

Novel Cytosolic Allergens of *Aspergillus fumigatus* Identified from Germinating Conidia

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Aspergillus fumigatus is the common cause of allergic broncho-pulmonary aspergillosis (ABPA) and most of the allergens have been described from its secreted fraction. In the present investigation, germinating conidial cytosolic proteins of *A. fumigatus* were extracted from a 16 h culture. The proteome from this fraction was developed, and immuno-blots were generated using pooled ABPA patients' sera. Well separated Immunoglobulin-E (IgE) and Immunoglobulin-G (IgG) reactive spots were picked from corresponding 2DE gels and subjected to mass spectrometric analysis. As a result, 66 immuno-reactive proteins were identified from two geographically different strains (190/96 and DAYA) of *A. fumigatus*. Only 3 out of 66 proteins reacted with IgG, and the remaining 63 proteins were found to be IgE reactive. These 63 IgE-reactive cytosolic proteins from germinating conidia included 2 already known (Asp f12 and Asp f22) and 4 predicted allergens (Hsp88, Hsp70, malate dehydrogenase, and alcohol dehydrogenase) based on their homology with other known fungal allergens. In view of this, the panel of presently identified IgE-reactive novel proteins holds the potential of providing a basis for the wider diagnostic application in assay for allergic aspergillosis. We could demonstrate that recombinantly expressed proteins from this panel showed consistent reactivity with IgE of individual sera of ABPA patients. The recombinantly expressed proteins may also be useful in desensitization therapy of allergic disorders including ABPA.

Keywords: *A. fumigatus* • germinating conidia • proteome • allergens • aspergillosis • diagnostics

Introduction

A. fumigatus is an ubiquitous filamentous fungal saprophyte, a primary and opportunistic pathogen, and also a major source of allergens. It is the prototypical airborne pathogen, affecting a wide range of susceptible patient groups.¹ Its conidial

production is so prolific that the human respiratory tract always remains at risk of acquiring *Aspergillus* infection.² While in the upper airways, the conidia may cause respiratory discomfort due to contact irritation and allergic responses. In a recent study, the importance of hydrophobic rodlet layer of dormant conidia in the prevention of immune recognition has been described, and the allergic responses may get induced after release of cellular proteins from the metabolically active germinating conidia.³ These responses may get more severe to develop allergic bronchopulmonary aspergillosis (ABPA), a disabling allergic disease⁴ presented with shortness of breath, cough, wheezing and pulmonary infiltrates, which does not respond to conventional antibiotics in asthma and cystic fibrosis sufferers.^{5,6} The prevalence of ABPA has been estimated to be from 16 to 38% in asthmatics,⁷ up to 15% among patients with cystic fibrosis⁸ and 25% in the pediatric patients with infection of HIV.^{9,10} In immuno-compromised individuals, *A. fumigatus* may invade the lung tissues and disseminate to other

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A. fumigatus Early Stage Allergens

body parts causing invasive aspergillosis (IA), a severe and usually fatal infection in 30–90% of patients even under treatment.¹¹

The germinating conidia and mycelia express number of surface associated, secretory and cytosolic proteins, most of which have been described as virulent factors that play a role in pathogenesis.¹² The germinating conidial proteins are expected to be released earlier in comparison to the mycelial and secreted proteins during *A. fumigatus* infection. Some of these proteins were found to be responsible for evoking initial allergic responses during first encounter with host defense system.¹³ The majority of ABPA patients have been shown to have increased polyclonal response to multiple allergens/antigens.¹⁴ The sensitization of host with allergens of *A. fumigatus* may result in elevated levels of total serum IgE and *Aspergillus* specific IgE and/or IgG antibodies and their detection in sera has been considered to be important immuno-diagnostic criteria for ABPA¹⁴ and IA.^{15–17} Some of the *A. fumigatus* allergens (rAsp f1, rAsp f2, rAsp f3, rAsp f4 and rAsp f6) from secreted and mycelial fraction have been cloned, expressed and also evaluated for their IgE binding and diagnostic utility.^{12,18–20} These proteins are currently used in commercially available ELISA based diagnostic test of ABPA (allergen components, *A. fumigatus*, ImmunoCAP, Phadia, Uppsala, Sweden). On the other hand crude extracts of *A. fumigatus* are still in use for the diagnosis of ABPA (Siemens, Germany). ELISA kits for detection of *Aspergillus* antigens like, mannan and galactomannan remained good in specificity with variable sensitivity for invasive aspergillosis.²¹ The detection of IgG antibodies also has been shown to be useful in diagnosis of ABPA in cystic fibrosis patients.²² However, use of other available *A. fumigatus* allergens/antigens demonstrated restricted diagnostic relevance mainly due to cross reactivity by sharing of common epitopes with other fungal and bacterial proteins leading to wrong diagnosis of aspergillosis.²³ Knowledge of the broad spectrum of antigens and exploration of other fractions of *A. fumigatus* is essential to improve the specificity of currently available diagnostic tests.

The release of 29.4 megabase size complete genome reported the presence of 9926 genes in *A. fumigatus*²⁴ and the products of many of these genes are just only predicted. This inspired us to identify molecules not known yet, but their sequences are present in *A. fumigatus* and play a crucial role in the development of *Aspergillus* induced allergic and invasive disorders. The review of recent literature showed that of the known secretory allergens of *A. fumigatus* single molecule may not be sufficient for universal use in diagnosis of ABPA at initial stages of infection.²⁵ Thus, the less explored cytosolic proteins may form a panel of potential key determinants for the selection of universally reacting molecules for wider application in early and more specific diagnosis of *A. fumigatus* induced allergic disorders.²⁶

The present study, therefore, was aimed at developing high resolution allergeno-proteome of germinating conidial (GC) cytosolic fraction of geographically different strains of *A. fumigatus* for identification and characterization of its novel allergens. Such molecules may be important for global use in diagnosis of allergic aspergillosis and possibly for desensitization of allergic patients.

Materials and Methods

Strains of *Aspergillus*. Two clinical isolates, 190/96 strain isolated from an ABPA patient and characterized at Vallabh

Patel Chest Institute, Delhi, India (further typed and authenticated at Indian Type Culture Collection, Indian Agriculture Research Institute, New Delhi, India and coded as ITCC 6604) and DAYA, a Germany derived strain (D141; NRRL 6585; U.S. Department of Agriculture Peoria, IL), which was isolated from an aspergilloma that had developed in a 45 years old man with tuberculosis, were used in the present study.

Preparation of GC Protein Fraction. Total GC proteins were prepared by using a slight modified method outlined by Carberry et al (2006)²⁷ and Asif et al (2006).²⁸ Both the strains of *A. fumigatus* were grown in a synthetic broth (L-asparagine medium²⁹) for 16 h at 37 °C with continuous shaking in a rotatory shaker (C25KC, incubator shaker, New Brunswick Scientific, Edison, NJ). The conidia were observed under light microscope (Phase Contrast 2, ELWD 0.3, Nikon, Japan) to determine the stage of their growth in the culture. The growth of cells was seized at a stage where the germ tube size was predominantly 5.0 µm, by placing flask on ice for 30 min. Fungal cells were separated from the liquid media by centrifugation at 6500× g in a fixed angle rotor centrifuge (5810R, eppendorf, Hamburg, Germany) for 10 min at 4 °C. The cells were washed twice with 10 mM sodium phosphate buffer (pH 6.0) containing 0.9% NaCl, and lysed by mechanical grinding with 0.4 vol of glass beads (0.5 mm) suspended in 5.0 mL of 50 mM Tris-HCl buffer (pH 7.0), in a pestle mortar for 1 h at 4 °C. The suspension was centrifuged at 18 000× g (5810R, eppendorf, Hamburg, Germany) for 30 min at 4 °C to collect the soluble proteins in the supernatant. The protein solution was further filtered through 0.2 µm membrane filter and stored at –70 °C until use. The protein content in the sample was estimated by the method described by Bradford (1976).³⁰

Patient's Sera. The blood samples (5.0 mL) were drawn from the clinically confirmed patients of ABPA (*n* = 13) and apparently healthy control individuals (*n* = 12) with their informed consent according to ethical guidelines. The serum samples were analyzed for the levels of circulating immunoglobulins (*Aspergillus* specific IgE and IgG) against *A. fumigatus* GC antigen and total serum IgE before pooling them for immunoblotting.

Determination of Serum Immunoglobulin Levels. The ELISA methods as described by Sharma and Sarma (1997)³¹ and Sepulveda et al. (1979)³² were used with slight modifications for the determination of *Aspergillus* specific IgG and IgE against GC antigen of *A. fumigatus* respectively. The levels of total serum IgE in the serum of ABPA patients were determined by using the standard kit procured from Bethyl Laboratories Inc., Montgomery, TX.

Two-Dimensional Gel Electrophoresis (2DE). Extracted GC protein samples of *A. fumigatus* strains 190/96 and DAYA were precipitated by 2D clean up kit (Catalogue No. 80–6484–51) purchased from GE Healthcare Biosciences Corp. (Piscataway, NJ). The protein pellet was dissolved in rehydration buffer (7 M Urea, 2 M Thiourea, 20 mM dithiothreitol, 0.5% Bioampholytes). A total of 40 µg purified protein was used for each loading on 7 cm IPG strips pH 3–10 and 4–7 obtained from BioRad (Hercules, CA). The separation of proteins in first dimension was achieved on IEF cell (BioRad, CA) by using the standard program initiated with 200 V for 2 h, followed by ramping at 500 V for 2 h, and final focusing at 4000 V for 5 h for a total of 20 000 Vh. The second dimension electrophoresis was carried out using 12.5% SDS polyacrylamide gel in Mini Protean assembly (BioRad, Hercules, CA). Gels were silver stained by a modified method described by Blum et al (1987).³³

Immunoblotting. The proteins from corresponding 2DE gels were transferred onto nitrocellulose membrane (Amersham Biosciences) in a Mini Protean transfer unit (BioRad, CA, USA) for overnight at 50 V, 4 °C. The unwanted sites on membrane were blocked with 2% BSA prepared in phosphate buffered saline containing 0.05% Tween 20 (PBST) with continuous shaking for 1.5 h at room temperature. Membrane was incubated with pooled sera samples diluted (1:100) in PBST and kept for shaking at room temperature for 3 h. Further, membranes were incubated with detection antibody, antihuman IgE (ϵ -chain specific, produced in goat, Sigma, St Louis, MO, Catalogue No. A3525) or antihuman IgG (γ -chain specific, F(ab')₂, produced in goat, Sigma, St Louis, MO, Catalogue No. A2290) conjugated with horse radish peroxidase (HRP), diluted in PBST (1:3000) for 1.5 h at room temperature with constant shaking. The excess secondary antibody was washed vigorously with PBST thrice, each for 10 min. Finally, the membrane was washed once with PBS for 5 min before developing. The conjugate that remained bound on the membrane was detected by chemiluminescence assay using the ECL system (Thermo Scientific, Rockford, IL). Autoradiographs were developed using Kodak imaging films in accordance with the protocol provided by the supplier.

Matching the Immuno-Reactive Spots. The immuno-reactive protein spots obtained after immuno-blotting with ABPA patients' sera were matched manually as well as with the help of Delta 2-DE v 4.0 (DECODON, Germany) to the corresponding silver stained 2DE gel. The Western blots were matched first with their own Ponceau stained images and then were manually compared with the subsequent silver stained gels using the landmarks inserted on the membrane during the 2DE immuno-blotting.

In order to confirm if the correct protein spots had been excised from the corresponding gels, the selected immuno-blots were repeated using PVDF membrane. The reactive spots were also picked up directly from the PVDF membrane for analysis. For this purpose selected 2DE blots were reproduced as described above in the methodology section of immunoblotting and antibodies were removed from PVDF membrane by washing with stripping buffer (62.5 mM Tris pH 6.8, 2% SDS, 100 mM 2- β mercaptoethanol) for 30 min followed by five washes each for 5 min with PBS. The immuno-reactive spot area was excised using the landmarks left on membranes during the procedure of 2DE immuno-blotting. The membrane spots were digested directly from the PVDF membrane.

Mass Spectrometry-Based Identification of Immuno-Reactive Proteins. The matched spots were excised from the gels and further processed for in-gel tryptic digestion and Q-TOF MS/MS analyses as described by Asif et al 2006.²⁸ Briefly the excised spots were dehydrated in a vacuum centrifuge (UNIVAP-150H, UniEquip, Martinsried, Germany). The gel slices were rehydrated and protein was in-gel digested with 40 μ L trypsin (10 ng/ μ L in 100 mM ammonium bicarbonate, pH 7.4; Promega, Mannheim, Germany) for overnight at 37 °C. Tryptic digestion of proteins from PVDF membrane pieces was achieved as described by Asif et al. (2010).³⁴ Excess trypsin solution was removed and replaced with the same volume of 100 mM ammonium bicarbonate without trypsin. Peptides were extracted by repeated cycles of sonication in 0.1% TFA/50% ACN aqueous solution, dried completely in a vacuum centrifuge and reconstituted in 0.1% (v/v) formic acid in water. The reconstituted peptide samples (1 μ L) were separated by HPLC using C18 reverse phase column and further analyzed in a Q-TOF

Ultima Global mass spectrometer (Micromass, Manchester, U.K.) and data were acquired with the MassLynx (v 4.0) software on a Windows NT PC and further processed using ProteinLynx Global Server (PLGS, v 2.2, Micromass, Manchester, U.K.) as PKL (peaklist) according to settings and details as described by Asif et al (2006).²⁸ The obtained peaklists were further searched using the available online MASCOT (<http://www.matrixscience.com>) algorithm against NCBI nr database. Retrieved data against the whole database with selected search parameters set as follows: enzyme, trypsin; allowance of up to one missed cleavage peptide; mass tolerance ± 0.5 Da and MS/MS tolerance ± 0.5 Da; modifications of cysteine carboxamidomethylation and methionine oxidation. Proteins were finally identified on the basis of their two or more peptide matches whose ion scores exceeded the threshold, $P < 0.05$, which indicated by the 95% confidence level for these peptides. Proteins were accepted as identified by their matches if the threshold was exceeded and the protein spot possessed the correct molecular mass and pI value for the *A. fumigatus* isoform in the corresponding gel electrophoresis. The proteins spots were excised and analyzed from more than one gels to ensure the accuracy of protein identification.

Functional Annotation and Prediction of Antigenic Index. A list of known and predicted allergens³⁵ of *A. fumigatus* was acquired from the *Aspergillus* database (www.aspergillus.org.uk) and functional annotation to all identified proteins was given by matching their accession number, obtained amino acid sequences at protein databases uniprot (www.uniprot.org) and Kognitor³⁶ (www.ncbi.nlm.nih.gov/COG/grace/kognitor). Amino acid sequences of all identified immuno-reactive proteins have been analyzed for prediction of antigenic index by *in-silico* sequence analysis tool DNASTAR (DNASTAR, windows 32 protean 5.07.1989–2003, DNASTAR Inc., Madison, WI).

Cloning, Expression, and Immunoreactivity of Recombinant Proteins. The genes coding for alcohol dehydrogenase and fructose-bisphosphate aldolase class-II were amplified from the previously constructed λ -ZAP cDNA library using primers; pair 1 (forward AAATTTGGATCCCCGGTCTGATGACATTC-TTG and reverse TATTATAAGCTTCTACGCTACGACTCGCAATCCCATC) and pair 2 (forward AAATTTGGATCCGTCACAAACGAGGACGTTGAC and reverse TATTATAAGCTTCTAGTTGAAGTCCTCCAGAGCAACC) respectively. Both amplicons, one of 512 bp (coding for 30–199 amino acid part of full length alcohol dehydrogenase, accession No. XP_754009) and another of 507 bp (coding for 187–354 amino acid region of complete fructose biphosphate aldolase-class-II sequence, accession No. XP_754452) coding for partial protein sequences were cloned in a prokaryotic expression vector pQE-30a (Qiagen, Hilden, Germany) in the *Bam*HI and *Hin*DI restriction sites of plasmid vector. The recombinant proteins were induced by isopropyl- α -D-thiogalactopyranoside (IPTG) and molecular weights of recombinant proteins were confirmed on 12.5% SDS polyacrylamide gel and purified in native form by metal affinity chromatography using Ni-NTA resin (Qiagen, Hilden, Germany) in nondenaturing conditions as recommended by manufacturer. Furthermore, the recombinant proteins (alcohol dehydrogenase and fructose-bisphosphate aldolase-class-II) were employed for the immunoblotting using sera of 10 ABPA patients along with previously used pooled serum. An amount of 0.3 μ g of purified protein was used for each loading and subsequently proteins were electro-transferred onto PVDF membrane (Amersham Biosciences). The membrane was blocked with 3% BSA prepared in Tris buffered saline containing 0.1% Tween 20, pH-7.4 and

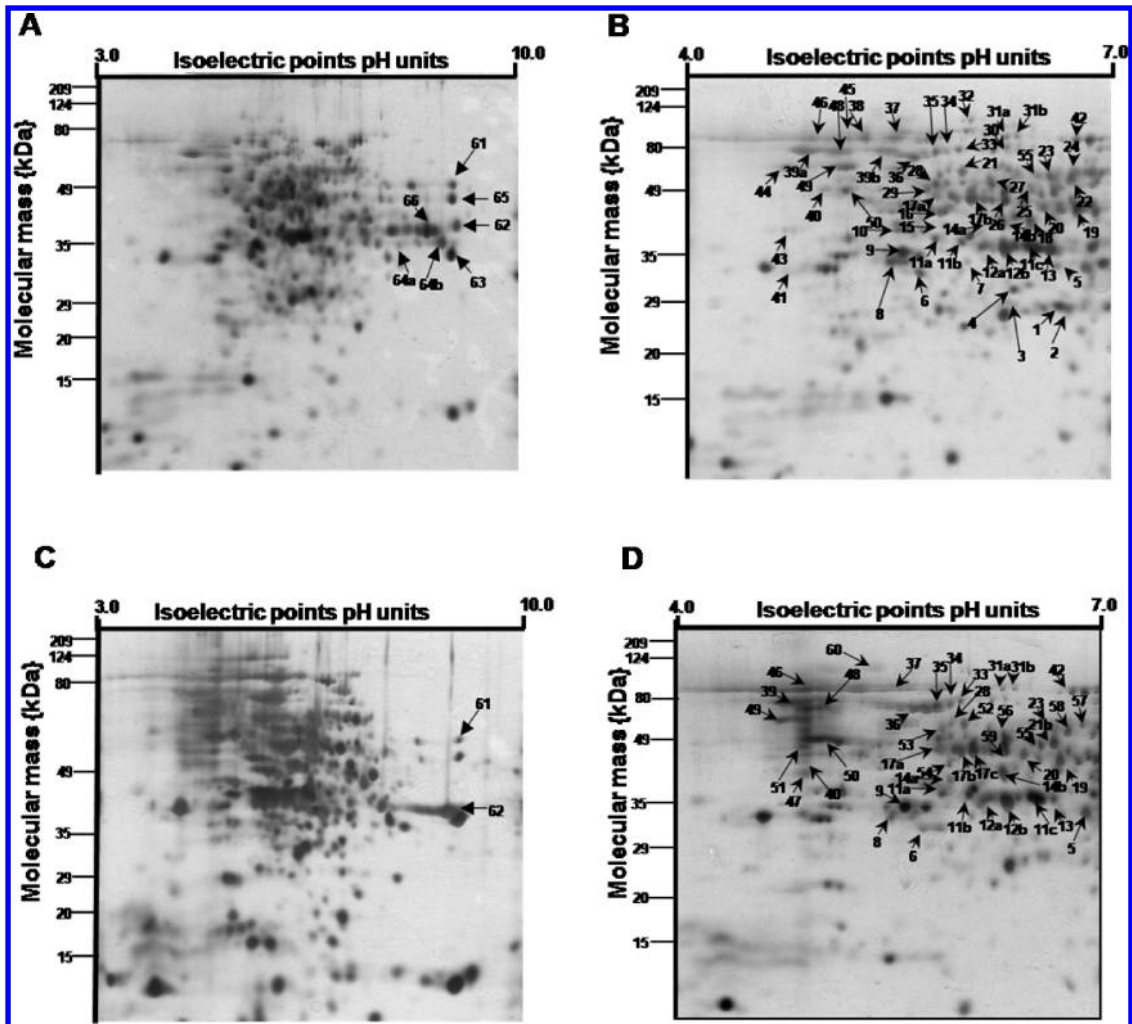


Figure 1. Silver stained 2DE polyacrylamide gels of *A. fumigatus* strains 190/96 (A and B) and DAYA (C and D), in pH ranges 3–10 (A and C) and pH 4–7 (B and D). GC proteins were prepared from 16 h culture by mechanical grinding of cells with glass beads. An amount of 40 μ g proteins was loaded on linear pH gradient strip and separated horizontally on the basis of their isoelectric points followed by vertical separation on 12.5% SDS polyacrylamide gels. Silver stained gels were compared with immunoblots for marking the spot numbers.

developed with patient's sera to detect the presence of IgE antibodies against recombinants. The antihuman IgE (ϵ -chain specific, produced in goat, Sigma, USA, Catalogue No. A3525) was used as secondary antibody and signals on membrane were detected by chemiluminescence (Thermo Scientific, Rockford, IL) in accordance with the supplier.

Results and Discussion

In the present work we have developed the immuno-proteomes of two geographically distinct strains of *A. fumigatus* (190/96 and DAYA). The silver stained 2DE gels demonstrated well separated protein profile of 190/96 and DAYA. There were large number of proteins that remained concentrated in the acidic to neutral pH range (Figure 1A and C). To get better separation of those clustered low pI proteins, we resolved GC fraction on narrow pH range strips (pH 4–7). This improved the separation of spots significantly, however, 2DE gels showed several isomeric proteins having pIs from 5.0 to 6.8 (Figure 1B and D). There were apparent differences in the proteomes of 190/96 and DAYA. A few proteins with pIs range of 4.8–5.3 appeared in DAYA exclusively. Although the spot pattern of GC proteins of two geographically diverse strains was found to be

Table 1. ABPA Patients and Control Subjects Included in the Study

	control individuals	ABPA patients
Numbers	12	13
Age, years (range)	25–65	28–60
Gender (M/F)	8/4	5/8
Total IgE (IU/mL) (M $\pm$ SE)	328.8 $\pm$ 48	1035.5 $\pm$ 170.8
Specific IgE against GC antigen (Abs. at 410 nm) (M $\pm$ SE)	0.075 $\pm$ 0.012	0.308 $\pm$ 0.050
Specific IgG against GC antigen (Abs. at 492 nm) (M $\pm$ SE)	0.015 $\pm$ 0.003	0.589 $\pm$ 0.029

different, there were several overlapping proteins in Indian and German strain (Figure 1A–D).

Serum samples obtained from clinically confirmed patients of ABPA ($n = 13$) having high titers of *Aspergillus* specific antibodies (IgG and IgE) against GC antigen of *A. fumigatus* and also elevated levels of total serum IgE antibodies (Table 1), were used to prepare the positive pool of serum for immuno-blotting. The negative pool was prepared from the sera of apparently healthy individuals ($n = 12$). Two dimensional IgE and IgG specific immunoblots of the GC proteome

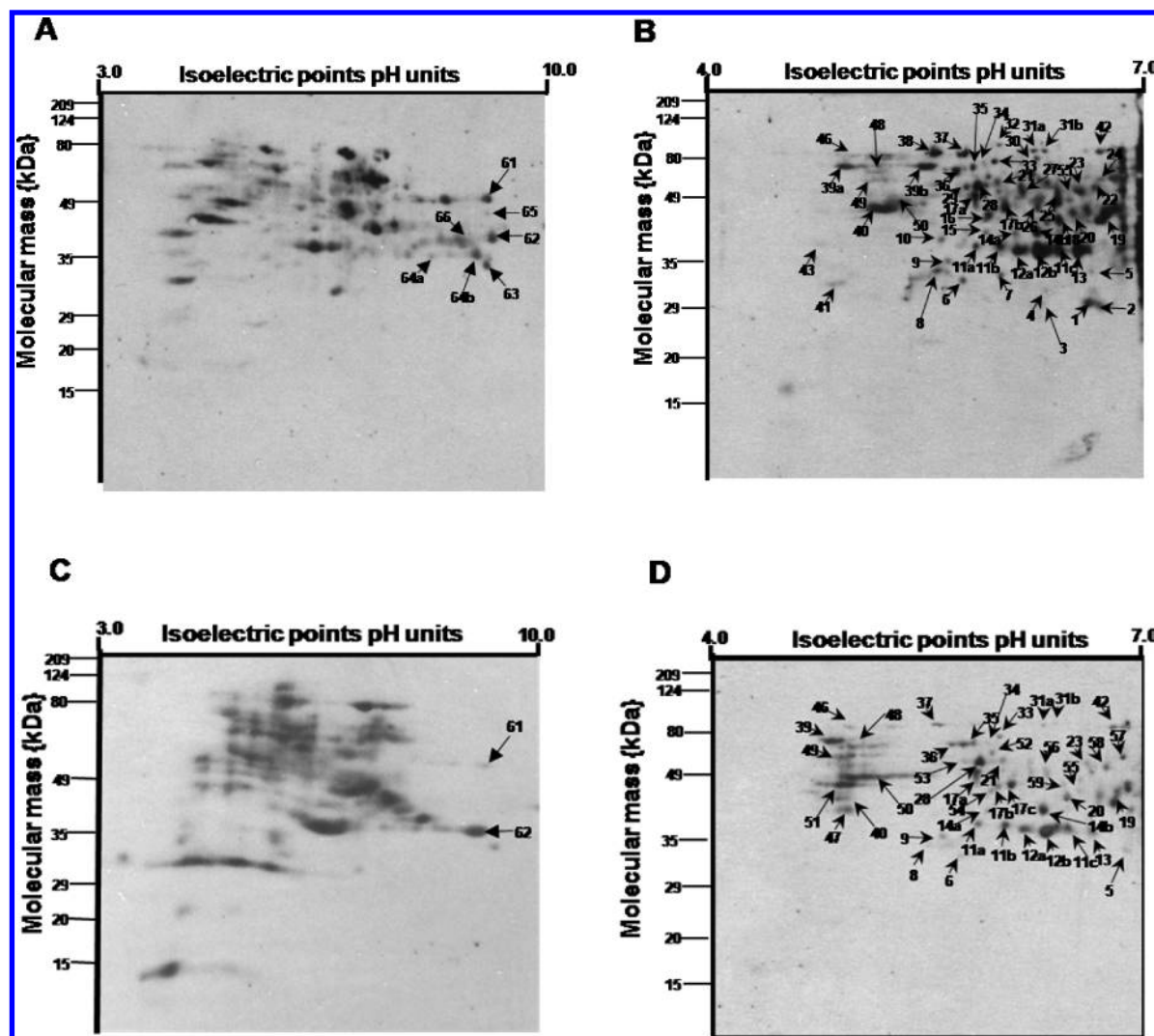


Figure 2. 2DE immuno-blots of GC proteomes of *A. fumigatus* strains 190/96 (A and B) and DAYA (C and D), in pH ranges 3–10 (A and C) and pH 4–7 (B and D) showing proteins which reacted with IgE antibodies of ABPA patients sera and probed with antihuman IgE conjugated with HRP. IgE blots were compared with 2DE gels and spots were excised from the gels on the basis of their appearance in the immuno-blots. Excised protein spots were in-gel digested and subjected to liquid chromatography coupled with tandem mass spectrometry for identification of proteins.

were developed with pooled ABPA patients' sera. Large number of unevenly distributed IgE reactive spots appeared on the blots (Figure 2A–D). The GC fraction of *A. fumigatus* had fewer number of IgG specific antigens and strong reactivity appeared in the area of low pI and high molecular weight (Figure 3A–D). We observed a significant number of common IgE reactive spots with variable intensity of signals on the immuno-blots of 190/96 and DAYA (Figure 2B and D).

Matching of immuno-blots with corresponding silver stained 2DE gels identified 111 protein spots, which were excised from the 2DE gels (Figure 1). These spots included 64 from 190/96 (7 from 2DE gel of pH 3–10 and 57 from 2DE gel of pH 4–7) and 47 spots from DAYA (2 from 2DE gel of pH 3–10 and 45 from 2DE gel of pH 4–7). All spots were subjected to tryptic digestion, peptide extraction and Q-TOF MS/MS analysis of extracted peptides by liquid chromatography coupled with tandem mass spectrometry. MASCOT search of the sequenced files from available databases (NCBIInr) led to identification of total 66 proteins with significant MASCOT scores ranging from 59 to 876. Sequence coverage in the identified proteins ranged between 5–57%. Out of these 66 proteins, 64 showed homology

with *A. fumigatus* proteins. One of remaining 2 proteins which corresponded to Spot No. 54, showed match with ACT_BOTCI actin of *A. nidulans* and other of Spot No. 16 showed match with elongation factor-Tu of *Klebsiella pneumoniae*. Although the MASCOT scores of Spot No. 16 with *K. pneumoniae* was significant, due to lack of homology with any protein of *Aspergillus*, it was not considered for further analysis. Proteomics has advanced with the introduction of 2DE, but several limitations remained associated with this separation technique, especially in the case of fungal proteins. Often hydrophobic, membranous, highly acidic or basic, and large-sized proteins are poorly separated by 2DE.³⁷ In the present study, too, we might have missed to resolve all *A. fumigatus* cytosolic proteins and it is possible that some cellular allergens may have been left unidentified in addition to 66 immunoreactive proteins described here.

Analysis of the identified spots showed presence of 63 IgE reactive proteins (Figure 2). Six proteins fell in category of *A. fumigatus* allergens, of which 2 proteins (Spot No. 17/Asp f22³⁸ and Spot No. 38/Asp f12³⁹) were known allergens and 4 were predicted allergens.³⁵ These predicted allergens recovered in

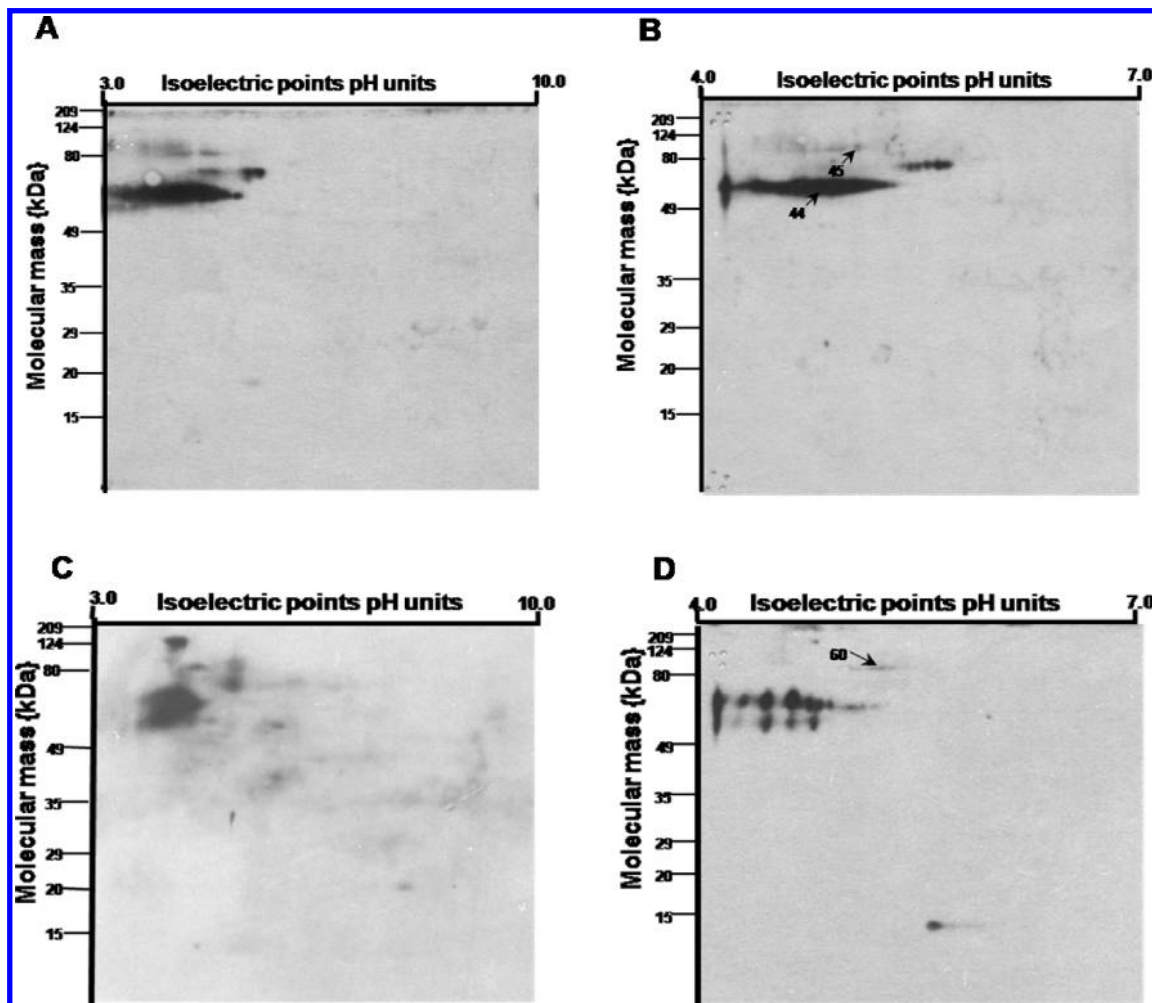


Figure 3. 2DE immuno-blots of GC proteome of *A. fumigatus* strains 190/96 (A and B) and DAYA (C and D), in pH ranges 3–10 (A and C) and pH 4–7 (B and D) showing proteins which reacted with IgG antibodies of ABPA patients sera and probed with antihuman IgG conjugated with HRP. IgG blots were compared with 2DE gels and matched spots were excised from the gels for further analyses by liquid chromatography coupled with tandem mass spectrometry for identification of proteins.

Spot Nos. 37, 39, 62, and 63 were identified as Hsp70 chaperone Hsp88, Hsp70, malate dehydrogenase NAD-dependent and Zn containing alcohol dehydrogenase putative respectively. However, the protein identified from Spot No. 43 was found to be PEP2, a vacuolar aspartic endopeptidase⁴⁰ previously reported in the literature but not so far as allergen. Interestingly, we were able to characterize only 3 proteins (2 in 190/96 and 1 in DAYA) that reacted with IgG antibodies (Figure 3), however, few more IgG reactive spots were visible on blots but their amount in corresponding protein spot had insufficient concentration of proteins for Q-TOF MS/MS analysis. Present study identified 62 proteins which were uncharacterized predicted molecules deduced from recently sequenced genome of *A. fumigatus* for their biological functions. Possible reason for getting a large number of unidentified immuno-reactive proteins may be that we used a less explored complex GC fraction of *A. fumigatus* for immuno-proteomics studies. The results of the present work demonstrated the physical presence of proteins that were predicted in *A. fumigatus* and also assigned at least one biological property of them being immunogenic and reactive specifically to IgE and IgG antibodies of ABPA patients' sera. It was not known until we observed that the distribution of IgE and IgG binding epitopes in antigens of *A. fumigatus* was so protein specific. Further, analysis of proteins by using DNASTar, *in-silico*

analysis tool (DNASTar, windows 32 protean 5.07.1989–2003, DNASTar Inc. Madison, WI) confirmed the presence of antigenic epitopes among all 66 identified immuno-reactive proteins. It was observed that out of 66 identified proteins 30 were common in both strains. Twenty-six proteins were specific for Indian strain (190/96) and 10 proteins were found to be specific for German strain (DAYA). These differences in the strain specific immuno-reactivity can be attributed to the fact that Indian ABPA patients' sera were used in the present study. A recently published proteome map⁴¹ of *A. fumigatus* also showed the presence of 24 common proteins that were found to be IgE reactive in the present study. Some of the proteins found to be allergenic in strains of *A. fumigatus* (190/96 and DAYA) were identified as potential drug targets (mitochondrial Hsp70 chaperone Ssc70 and Hsp70 chaperone Hsp88)⁴² or the molecules (malate dehydrogenase-NAD-dependent and mitochondrial aconitate hydratase) involved in the interaction between *A. fumigatus* conidia and host cells.⁴³ We have earlier developed conidial hyphal surface associated proteome which also showed presence of 3 common proteins (vacuolar aspartic endopeptidase PEP2, protein disulfide isomerase Pdi1 and alcohol dehydrogenase)²⁸ where they were reflected as potential vaccine candidates. Another recent study from our group identified a panel of *A. fumigatus* proteins reactive to IgG, IgM

and IgA antibodies present in the sera of rabbits which acquired protective immunity after experimentally induced invasive aspergillosis³⁴ indicating their role in conferring protection. Sixteen proteins [marked in Table 2 with asterisk (*)] of that panel were identified in GC fraction of *A. fumigatus* used in the present study and all of them were found to predominantly IgE reactive. Thus, these proteins will be important also in diagnosis of aspergillosis.

Present study described the immune responses of the host to the germinating conidial proteins. It was bit surprising to observe that majority of GC proteins reacted with IgE. The antigen antibody reaction is a complex phenomenon and resultant host immune responses to this fraction of *A. fumigatus* have not been studied so far. We consider that less explored cytosolic fraction of *A. fumigatus* had mainly the molecules that contained predominantly the allergenic epitopes for IgE binding. This might be the reason why only 3 proteins out of 66 exclusively reacted with IgG antibodies of ABPA patients' sera. These IgG reactive proteins were identified as protein disulfide isomerase Pdi1, translation elongation factor EF-2 subunit and assimilatory sulfite reductase from the Spot No. 44, 45, and 60 respectively. Among them, the Pdi1 has been considered as possible vaccine candidate from conidial hyphal wall associated proteome.²⁸ Few other studies have also demonstrated successful attempts of immuno-protection in experimental animal models of invasive aspergillosis by using *A. fumigatus* immunogenic proteins.^{44,45} In view of this, these 3 proteins may not have allergenic potential but could be evaluated for their immuno-therapeutic properties.

