Crystallized With Z

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1163.6099	1162.6026	1162.5982	0.0044	11	20	0	---	LIEDVNASFR
1343.6970	1342.6897	1342.6880	0.0017	37	48	1	---	TFEAAFTVSSKR
1343.6970	1342.6897	1342.6880	0.0017	37	48	1	16	TFEAAFTVSSKR
1459.8254	1458.8181	1458.8194	-0.0013	97	111	0	---	IIAGTPEVHAVKPGA
1550.8894	1549.8821	1549.8827	-0.0006	49	63	1	---	NLADAVSKAPQLVPK
1950.9766	1949.9693	1949.9694	-0.0000	4	20	1	120	ATTEEQKLIEDVNASFR
1950.9766	1949.9693	1949.9694	-0.0000	4	20	1	---	ATTEEQKLIEDVNASFR

No match to: 713.4088, 724.4957, 734.4910, 750.5148, 768.5228, 782.4743, 838.5289, 848.5228, 864.5468, 886.9863, 1007.6729, 1133.7175, 1161.5786, 1162.0762, 1279.7638, 1334.8838, 1387.6887, 1387.6887, 1388.7415, 1405.7415, 1439.7294, 1446.7434, 1448.9152, 1562.9551, 1618.0667, 1634.8578, 1678.8422, 1706.9818, 1732.1024, 1964.9863, 2136.0920, 2150.1096, 2231.2073, 2239.1594, 2304.1379, 2322.1589, 2322.1589, 2336.1721, 2382.0310, 2564.1943, 2824.3179, 2928.1455, 2973.5139, 2989.5269, 2989.5269, 3018.5291, 3033.5400

4. gi|3004465 **Mass:** 14592 **Score:** 56 **Expect:** 1.5 **Queries matched:** 5

Phl p6 allergen [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1343.6970	1342.6897	1342.6880	0.0017	64	75	1	---	TFEAAFTVSSKR
1343.6970	1342.6897	1342.6880	0.0017	64	75	1	16	TFEAAFTVSSKR
1550.8894	1549.8821	1549.8827	-0.0006	76	90	1	---	NLADAVSKAPQLVPK
1964.9863	1963.9790	1963.9850	-0.0060	31	47	1	---	ATTEEQKLIEDINASFR
3018.5291	3017.5218	3017.5903	-0.0685	1	30	1	---	MAAHKFMVAMFLAVAVVLGLATSPTAEGGK

No match to: 713.4088, 724.4957, 734.4910, 750.5148, 768.5228, 782.4743, 838.5289, 848.5228, 864.5468, 886.9863, 1007.6729, 1133.7175, 1161.5786, 1162.0762, 1163.6099, 1279.7638, 1334.8838, 1387.6887, 1387.6887, 1388.7415, 1405.7415, 1439.7294, 1446.7434, 1448.9152, 1459.8254, 1562.9551, 1618.0667, 1634.8578, 1678.8422, 1706.9818, 1732.1024, 1950.9766, 1950.9766, 2136.0920, 2150.1096, 2231.2073, 2239.1594, 2304.1379, 2322.1589, 2322.1589, 2336.1721, 2382.0310, 2564.1943, 2824.3179, 2928.1455, 2973.5139, 2989.5269, 2989.5269, 3033.5400

5. gi|147862150 **Mass:** 27700 **Score:** 44 **Expect:** 24 **Queries matched:** 7

hypothetical protein [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
713.4088	712.4015	712.4231	-0.0216	165	170	0	---	LPVTQR
1163.6099	1162.6026	1162.6267	-0.0241	219	228	1	---	ETILEKGVMK + Oxidation (M)
1387.6887	1386.6814	1386.7037	-0.0223	159	170	1	---	MQADGRLPVTQR + Oxidation (M)
1387.6887	1386.6814	1386.7037	-0.0223	159	170	1	---	MQADGRLPVTQR + Oxidation (M)

1405.7415	1404.7342	1404.7473	-0.0131	171 - 182	1	---	RNYQGVIDAITR
2150.1096	2149.1023	2149.1676	-0.0653	135 - 158	0	---	IAAGLVAGGIGAAVGNPADVAMVR
2824.3179	2823.3106	2823.4482	-0.1376	135 - 164	1	---	IAAGLVAGGIGAAVGNPADVAMVRMQADGR + Oxidation (M)

No match to: 724.4957, 734.4910, 750.5148, 768.5228, 782.4743, 838.5289, 848.5228, 864.5468, 886.9863, 1007.6729, 1133.7175, 1161.5786, 1162.0762, 1279.7638, 1334.8838, 1343.6970, 1343.6970, 1388.7415, 1439.7294, 1446.7434, 1448.9152, 1459.8254, 1550.8894, 1562.9551, 1618.0667, 1634.8578, 1678.8422, 1706.9818, 1732.1024, 1950.9766, 1950.9766, 1964.9863, 2136.0920, 2231.2073, 2239.1594, 2304.1379, 2322.1589, 2322.1589, 2336.1721, 2382.0310, 2564.1943, 2928.1455, 2973.5139, 2989.5269, 2989.5269, 3018.5291, 3033.5400

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 54

Protein View

Match to: **gi|1171011** Score: **203** Expect: **3e-015**
RecName: Full=Pollen allergen Phl p 6; AltName: Full=Allergen Phl p VI; AltName: Allergen=Phl p 6;

Nominal mass (M_r): **13912;** Calculated pI value: **5.31**
NCBI BLAST search of gi|1171011 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|414712 from Phleum pratense

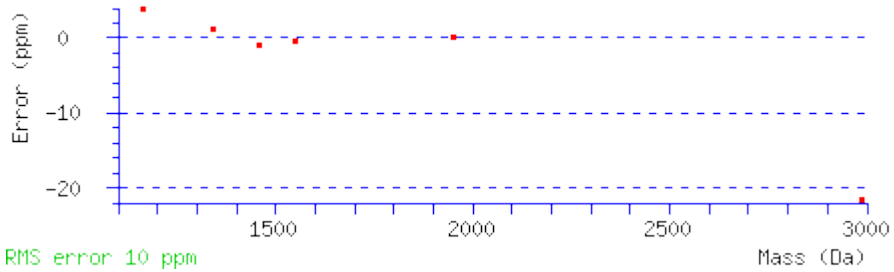
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **62%**

Matched peptides shown in **Bold Red**

```
   1 MVAMFLAVAV VLGLATSPTA EGGKATTEEQ KLIEDVNASF RAAMATTANV
  51 PPADKYKTFE AAFTVSSKRN LADAVSKAPQ LVPKLDEVYN AAYNAADHAA
 101 PEDKYEAFVL HFSEALRIIA GTPEVHAVKP GA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
2 - 31	2989.5269	2988.5196	2988.5840	-0.0644	1	VAMFLAVAVVLGLATSPTAEGGKATTEEQK	(No match)
2 - 31	2989.5269	2988.5196	2988.5840	-0.0644	1	VAMFLAVAVVLGLATSPTAEGGKATTEEQK	(No match)
25 - 41	1950.9766	1949.9693	1949.9694	-0.0000	1	ATTEEQKLIEDVNASFR	(Ions score 120)
25 - 41	1950.9766	1949.9693	1949.9694	-0.0000	1	ATTEEQKLIEDVNASFR	(No match)
32 - 41	1163.6099	1162.6026	1162.5982	0.0044	0	LIEDVNASFR	(No match)
58 - 69	1343.6970	1342.6897	1342.6880	0.0017	1	TFEAAFTVSSKR	(No match)
58 - 69	1343.6970	1342.6897	1342.6880	0.0017	1	TFEAAFTVSSKR	(Ions score 16)
70 - 84	1550.8894	1549.8821	1549.8827	-0.0006	1	NLADAVSKAPQLVPK	(No match)
118 - 132	1459.8254	1458.8181	1458.8194	-0.0013	0	IIAGTPEVHAVKPGA	(No match)



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	Accession	Mass	Score	Description
1.	gi|1171011	13912	161	RecName: Full=Pollen allergen Phl p 6; AltName: Full=Allergen Phl p VI; AltName: Allergen=Phl
2.	gi|28374059	11914	143	Chain A, Crystal Structure Of Phl P 6, A Major Timothy Grass Pollen Allergen Co-Crystallized
3.	gi|3004467	14597	140	Phl p6 allergen [Phleum pratense]
4.	gi|149770654	17243	50	LysM receptor kinase 3 [Medicago truncatula]
5.	gi|222848535	116633	41	predicted protein [Populus trichocarpa]
6.	gi|4835909	31670	41	cytosolic ascorbate peroxidase [Mesembryanthemum crystallinum]
7.	gi|1213340	11819	40	phosphoenolpyruvate carboxylase [Brassica napus]
8.	gi|1213342	12005	40	phosphoenolpyruvate carboxylase [Brassica napus]
9.	gi|222624472	13295	40	hypothetical protein OsJ_09942 [Oryza sativa Japonica Group]
10.	gi|18417634	34853	38	F-box family protein (FBL19) [Arabidopsis thaliana]

Results List

1. gi|1171011 **Mass:** 13912 **Score:** 161 **Expect:** 4.8e-011 **Queries matched:** 7

RecName: Full=Pollen allergen Phl p 6; AltName: Full=Allergen Phl p VI; AltName: Allergen=Phl p 6;

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1343.7107	1342.7034	1342.6880	0.0154	58	-	69	1	3	TFEAAFTVSSKR
1343.7107	1342.7034	1342.6880	0.0154	58	-	69	1	---	TFEAAFTVSSKR
1459.8140	1458.8067	1458.8194	-0.0127	118	-	132	0	---	IIAGTPEVHAVKPGA
1950.9869	1949.9796	1949.9694	0.0103	25	-	41	1	99	ATTEEQKLIEDVNASFR
1950.9869	1949.9796	1949.9694	0.0103	25	-	41	1	---	ATTEEQKLIEDVNASFR
2989.5295	2988.5222	2988.5840	-0.0618	2	-	31	1	---	VAMFLAVAVVLGLATSPTAEGGKATTEEQK
2989.5295	2988.5222	2988.5840	-0.0618	2	-	31	1	---	VAMFLAVAVVLGLATSPTAEGGKATTEEQK

No match to: 713.4027, 724.4924, 734.4845, 750.5166, 768.5164, 864.5140, 1350.6931, 1388.7948, 1791.7292, 2240.1506, 2383.9697, 2383.9697, 2795.3914, 2795.3914

2. gi|28374059 **Mass:** 11914 **Score:** 143 **Expect:** 3e-009 **Queries matched:** 5

Chain A, Crystal Structure Of Phl P 6, A Major Timothy Grass Pollen Allergen Co-Crystallized With Z

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1343.7107	1342.7034	1342.6880	0.0154	37	-	48	1	3	TFEAAFTVSSKR
1343.7107	1342.7034	1342.6880	0.0154	37	-	48	1	---	TFEAAFTVSSKR
1459.8140	1458.8067	1458.8194	-0.0127	97	-	111	0	---	IIAGTPEVHAVKPGA
1950.9869	1949.9796	1949.9694	0.0103	4	-	20	1	99	ATTEEQKLIEDVNASFR
1950.9869	1949.9796	1949.9694	0.0103	4	-	20	1	---	ATTEEQKLIEDVNASFR

No match to: 713.4027, 724.4924, 734.4845, 750.5166, 768.5164, 864.5140, 1350.6931, 1388.7948, 1791.7292, 2240.1506, 2383.9697, 2383.9697, 2795.3914, 2795.3914, 2989.5295, 2989.5295

3. gi|3004467 **Mass:** 14597 **Score:** 140 **Expect:** 6e-009 **Queries matched:** 5

Phl p6 allergen [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1343.7107	1342.7034	1342.6880	0.0154	64 -	75	1	3	TFEAAFTVSSKR
1343.7107	1342.7034	1342.6880	0.0154	64 -	75	1	---	TFEAAFTVSSKR
1459.8140	1458.8067	1458.8194	-0.0127	124 -	138	0	---	IIAGTPEVHAVKPGA
1950.9869	1949.9796	1949.9694	0.0103	31 -	47	1	99	ATTEEQKLIEDVNASFR
1950.9869	1949.9796	1949.9694	0.0103	31 -	47	1	---	ATTEEQKLIEDVNASFR

No match to: 713.4027, 724.4924, 734.4845, 750.5166, 768.5164, 864.5140, 1350.6931, 1388.7948, 1791.7292, 2240.1506, 2383.9697, 2383.9697, 2795.3914, 2795.3914, 2989.5295, 2989.5295

4. gi|149770654 **Mass:** 17243 **Score:** 50 **Expect:** 6.6 **Queries matched:** 6

LysM receptor kinase 3 [Medicago truncatula]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
713.4027	712.3954	712.3908	0.0047	134 -	138	1	---	YFQKK
1343.7107	1342.7034	1342.6921	0.0113	42 -	52	0	---	DYGLFVTYPLR
1343.7107	1342.7034	1342.6921	0.0113	42 -	52	0	---	DYGLFVTYPLR
1350.6931	1349.6858	1349.6575	0.0283	145 -	156	1	---	LPQTSRAFSTQD
1950.9869	1949.9796	1949.9747	0.0049	93 -	109	1	---	DQNGHFFPLYSRTGIAK
1950.9869	1949.9796	1949.9747	0.0049	93 -	109	1	---	DQNGHFFPLYSRTGIAK

No match to: 724.4924, 734.4845, 750.5166, 768.5164, 864.5140, 1388.7948, 1459.8140, 1791.7292, 2240.1506, 2383.9697, 2383.9697, 2795.3914, 2795.3914, 2989.5295, 2989.5295

5. gi|222848535 **Mass:** 116633 **Score:** 41 **Expect:** 48 **Queries matched:** 9

predicted protein [Populus trichocarpa]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
864.5140	863.5067	863.5228	-0.0161	504 -	511	1	---	KGPLPPQK
1343.7107	1342.7034	1342.6768	0.0266	308 -	318	1	---	GEDTIKLYYNK
1343.7107	1342.7034	1342.6768	0.0266	308 -	318	1	---	GEDTIKLYYNK
1791.7292	1790.7219	1790.8259	-0.1040	527 -	541	0	---	VPLDAYMMDFVFSEK
1950.9869	1949.9796	1949.9119	0.0678	932 -	948	1	---	TGGLFDTVFDVDHDKER
1950.9869	1949.9796	1949.9119	0.0678	932 -	948	1	---	TGGLFDTVFDVDHDKER
2240.1506	2239.1433	2239.0630	0.0803	864 -	882	0	---	VQNDFVNLANHLHSSHHDR
2795.3914	2794.3841	2794.2618	0.1224	527 -	550	1	---	VPLDAYMMDFVFSEKEDGGIFDNR
2795.3914	2794.3841	2794.2618	0.1224	527 -	550	1	---	VPLDAYMMDFVFSEKEDGGIFDNR

No match to: 713.4027, 724.4924, 734.4845, 750.5166, 768.5164, 1350.6931, 1388.7948, 1459.8140, 2383.9697, 2383.9697, 2989.5295, 2989.5295

6. gi|4835909 **Mass:** 31670 **Score:** 41 **Expect:** 54 **Queries matched:** 4

cytosolic ascorbate peroxidase [Mesembryanthemum crystallinum]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
713.4027	712.3954	712.3544	0.0410	142 -	146	0	---	DIFYR
1350.6931	1349.6858	1349.7190	-0.0332	239 -	251	1	---	KLSELGFTPSGSK

1950.9869	1949.9796	1949.9842	-0.0045	1 - 17	1	16	MAMPPVVDSVYLKEIDK + Oxidation (M)
1950.9869	1949.9796	1949.9842	-0.0045	1 - 17	1	---	MAMPPVVDSVYLKEIDK + Oxidation (M)

No match to: 724.4924, 734.4845, 750.5166, 768.5164, 864.5140, 1343.7107, 1343.7107, 1388.7948, 1459.8140, 1791.7292, 2240.1506, 2383.9697, 2383.9697, 2795.3914, 2795.3914, 2989.5295, 2989.5295

7. gi|1213340 **Mass:** 11819 **Score:** 40 **Expect:** 59 **Queries matched:** 5

phosphoenolpyruvate carboxylase [Brassica napus]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1343.7107	1342.7034	1342.6299	0.0735	40 -	50	1	---	RTPPTPQDEMR + Oxidation (M)
1343.7107	1342.7034	1342.6299	0.0735	40 -	50	1	---	RTPPTPQDEMR + Oxidation (M)
1350.6931	1349.6858	1349.7125	-0.0267	1 -	11	1	---	IRDCLAQLYAK
2989.5295	2988.5222	2988.3898	0.1324	41 -	66	1	---	TPPTPQDEMRAGMSYFHETIWNGVPK
2989.5295	2988.5222	2988.3898	0.1324	41 -	66	1	---	TPPTPQDEMRAGMSYFHETIWNGVPK

No match to: 713.4027, 724.4924, 734.4845, 750.5166, 768.5164, 864.5140, 1388.7948, 1459.8140, 1791.7292, 1950.9869, 1950.9869, 2240.1506, 2383.9697, 2383.9697, 2795.3914, 2795.3914

8. gi|1213342 **Mass:** 12005 **Score:** 40 **Expect:** 66 **Queries matched:** 5

phosphoenolpyruvate carboxylase [Brassica napus]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1343.7107	1342.7034	1342.6299	0.0735	40 -	50	1	---	RTPPTPQDEMR + Oxidation (M)
1343.7107	1342.7034	1342.6299	0.0735	40 -	50	1	---	RTPPTPQDEMR + Oxidation (M)
1350.6931	1349.6858	1349.7125	-0.0267	1 -	11	1	---	IRDCLAQLYAK
2989.5295	2988.5222	2988.3898	0.1324	41 -	66	1	---	TPPTPQDEMRAGMSYFHETIWNGVPK
2989.5295	2988.5222	2988.3898	0.1324	41 -	66	1	---	TPPTPQDEMRAGMSYFHETIWNGVPK

No match to: 713.4027, 724.4924, 734.4845, 750.5166, 768.5164, 864.5140, 1388.7948, 1459.8140, 1791.7292, 1950.9869, 1950.9869, 2240.1506, 2383.9697, 2383.9697, 2795.3914, 2795.3914

9. gi|222624472 **Mass:** 13295 **Score:** 40 **Expect:** 66 **Queries matched:** 4

hypothetical protein OsJ_09942 [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1350.6931	1349.6858	1349.6411	0.0448	1 -	11	0	---	MGRPHFNPHNK + Oxidation (M)
1791.7292	1790.7219	1790.7902	-0.0683	74 -	87	0	---	SNCQSLFLCCIYAR
2795.3914	2794.3841	2794.3426	0.0415	74 -	96	1	---	SNCQSLFLCCIYARFVVVMNSVK
2795.3914	2794.3841	2794.3426	0.0415	74 -	96	1	---	SNCQSLFLCCIYARFVVVMNSVK

No match to: 713.4027, 724.4924, 734.4845, 750.5166, 768.5164, 864.5140, 1343.7107, 1343.7107, 1388.7948, 1459.8140, 1950.9869, 1950.9869, 2240.1506, 2383.9697, 2383.9697, 2989.5295, 2989.5295

10. gi|18417634 **Mass:** 34853 **Score:** 38 **Expect:** 87 **Queries matched:** 4

F-box family protein (FBL19) [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
768.5164	767.5091	767.4766	0.0326	183 -	188	1	---	RNLLPR
1459.8140	1458.8067	1458.7943	0.0125	226 -	237	1	---	HLEIRYSTLTAR

2989.5295 2988.5222 2988.4333 0.0889 70 - 93 1 --- FLSFPESINWWTPEFEDKVDSFLR
2989.5295 2988.5222 2988.3997 0.1226 10 - 34 1 --- VEMGSGLYPDWSELTRECLLDIFSR + Oxidation (M)
No match to: 713.4027, 724.4924, 734.4845, 750.5166, 864.5140, 1343.7107, 1343.7107, 1350.6931, 1388.7948, 1791.7292, 1950.9869, 1950.9869, 2240.1506, 2383.9697, 2383.9697, 2795.3914, 2795.3914

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 21

Protein View

Match to: **gi|1171011** Score: **161** Expect: **4.8e-011**
RecName: Full=Pollen allergen Phl p 6; AltName: Full=Allergen Phl p VI; AltName: Allergen=Phl p 6;

Nominal mass (M_r): **13912**; Calculated pI value: **5.31**
NCBI BLAST search of gi|1171011 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|414712 from Phleum pratense

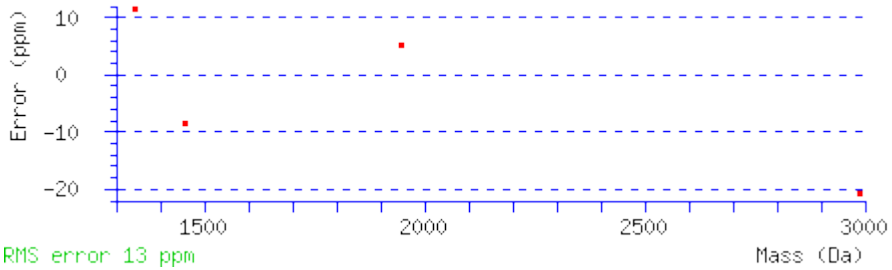
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **50%**

Matched peptides shown in **Bold Red**