The biological function annotation of presently identified proteins within uniprot databases (www.uniprot.org) and Kognitor³⁶ alienated 66 immuno-reactive proteins into 16 different categories (Supplemental Figure 3, Supporting Information). Major divisions of these functional categories were transport and/or metabolism of essential constituents (amino acid, carbohydrate, nucleotides and coenzymes), proteins that involved in energy conversion and/or production and stress proteins. The molecular chaperones and the proteins involved in secondary processing such as, posttranslational modifications which help in protein turnover constitutes the factors that may help the pathogen to survive under adverse conditions in the host. In the literature, 9 known and 8 predicted allergens³⁵ of *A. fumigatus* have been reported to occur in the category of adaptive stress proteins. Likewise, 11 IgE reactive proteins were also present in the same functional category, which have been identified from the Spot No. 2, 3, 28, 34–39, 43, and 44 listed as proteasome component-Prs2, proteasome component-Pre9, secretory pathway-gdp dissociation inhibitor, mitochondrial Hsp70 chaperone (Ssc70), heat shock protein (Sti1), Hsp70 chaperone (HscA), Hsp70 chaperone-Hsp88, Asp f12/-Heat shock protein-P90 (Hsp90),³⁸ molecular chaperone-Hsp70, aspartic endopeptidase-PEP2 and protein disulfide isomerase (Pdi1) respectively. It was interesting to observe that of these 11 proteins, 1 matched with a known (Spot No. 38³⁶) and 2 with predicted allergen³⁵ (Spot Nos. 37 and 39) in the same functional category. Amino acid transport and metabolism is one of major biological process at basal cellular level. We observed that there were 14 immuno-reactive proteins in *A. fumigatus* that belonged to this group but none of them showed homology with any known or predicted allergens. It was important to note that 4 of these novel proteins of *A. fumigatus* (Spot Nos. 26, 27, 47 and 61) reacted strongly with IgE antibodies (Figure 2). Another major group of proteins was

carbohydrate transport/metabolism which contained 12 proteins and 5 of them showed strong IgE reactivity in both strains. These 5 proteins were fructose-bisphosphate aldolase-class-II (Spot No. 12), transaldolase (Spot No. 13), Asp f22/enolase³⁷ (Spot No. 17), phosphoglycerate kinase (Spot No. 19) and mitochondrial aconitate hydratase (Spot No. 42). Energy has been the basic requirement of any cell and the energy production/conversion also covers the major category of cellular functions. There were 11 proteins in this category which included a predicted allergen malate dehydrogenase-NAD-dependent (Spot No. 62) and 2 other predicted proteins (Spot No. 9 and 23). These proteins reacted more strongly in 190/96 strain of *A. fumigatus* as compared to DAYA. Immuno-reactive proteins which could not be attributed to any of the major functional category also had few proteins with strong IgE reactivity. These proteins were nuclear binding protein Nap1, ran-GTPase activating protein, alcohol dehydrogenase and Zinc containing alcohol dehydrogenase-putative identified from the Spot Nos. 49, 50, 63, and 66 respectively. In the literature 3 proteins namely Asp f2, Asp f4 and Asp f7 have been reported as known allergens with unknown biological functions and 5 as the predicted allergens (RNA binding protein MSSP2, glucan 1,4- α glucosidase, aryl alcohol dehydrogenase, histidine acid phosphatase and NADH quinone oxidoreductase Pst2) which had only predicted biological functions.^{35,36} Six allergens (Spot Nos. 1, 11, 18, 21, 51 and 55) of the present study also belonged to the category of predicted and unknown functions according to Kognitor.³⁶ In this context, proteins that have unknown/predicted functions are also important in terms of immunogenicity.

In order to validate our results which demonstrated that majority of germinating conidial proteins are IgE reactive in nature, we selected 2 representative proteins (alcohol dehydrogenase, putative and fructose-bisphosphate aldolase-class-II) from the presently identified antigenic panel for recombinant expression. The selection of fructose-bisphosphate aldolase-class-II was based on its strong reactivity with immune sera of ABPA patients (Figure 2B and D, Spot No. 12a–b). The alcohol dehydrogenase was selected as it showed immunoreactivity with patient's sera (Figure 2A, Spot No. 63) and also has been a predicted allergen of *A. fumigatus*.³⁵ To achieve a better expression of both proteins, we selected suitable regions from amino acid sequences of these proteins for recombinant production. The partial sequence of both genes (512 bp for alcohol dehydrogenase and 507 bp for fructose-bisphosphate aldolase class-II) were cloned in plasmid vector, pQE-30a (Qiagen, Hilden, Germany) and expressed. Further recombinant proteins were purified (Figure 4) and examined for their IgE reactivity with sera of ABPA patients. The immunoreactivity of both recombinant proteins with 10 individual ABPA patients' sera (Figure 5) showed that these proteins are indeed IgE reactive. These results also confirmed their presence in *A. fumigatus* and the correct identification.

In conclusion, we have identified 63 IgE reactive proteins of *A. fumigatus* based on their immuno-reactivity with ABPA patients' sera. The study of IgE reactivity of this panel of antigens with a larger number of individual sera of ABPA patients will help in identifying *A. fumigatus* specific allergens. These molecules have potential to improve existing tests for diagnosis of ABPA which are only based on limited number of allergens and conventional crude antigenic preparations. Further, recombinant expression and detailed immunological characterization of such allergens will facilitate their diagnostic utility. On the other hand, allergens of this panel may also be

Table 2. Immuno-Reactive Proteins Analyzed by Mass Spectrometry (MS/MS) from GC Proteome^a

spot no.	accession no.	identification <i>A. fumigatus</i>	matches	sequence coverage (%)	MASCOT score	tht mass/pI (kDa)	obs mass/pI (kDa)	function	KOGs	IR	appeared signal in blots of Figures
1	XP_755878	Sorbitol/xylulose reductase Soul-like	10	33	278	28.2/5.96	29/6.1	Oxidoreductase	R	IgE	2B
2	XP_754489	Proteasome component Prs2	4	17	207	28.2/6.84	30/6.4	Hydrolase	O	IgE	2B
3	XP_750785	Proteasome component Pre9	5	16	171	28.2/5.80	28/5.8	Hydrolase, Threonine protease	O	IgE	2B
4	XP_001481696	6-phosphogluconolactonase	8	34	309	28.8/5.84	30/5.9	Hydrolase	G	IgE	2B
5	XP_753827	Pyridoxine biosynthesis protein	3	15	171	32.7/6.04	33/6.3	Catalytic activity	H	IgE	2B, D
6	XP_752719	Spermidine synthase	8	17	238	33.4/5.33	32/5.2	Transferase	E	IgE	2B, D
7	XP_754985	Phosphoribosyl- aminoimidazole- succinocarboxamide synthase	6	17	131	33.2/5.51	33/5.5	Ligase	F	IgE	2B
8	XP_754776	Inorganic diphosphatase	6	14	217	43.6/7.63	34/4.9	Hydrolase	C	IgE	2B, D
9	XP_750257	60S ribosomal protein P0	10	24	299	33.5/5.11	35/5.1	Ribosomal	J	IgE	2B, D
10	XP_753994	Adenosine kinase	2	6	82	36.8/5.02	38/5.0	Kinase, transferase	G	IgE	2B
11	a-c ^b	Thiamine biosynthesis protein (Nmt1)	8	26	295	38.3/6.04	38/5.4-6.0	Function not known	S	IgE	2B, D
12	a-b ^b	Fructose-bisphosphate aldolase, class II	13	22	438	39.7/5.55	38/5.5-5.9	Lyase	G	IgE	2B, D
13 ^b	XP_753716	Transaldolase	17	38	419	35.4/6.04	36/6.1	Transferase	G	IgE	2B, D
14	a-b	S-adenosylmethionine synthetase	10	26	343	42.1/5.67	42/5.5-5.8	Transferase, ATP, Mg, K, binding	H	IgE	2B, D
15	XP_751519	Glutamine synthetase	4	10	113	39.8/5.48	40/5.5	Ligase	E	IgE	2B
17	a-c ^b	Asp f22/Enolase	19	36	806	47.2/5.39	47/5.4-5.7	Lyase	G	IgE	2B, D
18	CAE17673	Putative flavohemoglobin	3	7	134	45.5/5.72	43/5.8	Electron carrier, Oxidoreductase	S	IgE	2B
19 ^b	XP_752401	Phosphoglycerate kinase PgkA	23	57	762	44.7/6.31	43/6.4	Oxygen transporter	G	IgE	2B, D
20	XP_752379	Adenosylhomocysteinase	23	38	677	48.4/5.82	47/6.0	Hydrolase	H	IgE	2B, D
21	XP_751658	Phosphatidyl synthase	13	23	452	67.0/6.11	63/5.7	Hydrolase	R	IgE	2B, D
22	EDP54506	Glucose-6-phosphate isomerase	15	31	447	61.3/5.85	58/6.4	Isomerase	G	IgE	2B
23	XP_750954	ATP citrate lyase subunit (Acl), putative	18	29	474	52.8/5.88	53/6.2	Lyase, Ligase	C	IgE	2B, D
24	Q4WFT3	GMP synthase	5	7	120	61.4/5.85	62/6.5	Ligase, ATP binding	F	IgE	2B
25 ^b	XP_750696	[glutamine-hydrolyzing] 6-phosphogluconate dehydrogenase Gnd1	19	31	876	55.7/5.86	55/5.8	Oxidoreductase, NADP binding	G	IgE	2B
26	XP_755071	Gamma-glutamyl phosphate reductase	6	14	112	48.7/5.60	48/5.6	Oxidoreductase, NADP binding	E	IgE	2B
27	XP_755056	Glutamatecarboxypeptidase	3	9	59	52.9/5.47	53/5	Carboxypeptidase, metalloproteinase, dimerization	E	IgE	2B

Table 2. Continued

spot no.	accession no.	identification <i>A. fumigatus</i>	matches	sequence coverage (%)	MASCOT score	tht mass/pI (kDa)	obs mass/pI (kDa)	function	KOGs	IR	appeared signal in blots of Figures
28	XP_755448	Secretory pathway gdp dissociation inhibitor	8	16	349	52.2/5.33	52/5.4	Rab-GDP dissociation	O	IgE	2B, D
29	XP_747854	Glucokinase GlkA	4	11	110	54.4/5.33	52/5.3	Kinase, ATP binding	G	IgE	2B
30	XP_755657	Bifunctional tryptophan synthase TRPB	9	14	376	78.7/5.66	80/5.7	Pyridoxal phosphate binding, binding	E	IgE	2B
31 a–b	XP_755459	3-isopropylmalate dehydratase	9	12	181	84.0/5.62	85/5.6–5.8	Iron sulfur cluster binding	E	IgE	2B, D
32	XP_752826	Phosphoribosyl-AMP cyclohydrolase	5	5	86	92.8/5.46	93/5.6	Dehydrogenase, Hydrolase, Phosphotase, Zn- binding	E	IgE	2B, D
33	XP_753831	Aminopeptidase P	4	8	15	72.6/5.93	78/5.4	Metallopeptidase, Hydrolase	E	IgE	2B
34 ^b	XP_755328	Mitochondrial Hsp70	17	28	673	74.4/6.02	77/5.3	ATP/unfolded protein binding	O	IgE	2B, D
35	XP_746746	Heat shock protein (Sti1)	4	9	102	64.9/5.83	75/5.3	Stress response	O	IgE	2B, D
36	XP_747200	Hsp70 chaperone (HscA)	13	27		66.9/5.30	63/5.2	ATP binding	O	IgE	2B, D
37	XP_752631	Hsp70 chaperone Hsp88	10	14	293	79.9/5.08	82/5.3	ATP binding	O	IgE	2B, D
38	XP_747926	Asp f 12/Heat shock protein P90/Molecular chaperone and allergen	13	20	613	80.5/4.95	83/4.9	ATP/unfolded protein binding	O	IgE	2B
39 a–b	XP_750490	Mod-E/Hsp90/Hsp1 Molecular chaperone	21	26	693	69.6/5.09	74/4.4–5.0	ATP binding	O	IgE	2B, D
40	XP_753589	ATP synthase F1, beta subunit	15	31	412	55.6/5.30	48/4.9	Hydrolase, ATP/metal ion binding	C	IgE	2B, D
41	XP_750312	40S ribosomal protein S3	12	56	615	29.1/9.18	31/4.5	Ribonucleoprotein, RNA binding	J	IgE	2B
42 ^b	XP_751171	Mitochondrial aconitate hydratase	17	21	389	85.4/6.26	86/6.5	Tricarboxylic acid cycle, Fe/S ion binding	G	IgE	2B, D
43	XP_754479	Aspartic endopeptidase PEP2	2	8	66	43.3/4.81	40/4.4	Hydrolase, protease	O	IgE	2B
44	XP_749744	Protein disulfide isomerase Pdi1	7	16	260	56.1/4.58	55/4.6	Ca ion binding, isomerase	O	IgG	3B
45	XP_755686	Translation elongation factor EF-2 subunit	4	5	58	93.1/6.51	93/5.6	GTPase, GTP binding	J	IgG	3B
46	XP_752090	Cobalamin-independent methionine synthase MetH/D	6	6	89	86.8/6.33	86/4.5	Methyltransferase, Zn ion binding	E	IgE	2B, D
47	XP_752650	Isocitrate dehydrogenase, NAD-dependent	7	17	281	41.7/8.72	42/4.7	Oxidoreductase	E	IgE	2D
48	XP_752056	Phosphoribosylaminoimidazole- carboxamide formyltransferase/IMP cyclohydrolase	2	3	63	64.9/6.39	72/4.9	Hydrolase, Transferase	F	IgE	2B, D
49	XP_754077	Nucleosome assembly protein Nap1	4	11	94	48.3/4.43	63/4.8	Nucleosome assembly	BD	IgE	2B, D
50	XP_754843	Ran GTPase activating protein 1 (RNAI protein)	5	12	99	46.2/4.62	47/4.7	Protein binding	AYT	IgE	2B, D

Table 2. Continued

spot no.	accession no.	identification <i>A. fumigatus</i>	matches	sequence coverage (%)	MASCOT score	tht mass/pI (kDa)	obs mass/pI (kDa)	function	KOGs	IR	appeared signal in blots of Figures
51	XP_756019	Curved DNA-binding protein	4	11	131	46.5/7.61	47/4.8	DNA binding, Hydrolase,	R	IgE	2D
52	XP_754690	Phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent	5	11	276	57.4/5.44	56/5.3	Aminopeptidase Isomerase, Mn ion binding	G	IgE	2D
53	XP_748938	Pyruvate dehydrogenase complex, dihydrolipoamide acetyltransferase component	4	11	101	52.0/6.25	52/5.1	Acetyl transferase/Protein binding	C	IgE	2D
54	XP_664146	ACT_BOTCI Actin <i>A. nidulans</i>	4	13	64	41.6/5.54	43/5.5	ATP/protein binding	Z	IgE	2D
55	XP_752265	UPF0160 domain protein MYG1	3	8	88	40.0/5.85	49/5.9	Function not known	R	IgE	2B, D
56	XP_751780	Homocitrate synthase	10	28	334	50.5/5.66	48/6.7	Acyltransferase	E	IgE	2D
57	XP_755754	Dihydroxy acid dehydratase Ilv3	10	18	284	64.7/7.55	60/6.6	Hydratase	E	IgE	2D
58 ^b	XP_749237	Myo-inositol-phosphate synthase	6	11	204	58.6/5.82	57/6.3	Isomerase	I	IgE	2D
59 ^b	XP_752164	Glutamate/Leucine/Phenylalanine/Valine dehydrogenase	10	24	481	49.3/5.79	48/6.0	Oxidoreductse	E	IgE	2D
60	XP_750781	Assimilatory sulfite reductase	9	10	283	114.5/5.03	110/4.9	Oxidoreductase, Electron carrier	C	IgG	3D
61 ^b	XP_754687	Serine hydroxymethyltransferase	4	8	131	51.8/7.64	53/7.6–8.6	Transferase, Pyridoxal phosphate	E	IgE	2A, C
62 ^b	XP_748936	Malate dehydrogenase, NAD-dependent	13	38	559	35.8/9.08	37/9.0	Oxidoreductase	C	IgE	2A, C
63 ^b	XP_754009	Alcohol dehydrogenase	11	31	381	37.1/7.55	33/8.4	Oxidoreductase, Zn ion binding	Q	IgE	2A
64 a–b ^b	XP_748145	Glyceraldehyde 3-phosphate dehydrogenase GpdA	12	28	162	36.2/6.96	36/7.0–7.9	Oxidoreductase, NAD binding	G	IgE	2A
65 ^b	XP_747920	Citrate synthase (CitI)	10	19	258	52.0/8.69	52/8.6	Acyltransferase	C	IgE	2A
66 ^b	EDP50202	Zinc-containing alcohol dehydrogenase, putative	8	20	286	36.8/7.01	36/7.6	Oxidoreductase, Zn ion binding	CR	IgE	2A

^a Matches = Number of peptides matched with protein in MS/MS query. Sequence coverage = Total percentage of proteins amino acid sequence covered by peptides in MS/MS analysis. MASCOT score = >40 indicate identification or extensive homology (*p* < 0.05). Tht = Theoretical. Obs = Observed. KOGs = functional categories of knogitor.³⁶ IR = Type of protein immuno-reactivity with antibodies of patients sera. ^b Identified in our previous study.³⁴

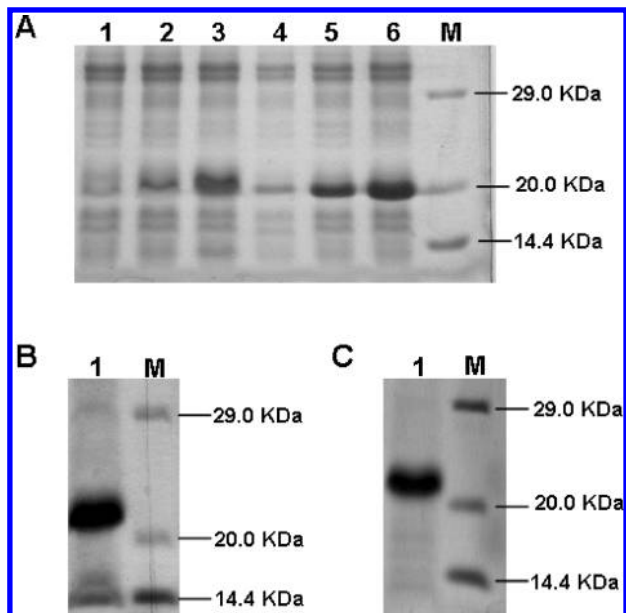


Figure 4. Commassie brilliant blue stained SDS gels showing inducible expression and purified fractions of recombinant proteins. (A) Induction of alcohol dehydrogenase, putative (Lanes 1–3) and fructose biphosphate aldolase, class-II (Lanes 4–6). (Lanes 1, 4) Uninduced control cell lysate of *E. coli*. (Lanes 2, 5) Induced cell lysate of *E. coli* with 1 mM of IPTG for 1 h. (Lanes 3, 6) Induced cell lysate of *E. coli* with 1 mM of IPTG for 3 h. (Lane M) Standard molecular weight protein marker. (B) (Lane 1) Purified fraction of alcohol dehydrogenase, putative. (Lane M) Standard molecular weight protein marker. (C) (Lane 1) Purified fraction of fructose biphosphate aldolase, class-II. (Lane M) Standard molecular weight protein marker.

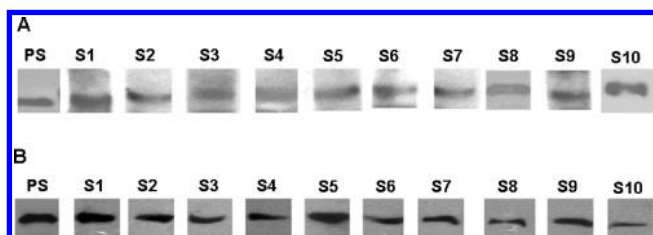


Figure 5. Immunoblots of recombinant proteins (A) alcohol dehydrogenase, putative and (B) fructose biphosphate aldolase, class-II showing IgE reactivity with pooled (PS) and individual ABPA patient's sera (S1–S10).

useful for desensitization therapies. Proteins of Spot Nos. 1, 5, 12, 13, and 25 corresponding to Sorbitol/xylulose reductase Sou1-like (Accession No. XP_755878), Pyridoxine biosynthesis protein (Accession No. XP_753827), Fructose-bisphosphate aldolase, class II (Accession No. XP_754452), Transaldolase (Accession No. XP_753716) and 6-phosphogluconate dehydrogenase Gnd1 (Accession No. XP_750696), are patent protected (Patent No. 1278/DEL/2010, IPMD, Delhi, India).

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Supporting Information Available: Control immunoblots of both the strains of *A. fumigatus* (190/96 and DAYA) developed using GC fraction and pooled sera of apparently healthy individuals. Pie charts showing functional categorization of 66 identified proteins in to 16 different groups according to Kognitor.³⁶ Table showing detailed analysis (MS/MS) on identification of proteins with number of matched peptides, percentage of sequence coverage, MASCOT score, molecular mass and isoelectric points. This material is available free of charge via the Internet at <http://pubs.acs.org>.

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SUPPLEMENTARY INFORMATION AVAILABLE:

Supplementary Figure Captions:

Supplementary Figure 1.

Control IgE immuno-blots of GC proteome of *A. fumigatus* strains 190/96 (A and B) and DAYA (C and D), in pH ranges 3-10 (A and C) and pH 4-7 (B and D) probed with anti-human IgE conjugated with HRP showing no reactivity with sera of apparently healthy controls individuals.

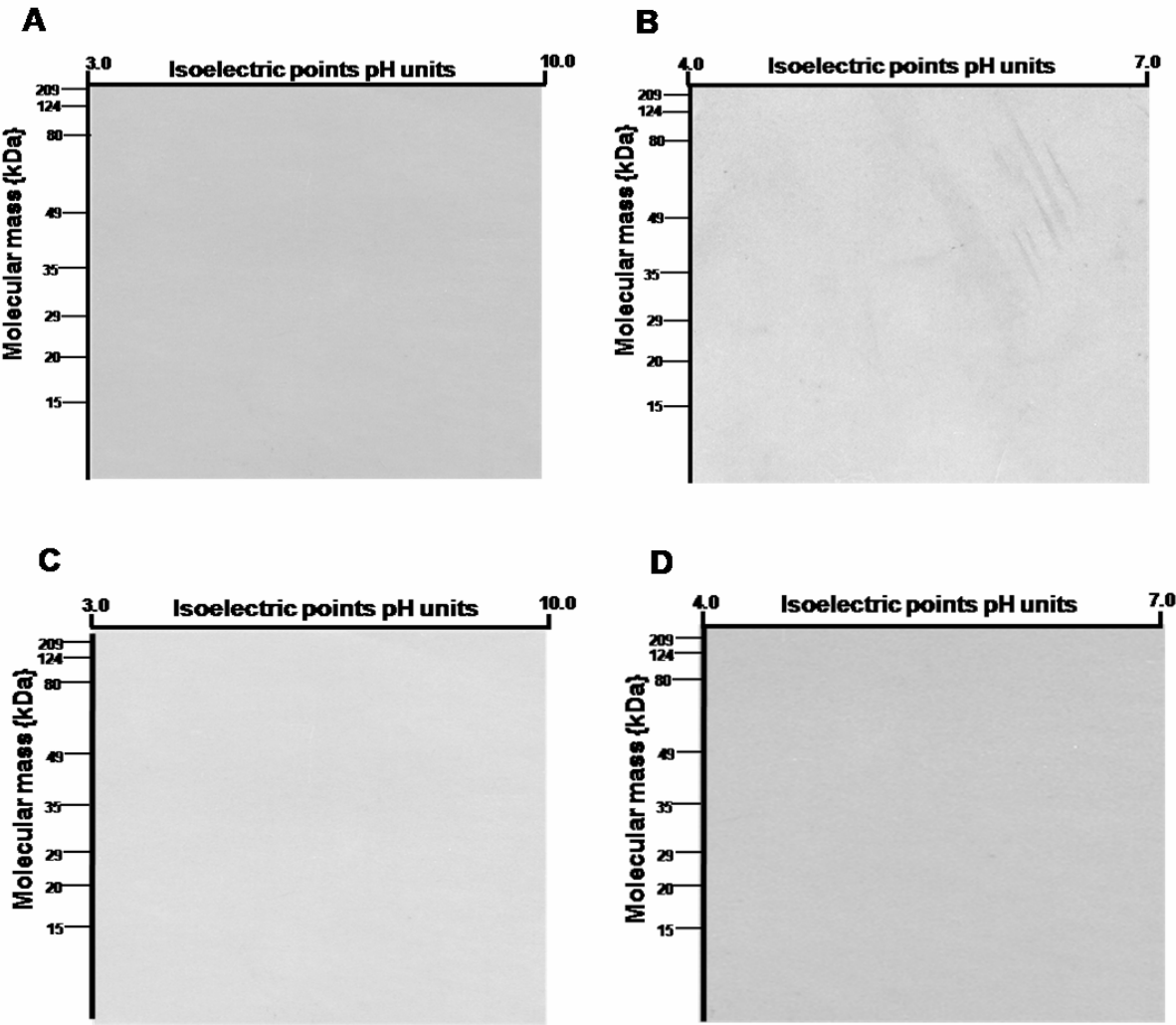
Supplementary Figure 2.

Control IgG immuno-blots of GC proteome of *A. fumigatus* strains 190/96 (A and B) and DAYA (C and D), in pH ranges 3-10 (A and C) and pH 4-7 (B and D) probed with anti-human IgE conjugated with HRP showing no reactivity with sera of apparently healthy controls individuals.

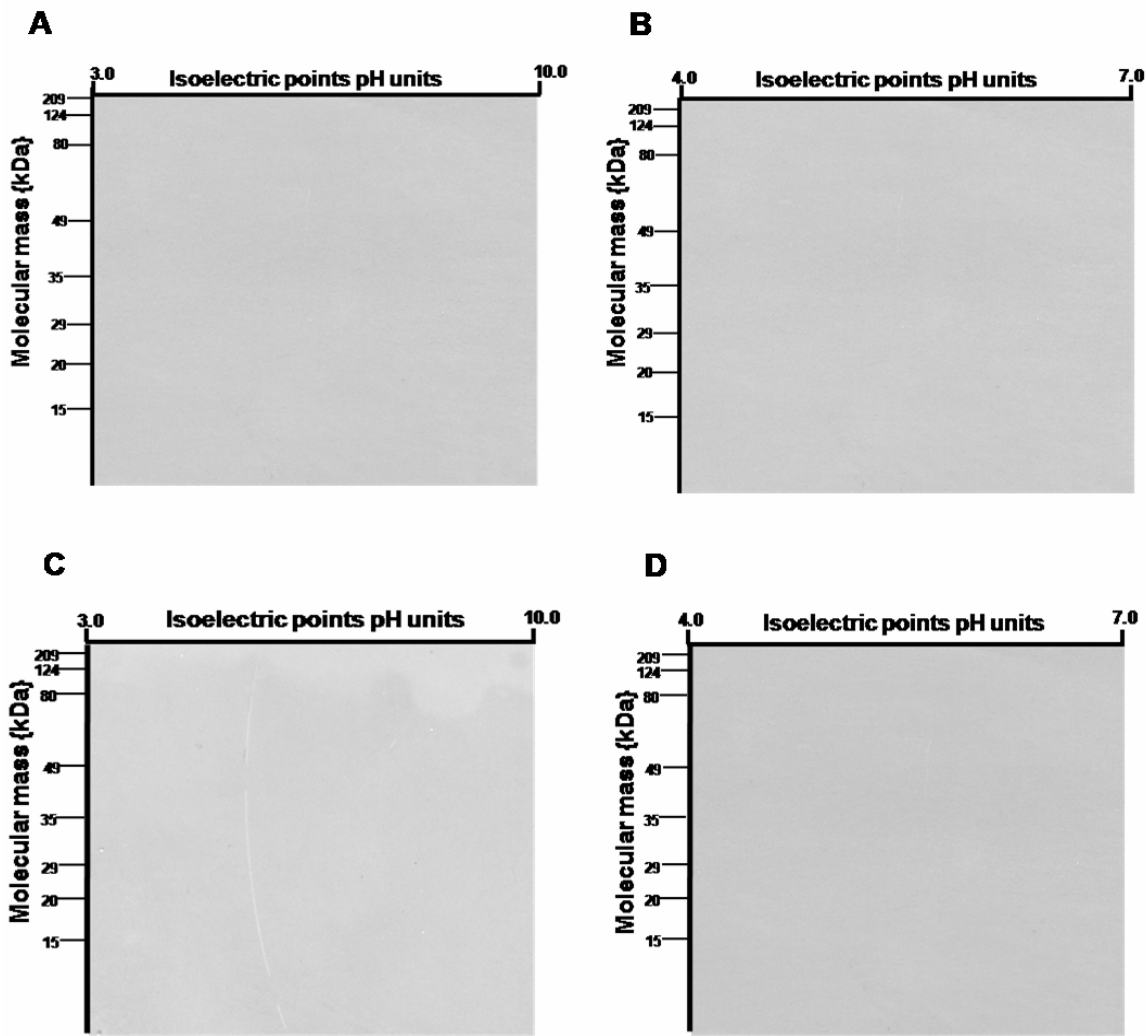
Supplementary Figure 3.

Pie chart showing functional categorization of 66 identified *A. fumigatus* cytosolic proteins with in Kognitor; a function annotation tool of NCBI database; (www.ncbi.nlm.nih.gov/COG/grace/kognitor).

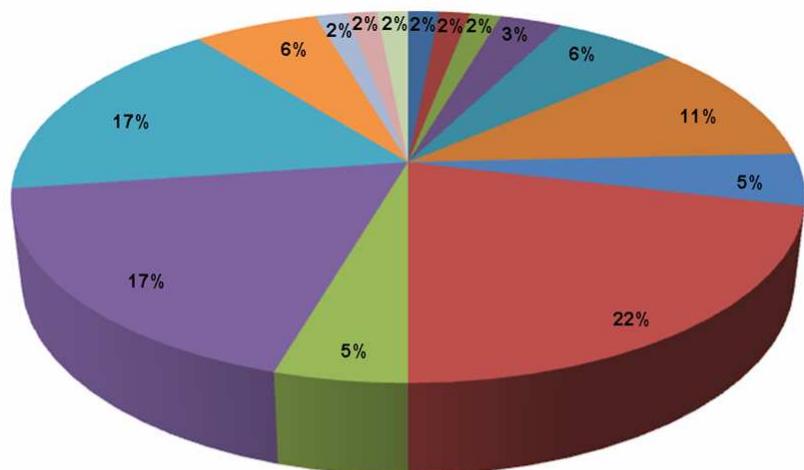
Supplementary Figure 1.



Supplementary Figure 2.



Supplementary Figure 3.



- Q (Secondary metabolites biosynthesis, transport and catabolism) 1
- I (Lipid transport and metabolism) 1
- Z (Cytoskeleton) 1
- S (Function unknown) 2
- J (Translation, ribosomal structure and biogenesis) 4
- C (Energy production and conversion) 7
- F (Nucleotide transport and metabolism) 3
- E (Amino acid transport and metabolism) 14
- H (Coenzyme transport and metabolism) 3
- G (Carbohydrate transport and metabolism) 12
- O (Posttranslational modification, protein turnover, chaperones) 11
- R (General function prediction only) 4
- CR (Energy production and conversion + General function prediction only) 1
- BD (Chromatin structure and dynamics + Cell cycle control, cell division, chromosome partitioning) 1
- AYT (RNA processing and modification + Nuclear structure + Signal transduction mechanisms) 1

Supplementary Table:

Table 1. MS/MS analysis table for reported proteins

Footnotes: ¹Mass 1 = Molecular mass of the protein observed in MASCOT search. ²MASCOT score 2 = >40 indicate identification or extensive homology (p<0.05). ³Peptide matched 3 = Number of peptides matched with protein in MS/MS query. ⁴pI 4 = Isoelectric point of the protein observed in MASCOT search.

Spot No.	Accession no.	Mass ¹ (kDa)	MASCOT Score ²	Peptide matched ³	pI ⁴	Protein name	MS/MS Analysis
1	XP_755878	28202	278	10	5.96	Sorbitol/xylulose reductase Sou1-like	Sequence Coverage: 33% 1 MPIPVPAAASS LLDLLSLKGK TVVVTGASGP RGMGIEAARG CAEMGANIAL 51 TYASRPEGGE KNAAEIAKTY GVKAKAYKCN VGDWESVQKL VADVIAEFGQ 101 IDAFIANAGR TASAGILDGS VNDWAEVIQT DLTGTFYCAK AVGPHFKERG 151 KGSFVITSSM SGHIANYPQE QTSYNVAKAG CIHFAKSLAN EWRDFARVNS 201 ISPGYIDTGL SDFVDKKTQD LWLSMIPMGR NGDAKELKGA YVYLCS DASS 251 YMTGTDLLID GGYCIR 2 - 18 867.5678 1733.1210 1733.0338 0.0872 0 M.PIPVPAAASSLLDLLSLK.G 21 - 31 522.3088 1042.6030 1042.5771 0.0259 0 K.TVVVTGASGPR.G 21 - 31 522.3173 1042.6200 1042.5771 0.0429 0 K.TVVVTGASGPR. 32 - 39 410.7115 819.4084 819.3909 0.0176 0 R.GMGIEAAR.G Oxidation (M) 90 - 110 730.7527 2189.2363 2189.1481 0.0882 0 K.LVADVIAEFGQIDAFIANAGR.T 198 - 216 1014.0510 2026.0874 2025.9895 0.0979 0 R.VNSISPGYIDTGLSDFVDK.K 198 - 216 1014.0542 2026.0938 2025.9895 0.1043 0 R.VNSISPGYIDTGLSDFVDK.K 198 - 217 719.0652 2154.1738 2154.0845 0.0893 1 R.VNSISPGYIDTGLSDFVDKK.T 198 - 217 719.0670 2154.1792 2154.0845 0.0947 1 R.VNSISPGYIDTGLSDFVDKK.T 218 - 230 790.4222 1578.8298 1578.7534 0.0764 0 K.TQDLWLSMIPMGR.N 2 Oxidation

							(M)
2	XP_754489	28202	207	4	6.84	Proteasome component Prs2	Sequence Coverage: 17% 1 MTDTLPSFQT RVACTKSFSS ICGLGPHQYA FKAITAANIT SIGVRGKNCA 51 VVLSQKKVAD KLIDPSSVSH IFRLSPSVGC VMTGSIADAR ASVDRARGEA 101 AEFYKYGYE MPCDVLAKRL ANINQVYTQR AYMRPLGVAM TLISVDDEKG 151 PQLYKCDPAG YYVGKATAS GPKQQEALNY LEKKLKNKDY AEGSWEEVVE 201 LGITALSNVL SVDFKKHELE IGIVGGPRAD GREGTDPFR ALTEDEIDER 251 LQAISEKD 33 - 45 643.9045 1285.7944 1285.7354 0.0591 0 K.AITAANITSIGVR. 120 - 130 660.3871 1318.7596 1318.6993 0.0603 0 R.LANINQVYTQR.A 174 - 183 618.3470 1234.6794 1234.6193 0.0601 0 K.QQEALNYLEK. 241 - 250 595.8098 1189.6050 1189.5462 0.0588 0 R.ALTEDEIDER.L
3	XP_750785	28188	171	5	5.80	Proteasome component Pre9	Sequence Coverage: 16% 1 MSRRYDSRTT IFSPEGRLYQ VEYALEAISH AGTALGILAK DGIVLAAEKK 51 VTSKLLEQDT SAEKLYTLND NMICAVAGMT ADANILINYA RQAAQRYLLT 101 YGEEIPCEQL VRRLCDLKQG YTQHGGLRPF GVSFIYAGYD PLREFQLYQS 151 NPSGNYGGWK ATSVGANNAS AQSLKQDYK EDCDLKEACA MAVKVLSKTM 201 DSTKLSSEKI EFATVGKTKE GKIYHHLWNA DEINALLKEH GLAKVDDEPE 251 AGDIK 9 - 17 504.2820 1006.5494 1006.5084 0.0411 0 R.TTIFSPEGR.L 9 - 17 504.2970 1006.5794 1006.5084 0.0711 0 R.TTIFSPEGR.L 55 - 64 567.3104 1132.6062 1132.5612 0.0451 0 K.LLEQDTSAEK.L 205 - 217 470.2768 1407.8086 1407.7609 0.0476 1 K.LSSEKIEFATVGK.T 245 - 255 594.2983 1186.5820 1186.5354 0.0467 0 K.VDDEPEAGDIK.-
4	XP_001481696	28820	309	8	5.84	6-phosphogluconolactonase	Sequence Coverage: 34% 1 MTGTSPNLYS LPNTDALAPH LRAYVLRCQN SAINRHNTFR VAVSGGSLPA 51 VLAKALLAPS NGSPEDTVRF

						DKWDVFFADE RAVPLDHPDS NYRLLKDELL 101 SKIPAEMGTP KVHPIDADHV NDDTQELADL YQEELMRSFA AKDSVKLPVF 151 DLILLGCGPD GHTCSLFPGH KLLREKDAWV AAETNSPKPP PKRITLTLPV 201 VTHAVSIAFV ATGAGKKEIL KQIFDAEEGR ELPSALVNQG AGEKVSFWD 251 HAAVDGVSFP RRGSL 2 - 22 746.7134 2237.1184 2237.1440 - 0.0257 0 M.TGTSPNLYSLPNTDALAPHLR.A 41 - 54 634.8778 1267.7410 1267.7500 - 0.0089 0 R.VAVSGGSLPAVLAK.A 55 - 69 763.8879 1525.7612 1525.7736 - 0.0124 0 K.ALLAPSNGSPEDTVR.F 55 - 69 763.8915 1525.7684 1525.7736 - 0.0052 0 K.ALLAPSNGSPEDTVR.F 94 - 102 529.8221 1057.6296 1057.6383 - 0.0086 1 R.LLKDELLSK.I 103 - 111 480.2419 958.4692 958.4794 - 0.0101 0 K.IPAEMGTPK.V Oxidation (M) 222 - 230 532.7511 1063.4876 1063.4934 - 0.0058 0 K.QIFDAEEGR.E 231 - 244 706.8649 1411.7152 1411.7307 - 0.0154 0 R.ELPSALVNQGAGEK.V
5	XP_7538 27	32716	171	3	6.04	Pyridoxine biosynthesis protein Sequence Coverage: 15% 1 MASNGTNGAS ASNSFTVKAG LAQMLKGGVI MDVVNAEQAR IAEEAGAAAV 51 MALERVPADI RAQGGVARMS DPSMIKEIMA AVTIPVMAKA RIGHFVECQI 101 LEAIGVDYID ESEVLTPADD VYHVKKHDYK VPFVCGCRNL GEALRRIAEG 151 AAMIRTKGEA GTGDVVEAVK HMRTVNSQIA RARSILQNST DPEIELRAYA 201 RELEVPEYELL RETAEKGRLP VVNFAAGGVA TPADAALMMQ LGCDGVFVGS 251 GIFKSGDAKK RAKAIVQAVT HYKDPKVLAE VSEGLGEAMV GINVSQMPEA 301 DRLAKRGW 156 - 170 487.6082 1459.8028 1459.7518 0.0509 1 R.TKGEAGTGDVVEAVK.H 174 - 181 444.7613 887.5080 887.4825 0.0256 0 R.TVNSQIAR.A) 184 - 197 807.9560 1613.8974 1613.8260 0.0714 0 R.SILQNSTDPEIELR.A
6	XP_7527 19	33424	238	8	5.33	Spermidine synthase Sequence Coverage: 17% 1 MSEITHPTIK DGWFSEQSDM WPGQAMNLKV NQILHHEKSK YQDVLVFEST