```
   1 MVAMFLAVAV VLGLATSPTA EGGKATTEEQ KLIEDVNASF RAAMATTANV
  51 PPADKYKTFE AAFTVSSKRN LADAVSKAPQ LVPKLDEVYN AAYNAADHAA
 101 PEDKYEAFVL HFSEALRIIA GTPEVHAVKP GA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
2 - 31	2989.5295	2988.5222	2988.5840	-0.0618	1	VAMFLAVAVVLGLATSPTAEGGKATTEEQK	(No match)
2 - 31	2989.5295	2988.5222	2988.5840	-0.0618	1	VAMFLAVAVVLGLATSPTAEGGKATTEEQK	(No match)
25 - 41	1950.9869	1949.9796	1949.9694	0.0103	1	ATTEEQKLIEDVNASFR	(Ions score 99)
25 - 41	1950.9869	1949.9796	1949.9694	0.0103	1	ATTEEQKLIEDVNASFR	(No match)
58 - 69	1343.7107	1342.7034	1342.6880	0.0154	1	TFEAAFTVSSKR	(Ions score 3)
58 - 69	1343.7107	1342.7034	1342.6880	0.0154	1	TFEAAFTVSSKR	(No match)
118 - 132	1459.8140	1458.8067	1458.8194	-0.0127	0	IIAGTPEVHAVKPGA	(No match)



Spot 137

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	Accession	Mass	Score	Description
1.	gi|1171011	13912	520	RecName: Full=Pollen allergen Phl p 6; AltName: Full=Allergen Phl p VI; AltName: Allergen=Phl
2.	gi|28374059	11914	486	Chain A, Crystal Structure Of Phl P 6, A Major Timothy Grass Pollen Allergen Co-Crystallized W
3.	gi|3004467	14597	476	Phl p6 allergen [Phleum pratense]
4.	gi|3004469	11392	202	Phl p6 IgE binding fragment [Phleum pratense]
5.	gi|3004465	14592	170	Phl p6 allergen [Phleum pratense]
6.	gi|3004471	8622	137	Phl p6 IgE binding fragment [Phleum pratense]
7.	gi|159484654	60577	57	chloroplast trigger factor [Chlamydomonas reinhardtii]
8.	gi|164664790	47926	56	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Leptochilus cantoniensis]
9.	gi|149384347	48495	56	ribulose-1,5-bisphosphate carboxylase/oxygenase [Deparia unifurcata]
10.	gi|15218569	52018	56	CKL2; casein kinase I/ kinase [Arabidopsis thaliana]

Results List

1. gi|1171011 **Mass:** 13912 **Score:** 520 **Expect:** 6e-047 **Queries matched:** 16

RecName: Full=Pollen allergen Phl p 6; AltName: Full=Allergen Phl p VI; AltName: Allergen=Phl p 6;

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
752.4548	751.4475	751.4592	-0.0117	78	84	0	---	APQLVPK
1163.6022	1162.5949	1162.5982	-0.0033	32	41	0	92	LIEDVNASFR
1163.6022	1162.5949	1162.5982	-0.0033	32	41	0	---	LIEDVNASFR
1187.5847	1186.5774	1186.5869	-0.0095	58	68	0	---	TFEAAFTVSSK
1343.6936	1342.6863	1342.6880	-0.0017	58	69	1	---	TFEAAFTVSSKR
1343.6936	1342.6863	1342.6880	-0.0017	58	69	1	92	TFEAAFTVSSKR
1459.8214	1458.8141	1458.8194	-0.0053	118	132	0	---	IIAGTPEVHAVKPGA
1550.8815	1549.8742	1549.8827	-0.0085	70	84	1	---	NLADAVSKAPQLVPK
1581.8187	1580.8114	1580.7986	0.0128	105	117	0	---	YEAFVLHFSEALR
1664.8286	1663.8213	1663.8239	-0.0026	42	57	1	---	AAMATTANVPPADKYK + Oxidation (M)
1950.9829	1949.9756	1949.9694	0.0063	25	41	1	156	ATTEEQKLIEDVNASFR
1950.9829	1949.9756	1949.9694	0.0063	25	41	1	---	ATTEEQKLIEDVNASFR
2349.1377	2348.1304	2348.2483	-0.1178	1	24	0	---	MVAMFLAVAVVLGLATSPTAEGGK + Oxidation (M)
2989.5410	2988.5337	2988.5840	-0.0503	2	31	1	---	VAMFLAVAVVLGLATSPTAEGGKATTEEQK
3739.8169	3738.8096	3738.7589	0.0507	85	117	1	2	LDEVYNAAYNAADHAAPEDKYEAFVLHFSEALR
3739.8169	3738.8096	3738.7589	0.0507	85	117	1	---	LDEVYNAAYNAADHAAPEDKYEAFVLHFSEALR

No match to: 713.4153, 722.3837, 808.4026, 818.4445, 899.4041, 1071.5961, 1177.6144, 1300.7369, 1309.7095, 1327.1334, 1365.6650, 1388.7817, 1475.7852, 1481.8082, 1572.8658, 1634.8553, 1706.9938, 1906.9666, 1908.0306, 1934.4407, 1964.9932, 1972.9672, 2136.1050, 2151.1206, 2305.1423, 2305.6104, 2322.1655, 2322.1655, 2336.1604, 2927.1677

2. gi|28374059 **Mass:** 11914 **Score:** 486 **Expect:** 1.5e-043 **Queries matched:** 14

Chain A, Crystal Structure Of Phl P 6, A Major Timothy Grass Pollen Allergen Co-Crystallized With Z

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
752.4548	751.4475	751.4592	-0.0117	57	63	0	---	APQLVPK
1163.6022	1162.5949	1162.5982	-0.0033	11	20	0	92	LIEDVNASFR
1163.6022	1162.5949	1162.5982	-0.0033	11	20	0	---	LIEDVNASFR
1187.5847	1186.5774	1186.5869	-0.0095	37	47	0	---	TFEAAFTVSSK
1343.6936	1342.6863	1342.6880	-0.0017	37	48	1	---	TFEAAFTVSSKR
1343.6936	1342.6863	1342.6880	-0.0017	37	48	1	92	TFEAAFTVSSKR
1459.8214	1458.8141	1458.8194	-0.0053	97	111	0	---	IIAGTPEVHAVKPGA
1550.8815	1549.8742	1549.8827	-0.0085	49	63	1	---	NLADAVSKAPQLVPK
1581.8187	1580.8114	1580.7986	0.0128	84	96	0	---	YEAFVLHFSEALR
1664.8286	1663.8213	1663.8239	-0.0026	21	36	1	---	AAMATTANVPPADKYK + Oxidation (M)
1950.9829	1949.9756	1949.9694	0.0063	4	20	1	156	ATTEEQKLIEDVNASFR
1950.9829	1949.9756	1949.9694	0.0063	4	20	1	---	ATTEEQKLIEDVNASFR
3739.8169	3738.8096	3738.7589	0.0507	64	96	1	2	LDEVYNAAYNAADHAAPEDKYEAFVLHFSEALR
3739.8169	3738.8096	3738.7589	0.0507	64	96	1	---	LDEVYNAAYNAADHAAPEDKYEAFVLHFSEALR

No match to: 713.4153, 722.3837, 808.4026, 818.4445, 899.4041, 1071.5961, 1177.6144, 1300.7369, 1309.7095, 1327.1334, 1365.6650, 1388.7817, 1475.7852, 1481.8082, 1572.8658, 1634.8553, 1706.9938, 1906.9666, 1908.0306, 1934.4407, 1964.9932, 1972.9672, 2136.1050, 2151.1206, 2305.1423, 2305.6104, 2322.1655, 2322.1655, 2336.1604, 2349.1377, 2927.1677, 2989.5410

3. gi|3004467 **Mass:** 14597 **Score:** 476 **Expect:** 1.5e-042 **Queries matched:** 14

Phl p6 allergen [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
752.4548	751.4475	751.4592	-0.0117	84	90	0	---	APQLVPK
1163.6022	1162.5949	1162.5982	-0.0033	38	47	0	92	LIEDVNASFR
1163.6022	1162.5949	1162.5982	-0.0033	38	47	0	---	LIEDVNASFR
1187.5847	1186.5774	1186.5869	-0.0095	64	74	0	---	TFEAAFTVSSK
1343.6936	1342.6863	1342.6880	-0.0017	64	75	1	---	TFEAAFTVSSKR
1343.6936	1342.6863	1342.6880	-0.0017	64	75	1	92	TFEAAFTVSSKR
1459.8214	1458.8141	1458.8194	-0.0053	124	138	0	---	IIAGTPEVHAVKPGA
1550.8815	1549.8742	1549.8827	-0.0085	76	90	1	---	NLADAVSKAPQLVPK
1581.8187	1580.8114	1580.7986	0.0128	111	123	0	---	YEAFVLHFSEALR
1664.8286	1663.8213	1663.8239	-0.0026	48	63	1	---	AAMATTANVPPADKYK + Oxidation (M)
1950.9829	1949.9756	1949.9694	0.0063	31	47	1	156	ATTEEQKLIEDVNASFR
1950.9829	1949.9756	1949.9694	0.0063	31	47	1	---	ATTEEQKLIEDVNASFR
3739.8169	3738.8096	3738.7589	0.0507	91	123	1	2	LDEVYNAAYNAADHAAPEDKYEAFVLHFSEALR
3739.8169	3738.8096	3738.7589	0.0507	91	123	1	---	LDEVYNAAYNAADHAAPEDKYEAFVLHFSEALR

No match to: 713.4153, 722.3837, 808.4026, 818.4445, 899.4041, 1071.5961, 1177.6144, 1300.7369, 1309.7095, 1327.1334, 1365.6650, 1388.7817, 1475.7852, 1481.8082, 1572.8658, 1634.8553, 1706.9938, 1906.9666, 1908.0306, 1934.4407, 1964.9932, 1972.9672, 2136.1050, 2151.1206, 2305.1423, 2305.6104, 2322.1655, 2322.1655, 2336.1604, 2349.1377, 2927.1677, 2989.5410

4. gi|3004469 **Mass:** 11392 **Score:** 202 **Expect:** 3.8e-015 **Queries matched:** 10

Phl p6 IgE binding fragment [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
752.4548	751.4475	751.4592	-0.0117	52	-	58	0	---	APQLVPK
1163.6022	1162.5949	1162.5982	-0.0033	6	-	15	0	92	LIEDVNASFR
1163.6022	1162.5949	1162.5982	-0.0033	6	-	15	0	---	LIEDVNASFR
1309.7095	1308.7022	1308.7037	-0.0015	32	-	43	1	---	TLEAAFTVSSKR
1459.8214	1458.8141	1458.8194	-0.0053	92	-	106	0	---	IIAGTPEVHAVKPGA
1550.8815	1549.8742	1549.8827	-0.0085	44	-	58	1	---	NLADAVSKAPQLVPK
1581.8187	1580.8114	1580.7986	0.0128	79	-	91	0	---	YEAFVLHFSEALR
1664.8286	1663.8213	1663.8239	-0.0026	16	-	31	1	---	AAMATTANVPPADKYK + Oxidation (M)
3739.8169	3738.8096	3738.7589	0.0507	59	-	91	1	2	LDEVYNAAYNAADHAAPEDKYEAFVLHFSEALR
3739.8169	3738.8096	3738.7589	0.0507	59	-	91	1	---	LDEVYNAAYNAADHAAPEDKYEAFVLHFSEALR

No match to: 713.4153, 722.3837, 808.4026, 818.4445, 899.4041, 1071.5961, 1177.6144, 1187.5847, 1300.7369, 1327.1334, 1343.6936, 1343.6936, 1365.6650, 1388.7817, 1475.7852, 1481.8082, 1572.8658, 1634.8553, 1706.9938, 1906.9666, 1908.0306, 1934.4407, 1950.9829, 1950.9829, 1964.9932, 1972.9672, 2136.1050, 2151.1206, 2305.1423, 2305.6104, 2322.1655, 2322.1655, 2336.1604, 2349.1377, 2927.1677, 2989.5410

5. gi|3004465 **Mass:** 14592 **Score:** 170 **Expect:** 6e-012 **Queries matched:** 8

Phl p6 allergen [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
752.4548	751.4475	751.4592	-0.0117	84	-	90	0	---	APQLVPK
1177.6144	1176.6071	1176.6138	-0.0067	38	-	47	0	---	LIEDINASFR
1187.5847	1186.5774	1186.5869	-0.0095	64	-	74	0	---	TFEAAFTVSSK
1343.6936	1342.6863	1342.6880	-0.0017	64	-	75	1	---	TFEAAFTVSSKR
1343.6936	1342.6863	1342.6880	-0.0017	64	-	75	1	92	TFEAAFTVSSKR
1550.8815	1549.8742	1549.8827	-0.0085	76	-	90	1	---	NLADAVSKAPQLVPK
1664.8286	1663.8213	1663.8239	-0.0026	48	-	63	1	---	AAMATTANVPPADKYK + Oxidation (M)
1964.9932	1963.9859	1963.9850	0.0009	31	-	47	1	---	ATTEEQKLIEDINASFR

No match to: 713.4153, 722.3837, 808.4026, 818.4445, 899.4041, 1071.5961, 1163.6022, 1163.6022, 1300.7369, 1309.7095, 1327.1334, 1365.6650, 1388.7817, 1459.8214, 1475.7852, 1481.8082, 1572.8658, 1581.8187, 1634.8553, 1706.9938, 1906.9666, 1908.0306, 1934.4407, 1950.9829, 1950.9829, 1972.9672, 2136.1050, 2151.1206, 2305.1423, 2305.6104, 2322.1655, 2322.1655, 2336.1604, 2349.1377, 2927.1677, 2989.5410, 3739.8169, 3739.8169

6. gi|3004471 **Mass:** 8622 **Score:** 137 **Expect:** 1.2e-008 **Queries matched:** 5

Phl p6 IgE binding fragment [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
752.4548	751.4475	751.4592	-0.0117	26	-	32	0	---	APQLVPK
1187.5847	1186.5774	1186.5869	-0.0095	6	-	16	0	---	TFEAAFTVSSK
1343.6936	1342.6863	1342.6880	-0.0017	6	-	17	1	---	TFEAAFTVSSKR
1343.6936	1342.6863	1342.6880	-0.0017	6	-	17	1	92	TFEAAFTVSSKR

1550.8815	1549.8742	1549.8827	-0.0085	18 - 32	1	---	NLADAVSKAPQLVPK

No match to: 713.4153, 722.3837, 808.4026, 818.4445, 899.4041, 1071.5961, 1163.6022, 1163.6022, 1177.6144, 1300.7369, 1309.7095, 1327.1334, 1365.6650, 1388.7817, 1459.8214, 1475.7852, 1481.8082, 1572.8658, 1581.8187, 1634.8553, 1664.8286, 1706.9938, 1906.9666, 1908.0306, 1934.4407, 1950.9829, 1950.9829, 1964.9932, 1972.9672, 2136.1050, 2151.1206, 2305.1423, 2305.6104, 2322.1655, 2322.1655, 2336.1604, 2349.1377, 2927.1677, 2989.5410, 3739.8169, 3739.8169

7. gi|159484654 **Mass:** 60577 **Score:** 57 **Expect:** 1.2 **Queries matched:** 11

chloroplast trigger factor [Chlamydomonas reinhardtii]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
752.4548	751.4475	751.3972	0.0503	1 -	6	0	---	MMLTLK + Oxidation (M)
818.4445	817.4372	817.4406	-0.0033	55 -	61	1	---	RSVDVSR
1475.7852	1474.7779	1474.7932	-0.0153	460 -	471	1	---	FNLAVDDIWVRK
1634.8553	1633.8480	1633.7981	0.0500	78 -	92	0	---	VEVSVAVEELGTCSR
1950.9829	1949.9756	1950.0535	-0.0779	146 -	161	1	---	FKTFCLEELLLEALPK
1950.9829	1949.9756	1950.0535	-0.0779	146 -	161	1	---	FKTFCLEELLLEALPK
2151.1206	2150.1133	2149.9911	0.1223	286 -	305	0	---	FSFDTEADVLGITSGMLGMK + 2 Oxidation (M)
2322.1655	2321.1582	2321.1936	-0.0354	385 -	406	1	---	ALEDAVVKAVADALDMPEVPPR + Oxidation (M)
2322.1655	2321.1582	2321.1936	-0.0354	385 -	406	1	---	ALEDAVVKAVADALDMPEVPPR + Oxidation (M)
2336.1604	2335.1531	2335.2470	-0.0939	124 -	145	0	---	GWQAGKPLPLSMVIQQVGGQNK
2989.5410	2988.5337	2988.6495	-0.1157	256 -	284	1	---	GLQLGDTLVIDLEITSKATGQALPGLTHK

No match to: 713.4153, 722.3837, 808.4026, 899.4041, 1071.5961, 1163.6022, 1163.6022, 1177.6144, 1187.5847, 1300.7369, 1309.7095, 1327.1334, 1343.6936, 1343.6936, 1365.6650, 1388.7817, 1459.8214, 1481.8082, 1550.8815, 1572.8658, 1581.8187, 1664.8286, 1706.9938, 1906.9666, 1908.0306, 1934.4407, 1964.9932, 1972.9672, 2136.1050, 2305.1423, 2305.6104, 2349.1377, 2927.1677, 3739.8169, 3739.8169

8. gi|164664790 **Mass:** 47926 **Score:** 56 **Expect:** 1.5 **Queries matched:** 10

ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Leptochilus cantoniensis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
808.4026	807.3953	807.4238	-0.0285	7 -	13	1	---	AGVKDYR
1177.6144	1176.6071	1176.5703	0.0369	14 -	22	0	---	LTYYTPEYK
1187.5847	1186.5774	1186.6570	-0.0796	278 -	287	0	---	DNGLLLHIHR
1309.7095	1308.7022	1308.6873	0.0149	298 -	308	1	---	NHGMHFRVLAK
1343.6936	1342.6863	1342.7581	-0.0718	277 -	287	1	---	RDNGLLLHIHR
1343.6936	1342.6863	1342.7581	-0.0718	277 -	287	1	---	RDNGLLLHIHR
1572.8658	1571.8585	1571.7837	0.0748	414 -	427	1	---	VALEACVQARNEGR
1664.8286	1663.8213	1663.7372	0.0841	194 -	207	1	---	DDENVNSQPFMRGR
1950.9829	1949.9756	1949.9087	0.0669	229 -	245	1	---	GHYLNATAGTCEEMLKR
1950.9829	1949.9756	1949.9087	0.0669	229 -	245	1	---	GHYLNATAGTCEEMLKR

No match to: 713.4153, 722.3837, 752.4548, 818.4445, 899.4041, 1071.5961, 1163.6022, 1163.6022, 1300.7369, 1327.1334, 1365.6650, 1388.7817, 1459.8214, 1475.7852, 1481.8082, 1550.8815, 1581.8187, 1634.8553, 1706.9938, 1906.9666, 1908.0306, 1934.4407, 1964.9932, 1972.9672, 2136.1050, 2151.1206, 2305.1423, 2305.6104, 2322.1655, 2322.1655, 2336.1604, 2349.1377, 2927.1677, 2989.5410, 3739.8169, 3739.8169

9. gi|149384347 **Mass:** 48495 **Score:** 56 **Expect:** 1.6 **Queries matched:** 10

ribulose-1,5-bisphosphate carboxylase/oxygenase [Deparia unifurcata]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
808.4026	807.3953	807.4238	-0.0285	6	12	1	---	AGVKDYR
1177.6144	1176.6071	1176.5703	0.0369	13	21	0	---	LTYYTPEYK
1187.5847	1186.5774	1186.6570	-0.0796	277	286	0	---	DNGLLLHIHR
1309.7095	1308.7022	1308.6873	0.0149	297	307	1	---	NHGMHFRVLAK
1343.6936	1342.6863	1342.7581	-0.0718	276	286	1	---	RDNGLLLHIHR
1343.6936	1342.6863	1342.7581	-0.0718	276	286	1	---	RDNGLLLHIHR
1481.8082	1480.8009	1480.7092	0.0917	311	325	0	---	MSGGDHIHAGTVVGK + Oxidation (M)
1572.8658	1571.8585	1571.7837	0.0748	413	426	1	---	VALEACVQARNEGR
1950.9829	1949.9756	1949.9087	0.0669	228	244	1	---	GHYLNATAGTCEEMLKR
1950.9829	1949.9756	1949.9087	0.0669	228	244	1	---	GHYLNATAGTCEEMLKR

No match to: 713.4153, 722.3837, 752.4548, 818.4445, 899.4041, 1071.5961, 1163.6022, 1163.6022, 1300.7369, 1327.1334, 1365.6650, 1388.7817, 1459.8214, 1475.7852, 1550.8815, 1581.8187, 1634.8553, 1664.8286, 1706.9938, 1906.9666, 1908.0306, 1934.4407, 1964.9932, 1972.9672, 2136.1050, 2151.1206, 2305.1423, 2305.6104, 2322.1655, 2322.1655, 2336.1604, 2349.1377, 2927.1677, 2989.5410, 3739.8169, 3739.8169

10. gi|15218569 **Mass:** 52018 **Score:** 56 **Expect:** 1.7 **Queries matched:** 9

CKL2; casein kinase I/ kinase [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1071.5961	1070.5888	1070.5607	0.0281	361	371	0	---	APVSSDPAISK
1187.5847	1186.5774	1186.6193	-0.0419	428	438	0	---	NSPIVSSEINK
1343.6936	1342.6863	1342.7245	-0.0381	44	54	1	---	TKHPQLLYESK
1343.6936	1342.6863	1342.7245	-0.0381	44	54	1	---	TKHPQLLYESK
1475.7852	1474.7779	1474.7602	0.0177	128	140	0	---	DIKPDNFLMGLGR
1572.8658	1571.8585	1571.9034	-0.0449	55	69	1	---	LYKVLQGGTGVPNVK
1634.8553	1633.8480	1633.8099	0.0381	452	465	1	---	NYEANLKGIESLHF
1908.0306	1907.0233	1906.9141	0.1092	279	293	0	---	EGFQFDYVFDWTILK
2336.1604	2335.1531	2335.1338	0.0193	171	191	1	---	NLTGTARYASMNTHLGIEQSR + Oxidation (M)

No match to: 713.4153, 722.3837, 752.4548, 808.4026, 818.4445, 899.4041, 1163.6022, 1163.6022, 1177.6144, 1300.7369, 1309.7095, 1327.1334, 1365.6650, 1388.7817, 1459.8214, 1481.8082, 1550.8815, 1581.8187, 1664.8286, 1706.9938, 1906.9666, 1934.4407, 1950.9829, 1950.9829, 1964.9932, 1972.9672, 2136.1050, 2151.1206, 2305.1423, 2305.6104, 2322.1655, 2322.1655, 2349.1377, 2927.1677, 2989.5410, 3739.8169, 3739.8169

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 46

Protein View

Match to: **gi|1171011** Score: **520** Expect: **6e-047**
RecName: Full=Pollen allergen Phl p 6; AltName: Full=Allergen Phl p VI; AltName: Allergen=Phl p 6;

Nominal mass (M_r): **13912;** Calculated pI value: **5.31**
NCBI BLAST search of gi|1171011 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|414712 from Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **100%**

Matched peptides shown in **Bold Red**

```
     1 MVAMFLAVAV VLGLATSPTA EGGKATTEEQ KLIEDVNASF RAAMATTANV
    51 PPADKYKTFE AAFTVSSKRN LADAVSKAPQ LVPKLDEVYN AAYNAADHAA
   101 PEDKYEAFVL HFSEALRIIA GTPEVHAVKP GA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
1 - 24	2349.1377	2348.1304	2348.2483	-0.1178	0	MVAMFLAVAVVLGLATSPTAEGGK Oxidation (M) (No match)
2 - 31	2989.5410	2988.5337	2988.5840	-0.0503	1	VAMFLAVAVVLGLATSPTAEGGKATTEEQK (No match)
25 - 41	1950.9829	1949.9756	1949.9694	0.0063	1	ATTEEQKLIEDVNASFR (Ions score 156)
25 - 41	1950.9829	1949.9756	1949.9694	0.0063	1	ATTEEQKLIEDVNASFR (No match)
32 - 41	1163.6022	1162.5949	1162.5982	-0.0033	0	LIEDVNASFR (Ions score 92)
32 - 41	1163.6022	1162.5949	1162.5982	-0.0033	0	LIEDVNASFR (No match)
42 - 57	1664.8286	1663.8213	1663.8239	-0.0026	1	AAMATTANVPPADKYK Oxidation (M) (No match)
58 - 68	1187.5847	1186.5774	1186.5869	-0.0095	0	TFEAAFTVSSK (No match)
58 - 69	1343.6936	1342.6863	1342.6880	-0.0017	1	TFEAAFTVSSKR (No match)
58 - 69	1343.6936	1342.6863	1342.6880	-0.0017	1	TFEAAFTVSSKR (Ions score 92)
70 - 84	1550.8815	1549.8742	1549.8827	-0.0085	1	NLADAVSKAPQLVPK (No match)
78 - 84	752.4548	751.4475	751.4592	-0.0117	0	APQLVPK (No match)
85 - 117	3739.8169	3738.8096	3738.7589	0.0507	1	LDEVYNAAYNAADHAAPEDKYEAFVLHFSEALR (Ions score 2)
85 - 117	3739.8169	3738.8096	3738.7589	0.0507	1	LDEVYNAAYNAADHAAPEDKYEAFVLHFSEALR (No match)
105 - 117	1581.8187	1580.8114	1580.7986	0.0128	0	YEAFVLHFSEALR (No match)
118 - 132	1459.8214	1458.8141	1458.8194	-0.0053	0	IIAGTPEVHAVKPGA (No match)

Spot 138

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	Accession	Mass	Score	Description
1.	gi|1171011	13912	418	RecName: Full=Pollen allergen Phl p 6; AltName: Full=Allergen Phl p VI; AltName: Allergen=Phl
2.	gi|28374059	11914	402	Chain A, Crystal Structure Of Phl P 6, A Major Timothy Grass Pollen Allergen Co-Crystallized
3.	gi|3004467	14597	396	Phl p6 allergen [Phleum pratense]
4.	gi|3004465	14592	185	Phl p6 allergen [Phleum pratense]
5.	gi|3004471	8622	148	Phl p6 IgE binding fragment [Phleum pratense]
6.	gi|3004469	11392	110	Phl p6 IgE binding fragment [Phleum pratense]
7.	gi|116056659	32595	54	50S ribosomal protein L28 (ISS) [Ostreococcus tauri]
8.	gi|53982307	133628	54	hypothetical protein [Oryza sativa (japonica cultivar-group)]
9.	gi|110288762	22085	54	hypothetical protein LOC_Os10g11570 [Oryza sativa (japonica cultivar-group)]
10.	gi|222630641	128362	53	hypothetical protein OsJ_17576 [Oryza sativa Japonica Group]

Results List

1. gi|1171011 **Mass:** 13912 **Score:** 418 **Expect:** 9.6e-037 **Queries matched:** 10

RecName: Full=Pollen allergen Phl p 6; AltName: Full=Allergen Phl p VI; AltName: Allergen=Phl p 6;

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1163.6050	1162.5977	1162.5982	-0.0005	32	-	41	0	77	LIEDVNASFR
1163.6050	1162.5977	1162.5982	-0.0005	32	-	41	0	---	LIEDVNASFR
1187.5869	1186.5796	1186.5869	-0.0073	58	-	68	0	---	TFEAAFTVSSK
1343.6920	1342.6847	1342.6880	-0.0033	58	-	69	1	---	TFEAAFTVSSKR
1343.6920	1342.6847	1342.6880	-0.0033	58	-	69	1	112	TFEAAFTVSSKR
1550.8738	1549.8665	1549.8827	-0.0162	70	-	84	1	---	NLADAVSKAPQLVPK
1664.8159	1663.8086	1663.8239	-0.0153	42	-	57	1	---	AAMATTANVPPADKYK + Oxidation (M)
1950.9691	1949.9618	1949.9694	-0.0075	25	-	41	1	---	ATTEEQKLIEDVNASFR
1950.9691	1949.9618	1949.9694	-0.0075	25	-	41	1	133	ATTEEQKLIEDVNASFR
2989.5276	2988.5203	2988.5840	-0.0637	2	-	31	1	---	VAMFLAVAVVLGLATSPTAEGGKATTEEQK

No match to: 707.3932, 713.4039, 768.5179, 818.4488, 936.5035, 1177.6178, 1300.7413, 1365.6750, 1387.6837, 1572.8719, 1634.8492, 1706.9885, 1964.9827, 2119.5452, 2135.0667, 2136.0928, 2136.0928, 2150.1055, 2150.1055, 2163.0752, 2927.2336, 3006.5198, 3740.7664

2. gi|28374059 **Mass:** 11914 **Score:** 402 **Expect:** 3.8e-035 **Queries matched:** 9

Chain A, Crystal Structure Of Phl P 6, A Major Timothy Grass Pollen Allergen Co-Crystallized With Z

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1163.6050	1162.5977	1162.5982	-0.0005	11	-	20	0	77	LIEDVNASFR
1163.6050	1162.5977	1162.5982	-0.0005	11	-	20	0	---	LIEDVNASFR
1187.5869	1186.5796	1186.5869	-0.0073	37	-	47	0	---	TFEAAFTVSSK
1343.6920	1342.6847	1342.6880	-0.0033	37	-	48	1	---	TFEAAFTVSSKR
1343.6920	1342.6847	1342.6880	-0.0033	37	-	48	1	112	TFEAAFTVSSKR

1550.8738	1549.8665	1549.8827	-0.0162	49 -	63	1	---	NLADAVSKAPQLVPK
1664.8159	1663.8086	1663.8239	-0.0153	21 -	36	1	---	AAMATTANVPPADKYK + Oxidation (M)
1950.9691	1949.9618	1949.9694	-0.0075	4 -	20	1	---	ATTEEQKLIEDVNASFR
1950.9691	1949.9618	1949.9694	-0.0075	4 -	20	1	133	ATTEEQKLIEDVNASFR

No match to: 707.3932, 713.4039, 768.5179, 818.4488, 936.5035, 1177.6178, 1300.7413, 1365.6750, 1387.6837, 1572.8719, 1634.8492, 1706.9885, 1964.9827, 2119.5452, 2135.0667, 2136.0928, 2136.0928, 2150.1055, 2150.1055, 2163.0752, 2927.2336, 2989.5276, 3006.5198, 3740.7664

3. gi|3004467 **Mass:** 14597 **Score:** 396 **Expect:** 1.5e-034 **Queries matched:** 9

Phl p6 allergen [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1163.6050	1162.5977	1162.5982	-0.0005	38 -	47	0	77	LIEDVNASFR
1163.6050	1162.5977	1162.5982	-0.0005	38 -	47	0	---	LIEDVNASFR
1187.5869	1186.5796	1186.5869	-0.0073	64 -	74	0	---	TFEAAFTVSSK
1343.6920	1342.6847	1342.6880	-0.0033	64 -	75	1	---	TFEAAFTVSSKR
1343.6920	1342.6847	1342.6880	-0.0033	64 -	75	1	112	TFEAAFTVSSKR
1550.8738	1549.8665	1549.8827	-0.0162	76 -	90	1	---	NLADAVSKAPQLVPK
1664.8159	1663.8086	1663.8239	-0.0153	48 -	63	1	---	AAMATTANVPPADKYK + Oxidation (M)
1950.9691	1949.9618	1949.9694	-0.0075	31 -	47	1	---	ATTEEQKLIEDVNASFR
1950.9691	1949.9618	1949.9694	-0.0075	31 -	47	1	133	ATTEEQKLIEDVNASFR

No match to: 707.3932, 713.4039, 768.5179, 818.4488, 936.5035, 1177.6178, 1300.7413, 1365.6750, 1387.6837, 1572.8719, 1634.8492, 1706.9885, 1964.9827, 2119.5452, 2135.0667, 2136.0928, 2136.0928, 2150.1055, 2150.1055, 2163.0752, 2927.2336, 2989.5276, 3006.5198, 3740.7664

4. gi|3004465 **Mass:** 14592 **Score:** 185 **Expect:** 1.9e-013 **Queries matched:** 7

Phl p6 allergen [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1177.6178	1176.6105	1176.6138	-0.0033	38 -	47	0	---	LIEDINASFR
1187.5869	1186.5796	1186.5869	-0.0073	64 -	74	0	---	TFEAAFTVSSK
1343.6920	1342.6847	1342.6880	-0.0033	64 -	75	1	---	TFEAAFTVSSKR
1343.6920	1342.6847	1342.6880	-0.0033	64 -	75	1	112	TFEAAFTVSSKR
1550.8738	1549.8665	1549.8827	-0.0162	76 -	90	1	---	NLADAVSKAPQLVPK
1664.8159	1663.8086	1663.8239	-0.0153	48 -	63	1	---	AAMATTANVPPADKYK + Oxidation (M)
1964.9827	1963.9754	1963.9850	-0.0096	31 -	47	1	---	ATTEEQKLIEDINASFR

No match to: 707.3932, 713.4039, 768.5179, 818.4488, 936.5035, 1163.6050, 1163.6050, 1300.7413, 1365.6750, 1387.6837, 1572.8719, 1634.8492, 1706.9885, 1950.9691, 1950.9691, 2119.5452, 2135.0667, 2136.0928, 2136.0928, 2150.1055, 2150.1055, 2163.0752, 2927.2336, 2989.5276, 3006.5198, 3740.7664

5. gi|3004471 **Mass:** 8622 **Score:** 148 **Expect:** 9.6e-010 **Queries matched:** 4

Phl p6 IgE binding fragment [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1187.5869	1186.5796	1186.5869	-0.0073	6 -	16	0	---	TFEAAFTVSSK

1343.6920	1342.6847	1342.6880	-0.0033	6 - 17	1	---	TFEAAFTVSSKR
1343.6920	1342.6847	1342.6880	-0.0033	6 - 17	1	112	TFEAAFTVSSKR
1550.8738	1549.8665	1549.8827	-0.0162	18 - 32	1	---	NLADAVSKAPQLVPK

No match to: 707.3932, 713.4039, 768.5179, 818.4488, 936.5035, 1163.6050, 1163.6050, 1177.6178, 1300.7413, 1365.6750, 1387.6837, 1572.8719, 1634.8492, 1664.8159, 1706.9885, 1950.9691, 1950.9691, 1964.9827, 2119.5452, 2135.0667, 2136.0928, 2136.0928, 2150.1055, 2150.1055, 2163.0752, 2927.2336, 2989.5276, 3006.5198, 3740.7664

6. gi|3004469 **Mass:** 11392 **Score:** 110 **Expect:** 6e-006 **Queries matched:** 4

Phl p6 IgE binding fragment [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1163.6050	1162.5977	1162.5982	-0.0005	6 -	15	0	77	LIEDVNASFR
1163.6050	1162.5977	1162.5982	-0.0005	6 -	15	0	---	LIEDVNASFR
1550.8738	1549.8665	1549.8827	-0.0162	44 -	58	1	---	NLADAVSKAPQLVPK
1664.8159	1663.8086	1663.8239	-0.0153	16 -	31	1	---	AAMATTANVPPADKYK + Oxidation (M)

No match to: 707.3932, 713.4039, 768.5179, 818.4488, 936.5035, 1177.6178, 1187.5869, 1300.7413, 1343.6920, 1343.6920, 1365.6750, 1387.6837, 1572.8719, 1634.8492, 1706.9885, 1950.9691, 1950.9691, 1964.9827, 2119.5452, 2135.0667, 2136.0928, 2136.0928, 2150.1055, 2150.1055, 2163.0752, 2927.2336, 2989.5276, 3006.5198, 3740.7664

7. gi|116056659 **Mass:** 32595 **Score:** 54 **Expect:** 2.4 **Queries matched:** 7

50S ribosomal protein L28 (ISS) [Ostreococcus tauri]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1187.5869	1186.5796	1186.5400	0.0396	83 -	93	0	---	IDADLHGMSGR + Oxidation (M)
1343.6920	1342.6847	1342.6411	0.0436	82 -	93	1	---	RIDADLHGMSGR + Oxidation (M)
1343.6920	1342.6847	1342.6411	0.0436	82 -	93	1	---	RIDADLHGMSGR + Oxidation (M)
1365.6750	1364.6677	1364.6935	-0.0258	10 -	23	0	---	LTNAFATGSDLGAK
1634.8492	1633.8419	1633.7981	0.0439	232 -	247	1	---	EAQLAKMDAAAATAEK + Oxidation (M)
1706.9885	1705.9812	1705.8933	0.0879	24 -	38	1	---	FRAACAVTTRPETVK
2927.2336	2926.2263	2926.3564	-0.1300	250 -	274	1	---	FAEANNMVLASNGRFCLDTMYSIFR

No match to: 707.3932, 713.4039, 768.5179, 818.4488, 936.5035, 1163.6050, 1163.6050, 1177.6178, 1300.7413, 1387.6837, 1550.8738, 1572.8719, 1664.8159, 1950.9691, 1950.9691, 1964.9827, 2119.5452, 2135.0667, 2136.0928, 2136.0928, 2150.1055, 2150.1055, 2163.0752, 2989.5276, 3006.5198, 3740.7664

8. gi|53982307 **Mass:** 133628 **Score:** 54 **Expect:** 2.4 **Queries matched:** 13

hypothetical protein [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
818.4488	817.4415	817.4922	-0.0507	700 -	705	1	---	FLNLRR
1163.6050	1162.5977	1162.6202	-0.0225	12 -	23	1	4	LGGKIMGMATGK
1163.6050	1162.5977	1162.6202	-0.0225	12 -	23	1	---	LGGKIMGMATGK
1343.6920	1342.6847	1342.7092	-0.0245	266 -	277	0	---	ADTVLLENALER
1343.6920	1342.6847	1342.7092	-0.0245	266 -	277	0	---	ADTVLLENALER
1550.8738	1549.8665	1549.8537	0.0128	1 -	15	1	---	MESALVSFALKLGGK
1634.8492	1633.8419	1633.8207	0.0212	1025 -	1038	1	---	AEKLPECFGVPMLK + Oxidation (M)

1664.8159	1663.8086	1663.7156	0.0930	838 - 850	0	---	WMQMMSAFTNLTR + 3 Oxidation (M)
1950.9691	1949.9618	1950.0210	-0.0592	1047 - 1063	1	---	RLFGLISLQDTTSEWGK
1950.9691	1949.9618	1950.0210	-0.0592	1047 - 1063	1	---	RLFGLISLQDTTSEWGK
1964.9827	1963.9754	1963.9091	0.0663	1148 - 1165	1	---	LRMCPAVLNQSSGTETNS
2136.0928	2135.0855	2135.0986	-0.0130	862 - 879	0	---	LPNGMGQLPFLDHLWIER
2136.0928	2135.0855	2135.0986	-0.0130	862 - 879	0	---	LPNGMGQLPFLDHLWIER

No match to: 707.3932, 713.4039, 768.5179, 936.5035, 1177.6178, 1187.5869, 1300.7413, 1365.6750, 1387.6837, 1572.8719, 1706.9885, 2119.5452, 2135.0667, 2150.1055, 2150.1055, 2163.0752, 2927.2336, 2989.5276, 3006.5198, 3740.7664

9. gi|110288762 **Mass:** 22085 **Score:** 54 **Expect:** 2.6 **Queries matched:** 6

hypothetical protein LOC_Os10g11570 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start - End	Miss	Ions	Peptide
1187.5869	1186.5796	1186.6393	-0.0597	92 - 100	1	---	LMAVQWRQR
1343.6920	1342.6847	1342.6775	0.0072	131 - 143	0	---	MATARPAGTQAPR + Oxidation (M)
1343.6920	1342.6847	1342.6775	0.0072	131 - 143	0	6	MATARPAGTQAPR + Oxidation (M)
1387.6837	1386.6764	1386.6673	0.0091	144 - 156	0	---	QGRPEMAVGTGER
1964.9827	1963.9754	1963.8904	0.0850	34 - 54	1	---	TGMAEGAAGVGADKTEGEAAR + Oxidation (M)
3740.7664	3739.7591	3739.8159	-0.0568	173 - 203	1	---	NTMIQYDLYIYGYTFLEFSWAVGKVLELGQY + Oxidation (M)

No match to: 707.3932, 713.4039, 768.5179, 818.4488, 936.5035, 1163.6050, 1163.6050, 1177.6178, 1300.7413, 1365.6750, 1550.8738, 1572.8719, 1634.8492, 1664.8159, 1706.9885, 1950.9691, 1950.9691, 2119.5452, 2135.0667, 2136.0928, 2136.0928, 2150.1055, 2150.1055, 2163.0752, 2927.2336, 2989.5276, 3006.5198

10. gi|222630641 **Mass:** 128362 **Score:** 53 **Expect:** 2.8 **Queries matched:** 13

hypothetical protein OsJ_17576 [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start - End	Miss	Ions	Peptide
818.4488	817.4415	817.4922	-0.0507	655 - 660	1	---	FLNLRR
1163.6050	1162.5977	1162.6202	-0.0225	12 - 23	1	4	LGGKIMGMATGK
1163.6050	1162.5977	1162.6202	-0.0225	12 - 23	1	---	LGGKIMGMATGK
1343.6920	1342.6847	1342.7092	-0.0245	266 - 277	0	---	ADTVLLENALER
1343.6920	1342.6847	1342.7092	-0.0245	266 - 277	0	---	ADTVLLENALER
1550.8738	1549.8665	1549.8537	0.0128	1 - 15	1	---	MESALVSFALKLGGK
1634.8492	1633.8419	1633.8207	0.0212	980 - 993	1	---	AEKLPECFGVPMLK + Oxidation (M)
1664.8159	1663.8086	1663.7156	0.0930	793 - 805	0	---	WMQMMSAFTNLTR + 3 Oxidation (M)
1950.9691	1949.9618	1950.0210	-0.0592	1002 - 1018	1	---	RLFGLISLQDTTSEWGK
1950.9691	1949.9618	1950.0210	-0.0592	1002 - 1018	1	---	RLFGLISLQDTTSEWGK
1964.9827	1963.9754	1963.9091	0.0663	1103 - 1120	1	---	LRMCPAVLNQSSGTETNS
2136.0928	2135.0855	2135.0986	-0.0130	817 - 834	0	---	LPNGMGQLPFLDHLWIER
2136.0928	2135.0855	2135.0986	-0.0130	817 - 834	0	---	LPNGMGQLPFLDHLWIER

No match to: 707.3932, 713.4039, 768.5179, 936.5035, 1177.6178, 1187.5869, 1300.7413, 1365.6750, 1387.6837, 1572.8719, 1706.9885, 2119.5452, 2135.0667, 2150.1055, 2150.1055, 2163.0752, 2927.2336, 2989.5276, 3006.5198, 3740.7664

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 33

Protein View

Match to: **gi|1171011** Score: **418** Expect: **9.6e-037**
RecName: Full=Pollen allergen Phl p 6; AltName: Full=Allergen Phl p VI; AltName: Allergen=Phl p 6;

Nominal mass (M_r): **13912;** Calculated pI value: **5.31**
NCBI BLAST search of gi|1171011 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|414712 from Phleum pratense

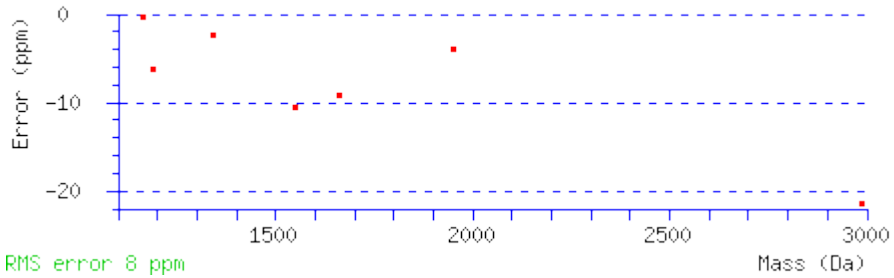
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **62%**

Matched peptides shown in **Bold Red**