						51 DYGTVLVLDN VIQCTERDEF SYQEMITHLA MNSHPNPKV LVIGGGDGGV 101 LREVVKHESV EEAILCDIDE AVIRVSKKYL PGMSIGFQHP NVKVHIGDGF 151 QFLKERKNEF DVIITDSSDP EGPAESLFQK PYFELLRDAL RDGGVITTQG 201 SENQWLHLSL ITDLKKACKE VFPVAEYAYT TIPTYPSGQI GFMVCKDAT 251 RNVREPVRTW SREEEERLCR YYNQDIHRAS FVLPNFARKA LDV 89 - 102 447.2879 1338.8419 1338.7984 0.0435 1 K.KVLVIGGGDGGVLR.E 90 - 102 606.3743 1210.7340 1210.7034 0.0306 0 K.VLVIGGGDGGVLR.E 90 - 102 606.3878 1210.7610 1210.7034 0.0576 0 K.VLVIGGGDGGVLR.E 144 - 154 420.9104 1259.7094 1259.6663 0.0431 0 K.VHIGDGFQFLK.E 144 - 154 630.8677 1259.7208 1259.6663 0.0546 0 K.VHIGDGFQFLK.E 252 - 258 435.2691 868.5236 868.4879 0.0358 1 R.NVREPVR.T 271 - 278 554.7820 1107.5494 1107.5097 0.0397 0 R.YYNQDIHR.A 279 - 288 561.3307 1120.6468 1120.6029 0.0439 0 R.ASFVLPNFAR.K
7	XP_754985	33240	131	6	5.51	Phosphoribosyl- aminoimidazole- succinocarboxami de synthase Sequence Coverage: 17% 1 MAEALTNTDL QGALPLIARG KVRDLYEVDD KTLLFIATDR ISAYDVIMEN 51 GIPNKGVLTT LCTKAWFKIL TDAIPSLRTH FITLDLPPQI PPSLRPALQN 101 RSMQVRKLKI LPIEAIVRGY ITGSAWNEYK KSGTVHGIKV APGLRESEAF 151 PDGPITYPST KAEQGEHDEN IHPDQAAAIL GEHASTVASL AVQLYKVAHA 201 YALSRGVIIA DTKFEFGVDE ETNEVVLADE VLTPDSSRFW PKDDYEVGRG 251 QQSFDKQFLR DWLVKEGLKG KEGVRMTEEV VQKTAEKYKE AWERITGGN 24 - 31 498.7505 995.4864 995.4447 0.0417 0 R.DLYEVDDK.T 32 - 40 525.3250 1048.6354 1048.5917 0.0438 0 K.TLLFIATDR.I 69 - 78 549.8499 1097.6852 1097.6444 0.0408 0 K.ILTDAIPSLR.T 110 - 118 512.3498 1022.6850 1022.6488 0.0363 0 K.ILPIEAIVR.G 110 - 118 512.3550 1022.6954 1022.6488 0.0467 0 K.ILPIEAIVR.G

							146 - 161 869.9517 1737.8888 1737.8097 0.0791 0 R.ESEAFDPGPIYTPSTK.A
8	XP_754776	43596	217	6	7.63	Inorganic diphosphatase	Sequence Coverage: 14% 1 MSPVALRMSS KALLPLSPLL RLSTASPALA RPCSPSPRTS ATLAPPTRQA 51 PPPSSLSSSS FSPSFSPQQA NLSSPSSSRV RSSVSSASTR AALLSRHFSS 101 YTPPQSPNMS YTVRKIGQAN TLEHRVYIEK DGVPISPFHD IPLYANPEQT 151 ILNMVVEIPR WTNAKQEISK EEFLNPIKQD VKKGKLRFVR NCFPHKGYLW 201 NYGAFFQTWE DPNVVHPETK AKGDNDPLDV CEIGELVGYP GQVKQVKVLG 251 VMALLDEEET DWKVIVIDIN DPLAPKLNDI EDVERHPLGL LRATNEWFRI 301 YKIPDGKPEN QFAFSGECKN KKYALDVIRE CADAWEKLIT GKSPRGDISL 351 ANTSVENSSD RADPAQLASI PKGENLPPAP IDGSIDKWFF ISGAAV 115 - 125 422.9172 1265.7298 1265.6840 0.0458 1 R.KIGQANTLEHR.V 264 - 276 703.9444 1405.8742 1405.8181 0.0562 0 K.VIVIDINDPLAPK.L 277 - 285 551.7962 1101.5778 1101.5302 0.0477 0 K.LNDIEDVER.H 286 - 292 403.2687 804.5228 804.4970 0.0259 0 R.HLPGLLR.A 323 - 329 425.2589 848.5032 848.4756 0.0277 0 K.YALDVIR.E 362 - 372 555.8337 1109.6528 1109.6080 0.0448 0 R.ADPAQLASIPK.G
9	XP_750257	33474	299	10	5.11	60S ribosomal protein P0	Sequence Coverage: 24% 1 MGGKSATKAA YFDKLKSLLD EYKTVFIVGV DNVSSQQMHE IRLALRGQAV 51 VLMGKNTMVR RAIKGFVADN PEYERLLPHV KGNVGFIFTN GDLKDVTKI 101 LANRVAAPAR AGAIAPADVW VPAGNTGMEP GKTSFFQALG VPTKIARGTI 151 EITTDLKLVE AGAKVGPSEA TLLNMLNISP FTYGMTITQV YDNGQCFPAH 201 VLDIEESQLL DAFSSAIKTI TTVSLALNYP TLPSVMHSLI NGYKKVLAVA 251 IETDYSWPEI EELKDRIANP DAYAAAAPVA AAPAAGGAAP AAEEKKEEEA 301 EESDEDMGFG LFD 65 - 75 648.8174 1295.6202 1295.5782 0.0420 0 K.GFVADNPEYER.L 65 - 75 648.8209 1295.6272 1295.5782

							0.0490 0 K.GFVADNPEYER.L 82 - 94 691.3812 1380.7478 1380.7038 0.0441 0 K.GNVGFIFTNGDLK.D 82 - 97 575.3206 1722.9400 1722.8941 0.0459 1 K.GNVGFIFTNGDLKDV.K.T 82 - 97 862.4805 1722.9464 1722.8941 0.0523 1 K.GNVGFIFTNGDLKDV.K.T 82 - 97 575.3236 1722.9490 1722.8941 0.0549 1 K.GNVGFIFTNGDLKDV.K.T 133 - 144 648.3787 1294.7428 1294.6922 0.0507 0 K.TSFFQALGVPTK.I 148 - 157 545.8188 1089.6230 1089.5918 0.0313 0 R.GTIEITDLK.L 267 - 295 859.8014 2576.3824 2576.2870 0.0954 0 R.IANPDYAAAAPVAAAPAAGGAAPAAEEK. K 267 - 295 859.8047 2576.3923 2576.2870 0.1053 0 R.IANPDYAAAAPVAAAPAAGGAAPAAEEK. K
10	XP_7539 94	36835	82	2	5.02	Adenosine kinase	Sequence Coverage: 6% 1 MAATQGY PFL CLENPLLDIQ AVGDAALLEK YGLKDNDAIL AEEKHMG LYD 51 ELLSRDAKLI AGGAAQNTAR GAQYMLPDNS VMYIGCVGKD KYADILKEAC 101 NQAGVHTEYR VDDVQPTGKC GVIITGHNRS MCTHLAAANE YKIDHLKQPH 151 VWSLVEKAQY YYVGGYHLTV CVPAILALAE EAAAKNKVFM LSLSAPFIPQ 201 FFKDQLDSVL PYTDYTCNE TEARAYAESH EWNTDDVVEI AKKLAQLPKK 251 NSSRPRVAIV TQGTLPITTA TVKPDGEVEV KEFPVHEISK SSINDTNGAG 301 DAFAGGFCAG VVQNKSL EES MDMGQWLASL SIQELGPS 59 - 70 571.8359 1141.6572 1141.6203 0.0369 0 K.LIAGGAAQNTAR.G 111 - 119 479.7577 957.5008 957.4767 0.0241 0 R.VDDVQPTGK.C
11a	XP_7480 95	38298	295	8	6.04	Thiamine biosynthesis protein (Nmt1)	Sequence Coverage: 26% 1 MSTDKITFLT NWHATPYHAP LYLAHSGKFF KEEGLK VAIL EPNDPSDVTE 51 IIGSGK VDMG FKAMIHTLAA KARNFPVTSI GSLLDEPFTG VVYLK DSGIT 101 EDFRSLKGKR IGYVGEFGKI QIDELTKYYG MTADDYTAVR CGMNVTKAII 151 RGDIDAGIGL ENVQMVELAE WLASQNRPRD DVQMLRIDQL AELGCCCFCS 201 ILYIANDAFL AANPDKVOKI

						MRAVKRATDY VLAEPAKAYE EYIDVKPIMG 251 TPVNRKIFER SFAYFSRDLK NVQRDWAKVT NYGKRLLGILD ANFEPNYTNK 301 YLSWDLADS TDPLGDQKRM AELQKQVAE GGFKRLHVSA SA 37 - 56 1027.5695 2053.1244 2053.0579 0.0665 0 K.VAILEPNDPSPDVTEIIGSGK.V 96 - 104 520.2540 1038.4934 1038.4618 0.0316 0 K.DSGITEDFR.S 111 - 119 485.2659 968.5172 968.4967 0.0205 0 R.IGYVGEFGK.I 120 - 127 480.2874 958.5602 958.5335 0.0268 0 K.IQIDELTK.Y 128 - 140 763.3618 1524.7090 1524.6555 0.0536 0 K.YYGMTADDYTAVR.C 227 - 237 589.3241 1176.6336 1176.6026 0.0310 0 R.ATDYVLAEPK.A 261 - 267 439.2237 876.4328 876.4130 0.0199 0 R.SFAYFSR.D 286 - 300 854.9590 1707.9034 1707.8468 0.0567 0 R.LGILDANFEPNYTNK.Y
11b	XP_7480 95	38298	235	8	6.04	Thiamine biosynthesis protein (Nmt1) Sequence Coverage: 25% 1 MSTDKITFLT NWHATPYHAP LYLAHSGGFF KEEGLKVAIL EPNDPSDVTE 51 IIGSGKVDMG FKAMIHTLAA KARNFPVTSI GSLLDEPFTG VVYLKDSGIT 101 EDFRSLKGKR IGYVGEFGKI QIDELTKYYG MTADDYTAVR CGMNVTKAII 151 RGDIDAGIGL ENVQMVELAE WLASQNRPRD DVQMLRIDQL AELGCCCCFS 201 ILYIANDAFL AANPDKVQKF MRAVKRATDY VLAEPKAYE EYIDVKPIMG 251 TPVNRKIFER SFAYFSRDLK NVQRDWAKVT NYGKRLLGILD ANFEPNYTNK 301 YLSWDLADS TDPLGDQKRM AELQKQVAE GGFKRLHVSA SA 28 - 36 527.7964 1053.5782 1053.5495 0.0288 1 K.GFFKEEGLK.V 37 - 56 1027.5746 2053.1346 2053.0579 0.0767 0 K.VAILEPNDPSPDVTEIIGSGK.V 96 - 104 520.2506 1038.4866 1038.4618 0.0248 0 K.DSGITEDFR.S 111 - 119 485.2672 968.5198 968.4967 0.0231 0 R.IGYVGEFGK.I 120 - 127 480.2850 958.5554 958.5335 0.0220 0 K.IQIDELTK.Y 227 - 237 589.3234 1176.6322 1176.6026 0.0296 0 R.ATDYVLAEPK.A 261 - 267 439.2215 876.4284 876.4130

							0.0155 0 R.SFAYFSR.D 286 - 300 854.9556 1707.8966 1707.8468 0.0499 0 R.LGILDANFEPNYTNK.Y
11c	XP_748095	38298	462	14	6.04	Thiamine biosynthesis protein (Nmt1)]	Sequence Coverage: 26% 1 MSTDKITFLT NWHATPYHAP LYLAHSKGFF KEEGLKVAIL EPNDPSDVT 51 IIGSGKVDMG FKAMIHTLAA KARNFPVTSI GSLLDEPFTG VVYLKDSGIT 101 EDFRSLKGKR IGYVGEFGKI QIDELTKYYG MTADDYTAVR CGMNVTKAII 151 RGDIDAGIGL ENVQMVELAE WLASQNRPRD DVQMLRIDQL AELGCCCFC 201 ILYIANDAFL AANPDKVQKF MRAVKRATDY VLAEPKAYE EYIDVKPIMG 251 TPVNRKIFER SFAYFSRDLK NVQRDWAKVT NYGKRLGILD ANFEPNYTNK 301 YLSWDLADS TDPLGDQKRM AELQKQVAAE GGFKRLHVS SA 28 - 36 527.7914 1053.5682 1053.5495 0.0188 1 K.GFFKEEGLK.V 37 - 56 685.3743 2053.1011 2053.0579 0.0432 0 K.VAILEPNDPSDVTIIGSGK.V 37 - 56 1027.5579 2053.1012 2053.0579 0.0433 0 K.VAILEPNDPSDVTIIGSGK.V 37 - 56 1027.5620 2053.1094 2053.0579 0.0515 0 K.VAILEPNDPSDVTIIGSGK.V 96 - 104 520.2471 1038.4796 1038.4618 0.0178 0 K.DSGITEDFR.S 96 - 104 520.2502 1038.4858 1038.4618 0.0240 0 K.DSGITEDFR.S 111 - 119 485.2477 968.4808 968.4967 - 0.0159 0 R.IGYVGEFGK.I 120 - 127 480.2622 958.5098 958.5335 - 0.0236 0 K.IQIDELTK.Y 226 - 237 445.2539 1332.7399 1332.7037 0.0361 1 K.RATDYVLAEPK.A 227 - 237 589.3192 1176.6238 1176.6026 0.0212 0 R.ATDYVLAEPK.A 227 - 237 589.3210 1176.6274 1176.6026 0.0248 0 R.ATDYVLAEPK.A 261 - 267 439.2151 876.4156 876.4130 0.0027 0 R.SFAYFSR.D 286 - 300 854.9557 1707.8968 1707.8468 0.0501 0 R.LGILDANFEPNYTNK.Y 286 - 300 854.9564 1707.8982 1707.8468 0.0515 0 R.LGILDANFEPNYTNK.Y
12a	XP_7544	39766	220	9	5.55	Fructose-bisphosphate	Sequence Coverage: 16%

	52					aldolase, class II	1 MGILDKLSRK SGVIVGDDVL RLFHEYAQEKN FAIPAVNVTS SSTVVACLEA 51 ARDQNCPIIL QVSQGGAAAYF AGKGVSN DGQ KASIAGSIAA AHYIRSIAPS 101 YGIPVVLHTD HCAKKLLPWL DGMLDEDERY FKQHGEPLFS SHMIDLSEEP 151 VDYNIE TTAK YLKRAAPMKQ WLEMEIGITG GEEDGVNNED VDNNSLYTQP 201 EDILAIYNAL APISPYFSIA AGFGNVHGVY KPGNVRLHPE LLSKHQAYVK 251 EKIGSNKDKP VYFVFHGGSG STKEEYKQAI SYGVVKVNLD TDMQYAYMSG 301 VRDYILNKKD YLMSAVGNPD GEDKPNKKYF DPRVWVREGE KTMSKR VQVA 351 LEDFNTAGQL 10 - 21 419.9170 1256.7292 1256.7089 0.0203 1 R.KSGVIVGDDVLR.L 11 - 21 565.3218 1128.6290 1128.6139 0.0151 0 K.SGVIVGDDVLR.L 22 - 29 514.2676 1026.5206 1026.5022 0.0185 0 R.LFEY AQEKN 82 - 95 467.6007 1399.7803 1399.7572 0.0231 0 K.ASIAGSIAAAHYIR.S 82 - 95 700.9099 1399.8052 1399.7572 0.0481 0 K.ASIAGSIAAAHYIR.S 278 - 286 482.7859 963.5572 963.5389 0.0183 0 K.QAISYGVVK.V 346 - 360 830.9594 1659.9042 1659.8580 0.0462 1 K.RVQVALEDFNTAGQL.- 346 - 360 830.9673 1659.9200 1659.8580 0.0620 1 K.RVQVALEDFNTAGQL.- 347 - 360 752.9063 1503.7980 1503.7569 0.0411 0 R.VQVALEDFNTAGQL.-
12b	XP_7544 52	39766	438	13	5.55	Fructose- biphosphate aldolase, class II	Sequence Coverage: 22% 1 MGILDKLSRK SGVIVGDDVL RLFHEYAQEKN FAIPAVNVTS SSTVVACLEA 51 ARDQNCPIIL QVSQGGAAAYF AGKGVSN DGQ KASIAGSIAA AHYIRSIAPS 101 YGIPVVLHTD HCAKKLLPWL DGMLDEDERY FKQHGEPLFS SHMIDLSEEP 151 VDYNIE TTAK YLKRAAPMKQ WLEMEIGITG GEEDGVNNED VDNNSLYTQP 201 EDILAIYNAL APISPYFSIA AGFGNVHGVY KPGNVRLHPE LLSKHQAYVK 251 EKIGSNKDKP VYFVFHGGSG STKEEYKQAI SYGVVKVNLD TDMQYAYMSG 301 VRDYILNKKD YLMSAVGNPD GEDKPNKKYF DPRVWVREGE

							KTMSKRVQVA 351 LEDFNTAGQL 10 - 21 419.9154 1256.7244 1256.7089 0.0155 1 R.KSGVIVGDDVLR.L 10 - 21 629.3725 1256.7304 1256.7089 0.0216 1 R.KSGVIVGDDVLR.L 11 - 21 565.3157 1128.6168 1128.6139 0.0029 0 K.SGVIVGDDVLR.L 22 - 29 514.2490 1026.4834 1026.5022 - 0.0187 0 R.LFEYAQEK.N 82 - 95 467.5998 1399.7776 1399.7572 0.0204 0 K.ASIAGSIAAAHYIR.S 82 - 95 700.9088 1399.8030 1399.7572 0.0459 0 K.ASIAGSIAAAHYIR.S 258 - 273 575.9697 1724.8873 1724.8522 0.0350 0 K.DKPVYFVFHGGSGSTK.E 278 - 286 482.7821 963.5496 963.5389 0.0107 0 K.QAISYGVVK.V 303 - 309 447.2638 892.5130 892.5018 0.0113 1 R.DYILNKK.D 303 - 309 447.2638 892.5130 892.5018 0.0113 1 R.DYILNKK.D 346 - 360 830.9579 1659.9012 1659.8580 0.0432 1 K.RVQVALEDFNTAGQL.- 346 - 360 830.9579 1659.9012 1659.8580 0.0432 1 K.RVQVALEDFNTAGQL.- 347 - 360 752.9050 1503.7954 1503.7569 0.0385 0 R.VQVALEDFNTAGQL.-
13	XP_7537 16	35426	419	17	6.04	Transaldolase	Sequence Coverage: 38% 1 MSSALEQLKA TGTVVVCD SG DFATIGK YKP QDATTNPSLI LAASKKPEYA 51 SLIDAAVQKG KKEGKTLDEQ VDATLDNLLV EFGKK ILEII PGKVSTEVDA 101 RFSFDTQASV DKALHIVKLY EQQGISKDRI LIKIASTWEG IKA AHILQSQ 151 HGINCNLTLM FSLVQAIAAA EAGAFLISPF VGRILDWYKA AHKR DFSPEE 201 DPGVKSVQSI FNYYKKG HGYK TIVMGASFRN TGEITELAGC DYLTISP NLL 251 EELYNSTASV PKKLDAASAA SLDIPKR SYI NDEAAFR FDF NEEAMAVEKL 301 REGISK FAAD AVTLKELLKQ KIQA 28 - 45 640.0280 1917.0622 1917.0207 0.0415 0 K.YKPQDATTNPSLILAASK.K 28 - 45 959.5454 1917.0762 1917.0207 0.0555 0 K.YKPQDATTNPSLILAASK.K 46 - 59 511.6237 1531.8493 1531.8246 0.0247 0 K.KPEYASLIDAAVQK.G

						86 - 101 580.6792 1739.0158 1738.9829 0.0329 1 K.ILEIIPGKVSTEVDAR.F 94 - 101 438.7287 875.4428 875.4349 0.0080 0 K.VSTEVDAR.F 102 - 112 622.8083 1243.6020 1243.5721 0.0300 0 R.FSFDTQASVDK.A 119 - 127 533.2903 1064.5660 1064.5502 0.0158 0 K.LYEQQGISK.D 119 - 129 446.2392 1335.6958 1335.6783 0.0175 1 K.LYEQQGISKDR.I 134 - 142 502.7865 1003.5584 1003.5338 0.0246 0 K.IASTWEGIK.A 195 - 205 610.2894 1218.5642 1218.5405 0.0238 0 R.DFSPEEDPGVK.S 206 - 215 624.8318 1247.6490 1247.6186 0.0304 0 K.SVQSIFNYYK.K 206 - 216 459.5841 1375.7305 1375.7136 0.0169 1 K.SVQSIFNYYKK.H 206 - 216 688.8820 1375.7494 1375.7136 0.0359 1 K.SVQSIFNYYKK.H 278 - 287 593.2908 1184.5670 1184.5462 0.0209 0 R.SYNDEAAFR.F 307 - 315 468.2704 934.5262 934.5124 0.0139 0 K.FAADAUTLK.E 307 - 319 473.6196 1417.8370 1417.8180 0.0189 1 K.FAADAUTLKELLK.Q 307 - 319 709.9361 1417.8576 1417.8180 0.0396 1 K.FAADAUTLKELLK.Q
14a	XP_7524 29	42170	343	10	5.67	S-adenosylmethionine synthetase Sequence Coverage: 26% 1 MGSVAKSNTF LFTSESVGEG HPDKIADQVS DAVLDACLA E DPLSKVACET 51 ATKTGMIMVF GEITNAKLD YQKIIRGAIK DIGYDDSDKG FDYKTCNVLV 101 AIEQQSPDIA QGLHYDEALE KLGAGDQGIM FGATDETPE LLPLTLLSH 151 KLNSAMTQAR KDGSIPWLRP DTKTQVTVEY AHDGGAVKPL RVDTVVVSQAQ 201 HSDDVSTEEL RTVIKEKIIK KVIPAELLDD RTIYHIQPSG RFVIGGPQGD 251 AGLTGRIIV DTYGGWGAHG GGAFTSGKDYS KVDRSAAYVG RWIAKSLVHA 301 GLARRVLVQL SYAIGVAEPL SIFVETYGTS EKSSDELVEI IRKNFDLRPG 351 VIVKELDLAK PIYFQTAKNG HFTNQSFPE KPKTLKF 81 - 89 514.2290 1026.4434 1026.4142 0.0293 0 K.DIGYDDSDK.G 81 - 94 546.5837 1636.7293 1636.6893 0.0400 1 K.DIGYDDSDKGFDYK.T

						192 - 211 729.3761 2185.1065 2185.0499 0.0566 0 R.VDTVVVSAQHSDDVSTEELR.T 222 - 231 570.8273 1139.6400 1139.6186 0.0214 0 K.VIPAELLDDR.T 232 - 241 586.3302 1170.6458 1170.6145 0.0313 0 R.TIYHIQPSGR.F 242 - 256 722.8976 1443.7806 1443.7471 0.0336 0 R.FVIGGPQGDAGLTGR.K 296 - 304 462.2853 922.5560 922.5348 0.0212 0 K.SLVHAGLAR.R 333 - 342 580.8231 1159.6316 1159.6084 0.0232 0 K.SSDELVEIIR.K 333 - 343 430.2486 1287.7240 1287.7034 0.0206 1 K.SSDELVEIIRK.N 355 - 368 546.3146 1635.9220 1635.8872 0.0348 0 K.ELDLAKPIYFQTAK.N
14b	XP_7524 29	42170	151	4	5.67	S-adenosylmethionine synthetase Sequence Coverage: 9% 1 MGSVAKSNTF LFTSESVGEG HPDKIADQVS DAVLDACLA E DPLSKVACET 51 ATKTGMIMVF GEITTNAKLD YQKIIRGAIK DIGYDDSDKG FDYKTCNVLV 101 AIEQQSPDIA QGLHYDEALE KLGAGDQGIM FGYATDETPE LLPLTLLSH 151 KLNSAMTQAR KDGSIPWLRP DTKTQVTVEY AHDGGAVKPL RVDTVVVSAQ 201 HSDDVSTEEL RTVIKEKIIK KVIPAELLDD RTIYHIQPSG RFVIGGPQGD 251 AGLTGRKIIV DTYGGWGAHG GGA FSGKDYS KVDRSAAYVG RWIAKSLVHA 301 GLARRVLVQL SYAIGVAEPL SIFVETYGTS EKSSDELVEIIRKNFDLRPG 351 VIVKELDLAK PIYFQTAKNG HFTNQSFWE KPKTLKF 222 - 231 570.8241 1139.6336 1139.6186 0.0150 0 K.VIPAELLDDR.T 242 - 256 722.8914 1443.7682 1443.7471 0.0212 0 R.FVIGGPQGDAGLTGR.K 333 - 342 580.8209 1159.6272 1159.6084 0.0188 0 K.SSDELVEIIR.K 333 - 343 644.8682 1287.7218 1287.7034 0.0184 1 K.SSDELVEIIRK.N
15	XP_7515 19	39874	113	4	5.48	Glutamine synthetase Sequence Coverage: 10% 1 MAETSTVVS N TENLMKYMSL DQRGHVQA EY VWIDAVGNCR CKTKTLSPV 51 KSVDELPEWN FDGSSTGQAP GDNSDVYLRP VAIFADPFRR GDNILVLCET 101 WSDGTPNKF NFRHEANRLM EIHAKKEFWF GLEQEYTLTG TDGWPGWPK 151 GGFPGAQGPY YCGVGTGKVY

						CRDIVEAHYR ACLYAGIKIS GINAEVMPSQ 201 WEYQVGPCQG IEMGDQLWMS RFLLRHVAEE FGVKISFEPK PIKGDWNGAG 251 LHTNVSTAAT RAEGGLKVIE AYMQLEARH NEHIAVYEGEG NEERLTGRHE 301 TGSIDKFSYG VADRGGGSIRI PRQVAKDGKG YFEDRRPASN ADPYQITGII 351 VETLCGGN 501.7632 1001.5118 1001.4930 0.0188 0 R.DIVEAHYR.A 227 - 234 439.7394 877.4642 877.4545 0.0097 0 R.VAEEFGVK.I 280 - 294 585.2807 1752.8203 1752.7815 0.0387 0 R.HNEHIAVYEGEGNEER.L 307 - 314 457.7331 913.4516 913.4294 0.0223 0 K.FSYGVADR.G
16	YP_0013 37378	43219	459	17	5.29	Elongation factor Tu [Klebsiella pneumoniae] Sequence Coverage: 32% 1 MSKEKFERTK PHVNVGTIGH VDHGKTTLTA AITTVLAKTY GGSARAFDQI 51 DNAPEEKARG ITINTSHVEY DTPTRHYAHV DCPGHADYVK NMITGAAQMD 101 GAILVVAATD GPMPQTREHI LLGRQVGVPI IIVFLNKCDM VDDEELLELV 151 EMEVRELLSQ YDFPGDDTPI VRGSALKALE GDAEWEAKII ELAGHLDTYI 201 PEPERAIDKP FLLPIEDVFS ISGRGT VVTG RVERGIKVG EEVEIVGIKE 251 TAKTTCTGVE MFRKLLDEGR AGENVGVLLR GIKREEIERG QVLAKPGTIN 301 PHTKFESEVY ILSKDEGGRH TPFFKGYRPQ FYFRTTDVTG TIELPEGVEM 351 VMPGDNIKMV VTLIHPIAMD DGLRFAIREG GRTVGAGVVA KVLG 26 - 38 652.4144 1302.8142 1302.7759 0.0384 0 K.TTLTAAITTVLAK.T 46 - 57 688.8384 1375.6622 1375.6255 0.0367 0 R.AFDQIDNAPEEK.A 118 - 124 419.2611 836.5076 836.4868 0.0208 0 R.EHILLGR.Q 125 - 137 745.4637 1488.9128 1488.8704 0.0424 0 R.QVGVPYIIVFLNK.C 156 - 172 983.0156 1964.0166 1963.9527 0.0639 0 R.ELLSQYDFPGDDTPIVR.G 156 - 172 983.0182 1964.0218 1963.9527 0.0691 0 R.ELLSQYDFPGDDTPIVR.G 189 - 205 656.0310 1965.0712 1965.0207 0.0505 0 K.IELAGHLDTYIPEPER.A 189 - 205 656.0335 1965.0787 1965.0207

						0.0580 0 K.IIELAGHLDTYIPEPER.A 239 - 249 586.3455 1170.6764 1170.6496 0.0269 0 K.VGEEVEIVGIK.E 239 - 249 586.3455 1170.6764 1170.6496 0.0269 0 K.VGEEVEIVGIK.E 239 - 253 534.3096 1599.9070 1599.8719 0.0350 1 K.VGEEVEIVGIKETAK.T 271 - 280 514.3099 1026.6052 1026.5822 0.0231 0 R.AGENVGVLRL.G 305 - 314 607.8337 1213.6528 1213.6230 0.0298 0 K.FESEVYILSK.D 305 - 319 576.9673 1727.8801 1727.8366 0.0435 1 K.FESEVYILSKDEGGR.H 326 - 334 411.8837 1232.6293 1232.6091 0.0202 0 K.GYRPQFYFR.T 326 - 334 617.3270 1232.6394 1232.6091 0.0304 0 K.GYRPQFYFR.T
17a	Q96X30	47276	806	20	5.39	Enolase/allergen Asp F 22 Sequence Coverage: 36% 1 MPISKIHARS VYDSRGNPTV EVDVVTETGL HRAIVPSGAS TGQHEAHEL 51 DGDKTQWGGK GVLKAVKNVN ETIGPALIKE NIDVKDQSKV DEFLNKLDGT 101 ANKSNL GANA ILGVSLAVAK AGAAEKG VPL YAHISDLAGT KKP YVLPVPF 151 QNV LN GGS HA GGRLAFQEFM IVPDSAPSFS EALRQGA EVY QKLKALAKKK 201 YGQSAGNVGD EGGVAPDIQT AEEALDLITE AIEQAGYT GK IKIAMDVASS 251 EFYKADVKKY DLDFKNPESD PSKWLT YEQ LADLYKSLAAK YPIVSIEDPF 301 AEDDWEAWSY FYKTSD FQIV GDDLTVTNPG RIKKAIELKS CNALLKVNQ 351 IGTLTESIQA AKDSYADNWG VMVSHRSGET EDVTIADIAV GLRSGQIKTG 401 APCR SERLAK LNQILRIEEE LGENAVYAGS KFR TAVNL 16 - 32 608.3249 1821.9529 1821.9221 0.0308 0 R.GNPTVEVDVVTETGLHR.A 16 - 32 911.9942 1821.9738 1821.9221 0.0517 0 R.GNPTVEVDVVTETGLHR.A 68 - 79 634.8787 1267.7428 1267.7136 0.0293 0 K.NVNETIGPALIK.E 68 - 79 634.8792 1267.7438 1267.7136 0.0303 0 K.NVNETIGPALIK.E 80 - 89 588.3108 1174.6070 1174.5830 0.0241 1 K.ENIDVKDQSK.V 90 - 96 432.7287 863.4428 863.4389 0.0040 0 K.VDEFLNK.L 90 - 103 521.9471 1562.8195 1562.7940

						0.0255 1 K.VDEFLNKLDGTANK.S 90 - 103 782.4279 1562.8412 1562.7940 0.0472 1 K.VDEFLNKLDGTANK.S 104 - 120 799.4887 1596.9628 1596.9199 0.0430 0 K.SNLGANAILGVSLAVAK.A 127 - 141 514.6233 1540.8481 1540.8249 0.0231 0 K.GVPLYAHISDLAGTK.K 127 - 141 771.4409 1540.8672 1540.8249 0.0423 0 K.GVPLYAHISDLAGTK.K 185 - 192 461.7368 921.4590 921.4556 0.0035 0 R.QGAENVYQK.L 314 - 331 968.0013 1933.9880 1933.9382 0.0499 0 K.TSDFQIVGDDTLVTNPGR.I 314 - 331 968.0177 1934.0208 1933.9382 0.0827 0 K.TSDFQIVGDDTLVTNPGR.I 348 - 362 786.9552 1571.8958 1571.8519 0.0440 0 K.VNQIGTLTESIQA.AK.D 377 - 393 873.4741 1744.9336 1744.8843 0.0493 0 R.SGETEDVTIADIAVGLR.S 377 - 393 873.4761 1744.9376 1744.8843 0.0533 0 R.SGETEDVTIADIAVGLR.S 417 - 431 804.8974 1607.7802 1607.7678 0.0124 0 R.IEEELGENAVYAGSK.F 417 - 431 804.9162 1607.8178 1607.7678 0.0500 0 R.IEEELGENAVYAGSK.F
17b	Q96X30	47276	114	3	5.39	Enolase /AspF22 Sequence Coverage: 10% 1 MPISKIHARS VYDSRGNPTV EVDVVTETGL HRAIVPSGAS TGQHEAHELK 51 DGDKTQWGGK GVLKAVKNVN ETIGPALIKE NIDVKDQSKV DEFLNKLDGT 101 ANKSNLGA NA ILGVSLAVAK AGAAEKG VPL YAHISDLAGT KKP YVLPVPF 151 QNV LN GGSHA GGRLAFQEFM IVPDSAPSFS EALRQGAENVY QKLKALAKKK 201 YGQSAGNVGD EGGVAPDIQT AEEALDLITE AIEQAGYT GK IKIAMDVASS 251 EFYKADVKKY DLDFKNPESD PSKWLTYEQL ADLYKSLAAK YPIVSIEDPF 301 AEDDWEAWSY FYKTSDFQIV GDDTLVTNPG RIKKAIELKS CNALLKVNQ 351 IGTLTESIQA AKDSYADN WG VMVSHRSGET EDVTIADIAV GLRSGQIKTG 401 APCR SERLAK LNQILRIEEE LGENAVYAGS K FRTAVNL 348 - 362 786.9449 1571.8752 1571.8519 0.0234 0 K.VNQIGTLTESIQA.AK.D 377 - 393 873.4615 1744.9084 1744.8843 0.0241 0 R.SGETEDVTIADIAVGLR.S 417 - 431 804.9011 1607.7876 1607.7678

							0.0198 0 R.IEEELGENAVYAGSK.F
17c	Q96X30	47276	772	19	5.39	Enolase/ Asp F22	Sequence Coverage: 40% 1 MPISKIHARS VYDSRGNPTV EVDVVTETGL HRAIVPSGAS TGQHEAHEL R 51 DGDKTQWGGK GVLKAVKNNV ETIGPALIKE NIDVKDQSKV DEFLNKLDGT 101 ANKSNL GANA ILGVSLAVAK AGAAEKGVPL YAHISDLAGT KKPYPVLPVPF 151 QNVLNNGGSHA GGRLAFQEFM IVPDSAPSF S EALRQGAEVY QKLKALAKKK 201 YGQSAGNVGD EGGVAPDIQT AEEALDLITE AIEQAGYT GK IKIAMDVASS 251 EFYKADVKKY DLD FKNPESD PSKWLTYEQL ADLYKSLAAK YPIVSIEDPF 301 AEDDWEAWSY FYKTSD FQIV GDDLTVTNPG RIKKAIELKS CNALLKVNQ 351 IGTLTESIQA AKDSYADN WG VMVSHRSGET EDVTIADIAV GLRSGQIKTG 401 APCR SERLAK LNQILRIEEE LGENAVYAGS K FRTAVNL 16 - 32 608.3074 1821.9004 1821.9221 - 0.0217 0 R.GNPTVEVDVVTETGLHR.A 16 - 32 608.3075 1821.9007 1821.9221 - 0.0214 0 R.GNPTVEVDVVTETGLHR.A 33 - 50 620.6436 1858.9090 1858.9286 - 0.0196 0 R.AIVPSGASTGQHEAHEL.R.D 68 - 79 634.8556 1267.6966 1267.7136 - 0.0169 0 K.NVNETIGPALIK.E 80 - 89 588.2962 1174.5778 1174.5830 - 0.0051 1 K.ENIDVKDQSK.V 90 - 103 521.9288 1562.7646 1562.7940 - 0.0295 1 K.VDEFLNKLDGTANK.S 90 - 103 782.4031 1562.7916 1562.7940 - 0.0024 1 K.VDEFLNKLDGTANK.S 104 - 120 799.4644 1596.9142 1596.9199 - 0.0056 0 K.SNLGANAILGVSLAVAK.A 104 - 120 799.4797 1596.9448 1596.9199 0.0250 0 K.SNLGANAILGVSLAVAK.A 127 - 141 514.6090 1540.8052 1540.8249 - 0.0198 0 K.GVPLYAHISDLAGTK.K 127 - 141 514.6102 1540.8088 1540.8249 - 0.0162 0 K.GVPLYAHISDLAGTK.K 185 - 192 461.7259 921.4372 921.4556 - 0.0183 0 R.QGAEVYQK.L 314 - 331 967.9717 1933.9288 1933.9382 - 0.0093 0 K.TSDFQIVGDDLTVTNPGR.I 314 - 331 967.9889 1933.9632 1933.9382 0.0251 0 K.TSDFQIVGDDLTVTNPGR.I 348 - 362 524.9501 1571.8285 1571.8519 -