```
     1 MVAMFLAVAV VLGLATSPTA EGGKATTEEQ KLIEDVNASF RAAMATTANV
    51 PPADKYKTFE AAFTVSSKRN LADAVSKAPQ LVPKLDEVYN AAYNAADHAA
   101 PEDKYEAFVL HFSEALRIIA GTPEVHAVKP GA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
2 - 31	2989.5276	2988.5203	2988.5840	-0.0637	1	**VAMFLAVAVVLGLATSPTAEGGKATTEEQK** (No match)
25 - 41	1950.9691	1949.9618	1949.9694	-0.0075	1	**ATTEEQKLIEDVNASFR** (No match)
25 - 41	1950.9691	1949.9618	1949.9694	-0.0075	1	**ATTEEQKLIEDVNASFR** (Ions score 133)
32 - 41	1163.6050	1162.5977	1162.5982	-0.0005	0	**LIEDVNASFR** (Ions score 77)
32 - 41	1163.6050	1162.5977	1162.5982	-0.0005	0	**LIEDVNASFR** (No match)
42 - 57	1664.8159	1663.8086	1663.8239	-0.0153	1	**AAMATTANVPPADKYK** Oxidation (M) (No match)
58 - 68	1187.5869	1186.5796	1186.5869	-0.0073	0	**TFEAAFTVSSK** (No match)
58 - 69	1343.6920	1342.6847	1342.6880	-0.0033	1	**TFEAAFTVSSKR** (No match)
58 - 69	1343.6920	1342.6847	1342.6880	-0.0033	1	**TFEAAFTVSSKR** (Ions score 112)
70 - 84	1550.8738	1549.8665	1549.8827	-0.0162	1	**NLADAVSKAPQLVPK** (No match)



Spot 139

Index

	Accession	Mass	Score	Description
1.	gi|3004465	14592	409	Phl p6 allergen [Phleum pratense]
2.	gi|1171011	13912	192	RecName: Full=Pollen allergen Phl p 6; AltName: Full=Allergen Phl p VI; AltName: Allergen=Phl p
3.	gi|28374059	11914	192	Chain A, Crystal Structure Of Phl P 6, A Major Timothy Grass Pollen Allergen Co-Crystallized Wit
4.	gi|3004467	14597	171	Phl p6 allergen [Phleum pratense]
5.	gi|3004471	8622	139	Phl p6 IgE binding fragment [Phleum pratense]

Results List

1. gi|3004465 **Mass:** 14592 **Score:** 409 **Expect:** 7.6e-036 **Queries matched:** 11

Phl p6 allergen [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
752.4576	751.4503	751.4592	-0.0089	84	90	0	---	APQLVPK
1177.6221	1176.6148	1176.6138	0.0010	38	47	0	92	LIEDINASFR
1177.6221	1176.6148	1176.6138	0.0010	38	47	0	---	LIEDINASFR
1187.5857	1186.5784	1186.5869	-0.0085	64	74	0	---	TFEAAFTVSSK
1343.6959	1342.6886	1342.6880	0.0006	64	75	1	---	TFEAAFTVSSKR
1343.6959	1342.6886	1342.6880	0.0006	64	75	1	97	TFEAAFTVSSKR
1550.8834	1549.8761	1549.8827	-0.0066	76	90	1	---	NLADAVSKAPQLVPK
1648.8330	1647.8257	1647.8290	-0.0033	48	63	1	---	AAMATTANVPPADKYK
1664.8256	1663.8183	1663.8239	-0.0056	48	63	1	---	AAMATTANVPPADKYK + Oxidation (M)
1964.9877	1963.9804	1963.9850	-0.0046	31	47	1	---	ATTEEQKLIEDINASFR
1964.9877	1963.9804	1963.9850	-0.0046	31	47	1	145	ATTEEQKLIEDINASFR

No match to: 707.3885, 713.4058, 768.5204, 805.3932, 818.4437, 822.4119, 951.4592, 966.5403, 991.4982, 1064.5447, 1075.5516, 1076.0488, 1118.5579, 1160.6046, 1163.6014, 1297.6753, 1299.6859, 1300.7334, 1325.6868, 1326.1599, 1327.1254, 1634.8530, 1706.9883, 1922.0277, 1948.4352, 1950.9659, 2093.0906, 2107.1646, 2133.5464, 2136.1023, 2149.0940, 2150.1182, 2150.1182, 2176.0854, 2221.1545, 2312.1770, 2321.1711, 2360.2859, 2927.2742, 2929.1658, 2973.5435, 2989.5583, 2989.5583, 3004.6113

2. gi|1171011 **Mass:** 13912 **Score:** 192 **Expect:** 3.8e-014 **Queries matched:** 11

RecName: Full=Pollen allergen Phl p 6; AltName: Full=Allergen Phl p VI; AltName: Allergen=Phl p 6;

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
752.4576	751.4503	751.4592	-0.0089	78	84	0	---	APQLVPK
1163.6014	1162.5941	1162.5982	-0.0041	32	41	0	---	LIEDVNASFR
1187.5857	1186.5784	1186.5869	-0.0085	58	68	0	---	TFEAAFTVSSK
1343.6959	1342.6886	1342.6880	0.0006	58	69	1	---	TFEAAFTVSSKR
1343.6959	1342.6886	1342.6880	0.0006	58	69	1	97	TFEAAFTVSSKR
1550.8834	1549.8761	1549.8827	-0.0066	70	84	1	---	NLADAVSKAPQLVPK

1648.8330	1647.8257	1647.8290	-0.0033	42 -	57	1	---	AAMATTANVPPADKYK
1664.8256	1663.8183	1663.8239	-0.0056	42 -	57	1	---	AAMATTANVPPADKYK + Oxidation (M)
1950.9659	1949.9586	1949.9694	-0.0107	25 -	41	1	---	ATTEEQKLIEDVNASFR
2989.5583	2988.5510	2988.5840	-0.0330	2 -	31	1	---	VAMFLAVAVVLGLATSPTAEGGKATTEEQK
2989.5583	2988.5510	2988.5840	-0.0330	2 -	31	1	---	VAMFLAVAVVLGLATSPTAEGGKATTEEQK

No match to: 707.3885, 713.4058, 768.5204, 805.3932, 818.4437, 822.4119, 951.4592, 966.5403, 991.4982, 1064.5447, 1075.5516, 1076.0488, 1118.5579, 1160.6046, 1177.6221, 1177.6221, 1297.6753, 1299.6859, 1300.7334, 1325.6868, 1326.1599, 1327.1254, 1634.8530, 1706.9883, 1922.0277, 1948.4352, 1964.9877, 1964.9877, 2093.0906, 2107.1646, 2133.5464, 2136.1023, 2149.0940, 2150.1182, 2150.1182, 2176.0854, 2221.1545, 2312.1770, 2321.1711, 2360.2859, 2927.2742, 2929.1658, 2973.5435, 3004.6113

3. gi|28374059 **Mass:** 11914 **Score:** 192 **Expect:** 3.8e-014 **Queries matched:** 10

Chain A, Crystal Structure Of Phl P 6, A Major Timothy Grass Pollen Allergen Co-Crystallized With Z

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
752.4576	751.4503	751.4592	-0.0089	57 -	63	0	---	APQLVPK
991.4982	990.4909	990.4981	-0.0072	2 -	10	1	---	GKATTEEQK
1163.6014	1162.5941	1162.5982	-0.0041	11 -	20	0	---	LIEDVNASFR
1187.5857	1186.5784	1186.5869	-0.0085	37 -	47	0	---	TFEAAFTVSSK
1343.6959	1342.6886	1342.6880	0.0006	37 -	48	1	---	TFEAAFTVSSKR
1343.6959	1342.6886	1342.6880	0.0006	37 -	48	1	97	TFEAAFTVSSKR
1550.8834	1549.8761	1549.8827	-0.0066	49 -	63	1	---	NLADAVSKAPQLVPK
1648.8330	1647.8257	1647.8290	-0.0033	21 -	36	1	---	AAMATTANVPPADKYK
1664.8256	1663.8183	1663.8239	-0.0056	21 -	36	1	---	AAMATTANVPPADKYK + Oxidation (M)
1950.9659	1949.9586	1949.9694	-0.0107	4 -	20	1	---	ATTEEQKLIEDVNASFR

No match to: 707.3885, 713.4058, 768.5204, 805.3932, 818.4437, 822.4119, 951.4592, 966.5403, 1064.5447, 1075.5516, 1076.0488, 1118.5579, 1160.6046, 1177.6221, 1177.6221, 1297.6753, 1299.6859, 1300.7334, 1325.6868, 1326.1599, 1327.1254, 1634.8530, 1706.9883, 1922.0277, 1948.4352, 1964.9877, 1964.9877, 2093.0906, 2107.1646, 2133.5464, 2136.1023, 2149.0940, 2150.1182, 2150.1182, 2176.0854, 2221.1545, 2312.1770, 2321.1711, 2360.2859, 2927.2742, 2929.1658, 2973.5435, 2989.5583, 2989.5583, 3004.6113

4. gi|3004467 **Mass:** 14597 **Score:** 171 **Expect:** 4.8e-012 **Queries matched:** 9

Phl p6 allergen [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
752.4576	751.4503	751.4592	-0.0089	84 -	90	0	---	APQLVPK
1163.6014	1162.5941	1162.5982	-0.0041	38 -	47	0	---	LIEDVNASFR
1187.5857	1186.5784	1186.5869	-0.0085	64 -	74	0	---	TFEAAFTVSSK
1343.6959	1342.6886	1342.6880	0.0006	64 -	75	1	---	TFEAAFTVSSKR
1343.6959	1342.6886	1342.6880	0.0006	64 -	75	1	97	TFEAAFTVSSKR
1550.8834	1549.8761	1549.8827	-0.0066	76 -	90	1	---	NLADAVSKAPQLVPK
1648.8330	1647.8257	1647.8290	-0.0033	48 -	63	1	---	AAMATTANVPPADKYK
1664.8256	1663.8183	1663.8239	-0.0056	48 -	63	1	---	AAMATTANVPPADKYK + Oxidation (M)
1950.9659	1949.9586	1949.9694	-0.0107	31 -	47	1	---	ATTEEQKLIEDVNASFR

No match to: 707.3885, 713.4058, 768.5204, 805.3932, 818.4437, 822.4119, 951.4592, 966.5403, 991.4982, 1064.5447,

1075.5516, 1076.0488, 1118.5579, 1160.6046, 1177.6221, 1177.6221, 1297.6753, 1299.6859, 1300.7334, 1325.6868, 1326.1599, 1327.1254, 1634.8530, 1706.9883, 1922.0277, 1948.4352, 1964.9877, 1964.9877, 2093.0906, 2107.1646, 2133.5464, 2136.1023, 2149.0940, 2150.1182, 2150.1182, 2176.0854, 2221.1545, 2312.1770, 2321.1711, 2360.2859, 2927.2742, 2929.1658, 2973.5435, 2989.5583, 2989.5583, 3004.6113

5. gi|3004471 **Mass:** 8622 **Score:** 139 **Expect:** 7.6e-009 **Queries matched:** 5

Phl p6 IgE binding fragment [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
752.4576	751.4503	751.4592	-0.0089	26	-	32	0	---	APQLVPK
1187.5857	1186.5784	1186.5869	-0.0085	6	-	16	0	---	TFEAAFTVSSK
1343.6959	1342.6886	1342.6880	0.0006	6	-	17	1	---	TFEAAFTVSSKR
1343.6959	1342.6886	1342.6880	0.0006	6	-	17	1	97	TFEAAFTVSSKR
1550.8834	1549.8761	1549.8827	-0.0066	18	-	32	1	---	NLADAVSKAPQLVPK

No match to: 707.3885, 713.4058, 768.5204, 805.3932, 818.4437, 822.4119, 951.4592, 966.5403, 991.4982, 1064.5447, 1075.5516, 1076.0488, 1118.5579, 1160.6046, 1163.6014, 1177.6221, 1177.6221, 1297.6753, 1299.6859, 1300.7334, 1325.6868, 1326.1599, 1327.1254, 1634.8530, 1648.8330, 1664.8256, 1706.9883, 1922.0277, 1948.4352, 1950.9659, 1964.9877, 1964.9877, 2093.0906, 2107.1646, 2133.5464, 2136.1023, 2149.0940, 2150.1182, 2150.1182, 2176.0854, 2221.1545, 2312.1770, 2321.1711, 2360.2859, 2927.2742, 2929.1658, 2973.5435, 2989.5583, 2989.5583, 3004.6113

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 55

Protein View

Match to: **gi|3004465** Score: **409** Expect: **7.6e-036**
Phl p6 allergen [Phleum pratense]

Nominal mass (M_r): **14592**; Calculated pI value: **5.68**
NCBI BLAST search of gi|3004465 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **43%**

Matched peptides shown in **Bold Red**

```
    1 MAAHKFMVAM FLAVAVVLGL ATSPTAEGGK ATTEEQKLIE DINASFRAAM
   51 ATTANVPPAD KYKTFEAAFT VSSKRNLADA VSKAPQLVPK LDEVYNAAYN
  101 AADHAAPEDK YEAFVLHFSE ALHIIAGTPE VHAVKPGA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
31 - 47	1964.9877	1963.9804	1963.9850	-0.0046	1	**ATTEEQKLIEDINASFR** (No match)
31 - 47	1964.9877	1963.9804	1963.9850	-0.0046	1	**ATTEEQKLIEDINASFR** (Ions score 145)
38 - 47	1177.6221	1176.6148	1176.6138	0.0010	0	**LIEDINASFR** (Ions score 92)
38 - 47	1177.6221	1176.6148	1176.6138	0.0010	0	**LIEDINASFR** (No match)
48 - 63	1648.8330	1647.8257	1647.8290	-0.0033	1	**AAMATTANVPPADKYK** (No match)
48 - 63	1664.8256	1663.8183	1663.8239	-0.0056	1	**AAMATTANVPPADKYK** Oxidation (M) (No match)
64 - 74	1187.5857	1186.5784	1186.5869	-0.0085	0	**TFEAAFTVSSK** (No match)
64 - 75	1343.6959	1342.6886	1342.6880	0.0006	1	**TFEAAFTVSSKR** (No match)
64 - 75	1343.6959	1342.6886	1342.6880	0.0006	1	**TFEAAFTVSSKR** (Ions score 97)
76 - 90	1550.8834	1549.8761	1549.8827	-0.0066	1	**NLADAVSKAPQLVPK** (No match)
84 - 90	752.4576	751.4503	751.4592	-0.0089	0	**APQLVPK** (No match)

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	Accession	Mass	Score	Description
1.	gi|27461140	12856	136	thioredoxin H [Triticum aestivum]
2.	gi|186972814	12916	121	Chain A, Crystal Structure Of Barley Thioredoxin H Isoform 1 Crystallized Using Ammonium Sulfa
3.	gi|5932426	13443	46	thioredoxin-like protein [Secale cereale]
4.	gi|23617005	5944	46	hypothetical protein [Oryza sativa Japonica Group]
5.	gi|24637237	14706	45	thioredoxin [Triticum aestivum]
6.	gi|27543511	14668	45	thioredoxin h [Leymus chinensis]
7.	gi|3982614	11399	42	disease resistance gene analog PIC11-1 [Zea mays]
8.	gi|223512123	34708	42	conserved hypothetical protein [Ricinus communis]
9.	gi|168002740	75846	38	predicted protein [Physcomitrella patens subsp. patens]
10.	gi|168065128	78825	38	predicted protein [Physcomitrella patens subsp. patens]

Results List

1. gi|27461140 **Mass:** 12856 **Score:** 136 **Expect:** 1.5e-008 **Queries matched:** 5

thioredoxin H [Triticum aestivum]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1020.6206	1019.6133	1019.6167	-0.0034	56	-	64	1	---	KFPGAIFLK
1207.6676	1206.6603	1206.6648	-0.0045	45	-	55	0	---	VIAPVFAEYAK
1207.6676	1206.6603	1206.6648	-0.0045	45	-	55	0	92	VIAPVFAEYAK
1335.8188	1334.8115	1334.7597	0.0518	45	-	56	1	---	VIAPVFAEYAKK
2210.0745	2209.0672	2209.0659	0.0013	26	-	44	1	---	ETGKLVIIDFTASWCGPCR

No match to: 713.4077, 734.4937, 736.4938, 750.5104, 768.5212, 886.9892, 1229.6549, 1237.5719, 1238.0715, 1276.7069, 1279.7593, 1334.8831, 1448.9189, 1492.7098, 1680.9435, 1809.0344, 1809.0344, 2014.9398, 2109.1863, 2395.1990, 2395.1990, 2427.1829, 2427.1829, 2473.1628, 2473.1628, 2658.2727, 2824.3169

2. gi|186972814 **Mass:** 12916 **Score:** 121 **Expect:** 4.8e-007 **Queries matched:** 4

Chain A, Crystal Structure Of Barley Thioredoxin H Isoform 1 Crystallized Using Ammonium Sulfate As

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1020.6206	1019.6133	1019.6167	-0.0034	56	-	64	1	---	KFPGAIFLK
1207.6676	1206.6603	1206.6648	-0.0045	45	-	55	0	---	VIAPVFAEYAK
1207.6676	1206.6603	1206.6648	-0.0045	45	-	55	0	92	VIAPVFAEYAK
1335.8188	1334.8115	1334.7597	0.0518	45	-	56	1	---	VIAPVFAEYAKK

No match to: 713.4077, 734.4937, 736.4938, 750.5104, 768.5212, 886.9892, 1229.6549, 1237.5719, 1238.0715, 1276.7069, 1279.7593, 1334.8831, 1448.9189, 1492.7098, 1680.9435, 1809.0344, 1809.0344, 2014.9398, 2109.1863, 2210.0745, 2395.1990, 2395.1990, 2427.1829, 2427.1829, 2473.1628, 2473.1628, 2658.2727, 2824.3169

3. gi|5932426 **Mass:** 13443 **Score:** 46 **Expect:** 16 **Queries matched:** 2

thioredoxin-like protein [Secale cereale]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1207.6676	1206.6603	1206.6495	0.0108	10	-	19	1	---	SIVEEKLDFK
1207.6676	1206.6603	1206.6318	0.0285	60	-	70	0	30	VIAPVYAEMSK

No match to: 713.4077, 734.4937, 736.4938, 750.5104, 768.5212, 886.9892, 1020.6206, 1229.6549, 1237.5719, 1238.0715, 1276.7069, 1279.7593, 1334.8831, 1335.8188, 1448.9189, 1492.7098, 1680.9435, 1809.0344, 1809.0344, 2014.9398, 2109.1863, 2210.0745, 2395.1990, 2395.1990, 2427.1829, 2427.1829, 2473.1628, 2473.1628, 2658.2727, 2824.3169

4. gi|23617005 **Mass:** 5944 **Score:** 46 **Expect:** 16 **Queries matched:** 4

hypothetical protein [Oryza sativa Japonica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
736.4938	735.4865	735.4755	0.0110	8	-	13	0	---	VVLLHR
2427.1829	2426.1756	2426.1821	-0.0064	29	-	53	1	---	GSGGATAACIFMTGAKSAIVLSLED
2427.1829	2426.1756	2426.1821	-0.0064	29	-	53	1	---	GSGGATAACIFMTGAKSAIVLSLED
2658.2727	2657.2654	2657.1671	0.0983	20	-	44	1	---	CDVEWPAERGSGGATAACIFMTGAK + Oxidation (M)

No match to: 713.4077, 734.4937, 750.5104, 768.5212, 886.9892, 1020.6206, 1207.6676, 1207.6676, 1229.6549, 1237.5719, 1238.0715, 1276.7069, 1279.7593, 1334.8831, 1335.8188, 1448.9189, 1492.7098, 1680.9435, 1809.0344, 1809.0344, 2014.9398, 2109.1863, 2210.0745, 2395.1990, 2395.1990, 2473.1628, 2473.1628, 2824.3169

5. gi|24637237 **Mass:** 14706 **Score:** 45 **Expect:** 21 **Queries matched:** 2

thioredoxin [Triticum aestivum]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1207.6676	1206.6603	1206.6495	0.0108	10	-	19	1	---	SIVEEKLDFK
1207.6676	1206.6603	1206.6318	0.0285	60	-	70	0	30	VIAPVYAEMSK

No match to: 713.4077, 734.4937, 736.4938, 750.5104, 768.5212, 886.9892, 1020.6206, 1229.6549, 1237.5719, 1238.0715, 1276.7069, 1279.7593, 1334.8831, 1335.8188, 1448.9189, 1492.7098, 1680.9435, 1809.0344, 1809.0344, 2014.9398, 2109.1863, 2210.0745, 2395.1990, 2395.1990, 2427.1829, 2427.1829, 2473.1628, 2473.1628, 2658.2727, 2824.3169

6. gi|27543511 **Mass:** 14668 **Score:** 45 **Expect:** 21 **Queries matched:** 2

thioredoxin h [Leymus chinensis]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1207.6676	1206.6603	1206.6495	0.0108	10	-	19	1	---	SIVEEKLDFK
1207.6676	1206.6603	1206.6318	0.0285	60	-	70	0	30	VIAPVYAEMSK

No match to: 713.4077, 734.4937, 736.4938, 750.5104, 768.5212, 886.9892, 1020.6206, 1229.6549, 1237.5719, 1238.0715, 1276.7069, 1279.7593, 1334.8831, 1335.8188, 1448.9189, 1492.7098, 1680.9435, 1809.0344, 1809.0344, 2014.9398, 2109.1863, 2210.0745, 2395.1990, 2395.1990, 2427.1829, 2427.1829, 2473.1628, 2473.1628, 2658.2727, 2824.3169

7. gi|3982614 **Mass:** 11399 **Score:** 42 **Expect:** 39 **Queries matched:** 4

disease resistance gene analog PIC11-1 [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1229.6549	1228.6476	1228.6703	-0.0227	1	-	10	0	---	LLILDDVWDK
1680.9435	1679.9362	1679.8617	0.0745	37	-	51	0	---	DVSSLAVDQYTIELK

1809.0344	1808.0271	1807.9567	0.0704	36 - 51	1	---	KDVSSLAVDQYTIELK
1809.0344	1808.0271	1807.9567	0.0704	36 - 51	1	7	KDVSSLAVDQYTIELK

No match to: 713.4077, 734.4937, 736.4938, 750.5104, 768.5212, 886.9892, 1020.6206, 1207.6676, 1207.6676, 1237.5719, 1238.0715, 1276.7069, 1279.7593, 1334.8831, 1335.8188, 1448.9189, 1492.7098, 2014.9398, 2109.1863, 2210.0745, 2395.1990, 2395.1990, 2427.1829, 2427.1829, 2473.1628, 2473.1628, 2658.2727, 2824.3169

8. gi|223512123 **Mass:** 34708 **Score:** 42 **Expect:** 41 **Queries matched:** 6

conserved hypothetical protein [Ricinus communis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
768.5212	767.5139	767.4766	0.0374	179 -	184	0	---	QRPVLR
1229.6549	1228.6476	1228.6485	-0.0009	1 -	11	0	---	MLPTDPISIAR + Oxidation (M)
1335.8188	1334.8115	1334.7975	0.0140	51 -	60	0	---	RPIWILVPWR
1492.7098	1491.7025	1491.7140	-0.0114	277 -	289	1	---	RDEVADAPMVSFR
2473.1628	2472.1555	2472.1642	-0.0086	98 -	122	0	---	GHHAPDAAAGDVHVAGLEGHAQAER
2473.1628	2472.1555	2472.1642	-0.0086	98 -	122	0	---	GHHAPDAAAGDVHVAGLEGHAQAER

No match to: 713.4077, 734.4937, 736.4938, 750.5104, 886.9892, 1020.6206, 1207.6676, 1207.6676, 1237.5719, 1238.0715, 1276.7069, 1279.7593, 1334.8831, 1448.9189, 1680.9435, 1809.0344, 1809.0344, 2014.9398, 2109.1863, 2210.0745, 2395.1990, 2395.1990, 2427.1829, 2427.1829, 2658.2727, 2824.3169

9. gi|168002740 **Mass:** 75846 **Score:** 38 **Expect:** 89 **Queries matched:** 4

predicted protein [Physcomitrella patens subsp. patens]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1207.6676	1206.6603	1206.6033	0.0571	64 -	73	0	---	TLHDNFVYAK
1207.6676	1206.6603	1206.6033	0.0571	64 -	73	0	29	TLHDNFVYAK
2473.1628	2472.1555	2472.2656	-0.1101	297 -	318	0	---	MNVLVMLHHGVAVGFYQGDILK + 2 Oxidation (M)
2473.1628	2472.1555	2472.2656	-0.1101	297 -	318	0	---	MNVLVMLHHGVAVGFYQGDILK + 2 Oxidation (M)

No match to: 713.4077, 734.4937, 736.4938, 750.5104, 768.5212, 886.9892, 1020.6206, 1229.6549, 1237.5719, 1238.0715, 1276.7069, 1279.7593, 1334.8831, 1335.8188, 1448.9189, 1492.7098, 1680.9435, 1809.0344, 1809.0344, 2014.9398, 2109.1863, 2210.0745, 2395.1990, 2395.1990, 2427.1829, 2427.1829, 2658.2727, 2824.3169

10. gi|168065128 **Mass:** 78825 **Score:** 38 **Expect:** 94 **Queries matched:** 4

predicted protein [Physcomitrella patens subsp. patens]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1207.6676	1206.6603	1206.6033	0.0571	86 -	95	0	---	TLHDNFVYAK
1207.6676	1206.6603	1206.6033	0.0571	86 -	95	0	29	TLHDNFVYAK
2473.1628	2472.1555	2472.2479	-0.0924	319 -	340	0	---	MNMLVMLHHGVAVGFYQGDILK
2473.1628	2472.1555	2472.2479	-0.0924	319 -	340	0	---	MNMLVMLHHGVAVGFYQGDILK

No match to: 713.4077, 734.4937, 736.4938, 750.5104, 768.5212, 886.9892, 1020.6206, 1229.6549, 1237.5719, 1238.0715, 1276.7069, 1279.7593, 1334.8831, 1335.8188, 1448.9189, 1492.7098, 1680.9435, 1809.0344, 1809.0344, 2014.9398, 2109.1863, 2210.0745, 2395.1990, 2395.1990, 2427.1829, 2427.1829, 2658.2727, 2824.3169

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 32

Protein View

Match to: **gi|27461140** Score: **136** Expect: **1.5e-008**
thioredoxin H [Triticum aestivum]

Nominal mass (M_r): **12856**; Calculated pI value: **5.29**
NCBI BLAST search of gi|27461140 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Triticum aestivum

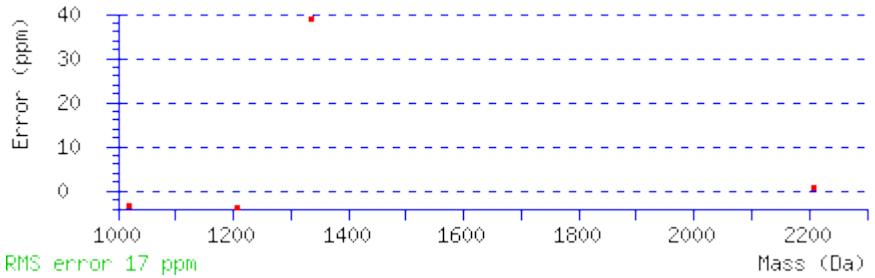
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **33%**

Matched peptides shown in **Bold Red**

```
     1 MAAEEGAVIA CHTKQEFDTH MANGK[ETGKL VIIDFTASWC GPCRVIAPVF
    51 AEYAKKFPGA IFLK]VDVDEL KDVAEAYNVE AMPTFLFIKD GAKVDTVVGG
   101 RKDDIHTKIV ALMGSASA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
26 - 44	2210.0745	2209.0672	2209.0659	0.0013	1	**ETGKLVIIDFTASWCGPCR**	(No match)
45 - 55	1207.6676	1206.6603	1206.6648	-0.0045	0	**VIAPVFAEYAK**	(No match)
45 - 55	1207.6676	1206.6603	1206.6648	-0.0045	0	**VIAPVFAEYAK**	(Ions score 92)
45 - 56	1335.8188	1334.8115	1334.7597	0.0518	1	**VIAPVFAEYAKK**	(No match)
56 - 64	1020.6206	1019.6133	1019.6167	-0.0034	1	**KFPGAIFLK**	(No match)