						0.0234 0 K.VNQIGTLTESIQAAK.D 348 - 362 786.9335 1571.8524 1571.8519 0.0006 0 K.VNQIGTLTESIQAAK.D 377 - 393 873.4526 1744.8906 1744.8843 0.0063 0 R.SGETEDVTIADIAVGLR.S 417 - 431 804.8896 1607.7646 1607.7678 - 0.0032 0 R.IEEELGENAVYAGSK.F 417 - 431 804.8900 1607.7654 1607.7678 - 0.0024 0 R.IEEELGENAVYAGSK.F
18	CAE17673	45546	134	3	5.72	Putative flavohaemoglobin Sequence Coverage: 7% 1 MPLTPEQVQI IKATVPVLAE HGTITITVFY KNMLTAHPEL NNVFNTTHQV 51 TGHQARALAG ALFAYASNID NLGALGPAVE LMCHKHASLY IKPDDYKIVG 101 KFLLEAMGQV LGDALTPEIL DAWATAYWQL ADIMIGREAQ LYEQAEGWTD 151 FRDFVVALKV PESSEITSFY LKPADGKPLP AFQPGQYISV QVHVPELNYL 201 QARQYSLSDM PRSDYYRISV KKESGLNPAE PGAKAHPGHV SNILHASVNE 251 GDTIKVSHPF GDDFLSDAKA AHPVVLLSAG VGLTPMTSIL NTLTSQAPER 301 KVSFIHGARN ARARAFKNHI TSLEQKLPNL KSTFFTSHPT EEDKEGDDYQ 351 FRGRVDLSQL DSNRDLFLDD ATTEYYVCGP DTFMTDMLNV LKSKGVSEDR 401 VKLELFGTGG VPH 2 - 12 633.3890 1264.7634 1264.7391 0.0244 0 M.PLTPEQVQIIK.A 223 - 234 585.3058 1168.5970 1168.5724 0.0247 0 K.ESGLNPAEPGAK.A 355 - 364 573.8049 1145.5952 1145.5677 0.0276 0 R.VDLSQLDSNR.D
19	XP_752401	44734	762	23	6.31	Phosphoglycerate kinase PgkA Sequence Coverage: 57% 1 MSLTNKLAIT DVDLKDKRVL IRVDFNVPLN EKKEVTNPQR IVGALPTIKY 51 AIEQGAKAVV LMSHLGRPDG KKNPKYSLKP VVPELEKLLG KSVIFTEDCV 101 GKEVEETVNK ASGGQVILE NLRFHPEEEG SYKDEEGKKV KADKEKVAEF 151 RKGLTALGDI YINDAFGTAH RAHSSMVGVD LPQKASGFLV KKELEYFAKA 201 LESPSRPFLA ILGGSKVSDK IQLIDNLLPK VNSLIITGGM AFTFKKTLEN 251 VKIGNSLFDE AGSKTVGDII EKAKKNNVKI VLPVDYITAD KFSADAKTGY 301 ATDEEGIPDG YMGLDVGDKS

						VKLYKETIAE AKTILWNGPP GVFEPEPFAN
						351 GTKQTLDAAV DAAKNGAIVI IGGGDTATVA AKYGAEKLS HVSTGGGASL
						401 ELLEGKELPG VAALSSK
						7 - 15 494.3047 986.5948 986.5648 0.0300 0 K.LAITDVDLK.D
						19 - 32 552.6723 1654.9951 1654.9406 0.0544 1 R.VLIRVDFNVPLNEK.K
						23 - 32 587.8250 1173.6354 1173.6030 0.0325 0 R.VDFNVPLNEK.K
						41 - 49 456.3173 910.6200 910.5851 0.0349 0 R.IVGALPTIK.Y
						58 - 71 499.2876 1494.8410 1494.7977 0.0433 0 K.AVVLMShLGRPDGK.K Oxidation (M)
						76 - 87 467.9474 1400.8204 1400.7915 0.0289 0 K.YSLKPVVPELEK.L
						76 - 87 701.4288 1400.8430 1400.7915 0.0516 0 K.YSLKPVVPELEK.L
						111 - 123 685.4166 1368.8186 1368.7725 0.0462 0 K.ASGGQVILLENLR.F
						153 - 171 669.0314 2004.0724 2004.0065 0.0659 0 K.GLtALGDIYINDAFGTAHR.A
						172 - 184 462.2453 1383.7141 1383.6817 0.0324 0 R.AHSSMVGVDLPQK.A Oxidation (M)
						172 - 184 692.8756 1383.7366 1383.6817 0.0550 0 R.AHSSMVGVDLPQK.A Oxidation (M)
						193 - 199 450.2427 898.4708 898.4436 0.0272 0 K.ELEYFAK.A
						217 - 230 532.6635 1594.9687 1594.9294 0.0393 1 K.VSDKIQLIDNLLPK.V
						231 - 246 581.6737 1741.9993 1741.9437 0.0556 1 K.VNSLIITGGMAFTFKK.T Oxidation (M)
						253 - 264 619.3207 1236.6268 1236.5986 0.0282 0 K.IGNSLFDEAGSK.T
						265 - 272 437.7579 873.5012 873.4807 0.0205 0 K.TVGDIIK.A
						280 - 291 673.9023 1345.7900 1345.7493 0.0407 0 K.IVLPVDYITADK.F
						280 - 291 673.9078 1345.8010 1345.7493 0.0517 0 K.IVLPVDYITADK.F
						280 - 297 656.0449 1965.1129 1965.0459 0.0670 1 K.IVLPVDYITADKFSADAK.T
						298 - 319 1160.0558 2318.0970 2317.9897 0.1074 0 K.TGYATDEEGIPDGYMGLDVGDK.S Oxidation (M)
						354 - 364 551.8043 1101.5940 1101.5666

						0.0275 0 K.QLDAAVDAAK.N 389 - 406 585.6675 1753.9807 1753.9210 0.0597 0 K.LSHVSTGGGASLELLEGGK.E 407 - 417 536.3262 1070.6378 1070.5972 0.0407 0 K.ELPGVAALSSK.-
20	XP_752379	48459	677	23	5.82	Adenosylhomocysteinase Sequence Coverage: 38% 1 MAAPAQKFKV ADISLAAFGR REIELAEIEM PGLMAIRRKY AEDQPLKGAR 51 IAGCLHMTIQ TAVLIETLTA LGAEVTWTSC NIFSTQDHAA AAIAASGVPV 101 FAWKGETEEE YQWCLEQQLN AFKDGQKLN ILDDGGDLTA LVHSKYPEML 151 KGCYGVSEET TTGVHHLYRM LKEGKLLVPA INVNSVTKS KFDNLYGCRE 201 SLIDGIKRAT DVMIAQKVAV VAGYGDVGKG CADALRSMGA RVLVTEIDPI 251 NALQAAVQGY QVVTMEEAAP QGQIFVTTTG CRDILVGKHF EVMRNDAIVC 301 NIGHFDIEID VAWLKANAKS VQNIKPQVDR YLMPNGRHII LLAEGRLVNL 351 GCATGHSSFV MSCSFSNQVL AQIALFKAED EAFGKKYVEF GTTGKKPVG 401 YVLPKILDEQ VALLHLEHVN AKLSKLTVPQ AEYLGGLDIAG PFKSDM 8 - 20 465.5890 1393.7452 1393.7718 - 0.0266 1 K.FKVADISLAAFGR.R 8 - 20 697.8864 1393.7582 1393.7718 - 0.0135 1 K.FKVADISLAAFGR.R 10 - 20 560.3039 1118.5932 1118.6084 - 0.0152 0 K.VADISLAAFGR.R 10 - 20 560.3195 1118.6244 1118.6084 0.0160 0 K.VADISLAAFGR.R 22 - 37 923.9560 1845.8974 1845.9216 - 0.0241 0 R.EIELAEIEMPGLMAIR.R 2 Oxidation (M) 22 - 37 923.9574 1845.9002 1845.9216 - 0.0213 0 R.EIELAEIEMPGLMAIR.R 2 Oxidation (M) 128 - 145 632.0074 1893.0004 1893.0207 - 0.0204 0 K.LNLILDDGGDLTALVHSK.Y 176 - 189 741.9138 1481.8130 1481.8453 - 0.0323 0 K.LLVPAINVNSVTK.S 176 - 189 741.9387 1481.8628 1481.8453 0.0175 0 K.LLVPAINVNSVTK.S 200 - 208 515.7914 1029.5682 1029.5818 - 0.0136 1 R.ESLIDGIKR.A 208 - 217 539.2856 1076.5566 1076.5648 - 0.0082 1 K.RATDVMIAQK.V Oxidation (M) 209 - 217 461.2349 920.4552 920.4637 -

						0.0085 0 R.ATDVMIA GK.V Oxidation (M) 218 - 229 567.8040 1133.5934 1133.6081 - 0.0146 0 K.VAVVAGYGDVGK.G 289 - 294 417.6919 833.3692 833.3854 - 0.0162 0 K.HFEV MR.N Oxidation (M) 320 - 330 428.5656 1282.6750 1282.6993 - 0.0244 0 K.SVQNIKPQVDR.Y 320 - 330 428.5689 1282.6849 1282.6993 - 0.0145 0 K.SVQNIKPQVDR.Y 338 - 346 511.3010 1020.5874 1020.6080 - 0.0205 0 R.HIILLAEGR.L 386 - 395 565.2932 1128.5718 1128.5815 - 0.0097 1 K.KYVEFGTTGK.K 387 - 395 501.2395 1000.4644 1000.4866 - 0.0221 0 K.YVEFGTTGK.K 396 - 405 550.3407 1098.6668 1098.6801 - 0.0133 0 K.KPVG VYVLPK.I 406 - 422 648.0227 1941.0463 1941.0683 - 0.0221 0 K.ILDEQVALLHLEHVNAK.L 426 - 443 966.5093 1931.0040 1931.0404 - 0.0364 0 K.LTPVQAEYLGLDIAGPFK.S 426 - 443 966.5135 1931.0124 1931.0404 - 0.0280 0 K.LTPVQAEYLGLDIAGPFK.S
21	XP_751658	67070	452	13	6.11	Phosphatidyl synthase Sequence Coverage: 23% 1 MPYMANTRTI PGPTAILPVG PEKGLDAGSA VPGRITMSLV LPIIGNNYSL 51 INTLISFIII LIFAFIHLFS SSPSFLIFSG SRLVNSSSNT DPAHPPPYKS 101 DIIYFSSLIT HSSPSYVSLT LLYVYILSRL SSIATMPRFD DADFGVEPAP 151 AGARSPRDAR GSASGSLPIP NEAGNTVEIP ATRSSISDAA QFMHNL SLSP 201 SMRDRRGSRN SFGTSLPIPR SPRVSR LSSV RKADAASVSR DILASQVQDM 251 SKEKVAAAKN MAFAFDIDGV LAHG NHA IPE AKEALKMLNG DNELGIKIPY 301 ILLTNGGGKT EASRCEQLSE ILEVPISTDQ FIQSHTPMQA LSEYYETVLV 351 LGGEGQKIRE VAENYGFKNV VHPKDILAWD PTISPWR TFT AEDRAEAKPR 401 DFSKIKFDAI LVFADSRDYA TDMQLIIDLL LAEDGKLLTR AKDPVSSRIP 451 IYFSQGDLLM PTDHKGPPRL TQGCFR IAVE AQYKALTGVD LERVVYGKPE 501 RATYTYADEV LKAWMEQIHN ENRLPKNIYM IGDNPQSDIV GGNMYGWNTC 551 LVRTGVFQGG ENDEHN PANF GVFPNVLEAV KAAVRKELGQ EFKFKWNPKV

						601 NPVTHGDGSS AVE 139 - 154 817.8704 1633.7262 1633.7373 - 0.0110 0 R.FDDADFGVEPAPAGAR.S 161 - 183 1119.5671 2237.1196 2237.1288 - 0.0091 0 R.GSASGSLPIPNEAGNTVEIPATR.S 210 - 220 594.8155 1187.6164 1187.6299 - 0.0134 0 R.NSFGTSLPIPR.S 241 - 252 675.8318 1349.6490 1349.6497 - 0.0006 0 R.DILASQVQDMSK.E Oxidation (M) 298 - 309 623.3599 1244.7052 1244.7129 - 0.0076 0 K.IPYILLTNGGGK.T 360 - 368 528.7513 1055.4880 1055.4924 - 0.0043 0 R.EVAENYGFK.N 388 - 394 420.1946 838.3746 838.3821 - 0.0074 0 R.TFTAEDR.A 405 - 417 747.9153 1493.8160 1493.8242 - 0.0082 1 K.IKFDAILVFADSR.D 477 - 484 461.2520 920.4894 920.4967 - 0.0073 0 R.IAVEAQYK.A 485 - 493 487.2698 972.5250 972.5240 0.0010 0 K.ALTGVDLER.V 502 - 512 637.3162 1272.6178 1272.6238 - 0.0059 0 R.ATYTYADEVLK.A 600 - 613 684.8210 1367.6274 1367.6317 - 0.0043 0 K.VNPVTHGDGSSAVE.-
22	EDP5450 6	61335	447	15	5.85	Glucose-6-phosphate isomerase Sequence Coverage: 31% 1 MPGFSQATEL GAWKELQEHH NSLGRNIVLK EYFEKDPQRF EKFSRTFANP 51 VDNTEILFDF SKNFLTEETL ALLVKLAREA GVEELRDAMF KGDPINFTED 101 RAVYHVALRN VTNEPMQVNG KSVVEDVNSV LEHMKEFTEQ VRSGEWWKGYT 151 GKKITTIINI GIGGSDLGPV MVTEALKPYG AEDMTLHFVS NIDGSHIAEA 201 LKHSDPETTL FLIASKTFTT AETTNANSA KKWFLESAKD EAHIAKHFVA 251 LSTNEEEVTK FGIDKKNMFG FASWVGGRYS VWSAIGLSVA LYIGFDNFHQ 301 FLAGAHAMDK HFRETPLEQN IPVLGGLLSV WYSDFFGAQT HLVAPFDQYL 351 HRFPAYLQQL SMESNGKAIT RTGEYVKYTT GPILFGEPAT NAQHSFFQLL 401 HQGTKLIPSD FIMAAESHNP VEGGKHQRML ASNFLAQSEA LMVGKTPEQV 451 KTEGAPDNLV PHKTFLGNRP TTSILAQKIT PSTLGALIAY YEHLTFTEGA 501 VWNINSFDQW GVELGKVLAK KIQKELETPG AGGDHDASTS GLLLAFKKKA

						551 NLA 46 - 62 979.5227 1957.0308 1956.9469 0.0839 0 R.TFANPVDNTEILFDFSK.N 46 - 62 979.5259 1957.0372 1956.9469 0.0903 0 R.TFANPVDNTEILFDFSK.N 63 - 75 745.9560 1489.8974 1489.8392 0.0583 0 K.NFLTEETLALLVK.L 79 - 86 451.7460 901.4774 901.4505 0.0270 0 R.EAGVEELR.D 92 - 101 582.3063 1162.5980 1162.5255 0.0726 0 K.GDPINFTEDR.A 110 - 121 673.8437 1345.6728 1345.6296 0.0432 0 R.NVTNEPMQVNGK.S Oxidation (M) 203 - 216 520.2913 1557.8521 1557.8039 0.0482 0 K.HSDPETTLFLIASK.T 217 - 231 779.4053 1556.7960 1556.7318 0.0642 0 K.TFTTAETTTNANSK.K 217 - 231 779.4058 1556.7970 1556.7318 0.0652 0 K.TFTTAETTTNANSK.K 247 - 260 535.2906 1602.8500 1602.7889 0.0610 0 K.HFVALSTNEEEVTK.F 406 - 425 710.0470 2127.1192 2127.0306 0.0885 0 K.LIPSDFIMAAESHNPVEGGK.H Oxidation (M) 406 - 425 710.0478 2127.1216 2127.0306 0.0909 0 K.LIPSDFIMAAESHNPVEGGK.H Oxidation (M) 452 - 463 426.5680 1276.6822 1276.6412 0.0410 0 K.TEGAPDNLVPHK.T 464 - 478 549.6653 1645.9741 1645.9151 0.0589 0 K.TFLGNRPPTSILAQK.I 525 - 547 762.7462 2285.2168 2285.1176 0.0992 0 K.ELETPGAGGDHDASTSGLLLAFK.K
23	XP_750954	52885	474	18	5.88	ATP citrate lyase subunit (Acl), putatibe Sequence Coverage: 29% 1 MSAKSILEAD GKAILNYHLT RAPVIKPTPL PPSSTHNPPP RLASIYPED 51 AAVKDVLDT EVVYPWLLTP GAKFVAKPDQ LIKRRGKSG LALNKTWPEA 101 REWIEARAGK EIKVETVTGV LRQFLVEPFV PHPQETEEYI NINSVREGDW 151 ILFTHEGGVD VGDVDAKAEK LLIPVNLARNY PSNEEIAAAL LSKVPKGVHN 201 VLVD FISRLY AVYVDCQFTY LEINPLVIP NAEGTSAEVH FLDLAAKLDQ 251 TAEFECGTKW AIARSPANLG LATVPQTDGK VNIDAGPPME FPAPFGRELS 301 KEEKFISDMD AKTGASLKLT VLNANGRIWT LVAGGGASVV YADAIASAGF 351 VSELANYGEY SGAPTETQTY

						NYAKTVLDLM LRAPMHPDGK VLFIGGGIAN 401 FTNVASTFKG VIRAIREVAP VLNEHNVQIW VRRAGPNYQE GLKNIKAVGE 451 ELGLKMHVYG PDMHVSIGVIP LALLGKKTDI KEFGSA 13 - 21 550.8359 1099.6572 1099.6138 0.0434 0 K.AILNYHLTR.A 74 - 83 579.8720 1157.7294 1157.6808 0.0486 0 K.FVAKPDQLIK.R 111 - 122 672.4186 1342.8226 1342.7820 0.0406 1 K.EIKVETVTGVLR.Q 114 - 122 487.3033 972.5920 972.5604 0.0316 0 K.VETVTGVLR.Q 171 - 178 469.3264 936.6382 936.6120 0.0262 0 K.LLIPVNL.R 171 - 178 469.3290 936.6434 936.6120 0.0314 0 K.LLIPVNL.R 179 - 193 810.4426 1618.8706 1618.8202 0.0505 0 R.NYPSNEEIAAALLSK.V 179 - 193 810.4478 1618.8810 1618.8202 0.0609 0 R.NYPSNEEIAAALLSK.V 197 - 208 452.6009 1354.7809 1354.7357 0.0451 0 K.GVHNVLVDFISR.L 197 - 208 678.4030 1354.7914 1354.7357 0.0557 0 K.GVHNVLVDFISR.L 197 - 208 678.4041 1354.7936 1354.7357 0.0579 0 K.GVHNVLVDFISR.L 265 - 280 784.9504 1567.8862 1567.8206 0.0657 0 R.SPANLGLATVPQTDGK.V 265 - 280 784.9531 1567.8916 1567.8206 0.0711 0 R.SPANLGLATVPQTDGK.V 281 - 297 915.9880 1829.9614 1829.8771 0.0844 0 K.VNIDAGPPMEFPAPFGR.E Oxidation (M) 305 - 312 471.7370 941.4594 941.4164 0.0430 0 K.FISDMDAK.T Oxidation (M) 319 - 327 479.2922 956.5698 956.5403 0.0295 0 K.LTVLNANGR.I 375 - 382 488.7997 975.5848 975.5423 0.0426 0 K.TVLDLMLR.A Oxidation (M) 391 - 409 978.5823 1955.1500 1955.0517 0.0984 0 K.VLFIGGGIANFTNVASTFK.G
24	Q4WFT3	61393	120	5	5.85	GMP synthase [glutamine- hydrolyzing] Sequence Coverage: 7% 1 MAEEQNPSAT FDTILTLDFG SQYTHLITRR LREIGVYSEM LPCTQKLADL 51 PFKPKGILS GGPYSVYEDG APHADPAVFE LGVPVLGICY GLQEIAAYRLG 101 KDNVVAGTAR EYGHADLNAQ RLDNQGHVDK LFAGLEEHVK

						VWMSHGDKLV 151 KLPEGFHTIA TTANSEYAGI AHETKPVYGI QFHPEVTHTP DGAKLLRNFA 201 VDICGANPNW TMSKFVDQEI LRIRKLVGET DHVLGAVSGG VDSTVAAKLM 251 KEAIGDRFHA VLVNNGCMRL NECETVAETL NKHLGINLTV VDASKRFLDG 301 LKGVTDPEKK RMFIGATFID VFEEEAIEKIE ALAENSGAKV KWFLQGTLYP 351 DVIESISFKG PSATIKTHHN VGALPKRMIE GQGMKLEPL RELFKDEVQR 401 LGRELGIAHE LVMRHPFPGP GIAIRVLGEV TPERVDIARK ADHIFISMIR 451 EAGLYDKISQ AYAALDPSKA VGVMGDKRVY AEIIILRAVE TTDCKLTLGI 501 DGDFVLRYY SVMTARAFPF DNEFLSKCAT RIINEVHGVS RVLYDISSKP 551 PATIEME 215 - 222 510.2953 1018.5760 1018.5447 0.0313 0 K.FVDQEILR.I 426 - 434 500.2962 998.5778 998.5397 0.0382 0 R.VLGEVTPER.V 426 - 439 518.6444 1552.9114 1552.8573 0.0541 1 R.VLGEVTPERVDIAR.K 458 - 469 632.3557 1262.6968 1262.6506 0.0462 0 K.ISQAYAALDPSK.A 479 - 487 545.3557 1088.6968 1088.6593 0.0375 0 R.VYAEIIILR.A
25	XP_7506 96	55764	876	19	5.86	6-phosphogluconate dehydrogenase Gnd1 Sequence Coverage: 31% 1 MSTQAVARLA GINVGAPARP LPSADFGLIG LAVMGQNLIL NVADHGFTVC 51 AYNRTTSKVD RFLANEAKGK SIVGAHSVEE FCAKLKPRRR IMLLVMAGKP 101 VDDFIESLLP HLEEGDIIID GGNSHFPSN RRTKYLKEKG IRFVGSGVSG 151 GEEGARYGPS LMPGGNEEAW PFIKDIFQSI AAKSDGEACC DWVGDEGAGH 201 FVKMVHNGIE YGDMQLICEA YDIMKRGLGM PVNEIADVFA KWNKGVLDSF 251 LIEITRDVLY FNDNDGTPLV EKILDKAGQK GTGKWTAINA LDLGMPVTLI 301 GEAVFARCLS AIKDERIRAS SLLDGPTPQF TGDKQAFIDD LEQALYASKI 351 ISYAQGFMLI QEAAREYGWK LNKPSIALMW RGGCIIRSVF LKDITNAYRN 401 NPDLENLLFD DFFKAAIQKA QQGWRNVVSK GALWGIPTPA FSTALSFYDG 451 YRTRDLPANL LQAQRDYFGA

						HTFRVKPECA NENYPEGKDI HVNWTGRGGD 501 VSASTYVV 143 - 156 654.8308 1307.6470 1307.6106 0.0364 0 R.FVGSGVSGGEEGAR.Y 175 - 183 496.7874 991.5602 991.5338 0.0264 0 K.DIFQSIAAK.S 227 - 241 788.9334 1575.8522 1575.7967 0.0556 0 R.GLGMPVNEIADVFAK.W Oxidation (M) 245 - 256 681.9071 1361.7996 1361.7555 0.0442 0 K.GVLDSFLIEITR.D 257 - 272 919.9794 1837.9442 1837.8734 0.0708 0 R.DVLYFNDNDGTPLVEK.I 319 - 334 817.4396 1632.8646 1632.7995 0.0651 0 R.ASSLLDGPTPQFTGDK.Q 319 - 334 817.4401 1632.8656 1632.7995 0.0661 0 R.ASSLLDGPTPQFTGDK.Q 335 - 349 856.4639 1710.9132 1710.8464 0.0668 0 K.QAFIDDLEQALYASK.I 350 - 365 609.6726 1825.9960 1825.9396 0.0564 0 K.IISYAQGFMLIQEAAR.E Oxidation (M) 350 - 365 914.0105 1826.0064 1825.9396 0.0668 0 K.IISYAQGFMLIQEAAR.E Oxidation (M) 350 - 365 914.0181 1826.0216 1825.9396 0.0820 0 K.IISYAQGFMLIQEAAR.E Oxidation (M) 388 - 399 476.2736 1425.7990 1425.7616 0.0374 1 R.SVFLKDITNAYR.N 388 - 399 713.9146 1425.8146 1425.7616 0.0531 1 R.SVFLKDITNAYR.N 393 - 399 426.7232 851.4318 851.4137 0.0181 0 K.DITNAYR.N 400 - 414 920.9688 1839.9230 1839.8679 0.0551 0 R.NNPDLLENLLFDDFFK.A 453 - 465 499.2953 1494.8641 1494.8266 0.0374 1 R.TRDLPANLLQAQR.D 455 - 465 619.8625 1237.7104 1237.6779 0.0326 0 R.DLPANLLQAQR.D 455 - 465 619.8661 1237.7176 1237.6779 0.0398 0 R.DLPANLLQAQR.D 466 - 474 557.2783 1112.5420 1112.5040 0.0381 0 R.DYFGAHTFR.V
26	XP_755071	48784	112	6	5.60	Gamma-glutamyl phosphate reductase Sequence Coverage: 14% 1 MSLTDSSAVE IARAASLASR QLATLPTIDR NDALTALHDA LLRNREILD 51 ANAKDVAIAS QAANNGSLSH SVLKRLDLSR PGKYDDMLKG ILSVRDLEDP 101 VGRVTLRTLL DDGLILERVS

						CPIGVLLIIF EARPEVIANI AALSIKSGNA 151 AILKGGKEST ESFIAISKVI SEAISGTRVP VASVQLVKTR DVVSSLLAQD 201 SLIDLVIPRG SNDLVRVKE NTKIPVLGHA DGLCSAYLHA DADPAIAVKV 251 IVDAKTDYPA ACNSLESLLV HEDALGTIFP AVAEALLAKG VRLRCDIQSK 301 SALLKNISSP PADLLEDAVD SDFDTEFLDL VLAVKTIPST SSPISAVEDA 351 ISHINSHSSK HTDLIVTESK EIAEYFMRGV DSAGVFWNAS TRFADGMRFG 401 FGTEVGISTN KIHTRGPVGL DGLTIYKYLL RGQGHRAGDY FEGEGGKKWK 451 HEHLVI 108 - 118 629.3752 1256.7358 1256.6976 0.0382 0 R.TLLDDGLILER.V 169 - 178 516.7999 1031.5852 1031.5611 0.0241 0 K.VISEAISGTR.V 179 - 188 520.3460 1038.6774 1038.6437 0.0337 0 R.VPVASVQLVK.T 361 - 370 571.8203 1141.6260 1141.5979 0.0281 0 K.HTDLIVTESK.E 399 - 411 678.8641 1355.7136 1355.6722 0.0415 0 R.FGFGTEVGISTNK.I 416 - 427 616.8666 1231.7186 1231.6812 0.0374 0 R.GPVGLDGLTIYK.Y
27	XP_7550 56	52982	59	3	5.47	Glutamate carboxypeptidase Sequence Coverage: 9% 1 MAPQLEPFFK QVDELSNSFI DRLRKAVAIP SISAHDENRK DVFRMAHFLA 51 SELEALGAEV EQRPLGKQPG KEHLDLPPVV IARYGNDKNK RTILVYGHYD 101 VQPALKDDGW ATEPFELTID DQGRMFGRGS TDDKGPVLGW LNVIEAHQKA 151 GVLPVNLLC CFEGMEEYGS EGLEEFIKSE SKKFFKDADA VCISDNYWLG 201 TEKPCLTYGL RGCNYYSVSI SGPAQDLHSG VFGGSTHEPM TDMVNILSKL 251 VDPKGNILIP GIMDLVAPLT EEENSLYSKI SYTMDNLHES LGSKTNIHET 301 KERTLMARWR YPSLSIHGIE GAFSAPGAKT VIPAKVIGKF SIRTVPNMES 351 DAVNKLVDY IKAFAKLNS KNTLDVWLQH DGKWWVASPK HWNFTAASKA 401 VKQVFGVEPD MTREGGSIPV TLSFEQATGK NVLLPMGSS TDAAHSVNEK 451 LDKKNYIEGT KLLGAYLHYV AEPPASEV 11 - 22 711.8683 1421.7220 1421.6787

						0.0434 0 K.QVDELSNSFIDR.L 414 - 430 860.9710 1719.9274 1719.8679 0.0595 0 R.EGGSIPVTLSEFQATGK.N 462 - 478 931.0040 1859.9934 1859.9305 0.0630 0 K.LLGAYLHYVAEEPASEV.-
28	XP_755448	52247	349	8	5.33	Secretory pathway gdp dissociation inhibitor Sequence Coverage: 16% 1 MEEIAPEYDV VVLGTGLTEC VLSGVLSVKG NKVLHIDRND HYGGEEAASVN 51 IETLFKKYGN VRPGEEPWKK YGRVNDWNID LVPKLLMANG ELTNILVSTD 101 VTRYLEFKQI AGSYVQQGKG PKATVAKVPS DAGEALRSSL MGMFEKRRAK 151 KFLEWVGEFK EDDPATHQGL NVAQCTMKEV YDKFGLEDNT RDFVGHSMAL 201 YPSDDYITTP GMAVETIHRI RLYVNSMARY GKSPYIPLY GLGELPQGFA 251 RLSAIYGGTY MLNTSVDEVL YDESGKVSGI KATMKDRDDN SEAMKFTTKT 301 KKIIADPSYF PGKVRVTGYL LKAICILNHP IEKTDGSDSL QLIPQSQVG 351 RKHDVYIAMV SSAHNVCPKG YYIAIVSTIA ETDANHHLEL EPGFERLGQI 401 EEKFFGPPIP LYEPDLSGEK DNIFISKSYD ATSHFETTTD DVRDLYKRAT 451 GEELVVEGLR EDQRLAED 109 - 119 589.8194 1177.6242 1177.6091 0.0151 0 K.QIAGSYVQQGK.G 128 - 137 507.7666 1013.5186 1013.5142 0.0045 0 K.VPSDAGEALR.S 179 - 191 529.2590 1584.7552 1584.7420 0.0132 1 K.EVYDKFGLEDNTR.D 184 - 191 476.2361 950.4576 950.4458 0.0119 0 K.FGLEDNTR.D 303 - 313 604.3318 1206.6490 1206.6285 0.0206 0 K.IIADPSYFPGK.V 303 - 313 604.3356 1206.6566 1206.6285 0.0282 0 K.IIADPSYFPGK.V 334 - 351 957.5198 1913.0250 1912.9854 0.0396 0 K.TDGSDSLQLIPQSQVGR.K 449 - 460 636.8495 1271.6844 1271.6721 0.0123 0 R.ATGEELVVEGLR.E
29	XP_747854	54420	110	4	5.33	Glucokinase GlkA Sequence Coverage: 11% 1 MSSPLVTEAT RIARQFDFSA EQIQSGVKEY IREMCEGLTK EHTTLSQIPT 51 YVTSVPNGTE KGLYLAVDLG GTNFRVCSID LHGDTTFNLT QSKIMIPREL 101 MASGTSKDLF LFLARQIEAF

						LRIHHNEHFE AHLRRRRREP N SEEELFDLGF 151 TFSFPVRQLG INKGTLRWT KGFNIPDAVG HDVCALLQNA IDELDLPVRV 201 AALVNDTVGT LMARSYTSPG DTSTFIGAIF GTGTNGAYVE KLDRTKLQT 251 IEHADYEKST GEMIINAEWG SFDNHLVLP NTKWDKELDE DSNNGIQMF 301 EKRVS GMFLG EILRRALLDM HKDEAFGLFK PNQSSKVVTP ENSPLYRQWG 351 IDTSFLSLVE ADKTDRMEEV KAALKDHLKI ENPSDAECQA VKVLVHAIGK 401 RAARLSAVPL AAILISTGKL ETDDMVDIGV DGSLVEFYFN FEGYIREALR 451 EVPEVGAAGE KKVIRIGISKD GSGVGAALIA LVASRNETGS GPK 15 - 28 792.3962 1582.7778 1582.7627 0.0151 0 R.QDFSAEQIQSGVK.E 337 - 347 637.8438 1273.6730 1273.6666 0.0064 0 K.VVTPENSPLYR.Q 405 - 419 727.4614 1452.9082 1452.8915 0.0167 0 R.LSAVPLAAILISTGK.L 447 - 461 518.9423 1553.8051 1553.8049 0.0002 1 R.EALREVPEVGAAGEK.K
30	XP_7556 57	78713	376	9	5.66	Bifunctional tryptophan synthase TRPB Sequence Coverage: 14% 1 MEGIKSTFAR CQEQRKRAALV AYITAGYPTV EETVDILLGL ENGGAGSLNA 51 NAIRWISTDI IELGIPFTDP IADGPTIQRA NTQALANGVT VTTVLNMVRQ 101 ARSRGLKAPL LLMGYYNPVL RYGEERMLKD CKEAGVNGFI MVDLPPEEAV 151 RFRDLCASNG MSYVPLIAPA TSEARMKLLC KIADSFYVV SRMGVTGATG 201 KLSSNLPELL KRVHQWSGNV PAALGFGVST REHFLSVQEL AEGVVIGSQI 251 ITVLGQAPAG QAAKHAE EYL SSVTGRKLER DAQGILTNEI NVLEAVEKAQ 301 VPAVSQPTAV VTEADTPDGP GLADQIDALN GTGNPAAQPS RFGEFGGQYV 351 PESLMDCLAE LERGFQEAVN DPTFWEEFRS YYPYMGRPSS LHLANRLTEY 401 VGGANIWLKR EDLNHTGSHK INNALGQILI ARRLGKTRII AETGAGQHGV 451 ATATVCAKFG MKCVVYMGAE DVRRQALNVF RMKLLGASVV AVDAGSRTL R 501 DAVNEALRAW VVDLDTTHYI IGSAIGPHPF PTIVRTFQSV IGEETKQMM 551 EAIGKLPAV VACVGGGSNA VGMFYFPAKD TSVKLVGVEA GGDGIDTNRH 601 SATLTGGSKG VLHGVRTYVL

						QDEHGQISET HSISAGLDYP GVGPELSSWK 651 DSDRARFIAA TDAEALIGFR TLAQTEGIIP ALESSHAVWG AMELAKSMKT 701 GDIVLNLSGR GDKDVQSVAD ELPRLGPKIG WDLRF 108 - 121 818.4405 1634.8664 1634.8854 - 0.0190 0 K.APLLLMGYYNPVLR.Y Oxidation (M) 182 - 192 635.3398 1268.6650 1268.6765 - 0.0114 0 K.IADSFYVVS.R 281 - 298 978.5051 1954.9956 1955.0211 - 0.0255 0 R.DAQGILTNEINVLEAVEK.A 421 - 432 648.3893 1294.7640 1294.7721 - 0.0080 0 K.INNALGQILAR.R 475 - 481 424.2388 846.4630 846.4712 - 0.0081 0 R.QALNVFR.M 484 - 497 657.8667 1313.7188 1313.7303 - 0.0115 0 K.LLGASVVAVDAGSR.T 501 - 508 444.2325 886.4504 886.4508 - 0.0004 0 R.DAVNEALR.A 657 - 670 747.8901 1493.7656 1493.7878 - 0.0222 0 R.FIAATDAEALIGFR.T 700 - 710 572.8140 1143.6134 1143.6248 -0.0113 0 K.TGDIVLNLSGR.G
31a	XP_7554 59	84023	181	9	5.62	3-isopropylmalate dehydratase Sequence Coverage: 12% 1 MPGVDDKKPKT LYDKVLDHII VNEQEDGTIL IYIDRHLVHE VTSPQAFEG 51 KNAGRKVRPP DCTLATVDHN IPTSSRKNF NVEEFIEETD SRLQCTTLEQ 101 NVKDFGLTYF GMGDKRQGIV HIIGPEQGFT LPGTTVVC GD SHTSTHGAFG 151 ALAFGIGTSE VEHVLATQTL LTRRSKNMRI QVDGELPPGV TSKDVLHII 201 GVIGTAGGTG AVIEFCGSVI RGLSMEARMS MCNMSIEAGA RAGMIAPDET 251 TFEYLKGRPL APKYDSA EWK RAVAFWSSLA SDEGAVYDKT VVLDGKDIIP 301 TVSWGTSPOD VVPITGVVPG PDDFEDENRK VACKRALEYM GLVAGTRI QD 351 IPVDKVFIGS CTNARIEDLR AAAKVVRGKK VAANIKRAMV VPGSGLVKQQ 401 AEAEGLD R VF TDAGFEWREA GCSMCLGMNP DILSPQERCA STSNRNFEGR 451 QGAGGRTHLM SPAMAAAAAI TGHADVREH LTASPLLA QPHLDIQEEH 501 EDPTTEDEFD RIMDM PADNE PHANSSAATA AAGSTAGLPK FTTLRGIAAP 551 MDRSNVD TDA IIPKQFLKTI KRTGLGSALF YELRYNPADG SENKSFVLNQ