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	Accession	Mass	Score	Description
1.	gi|39841264	10952	228	Phl p 3 allergen [Phleum pratense]
2.	gi|169404532	12218	227	Chain A, Solution Structure Of Phl P 3, A Major Allergen From Timothy Grass Pollen
3.	gi|14423759	10926	160	RecName: Full=Pollen allergen Dac g 3; AltName: Full=Allergen Dac g III; AltName: Allergen=Dac
4.	gi|168035127	73702	54	predicted protein [Physcomitrella patens subsp. patens]
5.	gi|157349758	43576	50	unnamed protein product [Vitis vinifera]
6.	gi|15241897	64256	48	SYNC1; ATP binding / aminoacyl-tRNA ligase/ asparagine-tRNA ligase/ aspartate-tRNA ligase/ nuc
7.	gi|147834192	51187	48	hypothetical protein [Vitis vinifera]
8.	gi|255561196	68961	45	Phosphoenolpyruvate carboxylase, putative [Ricinus communis]
9.	gi|225449527	25569	45	PREDICTED: hypothetical protein [Vitis vinifera]
10.	gi|168057923	28476	42	predicted protein [Physcomitrella patens subsp. patens]

Results List

1. gi|39841264 **Mass:** 10952 **Score:** 228 **Expect:** 9.6e-018 **Queries matched:** 8

Phl p 3 allergen [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
959.5234	958.5161	958.5235	-0.0074	49	-	56	1	---	KGNVWEVK
1348.7375	1347.7302	1347.7298	0.0004	57	-	68	0	68	SSKPLVGPFNFR
1348.7375	1347.7302	1347.7298	0.0004	57	-	68	0	---	SSKPLVGPFNFR
1440.6537	1439.6464	1439.6681	-0.0216	37	-	48	0	---	QHGSEEWEPLTK
1440.6537	1439.6464	1439.6681	-0.0216	37	-	48	0	44	QHGSEEWEPLTK
1605.8262	1604.8189	1604.8158	0.0032	23	-	36	0	---	YTRPGDSLAEVELR
1605.8262	1604.8189	1604.8158	0.0032	23	-	36	0	34	YTRPGDSLAEVELR
1857.9586	1856.9513	1856.9606	-0.0093	57	-	72	1	---	SSKPLVGPFNFRFMSK + Oxidation (M)

No match to: 768.5156, 1364.7294, 1370.7062, 1379.6990, 1379.6990, 1423.6528, 1796.8937, 1796.8937

2. gi|169404532 **Mass:** 12218 **Score:** 227 **Expect:** 1.2e-017 **Queries matched:** 8

Chain A, Solution Structure Of Phl P 3, A Major Allergen From Timothy Grass Pollen

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
959.5234	958.5161	958.5235	-0.0074	60	-	67	1	---	KGNVWEVK
1348.7375	1347.7302	1347.7298	0.0004	68	-	79	0	68	SSKPLVGPFNFR
1348.7375	1347.7302	1347.7298	0.0004	68	-	79	0	---	SSKPLVGPFNFR
1440.6537	1439.6464	1439.6681	-0.0216	48	-	59	0	---	QHGSEEWEPLTK
1440.6537	1439.6464	1439.6681	-0.0216	48	-	59	0	44	QHGSEEWEPLTK
1605.8262	1604.8189	1604.8158	0.0032	34	-	47	0	---	YTRPGDSLAEVELR
1605.8262	1604.8189	1604.8158	0.0032	34	-	47	0	34	YTRPGDSLAEVELR
1857.9586	1856.9513	1856.9606	-0.0093	68	-	83	1	---	SSKPLVGPFNFRFMSK + Oxidation (M)

No match to: 768.5156, 1364.7294, 1370.7062, 1379.6990, 1379.6990, 1423.6528, 1796.8937, 1796.8937

3. gi|14423759 **Mass:** 10926 **Score:** 160 **Expect:** 6.1e-011 **Queries matched:** 6

RecName: Full=Pollen allergen Dac g 3; AltName: Full=Allergen Dac g III; AltName: Allergen=Dac g 3

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1379.6990	1378.6917	1378.7132	-0.0215	76	87	0	---	NVFDEVIPTAFK
1379.6990	1378.6917	1378.7132	-0.0215	76	87	0	41	NVFDEVIPTAFK
1440.6537	1439.6464	1439.6681	-0.0216	36	47	0	---	QHGSEEWEPLTK
1440.6537	1439.6464	1439.6681	-0.0216	36	47	0	44	QHGSEEWEPLTK
1796.8937	1795.8864	1795.8926	-0.0062	72	87	1	32	GGMRNVFDEVIPTAFK + Oxidation (M)
1796.8937	1795.8864	1795.8926	-0.0062	72	87	1	---	GGMRNVFDEVIPTAFK + Oxidation (M)

No match to: 768.5156, 959.5234, 1348.7375, 1348.7375, 1364.7294, 1370.7062, 1423.6528, 1605.8262, 1605.8262, 1857.9586

4. gi|168035127 **Mass:** 73702 **Score:** 54 **Expect:** 2.5 **Queries matched:** 7

predicted protein [Physcomitrella patens subsp. patens]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
959.5234	958.5161	958.5559	-0.0398	60	67	1	---	IVSVRTER
1379.6990	1378.6917	1378.6948	-0.0031	47	59	1	---	KGLAMTMDVVNGK + Oxidation (M)
1379.6990	1378.6917	1378.6333	0.0584	30	41	1	---	MAAGLRMLDDDR + Oxidation (M)
1423.6528	1422.6455	1422.6343	0.0112	1	13	1	---	MACELASESGGRR
1440.6537	1439.6464	1439.7390	-0.0925	639	649	1	---	SFWKFWPAFPK
1440.6537	1439.6464	1439.7390	-0.0925	639	649	1	---	SFWKFWPAFPK
1857.9586	1856.9513	1856.9784	-0.0271	14	29	1	---	FFGLTEVSTGRVEFLR

No match to: 768.5156, 1348.7375, 1348.7375, 1364.7294, 1370.7062, 1605.8262, 1605.8262, 1796.8937, 1796.8937

5. gi|157349758 **Mass:** 43576 **Score:** 50 **Expect:** 6.7 **Queries matched:** 8

unnamed protein product [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1348.7375	1347.7302	1347.7510	-0.0208	95	106	0	0	SDIHINLPALQK
1348.7375	1347.7302	1347.7510	-0.0208	95	106	0	---	SDIHINLPALQK
1364.7294	1363.7221	1363.7281	-0.0060	295	305	1	---	AESLLFCLKQR
1379.6990	1378.6917	1378.6524	0.0393	173	183	1	---	HTRDCANQIHK
1379.6990	1378.6917	1378.6524	0.0393	173	183	1	---	HTRDCANQIHK
1423.6528	1422.6455	1422.6595	-0.0140	364	375	1	---	SVVEDMQNRMSK
1605.8262	1604.8189	1604.7439	0.0750	263	276	1	---	ACVAHSKSSWDMVK
1605.8262	1604.8189	1604.7439	0.0750	263	276	1	---	ACVAHSKSSWDMVK

No match to: 768.5156, 959.5234, 1370.7062, 1440.6537, 1440.6537, 1796.8937, 1796.8937, 1857.9586

6. gi|15241897 **Mass:** 64256 **Score:** 48 **Expect:** 8.8 **Queries matched:** 7

SYNC1; ATP binding / aminoacyl-tRNA ligase/ asparagine-tRNA ligase/ aspartate-tRNA ligase/ nucleic

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide

959.5234	958.5161	958.5348	-0.0187	55 - 63	1	---	IGGWVKSGR
1370.7062	1369.6989	1369.7816	-0.0827	419 - 431	1	---	AIELLEEAVAKGK
1379.6990	1378.6917	1378.7278	-0.0361	547 - 558	0	---	MILFATGLDNIR + Oxidation (M)
1379.6990	1378.6917	1378.7278	-0.0361	547 - 558	0	---	MILFATGLDNIR + Oxidation (M)
1796.8937	1795.8864	1795.9540	-0.0676	37 - 54	0	---	TILDRPDGGAGLAGQTVR
1796.8937	1795.8864	1795.9540	-0.0676	37 - 54	0	---	TILDRPDGGAGLAGQTVR
1857.9586	1856.9513	1856.9553	-0.0040	476 - 492	1	---	LNDDEKTVAAMDVLVPK

No match to: 768.5156, 1348.7375, 1348.7375, 1364.7294, 1423.6528, 1440.6537, 1440.6537, 1605.8262, 1605.8262

7. gi|147834192 **Mass:** 51187 **Score:** 48 **Expect:** 9.2 **Queries matched:** 8

hypothetical protein [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1348.7375	1347.7302	1347.7510	-0.0208	162 - 173	0	0		SDIHINLPALQK
1348.7375	1347.7302	1347.7510	-0.0208	162 - 173	0	---		SDIHINLPALQK
1364.7294	1363.7221	1363.7281	-0.0060	362 - 372	1	---		AESLLFCLKQR
1379.6990	1378.6917	1378.6524	0.0393	240 - 250	1	---		HTRDCANQIHK
1379.6990	1378.6917	1378.6524	0.0393	240 - 250	1	---		HTRDCANQIHK
1423.6528	1422.6455	1422.6595	-0.0140	431 - 442	1	---		SVVEDMQNRMSK
1605.8262	1604.8189	1604.7439	0.0750	330 - 343	1	---		ACVAHSKSSWDMVK
1605.8262	1604.8189	1604.7439	0.0750	330 - 343	1	---		ACVAHSKSSWDMVK

No match to: 768.5156, 959.5234, 1370.7062, 1440.6537, 1440.6537, 1796.8937, 1796.8937, 1857.9586

8. gi|255561196 **Mass:** 68961 **Score:** 45 **Expect:** 18 **Queries matched:** 7

Phosphoenolpyruvate carboxylase, putative [Ricinus communis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1364.7294	1363.7221	1363.7421	-0.0199	472 - 483	0	---		VTIDLVEMVFAK
1370.7062	1369.6989	1369.6812	0.0177	31 - 41	0	---		NSVFVQMNFIR + Oxidation (M)
1423.6528	1422.6455	1422.7255	-0.0800	392 - 402	1	---		EYRSIVFQEPR
1440.6537	1439.6464	1439.7303	-0.0839	348 - 358	1	---		EEHLCVRTLQR
1440.6537	1439.6464	1439.7303	-0.0839	348 - 358	1	---		EEHLCVRTLQR
1796.8937	1795.8864	1795.8913	-0.0049	582 - 597	0	---		SEYAPGLEDTLILTMK + Oxidation (M)
1796.8937	1795.8864	1795.8913	-0.0049	582 - 597	0	---		SEYAPGLEDTLILTMK + Oxidation (M)

No match to: 768.5156, 959.5234, 1348.7375, 1348.7375, 1379.6990, 1379.6990, 1605.8262, 1605.8262, 1857.9586

9. gi|225449527 **Mass:** 25569 **Score:** 45 **Expect:** 19 **Queries matched:** 7

PREDICTED: hypothetical protein [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1348.7375	1347.7302	1347.6645	0.0658	163 - 173	0	---		GCITFYVYAVR
1348.7375	1347.7302	1347.6645	0.0658	163 - 173	0	---		GCITFYVYAVR
1379.6990	1378.6917	1378.7390	-0.0473	146 - 157	1	---		LIRGLTGYEMAR
1379.6990	1378.6917	1378.7390	-0.0473	146 - 157	1	---		LIRGLTGYEMAR

1423.6528	1422.6455	1422.6561	-0.0106	175 - 187	0	---	VGNLGFSCADDLR
1605.8262	1604.8189	1604.8925	-0.0736	132 - 145	1	---	VWPPEIPLGEVNKK
1605.8262	1604.8189	1604.8925	-0.0736	132 - 145	1	---	VWPPEIPLGEVNKK

No match to: 768.5156, 959.5234, 1364.7294, 1370.7062, 1440.6537, 1440.6537, 1796.8937, 1796.8937, 1857.9586

10. gi|168057923 **Mass:** 28476 **Score:** 42 **Expect:** 37 **Queries matched:** 7

predicted protein [Physcomitrella patens subsp. patens]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1348.7375	1347.7302	1347.7431	-0.0129	67 -	78	0	---	ASSLLTIEVIMR + Oxidation (M)
1348.7375	1347.7302	1347.7431	-0.0129	67 -	78	0	---	ASSLLTIEVIMR + Oxidation (M)
1370.7062	1369.6989	1369.7024	-0.0034	1 -	12	0	---	MLTSQNQVPPQK
1379.6990	1378.6917	1378.6650	0.0267	172 -	183	0	---	LQSDIEISTDMK
1379.6990	1378.6917	1378.6650	0.0267	172 -	183	0	---	LQSDIEISTDMK
1796.8937	1795.8864	1795.8522	0.0342	130 -	146	1	---	SEKMPSSTHHSGAPLSK + Oxidation (M)
1796.8937	1795.8864	1795.8522	0.0342	130 -	146	1	---	SEKMPSSTHHSGAPLSK + Oxidation (M)

No match to: 768.5156, 959.5234, 1364.7294, 1423.6528, 1440.6537, 1440.6537, 1605.8262, 1605.8262, 1857.9586

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 16

Protein View

Match to: **gi|39841264** Score: **228** Expect: **9.6e-018**
Phl p 3 allergen [Phleum pratense]

Nominal mass (M_r): **10952**; Calculated pI value: **8.94**
NCBI BLAST search of gi|39841264 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

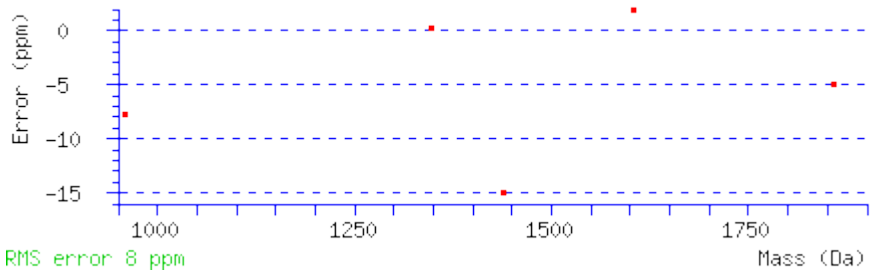
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **51%**