						601 EPYRNAKILV VTGPNFGCGS SREHAPWALL DFGIKCIAP SFADIFFNNT 651 FKNGLMPVVI SDPAVLATIA AEASAGREEIE VDLVNQEIKD AAGSKLASFE 701 VDAFRKHCLI NGLDDIGLTL QMEDKIRAFE AKRTLETPWL DSGGYLKRGV 751 RGGATMIQAA PVPKTNRGDV KTEPLEW 81 - 92 734.3340 1466.6534 1466.6525 0.0010 0 K.NVEEFIEETDSR.L 180 - 193 720.3961 1438.7776 1438.7668 0.0109 0 R.IQVDGELPPGVTSK.D 399 - 408 558.7718 1115.5290 1115.5207 0.0084 0 K.QQAEAGLDR.V 554 - 564 586.8144 1171.6142 1171.6085 0.0058 0 R.SNVDTDAIPK.Q 573 - 584 663.8622 1325.7098 1325.6979 0.0119 0 R.TGLGSALFYELR.Y 585 - 594 547.7415 1093.4684 1093.4676 0.0009 0 R.YNPADGSENK.S 595 - 604 626.8216 1251.6286 1251.6248 0.0039 0 K.SFVLNQEPYR.N 678 - 689 714.8877 1427.7608 1427.7507 0.0101 0 R.EIEVDLVNQEIK.D 696 - 705 577.7994 1153.5842 1153.5768 0.0075 0 K.LASFEVDAFR.K
31b	XP_7554 59	84023	80	3	5.62	3-isopropylmalate dehydratase Sequence Coverage: 4% 1 MPGVDDKKPKT LYDKVLDHHI VNEQEDGTIL IYDRHLVHE VTSPQAFEG 51 KNAGRKVRPP DCTLATVDHN IPTSSRKNF NVEEFIEETD SRLQCTTLEQ 101 NVKDFGLTYF GMGDKRQGIV HIIGPEQGFT LPGTTVCCGD SHTSTHGAFG 151 ALAFGIGTSE VEHVLATQTL LTRRSKNMRI QVDGELPPGV TSKDVVLHII 201 GVIGTAGGTG AVIEFCGSVI RGLSMEARMS MCNMSIEAGA RAGMIAPDET 251 TFEYLKGRPL APKYDSA EWK RAVAFWSSLA SDEGAVYDKT VVLDGKDIP 301 TVSWGTSPOD VVPITGVVPG PDDFEDENRK VACKRALEYM GLVAGTRI QD 351 IPVDKVFIGS CTNARIEDLR AAAKVVRGKK VAANIKRAMV VPGSLVKQQ 401 AEAEGLDRVF TDAGFEWREA GCSMCLGMNP DILSPQERCA STSNRNFEGR 451 QGAGGRTHLM SPAMAAAAAI TGHLADVREH LTASPLLAKA QPHLDIQEEH 501 EDPTTEDEFD RIMDMPADNE

						PHANSSAATA AAGSTAGLPK FTTLRGIAAP 551 MDRSNVDTD A IIPKQFLKTI KRTGLGSALF YELRYNPADG SENKSFVLNQ 601 EPYRNAKILV VTGPNFGCGS SREHAPWALL DFGIKCIAP SFADIFFNNT 651 FKNGMLPVVI SDPAVLATIA AEASAGREIE VDLVNQEIKD AAGSKLASFE 701 VDAFRKHCLI NGLDDIGLTL QMEDKIRAFE AKRTLETPWL DSGGYLKRGV 751 RGGATMIQAA PVPKTNRGDV KTEPLEW 399 - 408 558.7700 1115.5254 1115.5207 0.0048 0 K.QQAEAEGLDR.V 573 - 584 663.8600 1325.7054 1325.6979 0.0075 0 R.TGLGSALFYELR.Y 595 - 604 626.8239 1251.6332 1251.6248 0.0085 0 K.SFVLNQEPYR.N
32	XP_7528 26	92824	86	5	5.46	Phosphoribosyl- AMP cyclohydrolase Sequence Coverage: 5% 1 MATPILISYN PTSASSGLSL SQIAYFGRVL IKVSSLSQAE EFLRQNFRL 51 DVYVDATDIT SSGDIVDILN AGAAKAFISL DQLTSLSQEQ SVPSSRLVVY 101 TSSDSQVDAF QSWVGEDAER KEAGICTESA DVKTVADRLG LNLEAQNLVYR 151 TYTTSTVTED AVKETLKQGA VSIVSADALT LDHKNPSGKI AAAALVAARA 201 VADQSNGLYA TSVTDERGVC LGLVWSSDES IAEALRTGTG VYQSRKRGLW 251 YKGQSSGDVQ ELIRLGFDCD SDCLVFVVKQ IGRGFCHLGT ASCFGPYNGL 301 ARLQKTLQAR KADAPAGSYT ARLFNEPKLT QAKIMEEAD LCRATTKEEI 351 AFEAADLLYF ALTRCVAAGV SLEDIERNLD LKSLKVRRK GDAKGPWAEK 401 AGLTASPAET KPAGPAAPAK EAAKKDDSRM EMTRVVTAST PVDKVKEYLK 451 RPSQKSND AI VGLVRPIQD VRDGGDAAVL KYTHKFEKAT SLTSPVIRAP 501 FPPELMKLSP ETQE AIDVSI ANIKKFHSAQ KDSNDVLQVE TMPGVVCSRF 551 SRPIERVGLY VPGGTAVLPS TAMMLGVPAM VAGCQKIVLA SPPRADGSIS 601 PEIVYVAHKV GAESIVLAGG AQAVAAMAYG TESISKVDKI LGPGNQFVTA 651 AKMLVSNDTS AGVSIDMPAG PSEVLVIADK DANPAFVASD LLSQAEHGVD 701 SQVILAIIDL NESQLQAIED EVDAQARALP RMDIVRGLA HSVTFVVRDI 751 DEAMALSNEY APEHLILQVK

						NAESVVEKVV NAGSVFIGQW TPESVGDYSA 801 GVNHSLPTYG YAKQYSGVNL GSFLKHITSS NLTAEGLLGL SRTVEQLAAV 851 EGLDAHKRAV SIRVAAMKKN QA 33 - 44 683.3569 1364.6992 1364.6936 0.0057 0 K.VSSLSQAEEFLR.Q 190 - 199 463.7931 925.5716 925.5709 0.0008 0 K.IAAAALVAAR.A 253 - 264 644.8304 1287.6462 1287.6419 0.0044 0 K.GQSSGDVQELIR.L 489 - 498 522.8088 1043.6030 1043.5975 0.0055 0 K.ATSLTSPVIR.A 587 - 594 426.7669 851.5192 851.5229 - 0.0036 0 K.IVLASPPR.A
33	XP_7538 31	72634	151	4	5.93	Aminopeptidase P Sequence Coverage: 8% 1 MLGFRSPIRL CKLSALGSTR LLPISRPKLF STAVARYAAD METVNTTKRL 51 ARLRQLMQEH KIDVYIVPSE DSHQSEYIAP CDGRREFISG FSGSAGTAIV 101 SMTKAALSTD GRYFNQASKQ LDSNWELLKR GVENVPTWQE WTTEQAQGGK 151 VVGVDPALIT ASGARSLEET LKRNGSSLVG ISQNLVDLVW GKDRPAPPRE 201 KVRVHPDKFS GKTFQEKIAD LRKELEKKKT AGFVISMLDE IAWLFNLRGS 251 DIPYNPVFFA YAIITPTKAE LYIDDDKITP EVVAHLGQDV VIKPYNSIFA 301 DAKALSEARR KEAGETASKF LLSNKASWAL SLSLGEEHV EETRSPiADA 351 KAIKNEVELA GMRACHIRDG AALIEYFAWL ENELVNKKTV LDEVDAADKL 401 EQIRTKHDLF AGLSFDTISS TGPNGAVIHY KPEKGTCSII DPDAIYLCD 451 GAQYLDGTTD VTRTFHFGKP TELEKKAFTL VLKGLIAIDT AVFPKGTSGF 501 ALDALARQYL WKEGLDYLHG TGHGVGSYLN VHEGPiGIGT RVQYTEVPIA 551 PGNVISDEPG FYEDGKFGIR IENVIMAREV QTTHKFGDKP WLGFHVHTMA 601 PIGRNLIIPS LLSDELKQWV NDYHAEVWDK THHFFENDEF TRSWLQRETA 651 PITK 151 - 165 713.4113 1424.8080 1424.7987 0.0093 0 K.VVGVDPALITASGAR.S 389 - 404 605.6550 1813.9432 1813.9421 0.0010 1 K.TVLDEVDAADKLEQIR.T 484 - 495 622.8691 1243.7236 1243.7176

						0.0060 0 K.GLIAIDTAVFPK.G 496 - 507 589.8114 1177.6082 1177.6091 - 0.0009 0 K.GTSGFALDALAR.Q
34	XP_7553 28	74420	673	17	6.02	Mitochondrial Hsp70 chaperone (Ssc70) Sequence Coverage: 28% 1 MMPSRLVRV CPSSTGTSSR ARSSGLTLDF LHQLPRTART PAFRVPGASF 51 RRWNSTEGEK VKGQVIGIDL GTTNSAVAVM EGKTPKIIEN AEGARTTPSV 101 VAF AQDGERL VGIAAKRQAV VNPENTLFAT KRLIGRKFTD PEVQRDIKEV 151 PYKIVQHTNG DAWVEARGQK YSPSQIGGFI LQKMKETAEN YLSKPVKNV 201 VTVPAYFNDS QRQATKDAGQ IAGLNVLRVV NEPTAAALAY GLEKEADRVV 251 AVYDLGGGTF DISVLEIQKG VFEVKSTNGD THLGGEFDFI HLVRHIVQQF 301 KKDSGLDLSN DRMAIQRIRE AAEKAKIELS SSLQTEINLP FITADASGAK 351 HINLKMTRSQ LESLVEPLIN RTVEPV RKAL KDANLQASDI QDIILVGGMT 401 RMPKVAESVK SMFGRDPAKS VNPDEAVAIG AAIQGAVLAG EVTDVLLLDV 451 TPLSLGIETL GGVFTRLINR NTTIPTKKSQ TFSTAADFQT AVEIKVFQGE 501 RELVKDNKLL GNFQLVGIPP AHRGVPQIEV TFDIDADSIV HVAADKSTG 551 KDQSITIASG SGLSDAEIQS MVEDAKEYGE QDKERKAAIE AANRADSVLN 601 DTEKALKEFE DRLDKAEAEQ IREKIATLRE FVAKNQSGEG TATAEELKQK 651 TDELQTASLT LFDKMHKAQS EQQQSQGQQ GENKP 87 - 95 486.7551 971.4956 971.5036 - 0.0079 0 K.IIENAEGAR.T 96 - 109 739.3746 1476.7346 1476.7209 0.0138 0 R.TTPSVVAF AQDGER.L 118 - 131 766.4130 1530.8114 1530.8042 0.0072 0 R.QAVVNPENTLFATK.R 118 - 132 563.3167 1686.9283 1686.9053 0.0230 1 R.QAVVNPENTLFATKR.L 138 - 145 496.2477 990.4808 990.4771 0.0038 0 K.FTDPEVQR.D 171 - 183 719.3937 1436.7728 1436.7664 0.0065 0 K.YSPSQIGGFILQK.M) 198 - 212 840.9250 1679.8354 1679.8267 0.0087 0 K.NAVVTVPAYFNDSQR.Q 217 - 228 613.8484 1225.6822 1225.6779 0.0044 0 K.DAGQIAGLNVLR.V 229 - 244 823.4462 1644.8778 1644.8723

						0.0056 0 R.VVNEPTAAALAYGLEK.E 295 - 301 450.2551 898.4956 898.5025 - 0.0068 0 R.HIVQQFK.K 303 - 312 546.2505 1090.4864 1090.4891 - 0.0026 0 K.DSGLDLSNDR.M) 359 - 371 749.4215 1496.8284 1496.8198 0.0086 0 R.SQLESLVEPLINR.T 479 - 495 922.4645 1842.9144 1842.9000 0.0145 0 K.SQTFSTAADFQTAVEIK.V 509 - 523 544.6505 1630.9297 1630.9307 - 0.0011 0 K.LLGNFQLVGIPPAHR.G 635 - 648 717.8427 1433.6708 1433.6634 0.0075 0 K.NQSGEGTATAEELK.Q 635 - 650 564.2789 1689.8149 1689.8169 - 0.0021 1 K.NQSGEGTATAEELKQK.T 651 - 664 791.4071 1580.7996 1580.7934 0.0063 0 K.TDELQ TASLTLFDK.M
35	XP_746746	64991	102	4	5.83	Heat shock protein (Sti1) Sequence Coverage: 9% 1 MLPRSFQRCG TGFTTRKKTNL FVPRNSEKFTQAIELEPSNHILYSNRSVY 51 AAQSDYQKAL DDANKAIEIK PDWSKGYSRK GAACRGLGDL LGAHDAYEEA 101 LKLDPSNDQA KSGLNAVKRA IDGEARADGV NPAAGLGGIFNDPQMFQKLA 151 SNPKTSHLLA DADFMAKLQR LQQNPNSMSPQEIQDPRFLQVMSVLLGIDM 201 SFGAPPEAAG SSRAAAEAE DVPMPDAKPA AAEKKKEPEPAPQPEPEPED 251 EETIAKKKAQ EAGDAEKKIG NDFYKKKQFD EAIEHYTKAW ELNKDITYLN 301 NIGAAKFEKG DLQGAIEICQ KAVEEGRELRA DFKVIAKAFARIGTAYEKL 351 GDFTQAIEYY HKSLTEHRTP DALTKLRNAE KAKVKAEKEA YIDPVEAEKA 401 RELGQKKFQE ADWPGAVEAF TEMTRAPHD PRGFSNRAAA LIKLMAFPQA 451 VQDCDEAIRR DPKFIRAYIR KSQALVAMKE YSKALDACTE AAEQDDGTHT 501 REIDQQQKQC LEAQFSARAG ETEEQTMERIQNDPEIMSILQDPVMSILQ 551 QAKSDPAALQ EHMKNVQVRT KIQKLMAAGV IRLGR 29 - 46 711.3660 2131.0762 2131.0698 0.0064 0 K.FTQAIELEPSNHILYSNR.S 47 - 58 665.8228 1329.6310 1329.6201 0.0110 0 R.SAVYAAQSDYQK.A 295 - 306 646.8488 1291.6830 1291.6772 0.0059 0 K.DITYLNNIGAAK.F

							350 - 362 528.9258 1583.7556 1583.7620 - 0.0064 0 K.LGDFITQAIEYYHK.S
36	XP_747200	66932	478	13	5.30	Hsp70 chaperone (HscA)	Sequence Coverage: 27% 1 MSDEVYEGAI GIDLGTTYSC VANYEGTNVE IIANEQGSYT TPSFVSFTEK 51 ERLIGEAAKN QAAMNPKNIT FDIKRLIGR YEDPIVKDI ESWPFKVVDQ 101 GGNPVVEVEY LGETKTFSPQ EISSMVLMM KEVAETKLGK KVEKAVITVP 151 AYFNDNQRQA TKDAGAIAGL NVLRIINEPT AAAIAYGLGS GKSEKERNVL 201 IYDLGGGTFD VSLNLIQGGV FTVKATAGDT HLGQDFDTN LLEHFKKEFQ 251 KKTGKDLSGD ARALRRLRTA CERAKRTLSN ATQTTVEIDS LFDGEDFNSS 301 ITRARFEDLN AKAFSGTLEP VQQVLKDSGL EKSQVDEIVL VGGSTRIPRI 351 QKLLSDFFDG KKLEKSINPD EAVAYGAAVQ AGILSGKATS AETQDLLLLD 401 VVPLSLGVAM EGNIFAPVVP RGQTVPTIKK RFTTVVDNQ TTVQFPVYQG 451 ERTNCADNTS LGEFTLAPIP PMKAGEAALE VVFEVDVNGI LKVTATEKSS 501 GRSANITISN AVGKLSTTEI EQMINDAAKF KSSDEAFTKK FESRQQLSEY 551 ISRVEEIIISD PTMSLKLKRG NKEKIESALS DAMAQLEIED SAPEDYKKKE 601 LALKRLITKA MATR 80 - 87 510.2887 1018.5628 1018.5447 0.0181 1 R.RYEDPIVK.K 97 - 115 1016.5377 2031.0608 2031.0161 0.0448 0 K.VVDQGGNPVVEVEYLGETK.T 145 - 158 804.4228 1606.8310 1606.8103 0.0207 0 K.AVITVPAYFNDNQR.Q 163 - 174 585.3424 1168.6702 1168.6564 0.0138 0 K.DAGAIAGLNVLR.I 175 - 192 582.6591 1744.9555 1744.9359 0.0196 0 R.IINEPTAAAIAYGLGSGK.S 175 - 192 873.4902 1744.9658 1744.9359 0.0299 0 R.IINEPTAAAIAYGLGSGK.S 313 - 326 758.9335 1515.8524 1515.8297 0.0228 0 K.AFSGTLEPVQQVLK.D 313 - 332 716.0677 2145.1813 2145.1317 0.0495 1 K.AFSGTLEPVQQVLKDSGLEK.S 333 - 346 730.4066 1458.7986 1458.7678 0.0308 0 K.SQVDEIVLVGGSTR.I 353 - 361 521.2710 1040.5274 1040.5179 0.0096 0 K.LLSDFFDGK.K 366 - 387 711.0504 2130.1294 2130.0957

							0.0337 0 K.SINPDEAVAYGAAVQAGILSGK.A 432 - 452 810.7466 2429.2180 2429.1864 0.0316 0 R.TFTTVVDNQTTVPVYQGER.T 545 - 553 562.2959 1122.5772 1122.5669 0.0103 0 R.QQLESYISR.V
48	XP_752631	79995	293	10	5.08	Hsp70 chaperone Hsp88	Sequence Coverage: 14% 1 MSVVGIDFGA QSTKVGVARN KGIDIITNEV SNRSTPTLVG FGTR SRHIGE 51 GAKTQEMSNL KNTVGNLKR IGR SFNDPDV EIEQK YTSAA ICDVNGQAGV 101 EVSYLGKKEK FSATQLAAMY LTKIRDITSK ELKLPVSDVT ISVPAWFTDA 151 QRRAMIDAGE IAGLKVLRLI NDTTATALGY GITKLDLPGP EEKPR RVMFV 201 DIGHSDYTAS VVEFRKGELN VKATAYDRHF GGRDFDIALT EHFADEFKEK 251 FKIDVRSNPK AYARTVAAAE KMKKVLSANP AAPMSIESLM EDVDVRSIVK 301 REELETMVKP LLER VTIPIE EALAEAK LKP EDIDTIEMVG GCTRVPAIKE 351 AISKFFGK TL SFTLNQDEAI ARG CAFSCAI LSPVFRVRDF SVHDIVNYPI 401 EFTWEQSADI PDEDTS�TVF NRGNVMPSTK ILTFYRK QPF DLEAR YAKPD 451 MLPGKINPWI GRFSVKGVKA DANDDFMICK LKARLNLHGI LNVESGYVE 501 DVEVEEPVDE DKMDTDAPEG EQPKKTRKVK KQVRKGDLP STGTNSVDQT 551 VKETWIEREN AMYMEDKLIA ETDEKKNELE STIYELRDKI DGVYAEFASE 601 EEKDKLRAKL TDMEDWLYEE GEDTTKSVYV AKLDEIR FIA GPIVQR YKEK 651 IEAERQAILK AQEEEEAKKR AEEEEAKRKAEEAKKAEETK PDEEMKDAPA 701 EGEEAAPAEGE EKQQ 22 - 33 665.8676 1329.7206 1329.6888 0.0318 0 K.GIDIITNEVSNR.S 34 - 44 568.3215 1134.6284 1134.6033 0.0251 0 R.STPTLVGFGTR.S 74 - 85 710.8494 1419.6842 1419.6518 0.0325 0 R.SFNDPDVEIEQK.Y 169 - 184 826.4709 1650.9272 1650.8828 0.0444 0 R.LINDTTATALGYGITK.L 185 - 195 417.5722 1249.6948 1249.6666 0.0281 0 K.LDLPGPEEKPR.R 315 - 327 692.4089 1382.8032 1382.7657 0.0376 0 R.VTIPIEEALAEAK.L 315 - 327 692.4202 1382.8258 1382.7657

						0.0602 0 R.VTIPIEEALAEAK.L 359 - 372 789.9308 1577.8470 1577.8049 0.0421 0 K.TLSFTLNQDEAIAR.G 438 - 445 488.2589 974.5032 974.4821 0.0211 0 K.QPFDLEAR.Y 638 - 646 500.8084 999.6022 999.5865 0.0157 0 R.FIAGPIVQR.Y
38	XP_747926	80590	613	13	4.95	Asp f12/Heat shock protein P90/Molecular chaperone and allergen Mod-E/Hsp90/Hsp1 Sequence Coverage: 20% 1 MSSETFEFQA EISQLLSLII NTVYSNKEIF LRELISNASD ALDKIRYQSL 51 SDPTKLDTGK DLRIDIIPDK ENKTLTIRD T GIGMTKADLI NNLGTIARSG 101 TKQFMEALSA GADISMIGQF GVGFYSAYLV ADRVTTVVSKN NDDEQYIWES 151 AAGGTFTLTQ DTEGEQLGRG TKIILHLKDE QTDYLNESRI KEVVRKHSEF 201 ISYPIYLHVL KETEKEVPDE EAEETKEED EEKKAKIEEV DDEEEEEKKK 251 KKKTCTVKES KIEEEELNKT KPIWTRNPAD ITQEEYASFY KSLSNDWEDH 301 LAVKHFSVEG QLEFRAILYV PKRAPFDLFE TKTKNNIKL YVRRVFITDD 351 ATDLIPEWLG FIKGVVDS LPLNLSRETL QQNKIMKVIK KNIVKKTLEL 401 FNEIAEDREQ FDKFYSAFSK NIKLGIHEDA QNRQTLAKLL RYQSTKSGDE 451 ATSLADYVTR MPEHQKQIYY ITGESIKAVA KSPFLDSLKQ KNFEVLFLVD 501 PIDEYAFTQL KEFDGKKLVD ITKDFELEET EEEKAEREKE EKEYENLAKS 551 LKNILGDKVE KVVVSHKLVG SPCAIRTGQF GWSANMERIM KAQALRDTSM 601 SSYMSSKKT F EISPKSSIIK ELKKKVEADG ENDRTVKSIT QLLFETSLLV 651 SGFTIEEPAS FAERIHKLVS LGLNIDEEAE TTEEKATEEA APAEATTGES 701 AMEEVD 33 - 44 638.3338 1274.6530 1274.6354 0.0177 0 R.ELISNASDALDK.I 33 - 46 515.6200 1543.8382 1543.8205 0.0176 1 R.ELISNASDALDKIR.Y 87 - 98 635.8681 1269.7216 1269.7041 0.0176 0 K.ADLINNLGTIAR.S 173 - 189 696.3751 2086.1035 2086.0694 0.0340 1 K.IILHLKDEQTDYLNESR.I 277 - 291 888.4280 1774.8414 1774.8050 0.0365 0 R.NPADITQEEYASFYK.S 323 - 332 612.3378 1222.6610 1222.6346

						0.0264 1 K.RAPFDLFETK.K 324 - 332 534.2825 1066.5504 1066.5335 0.0169 0 R.APFDLFETK.K 364 - 377 757.4090 1512.8034 1512.7784 0.0251 0 K.GVVDSIEDLPLNLSR.E 397 - 408 725.3771 1448.7396 1448.7147 0.0250 0 K.TLELFNEIAEDR.E 424 - 433 576.8013 1151.5880 1151.5683 0.0197 0 K.LGIHEDAQNR.Q 447 - 460 742.8643 1483.7140 1483.6791 0.0350 0 K.SGDEATSLADYVTR.M 467 - 477 657.8640 1313.7134 1313.6867 0.0268 0 K.QIYYITGESIK.A 668 - 685 995.5217 1989.0288 1988.9790 0.0499 0 K.LVSLGLNIDEEAETTEK.A
39a	XP_750490	69618	336	13	5.09	Molecular chaperone Hsp70 Sequence Coverage: 21% 1 MAPAVGIDLG TTYSCVGVFR DDRIEIIAND QGNRTTPSFV AFTDTERLIG 51 DAAKNQVAMN PHNTVFDAGR LIGRRFQDAE VQSDMKHWPV KVVEKGGKPI 101 IEVEFKGETK QFTPEEISSM VLTKMRETAE AYLGGTVNNA VITVPAYFND 151 SQRQATKDAG LIAGLNVLRI INEPTAAAI A YGLDKKAEGE RNVLIFDLGG 201 GTFDVSLITI EEGIFEVKAT AGDTHLGGED FDNRLVNHFV NEFKRKHKKD 251 LTTNARALRR LRTACERAKR TLSSAAQTSI EIDSLFEGID FYTSITRARF 301 EELCQDLFRS TMEPVERVLR DAKLDKSSVH EIVLVGGSTR IPKIQRLVAD 351 FFNKEANKSI NPDEAVAYGA AVQAAILSGD TSSKSTNEIL LLDVAPLSLG 401 IETAGGVMTPLIKRNTTIPT KKSETFSTYS DNQPGVLIQV YEGERARTKD 451 NNLLGKFELT GIPPAPRGVP QIEVTFDVDA NGIMNVSAVE KGTGKTNKIT 501 ITNDKGRLSK EEIERMLADA EKYKEEDEAE AARIQAKNGLESYAYSLKNT 551 ISEGKLNISD ADKEKVSSKV EEISWLDNN QTATKDEYES QQKELESVAN 601 PIISAAYGGA AGAAPGGAAP GGATRTADEV EERPEELD 5 - 47 736.3688 1470.7230 1470.6991 0.0240 0 R.TTPSFVAFTDTER.L 158 - 169 606.3643 1210.7140 1210.7034 0.0107 0 K.DAGLIAGLNVLR.I) 219 - 234 559.2525 1674.7357 1674.7234 0.0123 0 K.ATAGDTHLGGEDFDNR.L 219 - 234 838.3826 1674.7506 1674.7234

						0.0272 0 K.ATAGDTHLGGEDFDNR.L 235 - 244 623.8430 1245.6714 1245.6506 0.0208 0 R.LVNHFVNEFK.R 235 - 244 416.2338 1245.6796 1245.6506 0.0290 0 R.LVNHFVNEFK.R 347 - 354 477.2595 952.5044 952.5018 0.0026 0 R.LVADFFNK.E 359 - 384 845.7736 2534.2990 2534.2500 0.0490 0 K.SINPDEAVAYGA AVQAAILSGDTSSK.S 457 - 467 599.3448 1196.6750 1196.6553 0.0197 0 K.FELTGIPPAPR.G 508 - 515 502.2818 1002.5490 1002.5345 0.0145 1 R.LSKEEIER.M 523 - 533 437.5370 1309.5892 1309.5786 0.0106 1 K.YKEEDEAEAAAR.I 538 - 548 622.8206 1243.6266 1243.6084 0.0182 0 K.NGLESYAYSLK.N 626 - 638 766.3547 1530.6948 1530.6685 0.0263 0 R.TADEVEERPEELD.-
39b	XP_750490	69618	5.09	21	693	Molecular chaperone Hsp70 Sequence Coverage: 26% 1 MAPAVGIDLG TTYSCVGVFR DDRIEIIAND QGNRTTPSFV AFTDTERLIG 51 DAAKNQVAMN PHNTVFDAKR LIGRRFQDAE VQSDMKHWPV KVVEKGGKPI 101 IEVEFKGETK QFTPEEISSM VLTKMRETAE AYLGGTVNNA VITVPAYFND 151 SQRQATKDAG LIAGLNLRI INEPTAAAI YGLDKKAEGE RNVLIFDLGG 201 GTFDVSLITI EEGIFEVKAT AGDTHLGGED FDNRLVNHFV NEFKRKHKKD 251 LTTNARALRR LRTACERAKR TLSSAAQTSI EIDSLFEGID FYTSITRARF 301 EELCQDLFRS TMEPVERVLR DAKLDKSSVH EIVLVGGSTR IPKIQRLVAD 351 FNKEANKSI NPDEAVAYGA AVQAAILSGD TSSKSTNEIL LLDVAPLSLG 401 IETAGGVMTPLIKRNTTIPT KKSETFSTYS DNQPGVLIQV YEGERARTKD 451 NNLLGKFELT GIPPAPRGVP QIEVTFDVDA NGIMNVSAVE KGTGKTNKIT 501 ITNDKGRLSK EEIERMLADA EKYKEEDEAE AARIQAKNGL ESYAYSLKNT 551 ISEGKLNISD ADKEKVSSKV EEIISWLDNN QTATKDEYES QQKELESVAN 601 PIISAAYGGA AGAAPGGAAP GGATRTADEV EERPEELD 24 - 34 621.8320 1241.6494 1241.6364 0.0131 0 R.IEIIANDQGNR.T

						35 - 47 736.3662 1470.7178 1470.6991 0.0188 0 R.TTPSFVAFDTER.L 158 - 169 606.3650 1210.7154 1210.7034 0.0121 0 K.DAGLIAGLNVLR.I 170 - 185 553.9749 1658.9029 1658.8879 0.0150 0 R.IINEPTAAAIAYGLDK.K 170 - 185 830.4614 1658.9082 1658.8879 0.0204 0 R.IINEPTAAAIAYGLDK.K 170 - 186 596.6722 1786.9948 1786.9828 0.0119 1 R.IINEPTAAAIAYGLDKK.A 219 - 234 559.2504 1674.7294 1674.7234 0.0060 0 K.ATAGDTHLGGEDFDNR.L 219 - 234 838.3850 1674.7554 1674.7234 0.0320 0 K.ATAGDTHLGGEDFDNR.L 235 - 244 623.8408 1245.6670 1245.6506 0.0164 0 R.LVNHFVNEFK.R 235 - 244 623.8414 1245.6682 1245.6506 0.0176 0 R.LVNHFVNEFK.R 235 - 244 416.2370 1245.6892 1245.6506 0.0386 0 R.LVNHFVNEFK.R 327 - 340 480.9323 1439.7751 1439.7733 0.0018 0 K.SSVHEIVLVGGSTR.I 327 - 340 720.9034 1439.7922 1439.7733 0.0190 0 K.SSVHEIVLVGGSTR.I 347 - 354 477.2532 952.4918 952.5018 - 0.0100 0 R.LVADFFNK.E 347 - 354 477.2624 952.5102 952.5018 0.0084 0 R.LVADFFNK.E 359 - 384 845.7729 2534.2969 2534.2500 0.0469 0 K.SINPDEAVAYGAAVQAAILSGDTSSK.S 457 - 467 599.3398 1196.6650 1196.6553 0.0097 0 K.FELTGIPPAPR.G 457 - 467 599.3604 1196.7062 1196.6553 0.0509 0 K.FELTGIPPAPR.G 508 - 515 502.2781 1002.5416 1002.5345 0.0071 1 R.LSKEEIER.M 538 - 548 622.8209 1243.6272 1243.6084 0.0188 0 K.NGLESYAYSLK.N) 626 - 638 766.3547 1530.6948 1530.6685 0.0263 0 R.TADEVEERPEELD.-
40	XP_753589	55586	412	15	5.30	ATP synthase F1, beta subunit Sequence Coverage: 31% 1 MFKSGGLARTF GRAAFARPS VARRAIQPVR YNGLPSLARF ASSEAGSVGK 51 IHQVIGAVVD VKFDGDNLPA ILNAJETENN GQKLVLVLEVSQ HLGENVVRTI 101 AMDGTEGLTR GAPARDTGAP IKIPVGPGTL GRIVNVTGDP IDERGPIKAT 151 KFAPIHAEAP EFTEQSTS AE

						ILVTGIKVVD LLAPYARGGK IGLFGGAGVG 201 KTVFIQELIN NIAKAHGGYS VFTGVGERTR EGNPLYHEMQ ETGVIQLEGE 251 SKVALVFGQM NEPPGARARV ALTGLTIAEY FRDEEGQDVL LFDNIFRFT 301 QAGSEVSALL GRIPSAVGYQ PTLAVDMGGM QERITTTKKG SITSVQAVYV 351 PADDLTD PAP ATTF AHL DAT TVLSRGISEL GIYP AVDPLD SKSRMLDPRI 401 VGEEHYAVAT RVQQMLQEYK SLQDI IAILG MDELSEADKL TVERARKLQR 451 FLSQPFTVAQ VFTGIEGKLV DLKDTIRSFK AIINGEGDDL PEA AFYMGD 501 FESARAKGEK ILAELEGKA 84 - 98 564.6611 1690.9615 1690.9366 0.0249 0 K.LVLEVSQHLGENVVR.T 116 - 132 550.3268 1647.9586 1647.9308 0.0278 1 R.DTGAPIKIPVGPGLGR.I 133 - 144 664.3539 1326.6932 1326.6779 0.0153 0 R.IVNVTGDPIDER.G 133 - 148 574.9902 1721.9488 1721.9312 0.0176 1 R.IVNVTGDPIDERGPIK.A 178 - 187 558.8283 1115.6420 1115.6339 0.0082 0 K.VVDLLAPYAR.G 191 - 201 488.2902 974.5658 974.5549 0.0109 0 K.IGLFGGAGVGK.T 202 - 214 751.9456 1501.8766 1501.8504 0.0262 0 K.TVFIQELINNIK.A 215 - 228 479.5700 1435.6882 1435.6844 0.0037 0 K.AHGGYSVFTGVGER.T 299 - 312 718.3895 1434.7644 1434.7467 0.0178 0 R.FTQAGSEVSALLGR.I 299 - 312 718.3974 1434.7802 1434.7467 0.0336 0 R.FTQAGSEVSALLGR.I 376 - 392 887.4830 1772.9514 1772.9196 0.0318 0 R.GISELGIYP AVDPLDSK.S 400 - 411 448.9020 1343.6842 1343.6834 0.0008 0 R.IVGEEHYAVATR.V 400 - 411 672.8567 1343.6988 1343.6834 0.0155 0 R.IVGEEHYAVATR.V 451 - 468 985.0487 1968.0828 1968.0357 0.0472 0 R.FLSQPFTVAQVFTGIEGK.L 511 - 519 472.2781 942.5416 942.5386 0.0031 1 K.ILAELEGKA.-
41	XP_750312	29183	615	12	9.18	40S ribosomal protein S3 Sequence Coverage: 56% 1 MAAVQGAISK RRKFVADGVF YAE LNEFFQR ELAEEGYSGV EVRVTPVTD 51 IIRATHTQE VLGEQGRIR ELTSLIQKRF

						KFPENSVS LY AAKVQNRGLS
						101 AVAQCESLR Y KLLNGLAVRR ACYGVLR FIM ESGAKGCEVV VSGKLRAARA
						151 KSMKFTDGF M IHSQPAKEF IDSATRHVLL RQGV LGIKVK IMRGSDPEGK
						201 AGPQK TLPDS VTIEPKKEEQ PVLQPM SQDY GAKALAAQQL AEQQRLAEQQ
						251 AAEGQEGAGA EAYAQE
						31 - 43 719.3351 1436.6556 1436.6783 - 0.0227 0 R.ELAEEGYSGVEVR.V
						44 - 54 614.3578 1226.7010 1226.7234 - 0.0224 0 R.VTPTVTDIIR.A
						44 - 54 614.3583 1226.7020 1226.7234 - 0.0214 0 R.VTPTVTDIIR.A
						55 - 67 475.9031 1424.6875 1424.7008 - 0.0133 0 R.ATHTQEV LGEQGR.R
						55 - 68 527.9338 1580.7796 1580.8019 - 0.0223 1 R.ATHTQEV LGEQGRR.I
						80 - 93 800.9128 1599.8110 1599.8297 - 0.0186 1 R.FKFPENSVS LYAAK.V
						98 - 109 645.8162 1289.6178 1289.6398 - 0.0219 0 R.GLSAVAQCESLR.Y Carbamidomethyl (C)
						112 - 119 428.2694 854.5242 854.5338 - 0.0095 0 K.LL NGLAVR.R)
						128 - 135 449.7114 897.4082 897.4266 - 0.0183 0 R.FIMESGAK.G Oxidation (M)
						136 - 144 467.7309 933.4472 933.4590 - 0.0117 0 K.GCEVVVSGK.L Carbamidomethyl (C)
						136 - 144 467.7334 933.4522 933.4590 - 0.0067 0 K.GCEVVVSGK.L Carbamidomethyl (C)
						155 - 168 517.9077 1550.7013 1550.7188 - 0.0175 0 K.FTDGFMIHSGQPAK.E Oxidation (M)
						169 - 176 469.7246 937.4346 937.4505 - 0.0159 0 K.EFIDSATR.H
						169 - 176 469.7295 937.4444 937.4505 - 0.0061 0 K.EFIDSATR.H
						206 - 217 656.8666 1311.7186 1311.7286 - 0.0099 0 K.TLPDSVTIIEPK.E
						206 - 217 656.8704 1311.7262 1311.7286 - 0.0023 0 K.TLPDSVTIIEPK.E
						218 - 233 918.4173 1834.8200 1834.8407 - 0.0207 0 K.EEQPVLQPM SQDYGAK.A Oxidation (M)
						234 - 245 663.8542 1325.6938 1325.7051 - 0.0113 0 K.ALAAQQLAEQQR.L
						234 - 245 663.8573 1325.7000 1325.7051 -

							0.0051 0 K.ALAAQQLAEEQQR.L
42	XP_751171	85475	389	17	6.26	Mitochondrial aconitate hydratase	Sequence Coverage: 21% 1 MISTRRLARAG ALAPKSRLFL GTRAFATVGD SPLDKKVEMA NTEKGNINY 51 KKMSENLDIV RRRLQRPLTY AEKVLVSHLD DPHGQEIERG KSYLKLRPDR 101 VACQDATAQM AILQFMSAGM PSVATPTTVH CDHLIEAQVG GDKDLARANE 151 INKEVYDFLA SATAKYNIGF WKPGSGIIHQ IVLENYAFPG GLMIGTDSHT 201 PNAGGLAMAA IGVGGADAVID VMAGLPWELK APKVIGVKLT GEMSGWTPK 251 DVILKVAGLL TVKGGTGAI EYHGPVTSLSCTGMGTICN MGAEIGATTS 301 MFPFNDRMVD YLKATKRQHI GDFAREYAKE LREDEGAEDY QLEINLSEL 351 EPHINGPFTP DLATPISKFK EAVETNKWPE ELKVGLIGSC TNSSYEDMSR 401 AASIARDALN HGLKAKSLFT VTPGSEQIRA TIERDGLQQT LEEFGGVILA 451 NACGPCIGQW DRRDVKKGEP NSIISSYNRN FTGRNDANPA THAFVASPDL 501 VVAMTIAGTL KFNPLTDKLK DKDGNFLLQ PPTGEGLPK GYDPGRDTYQ 551 APPADRSSVN VAVSPTSDRL QLLAGFEPWD GKDANGIPIL IKCQGKTTTD 601 HISMAGPWLK YRGHLDNISN NMLIGAVNAE NGKANSVKNK FTGEYDAVPA 651 TARDYKARGV KVVVIGDWN GEGSSREHAA LEPRHLGGLA IITRSFARIH 701 ETNLKKQGML PLTFADPADY DKINPEDTVD LLCTQLEVKG PMTLRVHPKD 751 GSAPFDISLN HTFNESQIEW FKDGSALNTM ARKSGAK 63 - 73 458.9341 1373.7805 1373.7779 0.0026 1 R.RLQRPLTYAEK.V 64 - 73 406.8962 1217.6668 1217.6768 - 0.0100 0 R.LQRPLTYAEK.V 74 - 89 636.6498 1906.9276 1906.9173 0.0102 0 K.VLYSHLDDPHGQEIER.G 148 - 165 662.0120 1983.0142 1982.9949 0.0193 1 R.ANEINKEVYDFLASATAK.Y 154 - 165 657.8387 1313.6628 1313.6503 0.0125 0 K.EVYDFLASATAK.Y 256 - 263 400.7673 799.5200 799.5167 0.0033 0 K.VAGLLTVK.G 417 - 429 717.8925 1433.7704 1433.7514 0.0190 0 K.SLFTVTPGSEQIR.A 512 - 520 538.3137 1074.6128 1074.6073

						0.0055 1 K.FNPLTDKLLK.D 521 - 540 709.3689 2125.0849 2125.0691 0.0157 1 K.DKDGNEFLLQPPTGEGLPAAK.G 523 - 540 941.9929 1881.9712 1881.9472 0.0240 0 K.DGNEFLLQPPTGEGLPAAK.G 541 - 556 593.6111 1777.8115 1777.8020 0.0095 1 K.GYDPGRDITYQAPPADR.S 557 - 569 659.8389 1317.6632 1317.6525 0.0108 0 R.SSVNVAVSPTSDDR.L 583 - 592 527.3240 1052.6334 1052.6230 0.0105 0 K.DANGIPIILK.C) 639 - 653 547.2748 1638.8026 1638.8002 0.0024 1 K.NKFTGEYDAVPATAR.D 641 - 653 699.3455 1396.6764 1396.6623 0.0142 0 K.FTGEYDAVPATAR.D 677 - 684 461.7411 921.4676 921.4668 0.0009 0 R.EHAALPR.H 685 - 694 525.8295 1049.6444 1049.6346 0.0099 0 R.HLGLAITR.S
43	XP_754479	43328	66	2	4.81	Aspartic endopeptidase Pep2 Sequence Coverage: 8% 1 MKSTSLTAS VLLGSASAAV HKLKLNVPL DEQLYTHNID AHVRALGQKY 51 MGIRPNVHQE LLEENSLNDM SRHDLVLDNF LNAQYFSEIS LGTPPQKFKV 101 VLDTGSSNLW VPGSDCSSIA CFLHNKYDSS ASSTYKANGT EFAIKYGSGE 151 LSGFVSQDTL QIGDLKVVKQ DFAEATNEPG LAFAFGRFDG ILGLGYDTIS 201 VNKIVPPFYN MLDQGLLDEP VFAFYLGDTN KEGDNSEASF GGVDKNHYTG 251 ELTKIPLRRK AYWEVDFDAI ALGDNVAELE NTGIILDTGT SLIALPSTLA 301 DLLNKEIGAK KGFTGQYSIE CDKRDSLPLD TFTLAGHNFT IGPYDYTLEV 351 QGSCISSFMG MDFPEPVGPL AILGDAFLRK WYSVYDLGNN AVGLAKAK 170 - 187 970.9763 1939.9380 1939.9064 0.0316 0 K.QDFAEATNEPGLAFAFGR.F 188 - 203 856.4617 1710.9088 1710.8829 0.0260 0 R.FDGILGLGYDTISVKN.I
44	XP_749744	56152	260	7	4.58	Protein disulfide isomerase Pdi1 Sequence Coverage: 16% 1 MRSFAPLVLS LLGASAVASA DATADTTSDV VSLTKDSFKD FMKEHDLVLA 51 EFYAPWCGHC KALAPKYEEA ATELKGNIP LVKVDCTEEE DLCKENGVEG 101 YPTLKIFRGP DSSKPYQGAR QADSIVSYMI KQSLPAVSTV TEENLEEIKT

						151 MDKIVVIGYF ASDDKAANDV FTSFAESQRD NYLFAATSDS AIAKAEGVKQ 201 PSIVLYKDFD EKKAVYDGA EQEAILSWVK TASTPLVGEI GPETYSSYIT 251 AGIPLAYIFA ETKEERDQYA EDFKPVAEKH KGAINIATID AKMFGAHAGN 301 LNLDPQTTPA FAIQDPEKNA KYPYDQSRREF NAKEIGKFIQ DVLDGKVEPS 351 IKSEPIPETQ EGPVTVVVVAH SYQDIVINND KDVLLIFYAP WCGHCKALAP 401 KYEELAALYA GDFKDKVTIA KIDATANDVP DSITGFPTIK LYPAGAKDSP 451 VEYSGSRTVE DLANFIKENG KVKVDALVAA SEKVEEGPDV TASPSATSTE 501 AEAPAAATGDE KGDHDEL 67 - 75 527.2641 1052.5136 1052.5026 0.0111 0 K.YEEAATELK.G 154 - 165 663.8634 1325.7122 1325.6867 0.0255 0 K.IVVIGYFASDDK.A 180 - 194 793.9009 1585.7872 1585.7624 0.0249 0 R.DNYLFAATSDSAIAK.A 282 - 292 543.8177 1085.6208 1085.6080 0.0128 0 K.GAINIATIDAK.M 322 - 328 464.7173 927.4200 927.4086 0.0114 0 K.YPYDQSR.E 422 - 440 988.0107 1974.0068 1973.9946 0.0123 0 K.IDATANDVPDSITGFPTIK.L 458 - 467 575.3217 1148.6288 1148.6077 0.0211 0 R.TVEDLANFIK.E
45	XP_7556 86	93139	58	4	6.51	Translation elongation factor EF-2 subunit Sequence Coverage: 5% 1 MVNFTIEIR SLMDRPTNIR NMSVIAHVDH GKSTLTDSMI QRAGIISAAC 51 AGEGRYMDTR PDEQDRGITI KSTAISLYAK FPDPEDLKEI PQKVDGAEFL 101 VNLIDSPGHV DFSSEVTAAL RVTDGALVVV DCVEGVVCVQT ETVLRQALTE 151 RIKPVLINK VDRALLELQV SKEDLYQSFS RTVESVNVII ATYHDKALGD 201 VQVYPDRGTV AFGSGLHGWA FTVRQFAVKY AKKFGVDRKK MLERLWGDNY 251 FNPQTKKWTk TGEPEQRAFN MFILDPIFKI FAAVNNDKTE EIHKLVEKLE 301 IKLASDEKDL KGKALLKVIM RKFLPAADAM LEMICHLPS PVTAQKYRAE 351 TLYEGPMDDE CAIGIRDCDP KAPLMYVSK MVPTSDKGRF YAFGRVFSGI 401 VKSGLKVRIQ GPNYIPGKKD DLFVKAIQRT ILMMGFRFVEP IEDVPAGNIV

						451 GLVGVDQFL KSGTLTTSET AHNLKVMKFS VSPVVQRGVE VKNAQDLPKL 501 VEGLKRLSKS DPCVLTMIN SGQHIVAGAG ELHLEICKD LEEDHAGVPL 551 RISDPVVSYSR ETVGGESSMT ALSKSPNKHNL RLYVTAQPLG EEVSLAIESG 601 KINPRDDFKA RARLLADDYG WDVTDARKIW CFGPDTTGAN LLVDQTKAVQ 651 YLNEIKDSFV SGFQWATREG PIAEPMRSI RFNILDVTLH ADAIHRGGGQ 701 IIPARRVLY AATLLAEP VPEQAMGGIY GVLTRRRGHV 751 YSEEQRPGTP LFNVKAYLPV NESFGFNGDL RQATGGQAFP QSVFDHWSIL 801 PGGSPLDPTT KPGQTVAEMR KRKGLKEQVP GYDNYDDKL 2 - 10 560.8113 1119.6080 1119.5924 0.0156 0 M.VNFTIEIR.S 197 - 207 616.8245 1231.6344 1231.6197 0.0147 0 K.ALGDVQVYPDR.G 462 - 475 487.2554 1458.7444 1458.7314 0.0129 0 K.SGTLTTSETAHNLK.V 479 - 487 509.7906 1017.5666 1017.5607 0.0059 0 K.FSVSPVVQR.G
46	XP_752090	86840	89	6	6.33	Cobalamin-independent methionine synthase MetH/D Sequence Coverage: 6% 1 MVQSAVLGFP RMGKLRDLKK ATEAYWGGKI SRDELLSEGG RLRAEHWKI 51 KDAGVDIIPS NDAFYDQVL DHIQLFGVVP ERYSKYNLDP LDEYFAMGRG 101 LQKPASEGQP AIDVPSLEMV KWFDSNYHYV KPTLQENQVF KLASNPKPVA 151 QFLEAKEAGI ITRPVILGPV SFLTAKADR GQKIDPIDKI NDLVPVYVDL 201 LAQLKAAGVE DVQIDEPVLV FDLPAKSKAA FKPVEYKIGA LGDKAPRVL 251 ATYFGDIVHN IDVLPALHNL HGIHVDLVRN PEQLDAVIAA LGPKQVLSAG 301 VVDGRNIWKT NFKAIEKVE HAIQKLGKDR VIVSTSSSL HVPHTLESEK 351 NLDPEVREWF SFAVEKTHEV VVIKAVTEG PAAVRDQLEA NAKSVQARAS 401 SARTNDPKVK ERQAAVTEEM HNRKSPFPVR LAEQSKSINL PLFPTTTIGS 451 FPQTKEIRIQ RNKFTKGEIT AEEYEKFIEQ ELAEVVKIQE ELDLDVLVHG 501 EPERNDMVQY FGERLTGYVF TTHAWVQSYG SRCVRPPIIV GDISRPAPMT 551 VKESKYAVSI SKKPMKGMLT GPITCLRWSF PRDDVHQSVM AQQLALALRD

						601 EVIDLEAAGV KVIQVDEPAL REGLPLRAGK EREDYLTWAV RAFRLATSGV 651 SDGTQIHSHF CYSEFQDFH AIAALDADVL SIENSKSDAK LLKVFVEEAY 701 PRHIGPGVYD IHSPRVPSEQ EIKDRIEEML PYLRPDQLWI NPDCGLKTRQ 751 WPETKAALTN MVNAAKFYRQ KYTK 2 - 11 537.3082 1072.6018 1072.6029 - 0.0011 0 M.VQSAVLGFPR.M 2 - 11 537.3125 1072.6104 1072.6029 0.0075 0 M.VQSAVLGFPR.M 376 - 385 485.7758 969.5370 969.5243 0.0127 0 K.AVTEGPAAVR.D 477 - 487 652.8705 1303.7264 1303.7023 0.0241 0 K.FIEQEIAEVVK.I 612 - 621 570.3284 1138.6422 1138.6346 0.0076 0 K.VIQVDEPALR.E 703 - 715 483.2498 1446.7276 1446.7368 - 0.0092 0 R.HIGPGVYDIHSPR.V
47	XP_7526 50	41701	281	7	8.72	Isocitrate dehydrogenase, NAD-dependent Sequence Coverage: 17% 1 MISARNFVAP ARQCLRTRRV SSGFASHLSQ LRGYASAADD RVAKFKGQKG 51 PDGKYTVTLI EGDGIGPEIA QSVKDIFAAA KAPIKWEPVD VTPILKDGTK 101 TIPEEAIKSV QKNYVALKGP LATPVGKGHV SLNLTLRRTF NLFANLRPCR 151 SVAGYKTPYD NVDTVLIREN TEGEYSGIEH VVVDGVVQSI KLITREASER 201 VLRFAFQYAR SVNKKKVRVV HKATIMKMSD GLFLNTAREI AKEFPDIEFD 251 AELLDNSCLK IVTDPTYND KVLVMPNLYG DILSDMCAGL IGGLGLTPSG 301 NIGDECSIFE AVHGSA PDIA GKGLANPTAL LLSSIMMLQH MGLHEHAARI 351 QKATFDTLAE GKTLTGDLGG KAKTHEYAEA ICKRL 100 - 108 501.2775 1000.5404 1000.5441 - 0.0036 0 K.TTIPEEAIK.S 157 - 168 703.3637 1404.7128 1404.7249 - 0.0121 0 K.TPYDNVDTVLIR.E 204 - 210 451.7187 901.4228 901.4446 - 0.0218 0 R.FAFQYAR.S 228 - 238 620.7956 1239.5766 1239.5918 - 0.0151 0 K.MSDGLFLNTAR.E Oxidation (M) 261 - 271 631.8155 1261.6164 1261.6190 - 0.0026 0 K.IVTDPTYNDK.V 353 - 362 526.7635 1051.5124 1051.5186 - 0.0061 0 K.ATFDTLAEGK.T 363 - 371 431.2336 860.4526 860.4604 -

						0.0077 0 K.TLTGDLGGK.A
48	XP_752056	64987	63	2	6.39	Phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase Sequence Coverage: 3% 1 MSQQKSAILS VYDKTGLLDL AKGLVKHNVR LLASGGTARM IREAGFPVED 51 VSAITHAPEM LGGRVKT LHP AVHGGILARD IESDEKDLAD QNISKVDFVV 101 CNLYPFKETV NKNVNTIAEA VEEIDIGGVT LLRAAAKNHA RVTILSDPQD 151 YPEFLKELEA GEISETSRKQ YALKAFEHTA DYDTAISGFF RKQYAGNGEQ 201 YLPLRYGANP HQKPASAYML HGKLPFKALN GSPGYINLLD ALNAWALVKE 251 LKQALGYPAAS FKHVSPAG AAVGVPLSEK ERKVYMVDDI AGIETSGLAQ 301 AYARARGADR MSSFGDLLAL SDVCDVPTAK IISREVS DGV IAAGYTPEAL 351 EILSKKKGGK YLVLMQMDENY VPASEETR TI YGVQLSQQRN DVVISPKQTF 401 NTIITPKDLK ALPDSALRDL TVATIALKYT QSNSVCYALN GQVIGLGAGQ 451 QSRIHCTRLA GDKADNWWMR FHDRV LNIKW KAGTKRADKS NAIDLLCSGQ 501 TPRNEVEKAE YERVFEVPA PFTQEERDSW LSKMGEVAVS SDAFFPFIDN 551 VFRAARSGAK YIAAPSGSQN DGPVFETA EK LGIVFVEQGT RLFHH 379 - 389 646.8580 1291.7014 1291.6884 0.0130 0 R.TYGVQLSQQR.N 581 - 591 609.8524 1217.6902 1217.6768 0.0134 0 K.LGIVFVEQGT.R.L
49	XP_754077	48306	94	4	4.43	Nucleosome assembly protein Nap1 Sequence Coverage: 11% 1 MSEPIRNKKA DFPVAPTQPN TPANNAPISS HAQQPGVASI KEESLDHATA 51 ASLFARNPGL VSMIQGKLGS LVGR SSGYIE SLPAPVRRRV AGLKGIQKEH 101 AKLEAQFQEE VLELEKKYFA KFTPLYQRRRA TIVNGAAEPT DDEVQAGKEE 151 EEEEEVDVKA EDERKQEEKD ITTPGIPEFW LSAMKNQISL AEMITDRDEE 201 ALKHLTDVRM EYLD RPPGFRL IFEFAENEFF TNKTISKTTY YKEESGYGGD 251 FIYDHAEGCK IDWKADKDLT VRVESKKQRN KNTKQTRVVK VTPVTESFFN 301 FFSPQPPTD DDDTIATDIE ER LELDYQLG EDIKEKLIPR AIDWFTGEAL 351 QFEELGDDMD ADEFDDDEDDE DEEDEDDEDD DRRSDRDVDD ESEEEVRFSS 401 LYASKYIFAS TPFFTMTAL PQS

						75 - 87 688.3735 1374.7324 1374.7143 0.0181 0 R.SSGYIESLPAPVR.R 103 - 116 852.9508 1703.8870 1703.8617 0.0253 0 K.LEAQFQEEVLELEK.K 122 - 128 462.7514 923.4882 923.4865 0.0018 0 K.FTPLYQR.R 323 - 336 564.9607 1691.8603 1691.8617 - 0.0015 1 R.LELDYQLGEDIKEK.L
50	XP_754843	46200	99	5	4.62	Ran GTPase activating protein 1 (RNA1 protein) Sequence Coverage: 12% 1 MAPPKVFSLE GKGLKLDTAE DIEAHIKPLI ESTDFTEIRL GGNTLGVPAS 51 ERLASVLASQ KSLEVADLAD IFTSRLLSEI PQALTALLNA LLEIKTLHTV 101 NLSDNAFGLN TQAPLVDFLS RHVPLRHLIL NNNGLGPAAG TLIADALTKL 151 AERKEEARKA GEEIPLLDSEI VCGRNRLENG SMEAWARAYK VHAAGIRSVK 201 MTQNGIRQEG ISLLKEGLR HASALEVLDL QDNTFTIMGS TALAGVVAGW 251 PSLRELGVGD CLLSARGGVK VAQALAEKGK QNIQTLRLQY NEITAEGVKL 301 FLHATKTALP SLRRIELNGN KFLEEDPNVT ELQEVLEARK EEHGTDDDPD 351 DMWGVDELDE LEESEEEEE AEEEEEEEEQ EEEERKADKF LKDNVKAEDE 401 KVAQRQDKDV DALAEALGKT AL 40 - 52 635.8472 1269.6798 1269.6677 0.0121 0 R.LGGNTLGVPASER.L 53 - 61 458.7786 915.5426 915.5389 0.0037 0 R.LASVLASQK.S 271 - 279 443.7540 885.4934 885.4920 0.0015 0 K.VAQALAEKGK.N 280 - 287 493.7731 985.5316 985.5305 0.0012 0 K.NQNIQTLR.L 288 - 299 682.8656 1363.7166 1363.6983 0.0183 0 R.LQYNEITAEGVK.L
51	XP_756019	46529	131	4	7.61	Curved DNA-binding protein Sequence Coverage: 11% 1 MEAWYQSHTL ASVRGHNIYF TMAENQAPEV DYTLNPNPDL TKYKTAAQIS 51 HKVLEAVTAL CSEGAKIVEI CQKGDELLEE ELTKVYKGKK ITKGIGHPTT 101 VSPSSYVTPY TPLVSDAQEA ETTLKAGEIV KIQLGAQIDG FGTIVCDMVV 151 VADKESPKDV VTGREADLIH ATHYANELLL RLMVPPGLLA SGTEEEKKKA 201 AAEKPPTQSQ ISALIEKVAK

						AYDCNVVENT TSWLFRNEI EGGKKIILAP 251 GSGVKGEVGP DVGEVWGVEV GLSLGSGKVK TLPHRATLHR RTTTYILKR 301 PSSRQTLSEI VKKFGTFPFS LRQLEDEKSA KVGVEVCVRG GVLRRQYEPAG 351 DADNAPVSRL LTTIAITKNG ITRLAAPNPP DLSKFQTDKK IEDEEILKIL 401 ERPLARNTGN KNKKKKKPTK DSKDEE 74 - 84 638.3303 1274.6460 1274.6241 0.0219 0 K.GDELLEELTK.V 246 - 255 477.8061 953.5976 953.5910 0.0067 0 K.IILAPGSGVK.G 345 - 359 795.3772 1588.7398 1588.7117 0.0281 0 R.QYEPAGDADNAPVSR.L 374 - 384 561.8163 1121.6180 1121.6080 0.0100 0 R.LAAPNPPDLSK.F
52	XP_754690	57418	276	5	5.44	Phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent Sequence Coverage: 11% 1 MTKVDHKVVL IVIDGWGIPG PDSPKGDGAI AAAETPYMSG FAEENSKTAQ 51 GYTELDASSL AVGLPEGLMG NSEVGHLNIG AGRVWQDSV RIDQTLKKGE 101 LNKVDNVVKS FTRAKEGNR LHLLGLVSDG GVHSNITHLV GLLKVAKEME 151 IPQVFIHFFG DGRDTPKSA IKYMQDLLDH TKEIGIGEIA TVVGRYYAMD 201 RDKRWDRVEV AMKGIVSGEG EESDPVKTI KERYEKGEND EFLKPIIVGG 251 KERRVQDNDT LFFFNYSRDR VREITQLLGD YDRSPKPDFP YPKNIQITTM 301 TQYKTDYTFP VAFPPQHMG VLAEWLSKKD IQQCHVAETE KYAHVTFFFN 351 GGIEKQFPGE VRDMIPSPKV PTYDHEPEMS AEA VGKKMAE RIAEGKFEFV 401 MNNFAPPDMV GHTGVYEA KGVAATDKAI GEIYQACKKH GYILFITADH 451 GNAEEMLTEK GTPKTSHTTN KVPFVLANAP EGWSLKKEEG VLGDVAPT VL 501 AAMGIEQPEE MSGKSLLVKA 84 - 91 494.7629 987.5112 987.5138 - 0.0025 0 R.VWQDSVR.I 183 - 195 657.3822 1312.7498 1312.7351 0.0148 0 K.EIGIGELATVVGR.Y 214 - 228 745.3665 1488.7184 1488.6944 0.0241 0 K.GIVSGEGEESDPVK.T 255 - 267 839.9080 1677.8014 1677.7787 0.0227 0 R.VQDNDTLFFFNYS 273 - 283 661.8368 1321.6590 1321.6514 0.0077 0 R.EITQLLDYDR.S

53	XP_748938	51999	101	4	6.25	Pyruvate dehydrogenase complex, dihydrolipoamide acetyltransferase component	Sequence Coverage: 11% 1 MVASAVRMRI PSAMLSKGGL YVRRPHVIHR FKDAVQPQLP ALSALSRFYA 51 SKSFPPHTII SMPALSPTMS AGNIGAWQKK AGDSLSPGDV LVEIETDKAQ 101 MDFEFQEEGV LAKVLKETGE KDVAVGTPIA VLVEEGTDVA PFESFTLEDA 151 GGDKGTAPPK ESKEEPKAEA APAPSTPEPA PAAQEPETST EKLQPSLDRE 201 PNISPAAKAL ALEKGVPIKA LKGTGRGGQI TKEDVEKYKP SISAAAAAPT 251 YEDIPLTSMR KTIATRLQQS MRENPHFFVS TTLSVTKLLK LRQALNASAE 301 GKYKLSVNDF LVKACAAALM KVPVAVNSSWR EENGQVVIRQ HNTVDISVAV 351 ATPNGLITPV VKNVHSLGLS SISNQIKDLG KRARENKLKP EEYQGGTFTI 401 SNMGMNPAVE RFTAVINPPQ AAILAVGTTR KVAVPVETEE GTSVEWDDQI 451 IVTGSFDHKV VDGAVGAEWI KELKKIVENP LELL 193 - 208 579.3189 1734.9349 1734.9264 0.0085 1 K.LQPSLDREPNISPAAK.A 227 - 237 401.8735 1202.5987 1202.6143 - 0.0156 1 R.GGQITKEDVEK.Y 331 - 339 522.2769 1042.5392 1042.5407 - 0.0015 0 R.EENGQVVIR.Q 412 - 430 970.5660 1939.1174 1939.0891 0.0284 0 R.FTAVINPPQAAILAVGTTR.K
54	XP_664146	41682	64	4	5.54	ACT_BOTCI Actin <i>A. nidulans</i>	Sequence Coverage: 13% 1 MPTEEVAALV IDNGSGMCKA GFAGDDAPRA VFPSIVGRPR HHGIMIGMQ 51 KDSYVGDEAQ SKRGILTTRY PIEHGVVTNW DDMEKIWHHT FYNELRVAPE 101 EHPVLLTEAP INPKSNREKM TQIVFETFNA PAFYVSIQAV LSLYASGRIT 151 GIVLDSGDGV THVVPYIEGF ALPHAISRVD MAGRDLTDYL MKILAERGYT 201 FSTTAEREIV RDIKEKLCYV ALDFEQEIQT ASQSSSLEKS YELPDGQVIT 251 IGNERFRAPE ALFQPSVLGL ESGGIHVTTF NSIMKCDVDV RKDLYGNIVM 301 SGGTTMYPGI SDRMQKEITA LAPSSMKVKI IAPPERKYSV WIGGSILASL 351 STFQQMWISK QEYDESGPSI VHRKCF 20 - 29 488.7349 975.4552 975.4410 0.0142 0 K.AGFAGDDAPR.A 240 - 255 895.9830 1789.9514 1789.8846

						0.0668 0 K.SYELPDGQVITIGNER.F 317 - 327 582.3156 1162.6166 1162.5903 0.0263 0 K.EITALAPSSMK.V Oxidation (M) 361 - 373 506.2470 1515.7192 1515.6954 0.0238 0 K.QEYDESGPSIVHR.K
55	XP_7522 65	40002	88	3	5.85	UPF0160 domain protein MYG1 Sequence Coverage: 8% 1 MADETVAKKL KTSPLIGTH NGHFHADEAL AVYLLRQLPT YASSPLIRTR 51 DPAQLATCHT VVDVGGEYDP ASNRYDHHQR TFSTTFPNHN TRLSAGLVY 101 MHFGRAlIAQ HTSLPLDHED VTLLYEKLYT DFIEAVDAND NGVSVYDPAA 151 LASANIEKRF RDGGITIASV VNDMNNPDPT CPPGEPQDED SLFNRASTFM 201 GHVFTRKLHH AFTSWLPARA TVGAAYQSR EVHPSGRIII LPQGGVPWKE 251 HLYNFEKEAS GAGDINPDEQ VYYVLYPESA TEGSKWRVQC VSVNEGSFES 301 RKPLPESWRG VRDADLDGCL AAEAESGKP KIPEGAVFVH ASGFIGGHKT 351 KEGAFAMAVR SLEL 37 - 48 673.3708 1344.7270 1344.7401 - 0.0131 0 R.QLPTYASSPLIR.T 220 - 229 512.2616 1022.5086 1022.5145 - 0.0058 0 R.ATVGAAAYQSR.R 352 - 360 484.2316 966.4486 966.4593 - 0.0106 0 K.EGAFAMAVR.S Oxidation (M)
56	XP_7517 80	50540	334	10	5.66	Homocitrate synthase Sequence Coverage: 28% 1 MCPGADNEPN GHTNGANGTV PHPGFTAVET RQNPSPASR NPYGHNVGVT 51 DFLSNVSRFK IESTLREGE QFANAFDTE KKIEIAKALD DFGVDYIELT 101 SPCASEQSRK DCEAICKLGL KAKILTHIRC HMDDARVAVE TGVGDGVDVVI 151 GTSSYLREHS HGKDMTYIKN TAIEVIEFVK SKGIEIRFSS EDSFRSDLVD 201 LLSIYSAVDK VGVNRVGIAD TVGCASPRQV YELVRVLRGV VSCDIETHFH 251 NDTGCAIANA YCALEAGATH IDTSVLGIGE RINGITPLGGL MARMMVADPE 301 YVKSKYKLEK LKDIEDLVAA AVEVNIPFNN YITGFCAFTH KAGIHAKAIL 351 NNPSTYEIIN PADFGMTRYV HFASRLTGWN AIKSRAQQLN IEMTDAQYKE 401 CTAKIKALAD IRPIAVDDAD SIIRAYYRNL KSGENKPLLD LTAEEQAQFA 451 AKEKELAGSG VIA 41 - 58 659.3185 1974.9337 1974.9548 -

						0.0211 0 R.NPYGHNVGVTDFLSNVSR.F 68 - 81 816.8560 1631.6974 1631.7104 - 0.0129 0 R.EGEQFANAFDTEK.K 137 - 157 1068.5507 2135.0868 2135.1111 - 0.0242 0 R.VAVETGVDGVDVVIGTSSYLRE 170 - 180 631.8462 1261.6778 1261.6918 - 0.0139 0 K.NTAIEVIEFVK.S 188 - 195 487.7136 973.4126 973.4141 - 0.0015 0 R.FSSEDSFR.S 196 - 210 819.4235 1636.8324 1636.8560 - 0.0235 0 R.SDLVDLLSIYSAVDK.V 229 - 235 453.7491 905.4836 905.4971 - 0.0134 0 R.QVYELVR.V 282 - 293 608.3268 1214.6390 1214.6441 - 0.0051 0 R.NGITPLGGLMAR.M Oxidation (M) 294 - 303 607.7679 1213.5212 1213.5359 - 0.0146 0 R.MMVADPEYK.S 2 Oxidation (M) 407 - 424 642.0159 1923.0259 1923.0425 - 0.0166 0 K.ALADIRPIAVDDADSIHR.A
57	XP_755754	64716	284	10	7.55	Dihydroxy acid dehydratase IIv3 Sequence Coverage: 18% 1 MLLSQTRGRL PSTLRSFSRR ALSTTLPRGK DSEETALNKV SRNVTQPISQ 51 GASQAMLYAT GLTEEDMNKA QVGISVWYN GNPCNMHLLD LSNRVREGVQ 101 KAGLVGFQFN TVGVSDAISM GTKGMRYSLQ SRDLIADSIE TVMGGQWYDA 151 NISIPGCDKN MPGVLMAMGR VNRPSLMVYG GTIKPGCART QNNADIDIVS 201 AFQAYGQFLT GEITENQRFD IIRNACPGGG ACGGMYTANT MATAIEVMGM 251 TLPGSSSNPA ESKAKDLECL AAGEAIKRLL KEDIRPSDIL TRQAFENAMI 301 VVNITGGSTN AVLHLIAIAD SVGIKLDIED FQKVSDRTPF LADLKPSGKY 351 VMADLHNIGG TPSLLKFLK EGVIDGSGMT VTGETLAKNL EKVPDFPADQ 401 KIIRPLSNPI KKTGHIQILR GSLAPGGSVG KITGKEGTRF VGKARVFDDE 451 DDFIAALERN EIKKEEKTVV VIRYTGPKGG PGMPEMLKPS SALMGAGLGS 501 SCALITDGRF SGGSHGFLIG HIVPEAAVGG PIGLVKDGDT ITIDAEKRLL 551 DLDVDETELA RRRKEWEALR DAGKLPQTGL TMRGTLGKYA RTVKDASHGC 601 ITDSVE 160 - 170 612.7891 1223.5636 1223.5461 0.0176 0 K.NMPGVLMAMGR.V 3 Oxidation (M)

						279 - 292 556.9983 1667.9731 1667.9570 0.0161 1 R.LLKEDIRPSDILTR.Q 338 - 349 425.2448 1272.7126 1272.7078 0.0048 0 R.TPFLADLKPSGK.Y 371 - 388 890.9545 1779.8944 1779.8561 0.0384 0 K.EGVIDGSGMTVTGETLAK.N Oxidation (M) 421 - 431 465.2571 928.4996 928.4978 0.0018 0 R.GSLAPGGSVGK.I 446 - 459 827.9002 1653.7858 1653.7522 0.0336 0 R.VFDEDDFIAALER.N 537 - 548 445.2258 1332.6556 1332.6521 0.0035 1 K.DGDTITIDAEKR.L 549 - 561 751.4067 1500.7988 1500.7671 0.0317 0 R.LLDLDVDETELAR.R 549 - 562 553.2981 1656.8725 1656.8682 0.0042 1 R.LLDLDVDETELARR.R 575 - 583 516.7834 1031.5522 1031.5434 0.0089 0 K.LPQTGLTMR.G Oxidation (M)
58	XP_749237	58635	204	6	5.82	Myo-inositol-phosphate synthase Sequence Coverage: 11% 1 MAPHATSDAV ANGAVNGSAR TTTAPLFTVN SPNVEYTDNE IKSRYAYHHT 51 DITRTAEGKM VATPKVTNYQ FKVDRKVGKV GMMLVGWGGN NGSTVTAGIL 101 ANRRRLVWET REGERAANY GSLVMSSTVK LGTDSKTGEE INIPFHDMLP 151 MIHPNDLVIG GWDISSMNLA DAMDR AQVLE PTLKQLVRKE MAEMKPLPSI 201 YYPDFIAANQ EDRADNVIEG NKASWAHVER IQQDIRDFKA QNGLDKVIVM 251 WTANTERYAD IIPGVNDTAD NLLNAIKAGH QEVAPSTVFA VACILENVFP 301 INGSPQNTFV PGAIQLAEKH GAFIGGDDFK SGQTKMKSAL VDFLINAGIK 351 LTSIASYNHL GNNDGKNLSS QKQFRSKEIS KSNVDDMV ANHLLYKEGE 401 HPDHTTVIKY MPAVGDNKRA LDEYYAEIFM GGHQTISLFN ICEDSLLASP 451 LIIDLVVIAE MMTRITWKSA DDEEYKGFHS VLSVLSYMLK APLTPPGTPV 501 VNALAKQRSA LTNIFRACVG LQPDSEMTLE HKLF 45 - 54 414.2033 1239.5881 1239.5884 - 0.0003 0 R.YAYHTTDITR.T 176 - 184 499.8025 997.5904 997.5808 0.0097 0 R.AQVLEPTLK.Q 214 - 222 480.2441 958.4736 958.4720 0.0017 0 R.ADNVIEGNK.A 320 - 330 582.2874 1162.5602 1162.5407

						0.0195 0 K.HGAFIGGDDFK.S 491 - 506 773.4732 1544.9318 1544.8926 0.0392 0 K.APLTPPGTPVVNALAK.Q 509 - 516 461.2667 920.5188 920.5080 0.0109 0 R.SALTNIFFR.A
59	XP_752164	49337	481	10	5.79	Glutamate/Leucine/Phenylalanine/V aline dehydrogenase Sequence Coverage: 24% 1 MSNLPHEPEF EQAYKELAST LENTLFEKN PEYRKALAVV SVPERVVQFR 51 VVWEDDNHQQV QINRGYRVQF NSALGPYKGG LRFHPSVNLS ILKFLGFEQI 101 FKNALTGLNM GGGKGGSDFD PKGKSDNEIR RFCVAFMTEL CKHIGADTDV 151 PAGDIGVTGR EIGFLFGQYR KIRNQWEGVL TGKGGSWGGS LIRPEATGYG 201 LVYYVDHMIK YVTKGAESFA GKRVAISGSG NVAQFAALKV IELGGSVVSL 251 SDSKGSLLVN GEGSFTPAEI DIIAQLKVDR KQLSEVATTE AFATKFKYIE 301 GARPWVHV GK VDVALPSATQ NEVSGEEAQA LIDAGCKFIA EGSNMGCTQA 351 AIDIFEHRQ ANPGAAAIWY APGKAANAGG VAVSGLEMAQ NSARISWTAE 401 EVDSRLKDIM ESCFRNGLDT AVKYATPAEG VLPSLVGTGSN IAGFTKVAEA 451 MKEQGDWW 35 - 45 584.8536 1167.6926 1167.6975 - 0.0049 1 R.KALAVVSVPER.V 36 - 45 520.8068 1039.5990 1039.6026 - 0.0035 0 K.ALAVVSVPER.V 68 - 78 612.3279 1222.6412 1222.6346 0.0066 0 R.VQFNSALGPYK.G 94 - 102 564.8085 1127.6024 1127.6015 0.0009 0 K.FLGFEQIFK.N 143 - 160 584.2945 1749.8617 1749.8646 - 0.0029 0 K.HIGADTDVPAGDIGVTGR.E 161 - 170 615.3186 1228.6226 1228.6241 - 0.0014 0 R.EIGFLFGQYR.K 215 - 223 461.7382 921.4618 921.4668 - 0.0050 1 K.GAESFAGKR.V 224 - 239 766.9347 1531.8548 1531.8358 0.0190 0 R.VAISGSGNVAQFAALK.V 240 - 254 745.4188 1488.8230 1488.8035 0.0195 0 K.VIELGGSVVSLSDSK.G 282 - 295 748.3948 1494.7750 1494.7566 0.0185 0 K.QLSEVATTEAFATK.F
60	XP_750781	114548	283	9	5.03	Assimilatory sulfite reductase Sequence Coverage: 10% 1 MMGSSSPSLS ALGGPTYVTA QTLIQQVAYI LSDKIFSYSP ESFDLDNALR