Matched peptides shown in **Bold Red**

```
    1 AVQVTFTVQK GSDPKKLVLD IKYTRPGDSL AEVELRQHGS EEWEPLTKKG
   51 NVWEVKSSKP LVGPFNFRFM SKGGMRNVFD EVIPTAFSIG KTYKPEE
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
23 - 36	1605.8262	1604.8189	1604.8158	0.0032	0	YTRPGDSLAEVELR (No match)
23 - 36	1605.8262	1604.8189	1604.8158	0.0032	0	YTRPGDSLAEVELR (Ions score 34)
37 - 48	1440.6537	1439.6464	1439.6681	-0.0216	0	QHGSEEWEPLTK (No match)
37 - 48	1440.6537	1439.6464	1439.6681	-0.0216	0	QHGSEEWEPLTK (Ions score 44)
49 - 56	959.5234	958.5161	958.5235	-0.0074	1	KGNVWEVK (No match)
57 - 68	1348.7375	1347.7302	1347.7298	0.0004	0	SSKPLVGPFNFR (Ions score 68)
57 - 68	1348.7375	1347.7302	1347.7298	0.0004	0	SSKPLVGPFNFR (No match)
57 - 72	1857.9586	1856.9513	1856.9606	-0.0093	1	SSKPLVGPFNFRFMSK Oxidation (M) (No match)



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	Accession	Mass	Score	Description
1.	gi|39841264	10952	166	Phl p 3 allergen [Phleum pratense]
2.	gi|169404532	12218	165	Chain A, Solution Structure Of Phl P 3, A Major Allergen From Timothy Grass Pollen
3.	gi|14423759	10926	117	RecName: Full=Pollen allergen Dac g 3; AltName: Full=Allergen Dac g III; AltName: Allergen=Da
4.	gi|157349758	43576	58	unnamed protein product [Vitis vinifera]
5.	gi|42565155	125495	58	MSH1 (MUTL PROTEIN HOMOLOG 1); ATP binding / catalytic/ damaged DNA binding / mismatched DNA
6.	gi|110737223	4669	58	hypothetical protein [Arabidopsis thaliana]
7.	gi|147834192	51187	57	hypothetical protein [Vitis vinifera]
8.	gi|255561196	68961	57	Phosphoenolpyruvate carboxylase, putative [Ricinus communis]
9.	gi|2315136	5452	54	larger subunit of Rubisco [Arabidopsis thaliana]
10.	gi|40643869	5438	54	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Iphigenia ledermannii]

Results List

1. gi|39841264 **Mass:** 10952 **Score:** 166 **Expect:** 1.5e-011 **Queries matched:** 6

Phl p 3 allergen [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1348.7418	1347.7345	1347.7298	0.0047	57	-	68	0	77	SSKPLVGPFNFR
1348.7418	1347.7345	1347.7298	0.0047	57	-	68	0	---	SSKPLVGPFNFR
1440.6825	1439.6752	1439.6681	0.0072	37	-	48	0	---	QHGSEEWEPLTK
1605.8389	1604.8316	1604.8158	0.0159	23	-	36	0	---	YTRPGDSLAEVELR
1605.8389	1604.8316	1604.8158	0.0159	23	-	36	0	28	YTRPGDSLAEVELR
1636.8561	1635.8488	1635.8507	-0.0019	77	-	91	0	---	NVFDEVIPTAFSIGK

No match to: 768.5148, 1364.7401, 1379.7140, 1379.7140, 1423.6637, 1510.7942, 1510.7942, 1677.9309, 1796.9043, 1796.9043, 2055.0437

2. gi|169404532 **Mass:** 12218 **Score:** 165 **Expect:** 1.9e-011 **Queries matched:** 6

Chain A, Solution Structure Of Phl P 3, A Major Allergen From Timothy Grass Pollen

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1348.7418	1347.7345	1347.7298	0.0047	68	-	79	0	77	SSKPLVGPFNFR
1348.7418	1347.7345	1347.7298	0.0047	68	-	79	0	---	SSKPLVGPFNFR
1440.6825	1439.6752	1439.6681	0.0072	48	-	59	0	---	QHGSEEWEPLTK
1605.8389	1604.8316	1604.8158	0.0159	34	-	47	0	---	YTRPGDSLAEVELR
1605.8389	1604.8316	1604.8158	0.0159	34	-	47	0	28	YTRPGDSLAEVELR
1636.8561	1635.8488	1635.8507	-0.0019	88	-	102	0	---	NVFDEVIPTAFSIGK

No match to: 768.5148, 1364.7401, 1379.7140, 1379.7140, 1423.6637, 1510.7942, 1510.7942, 1677.9309, 1796.9043, 1796.9043, 2055.0437

3. gi|14423759 **Mass:** 10926 **Score:** 117 **Expect:** 1.2e-006 **Queries matched:** 5

RecName: Full=Pollen allergen Dac g 3; AltName: Full=Allergen Dac g III; AltName: Allergen=Dac g 3

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1379.7140	1378.7067	1378.7132	-0.0065	76	-	87	0	---	NVFDEVIPTAFK
1379.7140	1378.7067	1378.7132	-0.0065	76	-	87	0	65	NVFDEVIPTAFK
1440.6825	1439.6752	1439.6681	0.0072	36	-	47	0	---	QHGSEEWEPLTK
1796.9043	1795.8970	1795.8926	0.0044	72	-	87	1	---	GGMRNVFDEVIPTAFK + Oxidation (M)
1796.9043	1795.8970	1795.8926	0.0044	72	-	87	1	11	GGMRNVFDEVIPTAFK + Oxidation (M)

No match to: 768.5148, 1348.7418, 1348.7418, 1364.7401, 1423.6637, 1510.7942, 1510.7942, 1605.8389, 1605.8389, 1636.8561, 1677.9309, 2055.0437

4. gi|157349758 **Mass:** 43576 **Score:** 58 **Expect:** 0.94 **Queries matched:** 8

unnamed protein product [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1348.7418	1347.7345	1347.7510	-0.0165	95	-	106	0	10	SDIHINLPALQK
1348.7418	1347.7345	1347.7510	-0.0165	95	-	106	0	---	SDIHINLPALQK
1364.7401	1363.7328	1363.7281	0.0047	295	-	305	1	---	AESLLFCLKQR
1379.7140	1378.7067	1378.6524	0.0543	173	-	183	1	---	HTRDCANQIHK
1379.7140	1378.7067	1378.6524	0.0543	173	-	183	1	---	HTRDCANQIHK
1423.6637	1422.6564	1422.6595	-0.0031	364	-	375	1	---	SVVEDMQNRMSK
1605.8389	1604.8316	1604.7439	0.0877	263	-	276	1	---	ACVAHSKSSWDMVK
1605.8389	1604.8316	1604.7439	0.0877	263	-	276	1	---	ACVAHSKSSWDMVK

No match to: 768.5148, 1440.6825, 1510.7942, 1510.7942, 1636.8561, 1677.9309, 1796.9043, 1796.9043, 2055.0437

5. gi|42565155 **Mass:** 125495 **Score:** 58 **Expect:** 0.98 **Queries matched:** 11

MSH1 (MUTL PROTEIN HOMOLOG 1); ATP binding / catalytic/ damaged DNA binding / mismatched DNA bindin

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1348.7418	1347.7345	1347.6717	0.0628	464	-	474	0	---	NVLDDVLHMHR
1348.7418	1347.7345	1347.6717	0.0628	464	-	474	0	---	NVLDDVLHMHR
1364.7401	1363.7328	1363.6666	0.0662	464	-	474	0	---	NVLDDVLHMHR + Oxidation (M)
1379.7140	1378.7067	1378.6728	0.0339	1037	-	1048	0	---	LYIGQTDDLEGR
1379.7140	1378.7067	1378.6728	0.0339	1037	-	1048	0	9	LYIGQTDDLEGR
1510.7942	1509.7869	1509.6922	0.0948	121	-	132	0	---	DGNLNWEMLQFK + Oxidation (M)
1510.7942	1509.7869	1509.6922	0.0948	121	-	132	0	---	DGNLNWEMLQFK + Oxidation (M)
1605.8389	1604.8316	1604.8456	-0.0140	462	-	474	1	---	IKNVLDDVLHMHR + Oxidation (M)
1605.8389	1604.8316	1604.8596	-0.0279	102	-	115	0	---	LMYTNLLGLDPSLR
1796.9043	1795.8970	1795.8774	0.0196	915	-	930	1	---	LTDGVCRESLAFETAK
1796.9043	1795.8970	1795.8774	0.0196	915	-	930	1	---	LTDGVCRESLAFETAK

No match to: 768.5148, 1423.6637, 1440.6825, 1636.8561, 1677.9309, 2055.0437

6. gi|110737223 **Mass:** 4669 **Score:** 58 **Expect:** 1 **Queries matched:** 9

hypothetical protein [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide

1348.7418	1347.7345	1347.7804	-0.0459	9 - 19	1	---	MTLRMVIMILK
1348.7418	1347.7345	1347.7804	-0.0459	9 - 19	1	---	MTLRMVIMILK
1364.7401	1363.7328	1363.7753	-0.0425	9 - 19	1	---	MTLRMVIMILK + Oxidation (M)
1379.7140	1378.7067	1378.7465	-0.0398	2 - 12	1	---	TMWISLKMTLR
1379.7140	1378.7067	1378.7465	-0.0398	2 - 12	1	---	TMWISLKMTLR
1510.7942	1509.7869	1509.7870	-0.0001	1 - 12	1	---	MTMWISLKMTLR
1510.7942	1509.7869	1509.7870	-0.0001	1 - 12	1	---	MTMWISLKMTLR
1605.8389	1604.8316	1604.8306	0.0010	23 - 36	0	---	TEIALVAWEMLAMK
1605.8389	1604.8316	1604.8306	0.0010	23 - 36	0	---	TEIALVAWEMLAMK

No match to: 768.5148, 1423.6637, 1440.6825, 1636.8561, 1677.9309, 1796.9043, 1796.9043, 2055.0437

7. gi|147834192 **Mass:** 51187 **Score:** 57 **Expect:** 1.3 **Queries matched:** 8

hypothetical protein [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1348.7418	1347.7345	1347.7510	-0.0165	162 - 173	0	10		SDIHINLPALQK
1348.7418	1347.7345	1347.7510	-0.0165	162 - 173	0	---		SDIHINLPALQK
1364.7401	1363.7328	1363.7281	0.0047	362 - 372	1	---		AESLLFCLKQR
1379.7140	1378.7067	1378.6524	0.0543	240 - 250	1	---		HTRDCANQIHK
1379.7140	1378.7067	1378.6524	0.0543	240 - 250	1	---		HTRDCANQIHK
1423.6637	1422.6564	1422.6595	-0.0031	431 - 442	1	---		SVVEDMQNRMSK
1605.8389	1604.8316	1604.7439	0.0877	330 - 343	1	---		ACVAHSKSSWDMVK
1605.8389	1604.8316	1604.7439	0.0877	330 - 343	1	---		ACVAHSKSSWDMVK

No match to: 768.5148, 1440.6825, 1510.7942, 1510.7942, 1636.8561, 1677.9309, 1796.9043, 1796.9043, 2055.0437

8. gi|255561196 **Mass:** 68961 **Score:** 57 **Expect:** 1.3 **Queries matched:** 8

Phosphoenolpyruvate carboxylase, putative [Ricinus communis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1364.7401	1363.7328	1363.7421	-0.0092	472 - 483	0	---		VTIDLVEMVFAK
1423.6637	1422.6564	1422.7255	-0.0691	392 - 402	1	---		EYRSIVFQEPR
1440.6825	1439.6752	1439.7303	-0.0551	348 - 358	1	---		EEHLCVRTLQR
1510.7942	1509.7869	1509.7874	-0.0005	31 - 42	1	---		NSVFVQMNFIRR
1510.7942	1509.7869	1509.7874	-0.0005	31 - 42	1	---		NSVFVQMNFIRR
1677.9309	1676.9236	1676.8634	0.0602	550 - 563	0	---		DPDYHVTLRPHLSK
1796.9043	1795.8970	1795.8913	0.0057	582 - 597	0	---		SEYAPGLEDTLILTMK + Oxidation (M)
1796.9043	1795.8970	1795.8913	0.0057	582 - 597	0	---		SEYAPGLEDTLILTMK + Oxidation (M)

No match to: 768.5148, 1348.7418, 1348.7418, 1379.7140, 1379.7140, 1605.8389, 1605.8389, 1636.8561, 2055.0437

9. gi|2315136 **Mass:** 5452 **Score:** 54 **Expect:** 2.6 **Queries matched:** 6

larger subunit of Rubisco [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1379.7140	1378.7067	1378.7092	-0.0025	2 - 14	1	---		SPQTETKASVGFK

1379.7140	1378.7067	1378.7092	-0.0025	2 - 14	1	---	SPQTETKASVGFK
1510.7942	1509.7869	1509.7497	0.0372	1 - 14	1	---	MSPQTETKASVGFK
1510.7942	1509.7869	1509.7497	0.0372	1 - 14	1	---	MSPQTETKASVGFK
1796.9043	1795.8970	1795.9468	-0.0498	33 - 49	1	---	DTDILAAFRVTPQPGVP
1796.9043	1795.8970	1795.9468	-0.0498	33 - 49	1	---	DTDILAAFRVTPQPGVP

No match to: 768.5148, 1348.7418, 1348.7418, 1364.7401, 1423.6637, 1440.6825, 1605.8389, 1605.8389, 1636.8561, 1677.9309, 2055.0437

10. gi|40643869 **Mass:** 5438 **Score:** 54 **Expect:** 2.6 **Queries matched:** 6

ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Iphigenia ledermannii]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1379.7140	1378.7067	1378.7092	-0.0025	2 - 14	1	---	SPQTETKASVGFK
1379.7140	1378.7067	1378.7092	-0.0025	2 - 14	1	---	SPQTETKASVGFK
1510.7942	1509.7869	1509.7497	0.0372	1 - 14	1	---	MSPQTETKASVGFK
1510.7942	1509.7869	1509.7497	0.0372	1 - 14	1	---	MSPQTETKASVGFK
1796.9043	1795.8970	1795.9468	-0.0498	33 - 49	1	---	DTDILAAFRVTPQPGVP
1796.9043	1795.8970	1795.9468	-0.0498	33 - 49	1	---	DTDILAAFRVTPQPGVP

No match to: 768.5148, 1348.7418, 1348.7418, 1364.7401, 1423.6637, 1440.6825, 1605.8389, 1605.8389, 1636.8561, 1677.9309, 2055.0437

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 17

Protein View

Match to: **gi|39841264** Score: **166** Expect: **1.5e-011**
Phl p 3 allergen [Phleum pratense]

Nominal mass (M_r): **10952**; Calculated pI value: **8.94**
NCBI BLAST search of gi|39841264 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

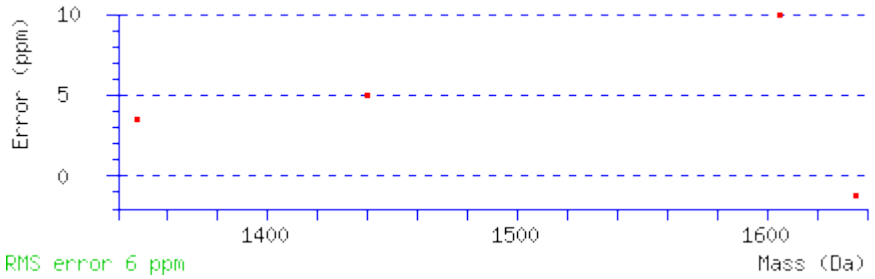
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **54%**

Matched peptides shown in **Bold Red**

```
     1 AVQVTFTVQK GSDPKKLVLD IKYTRPGDSL AEVELRQHGS EEWEPLTKKG
    51 NVWEVKSSKP LVGPFNFRFM SKGGMRNVFD EVIPTAFSIG KTYKPEE
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
23 - 36	1605.8389	1604.8316	1604.8158	0.0159	0	YTRPGDSLAEVELR	(No match)
23 - 36	1605.8389	1604.8316	1604.8158	0.0159	0	YTRPGDSLAEVELR	(Ions score 28)
37 - 48	1440.6825	1439.6752	1439.6681	0.0072	0	QHGSEEWEPLTK	(No match)
57 - 68	1348.7418	1347.7345	1347.7298	0.0047	0	SSKPLVGPFNFR	(Ions score 77)
57 - 68	1348.7418	1347.7345	1347.7298	0.0047	0	SSKPLVGPFNFR	(No match)
77 - 91	1636.8561	1635.8488	1635.8507	-0.0019	0	NVFDEVIPTAFSIGK	(No match)



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	Accession	Mass	Score	Description
1.	gi|39841264	10952	232	Phl p 3 allergen [Phleum pratense]
2.	gi|169404532	12218	231	Chain A, Solution Structure Of Phl P 3, A Major Allergen From Timothy Grass Pollen
3.	gi|14423759	10926	100	RecName: Full=Pollen allergen Dac g 3; AltName: Full=Allergen Dac g III; AltName: Allergen=Dac
4.	gi|22165102	54649	62	hypothetical protein [Oryza sativa (japonica cultivar-group)]
5.	gi|110737223	4669	55	hypothetical protein [Arabidopsis thaliana]
6.	gi|255561196	68961	54	Phosphoenolpyruvate carboxylase, putative [Ricinus communis]
7.	gi|2315136	5452	52	larger subunit of Rubisco [Arabidopsis thaliana]
8.	gi|40643869	5438	52	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Iphigenia ledermannii]
9.	gi|2323414	5424	52	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Nothofagus aequilateralis]
10.	gi|11620	5992	50	ribulose-1,5-bisphosphate-carboxylase [Mercurialis annua]

Results List

1. gi|39841264 **Mass:** 10952 **Score:** 232 **Expect:** 3.8e-018 **Queries matched:** 8

Phl p 3 allergen [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
959.5427	958.5354	958.5235	0.0119	49	56	1	---	KGNVWEVK
1348.7593	1347.7520	1347.7298	0.0222	57	68	0	81	SSKPLVGPFNFR
1348.7593	1347.7520	1347.7298	0.0222	57	68	0	---	SSKPLVGPFNFR
1440.6884	1439.6811	1439.6681	0.0131	37	48	0	---	QHGSEEWEPLTK
1605.8521	1604.8448	1604.8158	0.0291	23	36	0	54	YTRPGDSLAEVELR
1605.8521	1604.8448	1604.8158	0.0291	23	36	0	---	YTRPGDSLAEVELR
1636.8602	1635.8529	1635.8507	0.0022	77	91	0	---	NVFDEVIPTAFSIGK
2054.0505	2053.0432	2053.0302	0.0131	73	91	1	---	GGMRNVFDEVIPTAFSIGK + Oxidation (M)

No match to: 1364.7621, 1370.7422, 1374.8149, 1379.7351, 1379.7351, 1423.6783, 1510.8138, 1510.8138, 1619.8663, 1796.9231, 1796.9231

2. gi|169404532 **Mass:** 12218 **Score:** 231 **Expect:** 4.8e-018 **Queries matched:** 8

Chain A, Solution Structure Of Phl P 3, A Major Allergen From Timothy Grass Pollen

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
959.5427	958.5354	958.5235	0.0119	60	67	1	---	KGNVWEVK
1348.7593	1347.7520	1347.7298	0.0222	68	79	0	81	SSKPLVGPFNFR
1348.7593	1347.7520	1347.7298	0.0222	68	79	0	---	SSKPLVGPFNFR
1440.6884	1439.6811	1439.6681	0.0131	48	59	0	---	QHGSEEWEPLTK
1605.8521	1604.8448	1604.8158	0.0291	34	47	0	54	YTRPGDSLAEVELR
1605.8521	1604.8448	1604.8158	0.0291	34	47	0	---	YTRPGDSLAEVELR
1636.8602	1635.8529	1635.8507	0.0022	88	102	0	---	NVFDEVIPTAFSIGK
2054.0505	2053.0432	2053.0302	0.0131	84	102	1	---	GGMRNVFDEVIPTAFSIGK + Oxidation (M)

No match to: 1364.7621, 1370.7422, 1374.8149, 1379.7351, 1379.7351, 1423.6783, 1510.8138, 1510.8138, 1619.8663, 1796.9231, 1796.9231

3. gi|14423759 **Mass:** 10926 **Score:** 100 **Expect:** 6.1e-005 **Queries matched:** 6

RecName: Full=Pollen allergen Dac g 3; AltName: Full=Allergen Dac g III; AltName: Allergen=Dac g 3

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1379.7351	1378.7278	1378.7132	0.0146	76	87	0	35	NVFDEVIPTAFK
1379.7351	1378.7278	1378.7132	0.0146	76	87	0	---	NVFDEVIPTAFK
1440.6884	1439.6811	1439.6681	0.0131	36	47	0	---	QHGSEEWEPLTK
1619.8663	1618.8590	1618.8314	0.0276	22	35	0	---	YTRPGDTLAEVELR
1796.9231	1795.9158	1795.8926	0.0232	72	87	1	---	GGMRNVFDEVIPTAFK + Oxidation (M)
1796.9231	1795.9158	1795.8926	0.0232	72	87	1	8	GGMRNVFDEVIPTAFK + Oxidation (M)

No match to: 959.5427, 1348.7593, 1348.7593, 1364.7621, 1370.7422, 1374.8149, 1423.6783, 1510.8138, 1510.8138, 1605.8521, 1605.8521, 1636.8602, 2054.0505

4. gi|22165102 **Mass:** 54649 **Score:** 62 **Expect:** 0.35 **Queries matched:** 10

hypothetical protein [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1348.7593	1347.7520	1347.6895	0.0626	182	193	0	---	VGTHHSIENQVK
1348.7593	1347.7520	1347.6895	0.0626	182	193	0	---	VGTHHSIENQVK
1370.7422	1369.7349	1369.7201	0.0148	346	358	0	---	IVEQPIASDAATR
1379.7351	1378.7278	1378.7608	-0.0330	2	13	0	---	AVFNVIPSLTYR
1379.7351	1378.7278	1378.7608	-0.0330	2	13	0	---	AVFNVIPSLTYR
1510.8138	1509.8065	1509.8013	0.0052	1	13	0	---	MAVFNVIPSLTYR
1510.8138	1509.8065	1509.8013	0.0052	1	13	0	---	MAVFNVIPSLTYR
1605.8521	1604.8448	1604.7576	0.0872	406	418	1	---	QAETEIMQQERAR + Oxidation (M)
1605.8521	1604.8448	1604.7576	0.0872	406	418	1	---	QAETEIMQQERAR + Oxidation (M)
1619.8663	1618.8590	1618.7620	0.0970	404	416	1	---	EKQAETEIMQQER

No match to: 959.5427, 1364.7621, 1374.8149, 1423.6783, 1440.6884, 1636.8602, 1796.9231, 1796.9231, 2054.0505