						51 EWASRQETNA IGESTVVKAM ETRQGAGNIA LGYLFSDQDFD LKKRHVPQGI 101 VASSATLPYM RSALEQLSLL YSVASPVAAH VAAVDYAGEN GLVSDYASAL 151 SLAEELGLGL VSSASVHEAQ HMALLTTLLA SVLPSVHIYD GVRVGRETTR 201 VIDVLDQAGV ARTYEAIKKT LDESRNRHLD TQGVLELFA SLNGELGTDY 251 GLFEYHGHA E PVSVLVAFGT VEASLTAQVA RSLAKDGVRV GVVNVRYRVP 301 FVEEEFLRVL PQSTKTVGVL GQVTDEQDVQ EQGVRSALEY DVLAALTFAS 351 GREHAPTCVD IKYPRSQRWD LINTAAAFQL IFEKPIPAS GESAPLQLID 401 PATVQEYTFW DVDSSVCESA AAVLSEALAA DSASNVTTSK SYDNLIQGGGA 451 LRIDIRKSSK ILDTPYAITA ADTTYVGDIK LLGDIDVAAS IKNKGVIIIN 501 APGVKDDELE KKLPLGFRQA VAQREISLYI VDPSAAGASA PESSVLQSAF 551 LRVALPSQEG VGLKKLSSIT GDSETLETVA KDLDKLLRQV EIPESWRISE 601 EGTEVTQLSK DISINSFVPF DKDEAEAPL LNDWQAAAKG LAFKEAYGTK 651 KALRPETATK TFTVHVKENR RLTPVTYDRN IFHIEFDLGD SGLKYDIGEA 701 LGVHAENDPQ EVSEFITFYG LNPDDVVGVP SREDPAVLEN RTVYQALVQN 751 VDIFGRPPKR FYEALAEFAT DEKEKKDLLT LGGPEGAVEF KRRAEVDTIT 801 FADVLEFPS AHPDFQDLIR IVGPLKRREY SIASCQKVTP NSVALMIVAV 851 NWVDPGRDR FGLATRYLSR LQPGTPVTVS VKSSVMKLPP KSTQPLIMAG 901 LGTGLAPFRA FVQHRALEKA QGKEIGAVLL YMGRHQREE YCYGEEWEAY 951 QEAGVITLLG RAFSRDQPEK IYIQDRMRET LPEIIQAYIR EEGAFYLCGP 1001 TWPVPDVTAV LEEAIA TEAK NTGKKVDTRK EIEKLKDEER YVLEVY 201 - 212 628.3577 1254.7008 1254.6932 0.0076 0 R.VIDVLDQAGVAR.T 441 - 452 653.8477 1305.6808 1305.6677 0.0132 0 K.SYDNLIQGGALR.I 481 - 492 607.8539 1213.6932 1213.6918 0.0015 0 K.LLGDIDVAASIK.N 497 - 511 547.3056 1638.8950 1638.8828 0.0121 1 K.VIINAPGVKDDELEK.K 553 - 565 442.5987 1324.7743 1324.7714
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						0.0028 1 R.VALPSQEGVGLKK.L 598 - 610 710.8676 1419.7206 1419.7093 0.0114 0 R.ISEEGTEVTQLSK.D 672 - 679 482.7568 963.4990 963.5025 - 0.0035 0 R.LTPVTYDR.N 733 - 741 521.7685 1041.5224 1041.5091 0.0134 0 R.EDPAVLENR.T 871 - 882 613.3641 1224.7136 1224.7078 0.0058 0 R.LQPGTPVTVSVK.S
61	XP_754687	51841	131	4	7.64	Serine hydroxymethyltransferase Sequence Coverage: 8% 1 MATYALSQAH REQMEKSLVD SDPEIAQIME KEIQRQRESI LLIASENVTS 51 RAVFDALGSP MSNKYSEGYP GARYYGGNQH IDAIELTCQA RALKAFNLDP 101 EKWGVNVQCL SGSPANLEVY QALMRPHDRL MGLDLPHGGH LSHGYQTPSR 151 KISAVSTYFE TFPYRVNTET GIIDYDTLEA NAELYRPKCL VAGTSAYCRL 201 IDYGRMRKIA DKVGAYLIVD MAHISGLVAA GVIPSPEYA DVVTTTTHKS 251 LRGPRGAMIF FRKGVRSTDP KTGKEIMYDL EGPINFSVFP GHQGGPHNHT 301 ITALAVALKQ AATPEFRQYQ EQVLKNAKAL EVEFKALGHK LVSDGTDSDM 351 VLLDLRPKGL DGARVEAVLE QINIACNKNS IPGDKSALTP CGIRIGTPAM 401 TSRGMSEEDF KRVARIDQV INLCKSIQAD LPKEANKLKD FKAKVASGSV 451 PEILALRKEV AEWASTYPLP V 52 - 64 676.8318 1351.6490 1351.6442 0.0049 0 R.AVFDALGSPMSNK.Y Oxidation (M) 65 - 73 500.2264 998.4382 998.4457 - 0.0075 0 K.YSEGYPGAR.Y 95 - 102 467.2356 932.4566 932.4603 - 0.0037 0 K.AFNLDPEK.W 395 - 403 475.2436 948.4726 948.4699 0.0028 0 R.IGTPAMTSR.G Oxidation (M)
62	XP_748936	35876	559	13	9.08	Malate dehydrogenase, NAD-dependent Sequence Coverage: 38% 1 MFAARQSFNL LQKRAFSASA SQASKVAVLG AAGGIGQPLS LLLKLNPRVS 51 ELALYDIRGG PGVAADLSHI NTNSTVTGYD PTPSGLRDAL KGSEIVLIPA 101 GVPRKPGMTR DDLFNTNASI VRDLAKAAAE ASPEANILVI SNPVNSTVPI 151 VAEVFKSKGV YNPKRLEFGVT TLDVVRASRF ISQIKKTDPA KEAVPVVGGH 201 SGTIVPLLS QSNHPDIEGE

						TRDTLVNRIQ FGGDEVVKAK DGAGSATLSM 251 AMAGARFAES LLKAAQGEKG VIEPTFVESP LYKDQGVDFV ASRVELGPNG 301 VEKILEVGKV NAYEEKLIQA ALTDLKKNIQ KGRDFVAQNP 49 - 58 589.8170 1177.6194 1177.6343 - 0.0148 0 R.VSELALYDIR.G 88 - 104 579.0051 1733.9935 1734.0040 - 0.0105 1 R.DALKGSEIVLIPAGVPR.K 92 - 104 654.3834 1306.7522 1306.7609 - 0.0086 0 K.GSEIVLIPAGVPR.K 92 - 104 654.3902 1306.7658 1306.7609 0.0050 0 K.GSEIVLIPAGVPR.K 111 - 122 682.8453 1363.6760 1363.6732 0.0029 0 R.DDLFNTNASIVR.D 166 - 176 610.3547 1218.6948 1218.6972 - 0.0024 0 R.LFGVTTLDVVR.A 229 - 238 546.2822 1090.5498 1090.5659 - 0.0160 0 R.IQFGGDEVVK.A 241 - 256 749.8348 1497.6550 1497.6552 - 0.0001 0 K.DGAGSATLSMAMAGAR.F 2 Oxidation (M) 270 - 283 789.9274 1577.8402 1577.8341 0.0061 0 K.GVIEPTFVESPLYK.D 284 - 293 571.2678 1140.5210 1140.5200 0.0010 0 K.DQGVDFFASR.V 294 - 303 521.2324 1040.4502 1040.5502 - 0.1000 0 R.VELGPNGVEK.I 304 - 316 497.9310 1490.7712 1490.7980 - 0.0268 1 K.ILEVGVKNAYEEK.L 332 - 340 502.2418 1002.4690 1002.4883 - 0.0192 1 K.GRDFVAQNP.-
63	XP_754009	37156	381	11	7.55	Alcohol dehydrogenase Sequence Coverage: 31% 1 MTIPDKQWAQ VVLEKGSPPV YKEIPVPKPG PDDILVKLRY SGVCHTDLHA 51 MKGDWPLALK LPLVGGHEGV GVVVAKGELV TGFEIGDHAG IKWLNGSCME 101 CEFCKQSEEP LCPRATMSGY TVDGTFQQYC VAKATHASKI PNGVPLDAAA 151 PILCAGLTVY KGLKESGARP GQTVAIVGAG GGLGSLAQQY AKAMGLRVVA 201 IDGGDEKREM CEKLGAEAYI DFTKSTNVVE DVKAATPGGL GAHAVLLLAV 251 SEKPFQQATD YVRSRGTIVA IGMPAGAYLK APVFNTVVKM ITIKGSYVGN 301 RQDGVEAIDF FARGLINAPF KKAPLKDLPK IFELMEQGVV AGRYVLEIPE 351

						23 - 37 539.6475 1615.9207 1615.9185 0.0022 0 K.EIPVPKPGPDDILVK.L 61 - 76 510.9688 1529.8846 1529.8930 - 0.0084 0 K.LPLVGGHEGVGVVAK.G 77 - 92 548.2800 1641.8182 1641.8362 - 0.0181 0 K.GELVTGFEIGDHAGIK.W 77 - 92 821.9328 1641.8510 1641.8362 0.0148 0 K.GELVTGFEIGDHAGIK.W 198 - 208 579.8058 1157.5970 1157.6040 - 0.0070 1 R.VVAIDGGDEKR.E 214 - 224 614.3152 1226.6158 1226.6183 - 0.0024 0 K.LGAEAYIDFTK.S 266 - 280 739.4138 1476.8130 1476.8010 0.0120 0 R.GTIVAIGMPAGAYLK.A Oxidation (M) 295 - 313 701.0146 2100.0220 2100.0025 0.0195 1 K.GSYVGNRQDGVEAIDFFAR.G 302 - 313 684.3364 1366.6582 1366.6517 0.0065 0 R.QDGVEAIDFFAR.G 314 - 321 430.2508 858.4870 858.4963 - 0.0093 0 R.GLINAPFK.K 331 - 339 555.7706 1109.5266 1109.5427 - 0.0160 0 R.IFELMEQGK.V Oxidation (M)
64a	XP_748145	36292	341	12	6.96	Glyceraldehyde 3-phosphate dehydrogenase GpdA Sequence Coverage: 28% 1 MATPKVGING FGRIGRIIGL NSLSHGLVDV VAVNDPFIEV HYAAYMLKYD 51 TTHGQFKGTI ETYDQGLIVN GKKIRFYAEK DPSQIPWSET GAAYIVESTG 101 VFTTKEKASA HLKGGAKKVI ISAPSADAPM FVMGVNNTTY TSDIQVLSNA 151 SCTTNCLAPL AKVINDKFGE VEGLMTTVHS YTATQKVVD PSNKDWRGGR 201 TAAQNIIPSS TGAAKAVGKV IPSLNGKLTG MAMRVPTSNV SVVDLTCRLE 251 KGASYDEIKQ AIKAASEEGE LKNILGYTED DVVSSDLNGD ERSSIFDAKA 301 GISLNPNFVK LVAWYDNEWG YSRRVVDLIA YIAKVDSQ 6 - 13 410.2177 818.4208 818.4399 - 0.0190 0 K.VGINGFGR.I 58 - 72 804.4276 1606.8406 1606.8203 0.0204 0 K.GTIETYDQGLIVNGK.K 201 - 215 715.3840 1428.7534 1428.7572 - 0.0038 0 R.TAAQNIIPSTGAAK.A 228 - 234 406.1888 810.3630 810.3728 - 0.0097 0 K.LTGMAMR.V 2 Oxidation (M) 228 - 248 780.4000 2338.1782 2338.1443 0.0338 1 K.LTGMAMRVPTSNVSVVDLTCR.L Carbamidomethyl (C); 2 Oxidation (M)

						235 - 248 773.9117 1545.8088 1545.7821 0.0267 0 R.VPTSNVSVVDLTCR.L Carbamidomethyl (C) 264 - 272 467.2303 932.4460 932.4451 0.0010 0 K.AASEEGELK.N 300 - 310 580.3291 1158.6436 1158.6397 0.0040 0 K.AGISLNPNFVK.L 324 - 334 420.9211 1259.7415 1259.7601 - 0.0187 1 R.RVVDLIAIYIAK.V 324 - 334 630.8852 1259.7558 1259.7601 - 0.0043 1 R.RVVDLIAIYIAK.V 325 - 334 552.8303 1103.6460 1103.6590 - 0.0130 0 R.VVDLIAIYIAK.V 325 - 338 767.4362 1532.8578 1532.8450 0.0128 1 R.VVDLIAIYIAKVDSQ.
64b	XP_748145	36292	162	6	6.96	Glyceraldehyde 3-phosphate dehydrogenase GpdA Sequence Coverage: 23% 1 MATPKVGING FGRIGRIIGL NSLSHGLVDV VAVNDPFIEV HYAAYMLKYD 51 TTHGQFKGTI ETYDQGLIVN GKKIRFYAEK DPSQIPWSET GAAYIVESTG 101 VFTTKEKASA HLKGGAKKVI ISAPSADAPM FVMGVNNTTY TSDIQVLSNA 151 SCTTNCLAPL AKVINDKFGI VEGLMTTVHS YTATQKVVDA PSNKDWRGGR 201 TAAQNIIPSS TGAAKAVGKV IPSLNGKLTG MAMRVPTSNV SVVDLTCRLE 251 KGASYDEIKQ AIKAASEEGE LKNILGYTED DVVSSDLNGD ERSSIFDAKA 301 GISLNPNFVK LVAWYDNEWG YSRRVVDLIAIYIAKVDSQ 58 - 72 804.4311 1606.8476 1606.8203 0.0274 0 K.GTIETYDQGLIVNGK.K 187 - 194 415.2221 828.4296 828.4341 - 0.0045 0 K.VVDAPSNK.D 201 - 215 715.3871 1428.7596 1428.7572 0.0024 0 R.TAAQNIIPSTGAAK.A 264 - 272 467.2277 932.4408 932.4451 - 0.0042 0 K.AASEEGELK.N 300 - 310 580.3285 1158.6424 1158.6397 0.0028 0 K.AGISLNPNFVK.L 325 - 334 552.8398 1103.6650 1103.6590 0.0060 0 R.VVDLIAIYIAK.V
65	XP_747920	52079	258	10	8.69	Citrate synthase (Cit1) Sequence Coverage: 19% 1 MASTMRLGAF ALRSTSITAK PAVQSAAFNG LRCYSTGKAK SLKETFADKL 51 PGEIEKVKKL RKEHGSKVIG EVTLDQAYGG ARGVKCLVWE GSVLDSEEGI 101 RFRGYTIPEC QKLLPKAPGG

						EEPLPEGLFW LLLTGEIPTE QQVRDLSEAW 151 AARSDLPKFI EELIDRCPST LHPMAQFSLA VTALHEHESAF AKAYAKGINK 201 KDYWNYTYED SMDLIACLPT IAAKIYRNVF KDGGVAPIQK DKDYSFNLN 251 QLGYGDNNDV VELMRLYLTI HSDHEGGNVS AHTTHLVGSA LSSPMLSLAA 301 GLNGLAGPLH GLANQEVNLW LTKMKKSGN DLSDQAIKDY LWSTLNAGQV 351 VPGYGHAVLR KTDPRYVSQR EFALRKLPDD PMFKLVSVQVY KIAPGVLTEH 401 GKTKNPYPNV DAHSGVLLQY YGLTEANYYT VLFQVSRALG VLPQLIIDRA 451 LGAPIERPKS FSTEAYAKLV GAKL 68 - 82 774.9149 1547.8152 1547.7944 0.0209 0 K.VIGEVTLAQYGGAR.G 104 - 112 548.2610 1094.5074 1094.5066 0.0008 0 R.GYTIPECQK.L Carbamidomethyl (C) 159 - 166 517.7797 1033.5448 1033.5444 0.0005 0 K.FIEELIDR.C 159 - 166 517.7823 1033.5500 1033.5444 0.0057 0 K.FIEELIDR.C 228 - 234 404.2158 806.4170 806.4286 - 0.0116 1 R.NVFKDGK.V 376 - 384 553.7829 1105.5512 1105.5478 0.0035 1 R.KLPDDPMFK.L Oxidation (M) 392 - 402 561.3177 1120.6208 1120.6241 - 0.0032 0 K.IAPGVLTEHGK.T 438 - 449 654.4129 1306.8112 1306.7973 0.0140 0 R.ALGVLPQLIIDR.A 450 - 459 526.3135 1050.6124 1050.6185 - 0.0061 0 R.ALGAPIERP.KS 460 - 468 502.2373 1002.4600 1002.4658 - 0.0058 0 K.SFSTEAYAK.L
66	EDP5020 2	36847	286	8	7.01	Zinc-containing alcohol dehydrogenase, putative Sequence Coverage: 20% 1 MKQWVVADKE NGFDSLNFKE GPVPCGENE VLVKLRAASL NYRDLIIPK 51 MYPPINFPV VPGSDGAGEV VGVGSKVTQF KKGDKVVTLF NQLHQYGPVD 101 TRSTNSGLGG VLDGTLRQYG VFNENGLVRA PRNLNFLESS TLTCALTSW 151 NALYGMNALK PGEIVLVQGT GGVSMFALQF AKAAGATVIA TTSSDTKAKK 201 LKELGADHVI NYKTNPNWGE IARSLTPDNV GVDHIEVGG AGTLSQSLKC 251 IKFEGTISII GFLGGADPKG QPGMLEALNH ICTIRGVYVG SKALMNDMIR 301 AIEVNDIHPV VDEKVFRLDQ

							AKEAYEYMWA QKHLGKLAIE IE 50 - 76 898.4539 2692.3399 2692.3207 0.0191 0 K.GMYPPINFPVVPVPGSDGAGEVVGVGSK.V Oxidation (M) 103 - 117 723.8821 1445.7496 1445.7474 0.0022 0 R.STNSGLGGVLDGTLR.Q 103 - 117 723.8857 1445.7568 1445.7474 0.0094 0 R.STNSGLGGVLDGTLR.Q 103 - 117 723.8862 1445.7578 1445.7474 0.0104 0 R.STNSGLGGVLDGTLR.Q 103 - 117 723.8864 1445.7582 1445.7474 0.0108 0 R.STNSGLGGVLDGTLR.Q 118 - 129 698.3651 1394.7156 1394.6943 0.0214 0 R.QYGVFNENGLVR.A 253 - 269 861.4684 1720.9222 1720.9036 0.0187 0 K.FEGTISIIGFLGGADPK.G 293 - 300 498.2244 994.4342 994.4576 - 0.0233 0 K.ALMNDMIR.A 2 Oxidation (M)
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SUPPLEMENTARY INFORMATION AVAILABLE:

Supplementary Figure Captions:

Supplementary Figure 1.

Control IgE immuno-blots of GC proteome of *A. fumigatus* strains 190/96 (A and B) and DAYA (C and D), in pH ranges 3-10 (A and C) and pH 4-7 (B and D) probed with anti-human IgE conjugated with HRP showing no reactivity with sera of apparently healthy controls individuals.

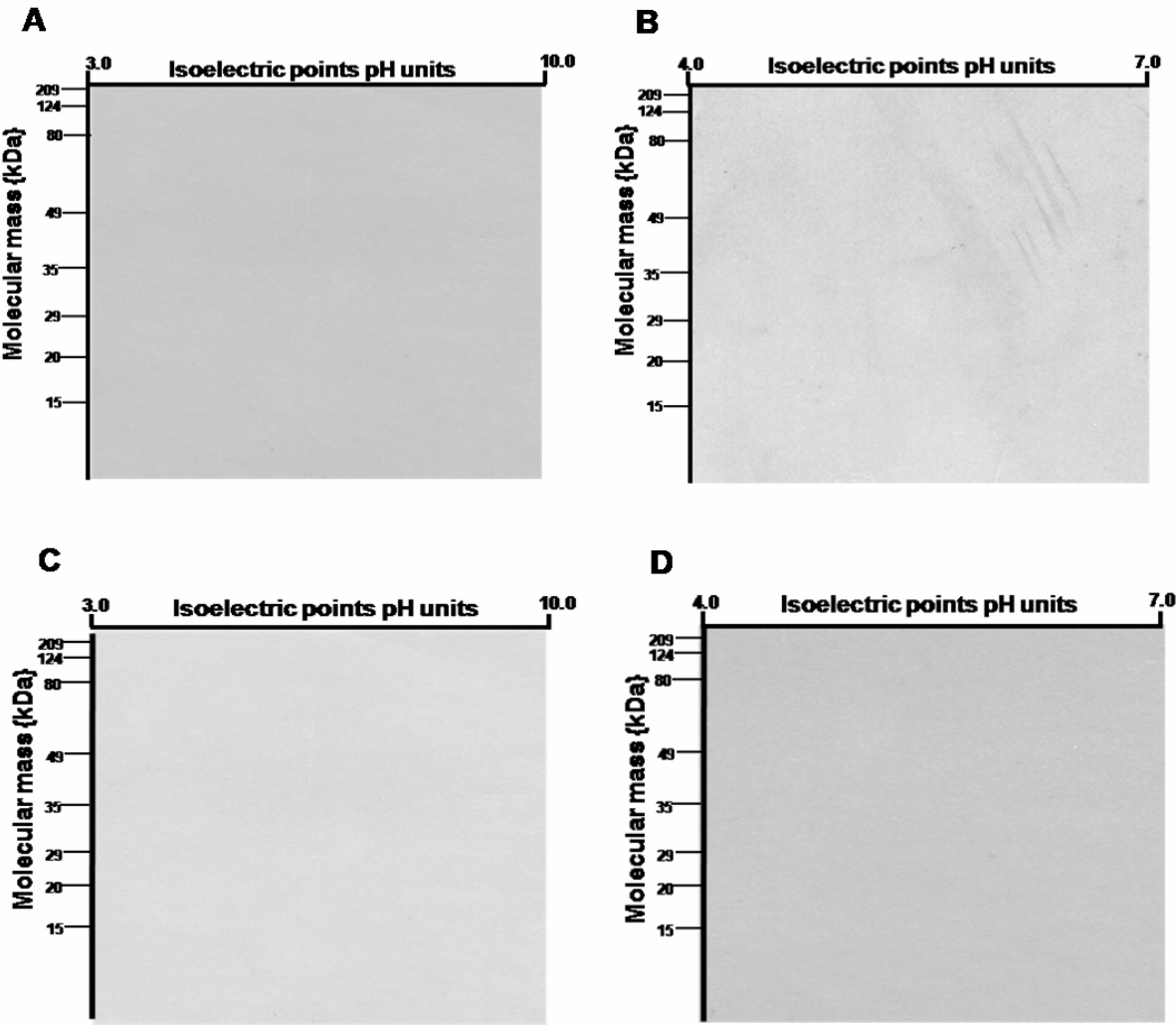
Supplementary Figure 2.

Control IgG immuno-blots of GC proteome of *A. fumigatus* strains 190/96 (A and B) and DAYA (C and D), in pH ranges 3-10 (A and C) and pH 4-7 (B and D) probed with anti-human IgE conjugated with HRP showing no reactivity with sera of apparently healthy controls individuals.

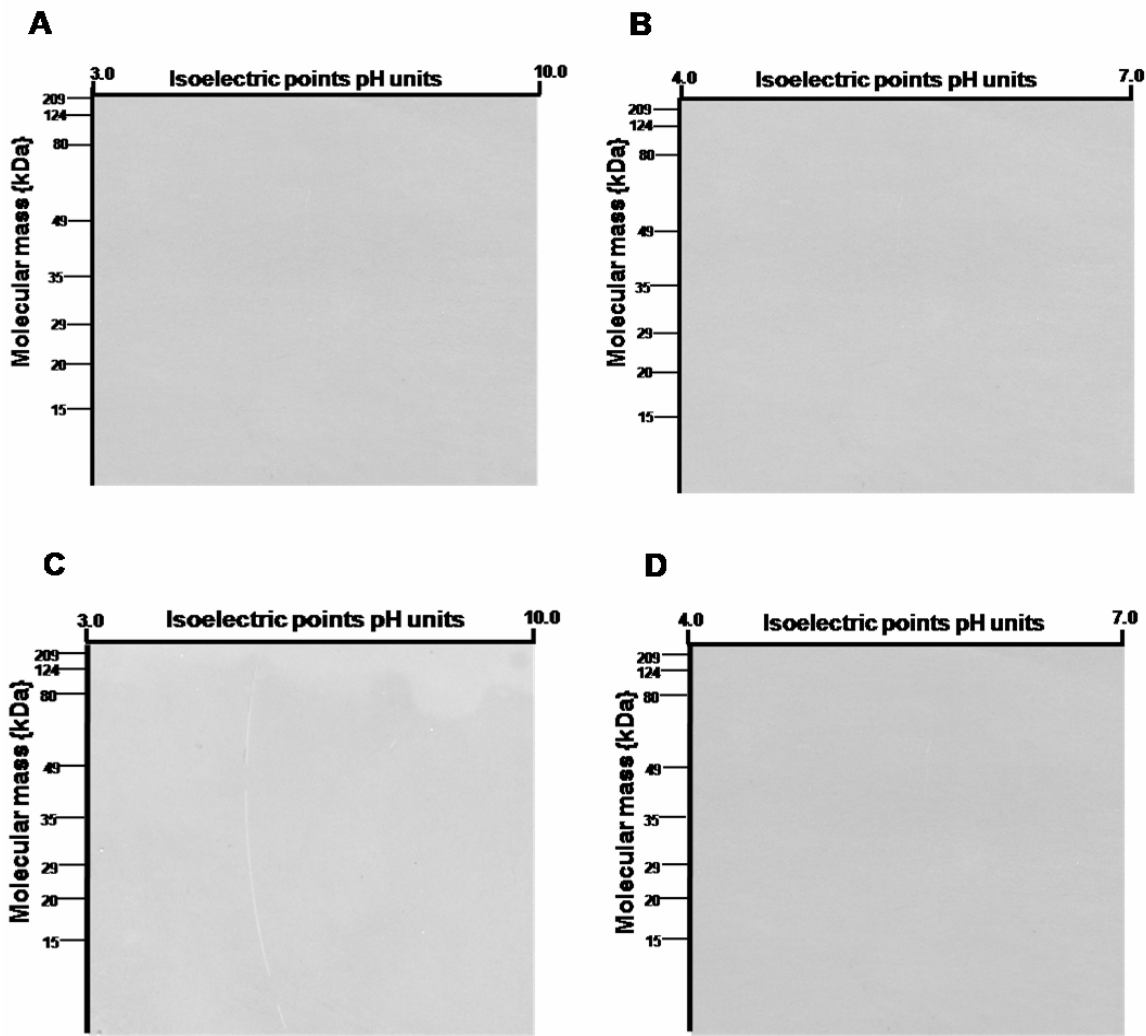
Supplementary Figure 3.

Pie chart showing functional categorization of 66 identified *A. fumigatus* cytosolic proteins with in Kognitor; a function annotation tool of NCBI database; (www.ncbi.nlm.nih.gov/COG/grace/kognitor).

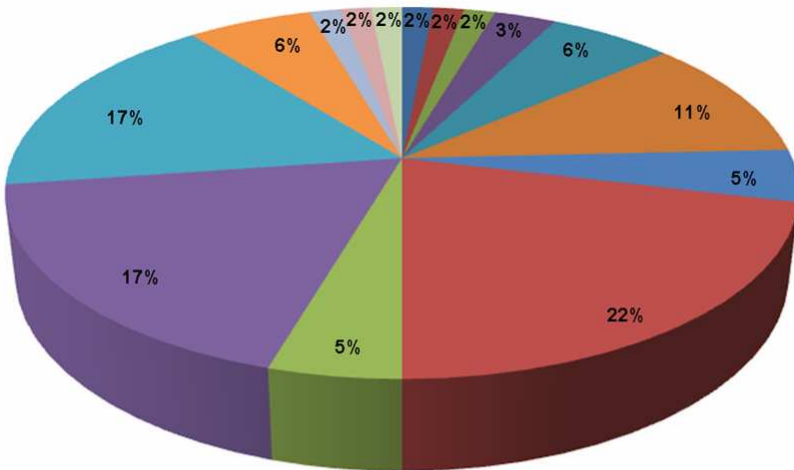
Supplementary Figure 1.



Supplementary Figure 2.



Supplementary Figure 3.



- Q (Secondary metabolites biosynthesis, transport and catabolism) 1
- I (Lipid transport and metabolism) 1
- Z (Cytoskeleton) 1
- S (Function unknown) 2
- J (Translation, ribosomal structure and biogenesis) 4
- C (Energy production and conversion) 7
- F (Nucleotide transport and metabolism) 3
- E (Amino acid transport and metabolism) 14
- H (Coenzyme transport and metabolism) 3
- G (Carbohydrate transport and metabolism) 12
- O (Posttranslational modification, protein turnover, chaperones) 11
- R (General function prediction only) 4
- CR (Energy production and conversion + General function prediction only) 1
- BD (Chromatin structure and dynamics + Cell cycle control, cell division, chromosome partitioning) 1
- AYT (RNA processing and modification + Nuclear structure + Signal transduction mechanisms) 1

Supplementary Table:

Table 1. MS/MS analysis table for reported proteins

Footnotes: ¹Mass 1 = Molecular mass of the protein observed in MASCOT search. ²MASCOT score 2 = >40 indicate identification or extensive homology (p<0.05). ³Peptide matched 3 = Number of peptides matched with protein in MS/MS query. ⁴pI 4 = Isoelectric point of the protein observed in MASCOT search.

Spot No.	Accession no.	Mass ¹ (kDa)	MASCOT Score ²	Peptide matched ³	pI ⁴	Protein name	MS/MS Analysis
1	XP_755878	28202	278	10	5.96	Sorbitol/xylulose reductase Sou1-like	Sequence Coverage: 33% 1 MPIPVPAAASS LLDLLSLKGK TVVVTGASGP RGMGIEAARG CAEMGANIAL 51 TYASRPEGGE KNAAEIAKTY GVKAKAYKCN VGDWESVQKL VADVIAEFGQ 101 IDAFIANAGR TASAGILDGS VNDWAEVIQT DLTGTFYCAK AVGPHFKERG 151 KGSFVITSSM SGHIANYPQE QTSYNVAKAG CIHFAKSLAN EWRDFARVNS 201 ISPGYIDTGL SDFVDKKTQD LWLSMIPMGR NGDAKELKGA YVYLCS DASS 251 YMTGTDLLID GGYCIR 2 - 18 867.5678 1733.1210 1733.0338 0.0872 0 M.PIPVPAAASSLLDLSLK.G 21 - 31 522.3088 1042.6030 1042.5771 0.0259 0 K.TVVVTGASGPR.G 21 - 31 522.3173 1042.6200 1042.5771 0.0429 0 K.TVVVTGASGPR. 32 - 39 410.7115 819.4084 819.3909 0.0176 0 R.GMGIEAAR.G Oxidation (M) 90 - 110 730.7527 2189.2363 2189.1481 0.0882 0 K.LVADVIAEFGQIDAFIANAGR.T 198 - 216 1014.0510 2026.0874 2025.9895 0.0979 0 R.VNSISPGYIDTGLSDFVDK.K 198 - 216 1014.0542 2026.0938 2025.9895 0.1043 0 R.VNSISPGYIDTGLSDFVDK.K 198 - 217 719.0652 2154.1738 2154.0845 0.0893 1 R.VNSISPGYIDTGLSDFVDKK.T 198 - 217 719.0670 2154.1792 2154.0845 0.0947 1 R.VNSISPGYIDTGLSDFVDKK.T 218 - 230 790.4222 1578.8298 1578.7534 0.0764 0 K.TQDLWLSMIPMGR.N 2 Oxidation

							(M)
2	XP_754489	28202	207	4	6.84	Proteasome component Prs2	Sequence Coverage: 17% 1 MTDTLPSFQT RVACTKSFSS ICGLGPHQYA FKAITAANIT SIGVRGKNCA 51 VVLSQKKVAD KLIDPSSVSH IFRLSPSVGC VMTGSIADAR ASVDRARGEA 101 AEFYKYGYE MPCDVLAKRL ANINQVYTQR AYMRPLGVAM TLISVDDEKG 151 PQLYKCDPAG YYVGKATAS GPKQQEALNY LEKKLKNKDY AEGSWEEVVE 201 LGITALSNVL SVDFKKHELE IGIVGGPRAD GREGTDPFR ALTEDEIDER 251 LQAISEKD 33 - 45 643.9045 1285.7944 1285.7354 0.0591 0 K.AITAANITSIGVR. 120 - 130 660.3871 1318.7596 1318.6993 0.0603 0 R.LANINQVYTQR.A 174 - 183 618.3470 1234.6794 1234.6193 0.0601 0 K.QQEALNYLEK. 241 - 250 595.8098 1189.6050 1189.5462 0.0588 0 R.ALTEDEIDER.L
3	XP_750785	28188	171	5	5.80	Proteasome component Pre9	Sequence Coverage: 16% 1 MSRRYDSRTT IFSPEGRLYQ VEYALEAISH AGTALGILAK DGIVLAAEKK 51 VTSKLLEQDT SAEKLYTLND NMICAVAGMT ADANILINYA RQAAQRYLLT 101 YGEEIPCEQL VRRLCDLKQG YTQHGGLRPF GVSFIYAGYD PLREFQLYQS 151 NPSGNYGGWK ATSVGANNAS AQSLKQDYK EDCDLKEACA MAVKVLSKTM 201 DSTKLSSEKI EFATVGKTKE GKIYHHLWNA DEINALLKEH GLAKVDDEPE 251 AGDIK 9 - 17 504.2820 1006.5494 1006.5084 0.0411 0 R.TTIFSPEGR.L 9 - 17 504.2970 1006.5794 1006.5084 0.0711 0 R.TTIFSPEGR.L 55 - 64 567.3104 1132.6062 1132.5612 0.0451 0 K.LLEQDTSAEK.L 205 - 217 470.2768 1407.8086 1407.7609 0.0476 1 K.LSSEKIEFATVGK.T 245 - 255 594.2983 1186.5820 1186.5354 0.0467 0 K.VDDEPEAGDIK.-
4	XP_001481696	28820	309	8	5.84	6-phosphogluconolactonase	Sequence Coverage: 34% 1 MTGTSPNLYS LPNTDALAPH LRAYVLRCQN SAINRHNTFR VAVSGGSLPA 51 VLAKALLAPS NGSPEDTVRF

						DKWDVFFADE RAVPLDHPDS NYRLLKDELL 101 SKIPAEMGTP KVHPIDADHV NDDTQELADL YQEELMRSFA AKDSVKLPVF 151 DLILLGCGPD GHTCSLFPGH KLLREKDAWV AAETNSPKPP PKRITLTLPV 201 VTHAVSIAFV ATGAGKKEIL KQIFDAEEGR ELPSALVNQG AGEKVSFWD 251 HAAVDGVSFP RRGSL 2 - 22 746.7134 2237.1184 2237.1440 - 0.0257 0 M.TGTSPNLYSLPNTDALAPHLR.A 41 - 54 634.8778 1267.7410 1267.7500 - 0.0089 0 R.VAVSGGSLPAVLAK.A 55 - 69 763.8879 1525.7612 1525.7736 - 0.0124 0 K.ALLAPSNGSPEDTVR.F 55 - 69 763.8915 1525.7684 1525.7736 - 0.0052 0 K.ALLAPSNGSPEDTVR.F 94 - 102 529.8221 1057.6296 1057.6383 - 0.0086 1 R.LLKDELLSK.I 103 - 111 480.2419 958.4692 958.4794 - 0.0101 0 K.IPAEMGTPK.V Oxidation (M) 222 - 230 532.7511 1063.4876 1063.4934 - 0.0058 0 K.QIFDAEEGR.E 231 - 244 706.8649 1411.7152 1411.7307 - 0.0154 0 R.ELPSALVNQGAGEK.V
5	XP_7538 27	32716	171	3	6.04	Pyridoxine biosynthesis protein Sequence Coverage: 15% 1 MASNGTNGAS ASNSFTVKAG LAQMLKGGVI MDVVNAEQAR IAEEAGAAAV 51 MALERVPADI RAQGGVARMS DPSMIKEIMA AVTIPVMAKA RIGHFVECQI 101 LEAIGVDYID ESEVLTPADD VYHVKKHDYK VPFVCGCRNL GEALRRIAEG 151 AAMIRTKGEA GTGDVVEAVK HMRTVNSQIA RARSILQNST DPEIELRAYA 201 RELEVPEYELL RETAEKGRLP VVNFAAGGVA TPADAALMMQ LGCDGVFVGS 251 GIFKSGDAKK RAKAIVQAVT HYKDPKVLAE VSEGLGEAMV GINVSQMPEA 301 DRLAKRGW 156 - 170 487.6082 1459.8028 1459.7518 0.0509 1 R.TKGEAGTGDVVEAVK.H 174 - 181 444.7613 887.5080 887.4825 0.0256 0 R.TVNSQIAR.A) 184 - 197 807.9560 1613.8974 1613.8260 0.0714 0 R.SILQNSTDPEIELR.A
6	XP_7527 19	33424	238	8	5.33	Spermidine synthase Sequence Coverage: 17% 1 MSEITHPTIK DGWFSEQSDM WPGQAMNLKV NQILHHEKSK YQDVLVFEST

						51 DYGTVLVLDN VIQCTERDEF SYQEMITHLA MNSHPNPKV LVIGGGDGGV 101 LREVVKHESV EEAILCDIDE AVIRVSKKYL PGMSIGFQHP NVKVHIGDGF 151 QFLKERKNEF DVIITDSSDP EGPAESLFQK PYFELLRDAL RDGGVITTQG 201 SENQWLHLSL ITDLKKACKE VFPVAEYAYT TIPTYPSGQI GFMVCKDAT 251 RNVREPVRTW SREEEERLCR YYNQDIHRAS FVLPNFARKA LDV 89 - 102 447.2879 1338.8419 1338.7984 0.0435 1 K.KVLVIGGGDGGVLR.E 90 - 102 606.3743 1210.7340 1210.7034 0.0306 0 K.VLVIGGGDGGVLR.E 90 - 102 606.3878 1210.7610 1210.7034 0.0576 0 K.VLVIGGGDGGVLR.E 144 - 154 420.9104 1259.7094 1259.6663 0.0431 0 K.VHIGDGFQFLK.E 144 - 154 630.8677 1259.7208 1259.6663 0.0546 0 K.VHIGDGFQFLK.E 252 - 258 435.2691 868.5236 868.4879 0.0358 1 R.NVREPVR.T 271 - 278 554.7820 1107.5494 1107.5097 0.0397 0 R.YYNQDIHR.A 279 - 288 561.3307 1120.6468 1120.6029 0.0439 0 R.ASFVLPNFAR.K
7	XP_754985	33240	131	6	5.51	Phosphoribosyl- aminoimidazole- succinocarboxami de synthase Sequence Coverage: 17% 1 MAEALTNTDL QGALPLIARG KVRDLYEVDD KTLLFIATDR ISAYDVIMEN 51 GIPNKGVLTT LCTKAWFKIL TDAIPSLRTH FITLDLPPQI PPSLRPALQN 101 RSMQVRKLKI LPIEAIVRGY ITGSAWNEYK KSGTVHGIKV APGLRESEAF 151 PDGPITYPST KAEQGEHDEN IHPDQAAAIL GEHASTVASL AVQLYKVAHA 201 YALSRGVIIA DTKFEFGVDE ETNEVVLADE VLTPDSSRFW PKDDYEVGRG 251 QQSFDKQFLR DWLVKEGLKG KEGVRMTEEV VQKTAEKYKE AWERITGGN 24 - 31 498.7505 995.4864 995.4447 0.0417 0 R.DLYEVDDK.T 32 - 40 525.3250 1048.6354 1048.5917 0.0438 0 K.TLLFIATDR.I 69 - 78 549.8499 1097.6852 1097.6444 0.0408 0 K.ILTDAIPSLR.T 110 - 118 512.3498 1022.6850 1022.6488 0.0363 0 K.ILPIEAIVR.G 110 - 118 512.3550 1022.6954 1022.6488 0.0467 0 K.ILPIEAIVR.G