5. gi|110737223 **Mass:** 4669 **Score:** 55 **Expect:** 2.1 **Queries matched:** 9

hypothetical protein [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1348.7593	1347.7520	1347.7804	-0.0284	9	19	1	---	MTLRMVIMILK
1348.7593	1347.7520	1347.7804	-0.0284	9	19	1	---	MTLRMVIMILK
1364.7621	1363.7548	1363.7753	-0.0205	9	19	1	---	MTLRMVIMILK + Oxidation (M)
1379.7351	1378.7278	1378.7465	-0.0187	2	12	1	---	TMWISLKMTLR
1379.7351	1378.7278	1378.7465	-0.0187	2	12	1	---	TMWISLKMTLR
1510.8138	1509.8065	1509.7870	0.0195	1	12	1	---	MTMWISLKMTLR
1510.8138	1509.8065	1509.7870	0.0195	1	12	1	---	MTMWISLKMTLR
1605.8521	1604.8448	1604.8306	0.0142	23	36	0	---	TEIALVAWEMLAMK
1605.8521	1604.8448	1604.8306	0.0142	23	36	0	---	TEIALVAWEMLAMK

No match to: 959.5427, 1370.7422, 1374.8149, 1423.6783, 1440.6884, 1619.8663, 1636.8602, 1796.9231, 1796.9231, 2054.0505

6. gi|255561196 **Mass:** 68961 **Score:** 54 **Expect:** 2.6 **Queries matched:** 8

Phosphoenolpyruvate carboxylase, putative [Ricinus communis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1364.7621	1363.7548	1363.7421	0.0128	472	483	0	---	VTIDLVEMVFAK
1370.7422	1369.7349	1369.6812	0.0537	31	41	0	---	NSVFVQMNFIR + Oxidation (M)
1423.6783	1422.6710	1422.7255	-0.0545	392	402	1	---	EYRSIVFQEPR
1440.6884	1439.6811	1439.7303	-0.0492	348	358	1	---	EEHLCVRTLQR
1510.8138	1509.8065	1509.7874	0.0191	31	42	1	---	NSVFVQMNFIRR
1510.8138	1509.8065	1509.7874	0.0191	31	42	1	---	NSVFVQMNFIRR
1796.9231	1795.9158	1795.8913	0.0245	582	597	0	---	SEYAPGLEDTLILTMK + Oxidation (M)
1796.9231	1795.9158	1795.8913	0.0245	582	597	0	---	SEYAPGLEDTLILTMK + Oxidation (M)

No match to: 959.5427, 1348.7593, 1348.7593, 1374.8149, 1379.7351, 1379.7351, 1605.8521, 1605.8521, 1619.8663, 1636.8602, 2054.0505

7. gi|2315136 **Mass:** 5452 **Score:** 52 **Expect:** 4.1 **Queries matched:** 6

larger subunit of Rubisco [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1379.7351	1378.7278	1378.7092	0.0186	2	14	1	---	SPQTETKASVGFK
1379.7351	1378.7278	1378.7092	0.0186	2	14	1	---	SPQTETKASVGFK
1510.8138	1509.8065	1509.7497	0.0568	1	14	1	---	MSPQTETKASVGFK
1510.8138	1509.8065	1509.7497	0.0568	1	14	1	---	MSPQTETKASVGFK
1796.9231	1795.9158	1795.9468	-0.0310	33	49	1	---	DTDILAAFRVTPQPGVP
1796.9231	1795.9158	1795.9468	-0.0310	33	49	1	---	DTDILAAFRVTPQPGVP

No match to: 959.5427, 1348.7593, 1348.7593, 1364.7621, 1370.7422, 1374.8149, 1423.6783, 1440.6884, 1605.8521, 1605.8521, 1619.8663, 1636.8602, 2054.0505

8. gi|40643869 **Mass:** 5438 **Score:** 52 **Expect:** 4.1 **Queries matched:** 6

ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Iphigenia ledermannii]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1379.7351	1378.7278	1378.7092	0.0186	2	14	1	---	SPQTETKASVGFK
1379.7351	1378.7278	1378.7092	0.0186	2	14	1	---	SPQTETKASVGFK
1510.8138	1509.8065	1509.7497	0.0568	1	14	1	---	MSPQTETKASVGFK
1510.8138	1509.8065	1509.7497	0.0568	1	14	1	---	MSPQTETKASVGFK
1796.9231	1795.9158	1795.9468	-0.0310	33	49	1	---	DTDILAAFRVTPQPGVP
1796.9231	1795.9158	1795.9468	-0.0310	33	49	1	---	DTDILAAFRVTPQPGVP

No match to: 959.5427, 1348.7593, 1348.7593, 1364.7621, 1370.7422, 1374.8149, 1423.6783, 1440.6884, 1605.8521, 1605.8521, 1619.8663, 1636.8602, 2054.0505

9. gi|2323414 **Mass:** 5424 **Score:** 52 **Expect:** 4.1 **Queries matched:** 6

ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Nothofagus aequilateralis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1379.7351	1378.7278	1378.7092	0.0186	2 -	14	1	---	SPQTETKASVGFK
1379.7351	1378.7278	1378.7092	0.0186	2 -	14	1	---	SPQTETKASVGFK
1510.8138	1509.8065	1509.7497	0.0568	1 -	14	1	---	MSPQTETKASVGFK
1510.8138	1509.8065	1509.7497	0.0568	1 -	14	1	---	MSPQTETKASVGFK
1796.9231	1795.9158	1795.9468	-0.0310	33 -	49	1	---	DTDILAAFRVTPQPGVP
1796.9231	1795.9158	1795.9468	-0.0310	33 -	49	1	---	DTDILAAFRVTPQPGVP

No match to: 959.5427, 1348.7593, 1348.7593, 1364.7621, 1370.7422, 1374.8149, 1423.6783, 1440.6884, 1605.8521, 1605.8521, 1619.8663, 1636.8602, 2054.0505

10. gi|11620 **Mass:** 5992 **Score:** 50 **Expect:** 5.7 **Queries matched:** 6

ribulose-1,5-bisphosphate-carboxylase [Mercurialis annua]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1348.7593	1347.7520	1347.6670	0.0850	42 -	55	0	---	VTPQPGVPPEEAGA
1348.7593	1347.7520	1347.6670	0.0850	42 -	55	0	---	VTPQPGVPPEEAGA
1379.7351	1378.7278	1378.7092	0.0186	2 -	14	1	---	SPQTETKASVGFK
1379.7351	1378.7278	1378.7092	0.0186	2 -	14	1	---	SPQTETKASVGFK
1510.8138	1509.8065	1509.7497	0.0568	1 -	14	1	---	MSPQTETKASVGFK
1510.8138	1509.8065	1509.7497	0.0568	1 -	14	1	---	MSPQTETKASVGFK

No match to: 959.5427, 1364.7621, 1370.7422, 1374.8149, 1423.6783, 1440.6884, 1605.8521, 1605.8521, 1619.8663, 1636.8602, 1796.9231, 1796.9231, 2054.0505

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 19

Protein View

Match to: **gi|39841264** Score: **232** Expect: **3.8e-018**
Phl p 3 allergen [Phleum pratense]

Nominal mass (M_r): **10952**; Calculated pI value: **8.94**
NCBI BLAST search of gi|39841264 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

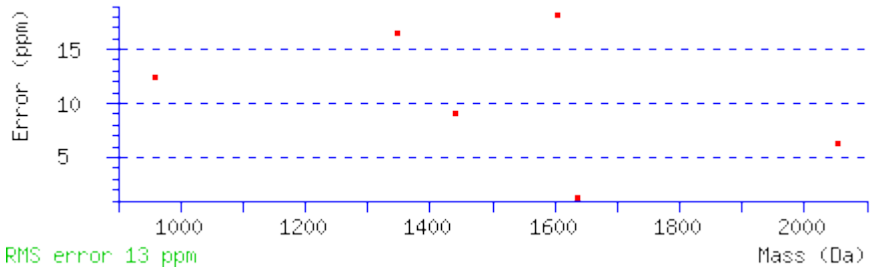
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **67%**

Matched peptides shown in **Bold Red**

```
    1 AVQVTFTVQK GSDPKKLVLD IKYTRPGDSL AEVELRQHGS EEWEPLTKKG
   51 NVWEVKSSKP LVGPFNFRFM SKGGMRNVFD EVIPTAFSIG KTYKPEE
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
23 - 36	1605.8521	1604.8448	1604.8158	0.0291	0	**YTRPGDSLAEVELR** (Ions score 54)
23 - 36	1605.8521	1604.8448	1604.8158	0.0291	0	**YTRPGDSLAEVELR** (No match)
37 - 48	1440.6884	1439.6811	1439.6681	0.0131	0	**QHGSEEWEPLTK** (No match)
49 - 56	959.5427	958.5354	958.5235	0.0119	1	**KGNVWEVK** (No match)
57 - 68	1348.7593	1347.7520	1347.7298	0.0222	0	**SSKPLVGPFNFR** (Ions score 81)
57 - 68	1348.7593	1347.7520	1347.7298	0.0222	0	**SSKPLVGPFNFR** (No match)
73 - 91	2054.0505	2053.0432	2053.0302	0.0131	1	**GGMRNVFDEVIPTAFSIGK** Oxidation (M) (No match)
77 - 91	1636.8602	1635.8529	1635.8507	0.0022	0	**NVFDEVIPTAFSIGK** (No match)



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	Accession	Mass	Score	Description
1.	gi|39841264	10952	158	Phl p 3 allergen [Phleum pratense]
2.	gi|169404532	12218	157	Chain A, Solution Structure Of Phl P 3, A Major Allergen From Timothy Grass Pollen
3.	gi|115458908	52678	66	Os04g0471100 [Oryza sativa (japonica cultivar-group)]
4.	gi|255594898	17624	58	malic enzyme, putative [Ricinus communis]
5.	gi|223945285	25324	54	unknown [Zea mays]
6.	gi|21539551	31763	50	putative protein phosphatase type 2C [Arabidopsis thaliana]
7.	gi|152126071	34654	49	RecName: Full=Probable 6-phosphogluconolactonase 4, chloroplastic; Short=6PGL 4; Flags: Precur
8.	gi|125563624	28877	48	hypothetical protein OsI_31266 [Oryza sativa Indica Group]
9.	gi|115466854	41313	46	Os06g0190900 [Oryza sativa (japonica cultivar-group)]
10.	gi|157358822	29066	46	unnamed protein product [Vitis vinifera]

Results List

1. gi|39841264 **Mass:** 10952 **Score:** 158 **Expect:** 9.6e-011 **Queries matched:** 4

Phl p 3 allergen [Phleum pratense]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1348.7465	1347.7392	1347.7298	0.0094	57	-	68	0	---	SSKPLVGPFNFR
1348.7465	1347.7392	1347.7298	0.0094	57	-	68	0	66	SSKPLVGPFNFR
1605.8324	1604.8251	1604.8158	0.0094	23	-	36	0	---	YTRPGDSLAEVELR
1605.8324	1604.8251	1604.8158	0.0094	23	-	36	0	53	YTRPGDSLAEVELR

No match to: 1364.7468, 1619.8506

2. gi|169404532 **Mass:** 12218 **Score:** 157 **Expect:** 1.2e-010 **Queries matched:** 4

Chain A, Solution Structure Of Phl P 3, A Major Allergen From Timothy Grass Pollen

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1348.7465	1347.7392	1347.7298	0.0094	68	-	79	0	---	SSKPLVGPFNFR
1348.7465	1347.7392	1347.7298	0.0094	68	-	79	0	66	SSKPLVGPFNFR
1605.8324	1604.8251	1604.8158	0.0094	34	-	47	0	---	YTRPGDSLAEVELR
1605.8324	1604.8251	1604.8158	0.0094	34	-	47	0	53	YTRPGDSLAEVELR

No match to: 1364.7468, 1619.8506

3. gi|115458908 **Mass:** 52678 **Score:** 66 **Expect:** 0.17 **Queries matched:** 6

Os04g0471100 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1348.7465	1347.7392	1347.6895	0.0498	80	-	91	0	---	VGTHHSIENQVK
1348.7465	1347.7392	1347.6895	0.0498	80	-	91	0	4	VGTHHSIENQVK
1364.7468	1363.7395	1363.7135	0.0260	125	-	136	0	---	FIDVPEATIFGR
1605.8324	1604.8251	1604.7576	0.0675	386	-	398	1	---	QAETEIMQQERAR + Oxidation (M)

1605.8324	1604.8251	1604.7576	0.0675	386 - 398	1	---	QAETEIMQQERAR + Oxidation (M)
1619.8506	1618.8433	1618.7620	0.0813	384 - 396	1	---	EKQAETEIMQQER

4. gi|255594898 **Mass:** 17624 **Score:** 58 **Expect:** 0.9 **Queries matched:** 5

malic enzyme, putative [Ricinus communis]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1348.7465	1347.7392	1347.6751	0.0642	92 - 103	1	---	RACVVALADMAR + Oxidation (M)
1348.7465	1347.7392	1347.6751	0.0642	92 - 103	1	---	RACVVALADMAR + Oxidation (M)
1605.8324	1604.8251	1604.7762	0.0489	93 - 107	1	---	ACVVALADMARSDAR
1605.8324	1604.8251	1604.7762	0.0489	93 - 107	1	---	ACVVALADMARSDAR
1619.8506	1618.8433	1618.8718	-0.0285	108 - 121	1	---	FSKDYIVPGLLDPR

No match to: 1364.7468

5. gi|223945285 **Mass:** 25324 **Score:** 54 **Expect:** 2.4 **Queries matched:** 5

unknown [Zea mays]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1348.7465	1347.7392	1347.7373	0.0020	199 - 209	0	---	VMPTGWFLLLR + Oxidation (M)
1348.7465	1347.7392	1347.7373	0.0020	199 - 209	0	---	VMPTGWFLLLR + Oxidation (M)
1605.8324	1604.8251	1604.8925	-0.0674	94 - 108	1	---	EALPPVEVPAAAKWK
1605.8324	1604.8251	1604.8925	-0.0674	94 - 108	1	---	EALPPVEVPAAAKWK
1619.8506	1618.8433	1618.7660	0.0773	1 - 16	0	---	MASAAAWEGPTAAELK + Oxidation (M)

No match to: 1364.7468

6. gi|21539551 **Mass:** 31763 **Score:** 50 **Expect:** 6.8 **Queries matched:** 5

putative protein phosphatase type 2C [Arabidopsis thaliana]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1348.7465	1347.7392	1347.6571	0.0822	185 - 197	0	---	GGFVSNFPGDVPR
1348.7465	1347.7392	1347.6571	0.0822	185 - 197	0	---	GGFVSNFPGDVPR
1364.7468	1363.7395	1363.7724	-0.0329	39 - 50	1	---	QITHGFHLVKGK
1605.8324	1604.8251	1604.8198	0.0054	49 - 62	1	---	GKAFHEIEDYVVAK
1605.8324	1604.8251	1604.8198	0.0054	49 - 62	1	---	GKAFHEIEDYVVAK

No match to: 1619.8506

7. gi|152126071 **Mass:** 34654 **Score:** 49 **Expect:** 8.4 **Queries matched:** 5

RecName: Full=Probable 6-phosphogluconolactonase 4, chloroplastic; Short=6PGL 4; Flags: Precursor

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1348.7465	1347.7392	1347.7761	-0.0369	104 - 117	0	---	GAFTVVLSGGSLIK
1348.7465	1347.7392	1347.7761	-0.0369	104 - 117	0	---	GAFTVVLSGGSLIK
1605.8324	1604.8251	1604.7286	0.0965	53 - 70	0	---	APAMATDCAAAAAAAGSK
1605.8324	1604.8251	1604.7286	0.0965	53 - 70	0	---	APAMATDCAAAAAAAGSK
1619.8506	1618.8433	1618.7878	0.0555	122 - 135	0	---	LAEPPYLDSVDWSK

No match to: 1364.7468

8. gi|125563624 **Mass:** 28877 **Score:** 48 **Expect:** 9.4 **Queries matched:** 4

hypothetical protein OsI_31266 [Oryza sativa Indica Group]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1364.7468	1363.7395	1363.7135	0.0260	156 -	167	0	---	YADPLVYTGPIR
1605.8324	1604.8251	1604.8926	-0.0674	154 -	167	1	---	IKYADPLVYTGPIR
1605.8324	1604.8251	1604.8926	-0.0674	154 -	167	1	---	IKYADPLVYTGPIR
1619.8506	1618.8433	1618.8831	-0.0397	156 -	169	1	---	YADPLVYTGPIRVR

No match to: 1348.7465, 1348.7465

9. gi|115466854 **Mass:** 41313 **Score:** 46 **Expect:** 14 **Queries matched:** 5

Os06g0190900 [Oryza sativa (japonica cultivar-group)]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1348.7465	1347.7392	1347.6895	0.0498	80 -	91	0	---	VGTHHSIENQVK
1348.7465	1347.7392	1347.6895	0.0498	80 -	91	0	4	VGTHHSIENQVK
1605.8324	1604.8251	1604.7576	0.0675	287 -	299	1	---	QAETEIMQQERAR + Oxidation (M)
1605.8324	1604.8251	1604.7576	0.0675	287 -	299	1	---	QAETEIMQQERAR + Oxidation (M)
1619.8506	1618.8433	1618.7620	0.0813	285 -	297	1	---	EKQAETEIMQQER

No match to: 1364.7468

10. gi|157358822 **Mass:** 29066 **Score:** 46 **Expect:** 14 **Queries matched:** 4

unnamed protein product [Vitis vinifera]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1364.7468	1363.7395	1363.6731	0.0664	171 -	183	0	---	IGSPITGYGQESR
1605.8324	1604.8251	1604.7756	0.0496	244 -	258	0	---	SPSPAQLMLESYVPA + Oxidation (M)
1605.8324	1604.8251	1604.7756	0.0496	244 -	258	0	---	SPSPAQLMLESYVPA + Oxidation (M)
1619.8506	1618.8433	1618.8426	0.0007	169 -	183	1	---	VRIGSPITGYGQESR

No match to: 1348.7465, 1348.7465

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries : 6

Protein View

Match to: **gi|39841264** Score: **158** Expect: **9.6e-011**
Phl p 3 allergen [Phleum pratense]

Nominal mass (M_r): **10952**; Calculated pI value: **8.94**
NCBI BLAST search of gi|39841264 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Phleum pratense

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **26%**

Matched peptides shown in **Bold Red**

```
    1 AVQVTFTVQK GSDPKKLVLD IKYTRPGDSL AEVELRQHGS EEWEPLTKKG
   51 NVWEVKSSKP LVGPFNFRFM SKGGMRNVFD EVIPTAFSIG KTYKPEE
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
23 - 36	1605.8324	1604.8251	1604.8158	0.0094	0	YTRPGDSLAEVELR	(No match)
23 - 36	1605.8324	1604.8251	1604.8158	0.0094	0	YTRPGDSLAEVELR	(Ions score 53)
57 - 68	1348.7465	1347.7392	1347.7298	0.0094	0	SSKPLVGPFNFR	(No match)
57 - 68	1348.7465	1347.7392	1347.7298	0.0094	0	SSKPLVGPFNFR	(Ions score 66)