							146 - 161 869.9517 1737.8888 1737.8097 0.0791 0 R.ESEAFDPGPIYTPSTK.A
8	XP_754776	43596	217	6	7.63	Inorganic diphosphatase	Sequence Coverage: 14% 1 MSPVALRMSS KALLPLSPLL RLSTASPALA RPCSPSPRTS ATLAPPTRQA 51 PPPSSLSSSS FSPSFSPQQA NLSSPSSSRV RSSVSSASTR AALLSRHFSS 101 YTPPQSPNMS YTVRKIGQAN TLEHRVYIEK DGVPISPFHD IPLYANPEQT 151 ILNMVVEIPR WTNAKQEISK EEFLNPIKQD VKKGKLRFRV NCFPHKGYLW 201 NYGAFFQTWE DPNVVHPETK AKGDNDPLDV CEIGELVGYP GQVKQVKVLG 251 VMALLDEEET DWKVIVIDIN DPLAPKLNDI EDVERHPLGL LRATNEWFRI 301 YKIPDGKPEN QFAFSGECKN KKYALDVIRE CADAWEKLIT GKSPRGDISL 351 ANTSVENSSD RADPAQLASI PKGENLPPAP IDGSIDKWFF ISGAAV 115 - 125 422.9172 1265.7298 1265.6840 0.0458 1 R.KIGQANTLEHR.V 264 - 276 703.9444 1405.8742 1405.8181 0.0562 0 K.VIVIDINDPLAPK.L 277 - 285 551.7962 1101.5778 1101.5302 0.0477 0 K.LNDIEDVER.H 286 - 292 403.2687 804.5228 804.4970 0.0259 0 R.HLPGLLR.A 323 - 329 425.2589 848.5032 848.4756 0.0277 0 K.YALDVIR.E 362 - 372 555.8337 1109.6528 1109.6080 0.0448 0 R.ADPAQLASIPK.G
9	XP_750257	33474	299	10	5.11	60S ribosomal protein P0	Sequence Coverage: 24% 1 MGGKSATKAA YFDKLKSLLD EYKTVFIVGV DNVSSQQMHE IRLALRGQAV 51 VLMGKNTMVR RAIKGFVADN PEYERLLPHV KGNVGFIFTN GDLKDVTKI 101 LANRVAAPAR AGAIAPADVW VPAGNTGMEP GKTSFFQALG VPTKIARGTI 151 EITTDLKLVE AGAKVGPSEA TLLNMLNISP FTYGMTITQV YDNGQCFPAH 201 VLDIEESQLL DAFSSAIKTI TTVSLALNYP TLPVMHSLI NGYKKVLAVA 251 IETDYSWPEI EELKDRIANP DAYAAAAPVA AAPAAGGAAP AAEEKKEEEA 301 EESDEDMGFG LFD 65 - 75 648.8174 1295.6202 1295.5782 0.0420 0 K.GFVADNPEYER.L 65 - 75 648.8209 1295.6272 1295.5782

							0.0490 0 K.GFVADNPEYER.L 82 - 94 691.3812 1380.7478 1380.7038 0.0441 0 K.GNVGFIFTNGDLK.D 82 - 97 575.3206 1722.9400 1722.8941 0.0459 1 K.GNVGFIFTNGDLKDV.K.T 82 - 97 862.4805 1722.9464 1722.8941 0.0523 1 K.GNVGFIFTNGDLKDV.K.T 82 - 97 575.3236 1722.9490 1722.8941 0.0549 1 K.GNVGFIFTNGDLKDV.K.T 133 - 144 648.3787 1294.7428 1294.6922 0.0507 0 K.TSFFQALGVPTK.I 148 - 157 545.8188 1089.6230 1089.5918 0.0313 0 R.GTIEITDLK.L 267 - 295 859.8014 2576.3824 2576.2870 0.0954 0 R.IANPDYAAAAPVAAAPAAGGAAPAAEEK. K 267 - 295 859.8047 2576.3923 2576.2870 0.1053 0 R.IANPDYAAAAPVAAAPAAGGAAPAAEEK. K
10	XP_7539 94	36835	82	2	5.02	Adenosine kinase	Sequence Coverage: 6% 1 MAATQGY PFL CLENPLLDIQ AVGDAALLEK YGLKDNDAIL AEEKHMG LYD 51 ELLSRDAKLI AGGAAQNTAR GAQYMLPDNS VMYIGCVGKD KYADILKEAC 101 NQAGVHTEYR VDDVQPTGKC GVIITGHNRS MCTHLAAANE YKIDHLKQPH 151 VWSLVEKAQY YYVGGYHLTV CVPAILALAE EAAAKNKVFM LSLSAPFIPQ 201 FFKDQLDSVL PYTDYTFCNE TEARAYAESH EWNTDDVVEI AKKLAQLPKK 251 NSSRPRVAIV TQGTLPITTA TVKPDGEVEV KEFPVHEISK SSINDTNGAG 301 DAFAGGFCAG VVQNKSL EES MDMGQWLASL SIQELGPS 59 - 70 571.8359 1141.6572 1141.6203 0.0369 0 K.LIAGGAAQNTAR.G 111 - 119 479.7577 957.5008 957.4767 0.0241 0 R.VDDVQPTGK.C
11a	XP_7480 95	38298	295	8	6.04	Thiamine biosynthesis protein (Nmt1)	Sequence Coverage: 26% 1 MSTDKITFLT NWHATPYHAP LYLAHSGKFF KEEGLK VAIL EPNDPSDVTE 51 IIGSGK VDMG FKAMIHTLAA KARNFPVTSI GSLLDEPFTG VVYLKDSGIT 101 EDFRSLKGKR IGYVGEFGKI QIDELTKYYG MTADDYTAVR CGMNVTKAII 151 RGDIDAGIGL ENVQMVELAE WLASQNRPRD DVQMLRIDQL AELGCCCFCS 201 ILYIANDAFL AANPDKVOKI

						MRAVKRATDY VLAEPAKAYE EYIDVKPIMG 251 TPVNRKIFER SFAYFSRDLK NVQRDWAKVT NYGKRLLGILD ANFEPNYTNK 301 YLSWDLADS TDPLGDQKRM AELQKQVAE GGFKRLHVSA SA 37 - 56 1027.5695 2053.1244 2053.0579 0.0665 0 K.VAILEPNDPSPDVTEIIGSGK.V 96 - 104 520.2540 1038.4934 1038.4618 0.0316 0 K.DSGITEDFR.S 111 - 119 485.2659 968.5172 968.4967 0.0205 0 R.IGYVGEFGK.I 120 - 127 480.2874 958.5602 958.5335 0.0268 0 K.IQIDELTK.Y 128 - 140 763.3618 1524.7090 1524.6555 0.0536 0 K.YYGMTADDYTAVR.C 227 - 237 589.3241 1176.6336 1176.6026 0.0310 0 R.ATDYVLAEPK.A 261 - 267 439.2237 876.4328 876.4130 0.0199 0 R.SFAYFSR.D 286 - 300 854.9590 1707.9034 1707.8468 0.0567 0 R.LGILDANFEPNYTNK.Y
11b	XP_7480 95	38298	235	8	6.04	Thiamine biosynthesis protein (Nmt1) Sequence Coverage: 25% 1 MSTDKITFLT NWHATPYHAP LYLAHSGGFF KEEGLKVAIL EPNDPSDVTE 51 IIGSGKVDMG FKAMIHTLAA KARNFPVTSI GSLLDEPFTG VVYLKDSGIT 101 EDFRSLKGKR IGYVGEFGKI QIDELTKYYG MTADDYTAVR CGMNVTKAII 151 RGDIDAGIGL ENVQMVELAE WLASQNRPRD DVQMLRIDQL AELGCCCCFS 201 ILYIANDAFL AANPDKVQKF MRAVKRATDY VLAEPAKAYE EYIDVKPIMG 251 TPVNRKIFER SFAYFSRDLK NVQRDWAKVT NYGKRLLGILD ANFEPNYTNK 301 YLSWDLADS TDPLGDQKRM AELQKQVAE GGFKRLHVSA SA 28 - 36 527.7964 1053.5782 1053.5495 0.0288 1 K.GFFKEEGLK.V 37 - 56 1027.5746 2053.1346 2053.0579 0.0767 0 K.VAILEPNDPSPDVTEIIGSGK.V 96 - 104 520.2506 1038.4866 1038.4618 0.0248 0 K.DSGITEDFR.S 111 - 119 485.2672 968.5198 968.4967 0.0231 0 R.IGYVGEFGK.I 120 - 127 480.2850 958.5554 958.5335 0.0220 0 K.IQIDELTK.Y 227 - 237 589.3234 1176.6322 1176.6026 0.0296 0 R.ATDYVLAEPK.A 261 - 267 439.2215 876.4284 876.4130

							0.0155 0 R.SFAYFSR.D 286 - 300 854.9556 1707.8966 1707.8468 0.0499 0 R.LGILDANFEPNYTNK.Y
11c	XP_748095	38298	462	14	6.04	Thiamine biosynthesis protein (Nmt1)]	Sequence Coverage: 26% 1 MSTDKITFLT NWHATPYHAP LYLAHSK GFF KEEGLKVAIL EPNDPSD TE 51 IIGSGK VDMG FKAMIHTLAA KARNFPVTSI GSLLDEPFTG VVYLK DSGIT 101 EDFR SLKGKR IGYVGEFGKI QIDELTK YYG MTADDYTAVR CGMNVTKAII 151 RGDIDAGIGL ENVQMVELAE WLASQNRPRD DVQMLRIDQL AELGCCCFC 201 ILYIANDAFL AANPDKVQKF MRAVK RATDY VLAEP AKAYE EYIDVKPIMG 251 TPVNRKIFER SFAYFSR DLK NVQRDWAKVT NYGKRL LGILD ANFEPNYTNK 301 YLSWDLADS TDPLGDQKRM AELQKQVAEE GGFKRLHVS SA 28 - 36 527.7914 1053.5682 1053.5495 0.0188 1 K.GFFKEEGLK.V 37 - 56 685.3743 2053.1011 2053.0579 0.0432 0 K.VAILEPNDPSDVTEIIGSGK.V 37 - 56 1027.5579 2053.1012 2053.0579 0.0433 0 K.VAILEPNDPSDVTEIIGSGK.V 37 - 56 1027.5620 2053.1094 2053.0579 0.0515 0 K.VAILEPNDPSDVTEIIGSGK.V 96 - 104 520.2471 1038.4796 1038.4618 0.0178 0 K.DSGITEDFR.S 96 - 104 520.2502 1038.4858 1038.4618 0.0240 0 K.DSGITEDFR.S 111 - 119 485.2477 968.4808 968.4967 - 0.0159 0 R.IGYVGEFGK.I 120 - 127 480.2622 958.5098 958.5335 - 0.0236 0 K.IQIDELTK.Y 226 - 237 445.2539 1332.7399 1332.7037 0.0361 1 K.RATDYVLAEPK.A 227 - 237 589.3192 1176.6238 1176.6026 0.0212 0 R.ATDYVLAEPK.A 227 - 237 589.3210 1176.6274 1176.6026 0.0248 0 R.ATDYVLAEPK.A 261 - 267 439.2151 876.4156 876.4130 0.0027 0 R.SFAYFSR.D 286 - 300 854.9557 1707.8968 1707.8468 0.0501 0 R.LGILDANFEPNYTNK.Y 286 - 300 854.9564 1707.8982 1707.8468 0.0515 0 R.LGILDANFEPNYTNK.Y
12a	XP_7544	39766	220	9	5.55	Fructose-bisphosphate	Sequence Coverage: 16%

	52					aldolase, class II	1 MGILDKLSRK SGVIVGDDVL RLFHEYAQEKN FAIPAVNVTS SSTVVACLEA 51 ARDQNCPIIL QVSQGGAAAYF AGKGVSN DGQ KASIAGSIAA AHYIRSIAPS 101 YGIPVVLHTD HCAKKLLPWL DGMLDEDERY FKQHGEPLFS SHMIDLSEEP 151 VDYNIE TTAK YLKRAAPMKQ WLEMEIGITG GEEDGVNNED VDNNSLYTQP 201 EDILAIYNAL APISPYFSIA AGFGNVHGVY KPGNVRLHPE LLSKHQAYVK 251 EKIGSNKDKP VYFVFHGGSG STKEEYKQAI SYGVVKVNLD TDMQYAYMSG 301 VRDYILNKKD YLMSAVGNPD GEDKPNKKYF DPRVWVREGE KTMSKR VQVA 351 LEDFNTAGQL 10 - 21 419.9170 1256.7292 1256.7089 0.0203 1 R.KSGVIVGDDVLR.L 11 - 21 565.3218 1128.6290 1128.6139 0.0151 0 K.SGVIVGDDVLR.L 22 - 29 514.2676 1026.5206 1026.5022 0.0185 0 R.LFEY AQEKN 82 - 95 467.6007 1399.7803 1399.7572 0.0231 0 K.ASIAGSIAAAHYIR.S 82 - 95 700.9099 1399.8052 1399.7572 0.0481 0 K.ASIAGSIAAAHYIR.S 278 - 286 482.7859 963.5572 963.5389 0.0183 0 K.QAISYGVVK.V 346 - 360 830.9594 1659.9042 1659.8580 0.0462 1 K.RVQVALEDFNTAGQL.- 346 - 360 830.9673 1659.9200 1659.8580 0.0620 1 K.RVQVALEDFNTAGQL.- 347 - 360 752.9063 1503.7980 1503.7569 0.0411 0 R.VQVALEDFNTAGQL.-
12b	XP_7544 52	39766	438	13	5.55	Fructose- biphosphate aldolase, class II	Sequence Coverage: 22% 1 MGILDKLSRK SGVIVGDDVL RLFHEYAQEKN FAIPAVNVTS SSTVVACLEA 51 ARDQNCPIIL QVSQGGAAAYF AGKGVSN DGQ KASIAGSIAA AHYIRSIAPS 101 YGIPVVLHTD HCAKKLLPWL DGMLDEDERY FKQHGEPLFS SHMIDLSEEP 151 VDYNIE TTAK YLKRAAPMKQ WLEMEIGITG GEEDGVNNED VDNNSLYTQP 201 EDILAIYNAL APISPYFSIA AGFGNVHGVY KPGNVRLHPE LLSKHQAYVK 251 EKIGSNKDKP VYFVFHGGSG STKEEYKQAI SYGVVKVNLD TDMQYAYMSG 301 VRDYILNKKD YLMSAVGNPD GEDKPNKKYF DPRVWVREGE

							KTMSKRVQVA 351 LEDFNTAGQL 10 - 21 419.9154 1256.7244 1256.7089 0.0155 1 R.KSGVIVGDDVLR.L 10 - 21 629.3725 1256.7304 1256.7089 0.0216 1 R.KSGVIVGDDVLR.L 11 - 21 565.3157 1128.6168 1128.6139 0.0029 0 K.SGVIVGDDVLR.L 22 - 29 514.2490 1026.4834 1026.5022 - 0.0187 0 R.LFEYAQEK.N 82 - 95 467.5998 1399.7776 1399.7572 0.0204 0 K.ASIAGSIAAAHYIR.S 82 - 95 700.9088 1399.8030 1399.7572 0.0459 0 K.ASIAGSIAAAHYIR.S 258 - 273 575.9697 1724.8873 1724.8522 0.0350 0 K.DKPVYFVFHGGSGSTK.E 278 - 286 482.7821 963.5496 963.5389 0.0107 0 K.QAISYGVVK.V 303 - 309 447.2638 892.5130 892.5018 0.0113 1 R.DYILNKK.D 303 - 309 447.2638 892.5130 892.5018 0.0113 1 R.DYILNKK.D 346 - 360 830.9579 1659.9012 1659.8580 0.0432 1 K.RVQVALEDFNTAGQL.- 346 - 360 830.9579 1659.9012 1659.8580 0.0432 1 K.RVQVALEDFNTAGQL.- 347 - 360 752.9050 1503.7954 1503.7569 0.0385 0 R.VQVALEDFNTAGQL.-
13	XP_7537 16	35426	419	17	6.04	Transaldolase	Sequence Coverage: 38% 1 MSSALEQLKA TGTVVVCD SG DFATIGKYKP QDATTNPSLI LAASKKPEYA 51 SLIDAAVQKG KKEGKTLDEQ VDATLDNLLV EFGKKILEII PGKVSTEVDA 101 RFSFDTQASV DKALHIVKLY EQQGISKDRI LIKIASTWEG IKAAHILQSQ 151 HGINCNLTLM FSLVQAIAAA EAGAFLISPF VGRILDWYKA AHKRDFSPEE 201 DPGVKSVQSI FNYYKKHGYK TIVMGASFRN TGEITELAGC DYLTISPNLL 251 EELYNSTASV PKKLDAASAA SLDIPKRSYI NDEAAFRFDF NEEAMAVEKL 301 REGISKFAAD AVTLKELLKQ KIQA 28 - 45 640.0280 1917.0622 1917.0207 0.0415 0 K.YKPQDATTNPSLILAASK.K 28 - 45 959.5454 1917.0762 1917.0207 0.0555 0 K.YKPQDATTNPSLILAASK.K 46 - 59 511.6237 1531.8493 1531.8246 0.0247 0 K.KPEYASLIDAAVQK.G

						86 - 101 580.6792 1739.0158 1738.9829 0.0329 1 K.ILEIIPGKVSTEVDAR.F 94 - 101 438.7287 875.4428 875.4349 0.0080 0 K.VSTEVDAR.F 102 - 112 622.8083 1243.6020 1243.5721 0.0300 0 R.FSFDTQASVDK.A 119 - 127 533.2903 1064.5660 1064.5502 0.0158 0 K.LYEQQGISK.D 119 - 129 446.2392 1335.6958 1335.6783 0.0175 1 K.LYEQQGISKDR.I 134 - 142 502.7865 1003.5584 1003.5338 0.0246 0 K.IASTWEGIK.A 195 - 205 610.2894 1218.5642 1218.5405 0.0238 0 R.DFSPEEDPGVK.S 206 - 215 624.8318 1247.6490 1247.6186 0.0304 0 K.SVQSIFNYYK.K 206 - 216 459.5841 1375.7305 1375.7136 0.0169 1 K.SVQSIFNYYKK.H 206 - 216 688.8820 1375.7494 1375.7136 0.0359 1 K.SVQSIFNYYKK.H 278 - 287 593.2908 1184.5670 1184.5462 0.0209 0 R.SYNDEAAFR.F 307 - 315 468.2704 934.5262 934.5124 0.0139 0 K.FAADAUTLK.E 307 - 319 473.6196 1417.8370 1417.8180 0.0189 1 K.FAADAUTLKELLK.Q 307 - 319 709.9361 1417.8576 1417.8180 0.0396 1 K.FAADAUTLKELLK.Q
14a	XP_752429	42170	343	10	5.67	S-adenosylmethionine synthetase Sequence Coverage: 26% 1 MGSVAKSNTF LFTSESVGEG HPDKIADQVS DAVLDACLA E DPLSKVACET 51 ATKTGMIMVF GEITNAKLD YQKIIRGAIK DIGYDDSDKG FDYKTCNVLV 101 AIEQQSPDIA QGLHYDEALE KLGAGDQGIM FGATDETPE LLPLTLLSH 151 KLNSAMTQAR KDGSIPWLRP DTKTQVTVEY AHDGGAVKPL RVDTVVVSQAQ 201 HSDDVSTEEL RTVIKEKIIK KVIPAELLDD RTIYHIQPSG RFVIGGPQGD 251 AGLTGRKIIV DTYGGWGAHG GGAFGSKDYS KVDRSAAYVG RWIAKSLVHA 301 GLARRVLVQL SYAIGVAEPL SIFVETYGTS EKSSDELVEI IRKNFDLRPG 351 VIVKELDLAK PIYFQTAKNG HFTNQSFWE KPKTLKF 81 - 89 514.2290 1026.4434 1026.4142 0.0293 0 K.DIGYDDSDK.G 81 - 94 546.5837 1636.7293 1636.6893 0.0400 1 K.DIGYDDSDKGFDYK.T

						192 - 211 729.3761 2185.1065 2185.0499 0.0566 0 R.VDTVVVSAQHSDDVSTEELR.T 222 - 231 570.8273 1139.6400 1139.6186 0.0214 0 K.VIPAELLDDR.T 232 - 241 586.3302 1170.6458 1170.6145 0.0313 0 R.TIYHIQPSGR.F 242 - 256 722.8976 1443.7806 1443.7471 0.0336 0 R.FVIGGPQGDAGLTGR.K 296 - 304 462.2853 922.5560 922.5348 0.0212 0 K.SLVHAGLAR.R 333 - 342 580.8231 1159.6316 1159.6084 0.0232 0 K.SSDELVEIIR.K 333 - 343 430.2486 1287.7240 1287.7034 0.0206 1 K.SSDELVEIIRK.N 355 - 368 546.3146 1635.9220 1635.8872 0.0348 0 K.ELDLAKPIYFQTAK.N
14b	XP_7524 29	42170	151	4	5.67	S-adenosylmethionine synthetase Sequence Coverage: 9% 1 MGSVAKSNTF LFTSESVGEG HPDKIADQVS DAVLDACLA E DPLSKVACET 51 ATKTGMIMVF GEITNAKLD YQKIIRGAIK DIGYDDSDKG FDYKTCNVLV 101 AIEQQSPDIA QGLHYDEALE KLGAGDQGIM FGYATDETPE LLPLTLLSH 151 KLNSAMTQAR KDGSIPWLRP DTKTQVTVEY AHDGGAVKPL RVDTVVVSAQ 201 HSDDVSTEEL RTVIKEKIIK KVIPAELLDD RTIYHIQPSG RFVIGGPQGD 251 AGLTGRKIIV DTYGGWGAHG GGA FSGKDYS KVDRSAAYVG RWIAKSLVHA 301 GLARRVLVQL SYAIGVAEPL SIFVETYGTS EKSSDELVEIIRKNFDLRPG 351 VIVKELDLAK PIYFQTAKNG HFTNQSFWE KPKTLKF 222 - 231 570.8241 1139.6336 1139.6186 0.0150 0 K.VIPAELLDDR.T 242 - 256 722.8914 1443.7682 1443.7471 0.0212 0 R.FVIGGPQGDAGLTGR.K 333 - 342 580.8209 1159.6272 1159.6084 0.0188 0 K.SSDELVEIIR.K 333 - 343 644.8682 1287.7218 1287.7034 0.0184 1 K.SSDELVEIIRK.N
15	XP_7515 19	39874	113	4	5.48	Glutamine synthetase Sequence Coverage: 10% 1 MAETSTVVS N TENLMKYMSL DQRGHVQA EY VWIDAVGNCR CKTKTLSPV 51 KSVDELPEWN FDGSSTGQAP GDNSDVYLRP VAIFADPFRR GDNILVLCET 101 WSDSGTPNKF NFRHEANRLM EIHAKKEFWF GLEQEYTLTG TDGWPGWPK 151 GGFPGAQGPY YCGVGTGKVY

						CRDIVEAHYR ACLYAGIKIS GINAEVMPSQ 201 WEYQVGPCQG IEMGDQLWMS RFLLRHVAEE FGVKISFEPK PIKGDWNGAG 251 LHTNVSTAAT RAEGGLKVIE AYMQKLEARH NEHIAVYEGEG NEERLTGRHE 301 TGSIDKFSYG VADRGGGSIRI PRQVAKDGKG YFEDRRPASN ADPYQITGII 351 VETLCGGN 501.7632 1001.5118 1001.4930 0.0188 0 R.DIVEAHYR.A 227 - 234 439.7394 877.4642 877.4545 0.0097 0 R.VAEEFGVK.I 280 - 294 585.2807 1752.8203 1752.7815 0.0387 0 R.HNEHIAVYEGEGNEER.L 307 - 314 457.7331 913.4516 913.4294 0.0223 0 K.FSYGVADR.G
16	YP_0013 37378	43219	459	17	5.29	Elongation factor Tu [Klebsiella pneumoniae] Sequence Coverage: 32% 1 MSKEKFERTK PHVNVGTIGH VDHGKTTLTA AITTVLAKTY GGSARAFDQI 51 DNAPEEKARG ITINTSHVEY DTPTRHYAHV DCPGHADYVK NMITGAAQMD 101 GAILVVAATD GPMPQTREHI LLGRQVGVPI IIVFLNKCDM VDDEELLELV 151 EMEVRELLSQ YDFPGDDTPI VRGSALKALE GDAEWEAKII ELAGHLDTYI 201 PEPERAIDKP FLLPIEDVFS ISGRGT VVTG RVERGIKVG EEVEIVGIKE 251 TAKTTCTGVE MFRKLLDEGR AGENVGVLLR GIKREEIERG QVLAKPGTIN 301 PHTKFESEVY ILSKDEGGRH TPFFKGYRPQ FYFRTTDVTG TIELPEGVEM 351 VMPGDNIKMV VTLIHPIAMD DGLRFAIREG GRTVGAGVVA KVLG 26 - 38 652.4144 1302.8142 1302.7759 0.0384 0 K.TTLTAAITTVLAK.T 46 - 57 688.8384 1375.6622 1375.6255 0.0367 0 R.AFDQIDNAPEEK.A 118 - 124 419.2611 836.5076 836.4868 0.0208 0 R.EHILLGR.Q 125 - 137 745.4637 1488.9128 1488.8704 0.0424 0 R.QVGVPYIIVFLNK.C 156 - 172 983.0156 1964.0166 1963.9527 0.0639 0 R.ELLSQYDFPGDDTPIVR.G 156 - 172 983.0182 1964.0218 1963.9527 0.0691 0 R.ELLSQYDFPGDDTPIVR.G 189 - 205 656.0310 1965.0712 1965.0207 0.0505 0 K.IELAGHLDTYIPEPER.A 189 - 205 656.0335 1965.0787 1965.0207

						0.0580 0 K.IIELAGHLDTYIPEPER.A 239 - 249 586.3455 1170.6764 1170.6496 0.0269 0 K.VGEEVEIVGIK.E 239 - 249 586.3455 1170.6764 1170.6496 0.0269 0 K.VGEEVEIVGIK.E 239 - 253 534.3096 1599.9070 1599.8719 0.0350 1 K.VGEEVEIVGIKETAK.T 271 - 280 514.3099 1026.6052 1026.5822 0.0231 0 R.AGENVGVLRL.G 305 - 314 607.8337 1213.6528 1213.6230 0.0298 0 K.FESEVYILSK.D 305 - 319 576.9673 1727.8801 1727.8366 0.0435 1 K.FESEVYILSKDEGGR.H 326 - 334 411.8837 1232.6293 1232.6091 0.0202 0 K.GYRPQFYFR.T 326 - 334 617.3270 1232.6394 1232.6091 0.0304 0 K.GYRPQFYFR.T
17a	Q96X30	47276	806	20	5.39	Enolase/allergen Asp F 22 Sequence Coverage: 36% 1 MPISKIHARS VYDSRGNPTV EVDVVTETGL HRAIVPSGAS TGQHEAHEL 51 DGDKTQWGGK GVLKAVKNVN ETIGPALIKE NIDVKDQSKV DEFLNKLDGT 101 ANKSNL GANA ILGVSLAVAK AGAAEKGVPL YAHISDLAGT KKPYPVLPVF 151 QNVLN GSHA GGRLAFQEFM IVPDSAPSFS EALRQGAENVY QKLKALAKKK 201 YGQSAGNVGD EGGVAPDIQT AEEALDLITE AIEQAGYTGK IKIAMDVASS 251 EFYKADVKKY DLDFKNPESD PSKWLTYEQL ADLYKSLAAK YPIVSIEDPF 301 AEDDWEAWSY FYKTSD FQIV GDDLTVTNPG RIKKAIELKS CNALLKVNQ 351 IGTLTESIQA AKDSYADNWG VMVSHRSGET EDVTIADIAV GLRSGQIKTG 401 APCRSERLAK LNQILRIEEE LGENAVYAGS KFRTAVNL 16 - 32 608.3249 1821.9529 1821.9221 0.0308 0 R.GNPTVEVDVVTETGLHR.A 16 - 32 911.9942 1821.9738 1821.9221 0.0517 0 R.GNPTVEVDVVTETGLHR.A 68 - 79 634.8787 1267.7428 1267.7136 0.0293 0 K.NVNETIGPALIK.E 68 - 79 634.8792 1267.7438 1267.7136 0.0303 0 K.NVNETIGPALIK.E 80 - 89 588.3108 1174.6070 1174.5830 0.0241 1 K.ENIDVKDQSK.V 90 - 96 432.7287 863.4428 863.4389 0.0040 0 K.VDEFLNK.L 90 - 103 521.9471 1562.8195 1562.7940

						0.0255 1 K.VDEFLNKLDGTANK.S 90 - 103 782.4279 1562.8412 1562.7940 0.0472 1 K.VDEFLNKLDGTANK.S 104 - 120 799.4887 1596.9628 1596.9199 0.0430 0 K.SNLGANAILGVSLAVAK.A 127 - 141 514.6233 1540.8481 1540.8249 0.0231 0 K.GVPLYAHISDLAGTK.K 127 - 141 771.4409 1540.8672 1540.8249 0.0423 0 K.GVPLYAHISDLAGTK.K 185 - 192 461.7368 921.4590 921.4556 0.0035 0 R.QGAENVYQK.L 314 - 331 968.0013 1933.9880 1933.9382 0.0499 0 K.TSDFQIVGDDTLVTNPGR.I 314 - 331 968.0177 1934.0208 1933.9382 0.0827 0 K.TSDFQIVGDDTLVTNPGR.I 348 - 362 786.9552 1571.8958 1571.8519 0.0440 0 K.VNQIGTLTESIQA.AK.D 377 - 393 873.4741 1744.9336 1744.8843 0.0493 0 R.SGETEDVTIADIAVGLR.S 377 - 393 873.4761 1744.9376 1744.8843 0.0533 0 R.SGETEDVTIADIAVGLR.S 417 - 431 804.8974 1607.7802 1607.7678 0.0124 0 R.IEEELGENAVYAGSK.F 417 - 431 804.9162 1607.8178 1607.7678 0.0500 0 R.IEEELGENAVYAGSK.F
17b	Q96X30	47276	114	3	5.39	Enolase /AspF22 Sequence Coverage: 10% 1 MPISKIHARS VYDSRGNPTV EVDVVTETGL HRAIVPSGAS TGQHEAHELK 51 DGDKTQWGGK GVLKAVKNVN ETIGPALIKE NIDVKDQSKV DEFLNKLDGT 101 ANKSNLGAANA ILGVSLAVAK AGAAEKGVPL YAHISDLAGT KKPYPVLPVPF 151 QNVNLGGSHA GGRLAFQEFM IVPDSAPSFS EALRQGAENVY QKLKALAKKK 201 YGQSAGNVGD EGGVAPDIQT AEEALDLITE AIEQAGYTGK IKIAMDVASS 251 EFYKADVKKY DLDFKNPESD PSKWLTYEQL ADLYKSLAAK YPIVSIEDPF 301 AEDDWEAWSY FYKTSDFQIV GDDTLVTNPG RIKKAIELKS CNALLKVNQ 351 IGTLTESIQA AKDSYADNWG VMVSHRSGET EDVTIADIAV GLRSGQIKTG 401 APCRSERLAK LNQILRIEEE LGENAVYAGS KFR TAVNL 348 - 362 786.9449 1571.8752 1571.8519 0.0234 0 K.VNQIGTLTESIQA.AK.D 377 - 393 873.4615 1744.9084 1744.8843 0.0241 0 R.SGETEDVTIADIAVGLR.S 417 - 431 804.9011 1607.7876 1607.7678

							0.0198 0 R.IEEELGENAVYAGSK.F
17c	Q96X30	47276	772	19	5.39	Enolase/ Asp F22	Sequence Coverage: 40% 1 MPISKIHARS VYDSRGNPTV EVDVVTETGL HRAIVPSGAS TGQHEAHEL R 51 DGDKTQWGGK GVLKAVKNNV ETIGPALIKE NIDVKDQSKV DEFLNKLDGT 101 ANKSNL GANA ILGVSLAVAK AGAAEKG VPL YAHISDLAGT KKPYPVLPVPF 151 QNVLN GGS HA GGRLAFQEFM IVPDSAPSF S EALRQGA EVY QKLKALAKKK 201 YGQSAGNVGD EGGVAPDIQT AEEALDLITE AIEQAGYT GK IKIAMDVASS 251 EFYKADVKKY DLD FKNPESD PSKWLTYEQL ADLYKSLAAK YPIVSIEDPF 301 AEDDWEAWSY FYKTSD FQIV GDDLTVTNPG RIKKAIELKS CNALLLVNQ 351 IGTLTESIQA AKDSYADNWG VMVSHRSGET EDVTIADIAV GLRSGQIKTG 401 APCRSERLAK LNQILRIEEE LGENAVYAGS K FRTAVNL 16 - 32 608.3074 1821.9004 1821.9221 - 0.0217 0 R.GNPTVEVDVVTETGLHR.A 16 - 32 608.3075 1821.9007 1821.9221 - 0.0214 0 R.GNPTVEVDVVTETGLHR.A 33 - 50 620.6436 1858.9090 1858.9286 - 0.0196 0 R.AIVPSGASTGQHEAHEL.R.D 68 - 79 634.8556 1267.6966 1267.7136 - 0.0169 0 K.NVNETIGPALIK.E 80 - 89 588.2962 1174.5778 1174.5830 - 0.0051 1 K.ENIDVKDQSK.V 90 - 103 521.9288 1562.7646 1562.7940 - 0.0295 1 K.VDEFLNKLDGTANK.S 90 - 103 782.4031 1562.7916 1562.7940 - 0.0024 1 K.VDEFLNKLDGTANK.S 104 - 120 799.4644 1596.9142 1596.9199 - 0.0056 0 K.SNLGANAILGVSLAVAK.A 104 - 120 799.4797 1596.9448 1596.9199 0.0250 0 K.SNLGANAILGVSLAVAK.A 127 - 141 514.6090 1540.8052 1540.8249 - 0.0198 0 K.GVPLYAHISDLAGTK.K 127 - 141 514.6102 1540.8088 1540.8249 - 0.0162 0 K.GVPLYAHISDLAGTK.K 185 - 192 461.7259 921.4372 921.4556 - 0.0183 0 R.QGA EVYQK.L 314 - 331 967.9717 1933.9288 1933.9382 - 0.0093 0 K.TSDFQIVGDDLTVTNPGR.I 314 - 331 967.9889 1933.9632 1933.9382 0.0251 0 K.TSDFQIVGDDLTVTNPGR.I 348 - 362 524.9501 1571.8285 1571.8519 -

						0.0234 0 K.VNQIGTLTESIQAAK.D 348 - 362 786.9335 1571.8524 1571.8519 0.0006 0 K.VNQIGTLTESIQAAK.D 377 - 393 873.4526 1744.8906 1744.8843 0.0063 0 R.SGETEDVTIADIAVGLR.S 417 - 431 804.8896 1607.7646 1607.7678 - 0.0032 0 R.IEEELGENAVYAGSK.F 417 - 431 804.8900 1607.7654 1607.7678 - 0.0024 0 R.IEEELGENAVYAGSK.F
18	CAE17673	45546	134	3	5.72	Putative flavohaemoglobin Sequence Coverage: 7% 1 MPLTPEQVQI IKATVPVLAE HGTITITVFY KNMLTAHPEL NNVFNTTHQV 51 TGHQARALAG ALFAYASNID NLGALGPAVE LMCHKHASLY IKPDDYKIVG 101 KFLLEAMGQV LGDALTPEIL DAWATAYWQL ADIMIGREAQ LYEQAEGWTD 151 FRDFVVALKV PESSEITSFY LKPADGKPLP AFQPGQYISV QVHVPELNYL 201 QARQYSLSDM PRSDYYRISV KKESGLNPAE PGAKAHPGHV SNILHASVNE 251 GDTIKVSHPF GDDFLSDAKA AHPVVLLSAG VGLTPMTSIL NTLTSQAPER 301 KVSFIHGARN ARARAFKNHI TSLEQKLPNL KSTFFTSHPT EEDKEGDDYQ 351 FRGRVDLSQL DSNRDLFLDD ATTEYYVCGP DTFMTDMLNV LKSKGVSEDR 401 VKLELFGTGG VPH 2 - 12 633.3890 1264.7634 1264.7391 0.0244 0 M.PLTPEQVQIIK.A 223 - 234 585.3058 1168.5970 1168.5724 0.0247 0 K.ESGLNPAEPGAK.A 355 - 364 573.8049 1145.5952 1145.5677 0.0276 0 R.VDLSQLDSNR.D
19	XP_752401	44734	762	23	6.31	Phosphoglycerate kinase PgkA Sequence Coverage: 57% 1 MSLTNKLAIT DVDLKDKRVL IRVDFNVPLN EKKEVTNPQR IVGALPTIKY 51 AIEQGAKAVV LMSHLGRPDG KKNPKYSLKP VVPELEKLLG KSVIFTEDCV 101 GKEVEETVNK ASGGQVILE NLRFHPEEEG SYKDEEGKKV KADKEKVAEF 151 RKGLTALGDI YINDAFGTAH RAHSSMVGVD LPQKASGFLV KKELEYFAKA 201 LESPSRPFLA ILGGSKVSDK IQLIDNLLPK VNSLIITGGM AFTFKKTLEN 251 VKIGNSLFDE AGSKTVGDII EKAKKNNVKI VLPVDYITAD KFSADAKTGY 301 ATDEEGIPDG YMGLDVGDKS

						VKLYKETIAE AKTILWNGPP GVFEPEPFAN
						351 GTKQTLDAAV DAAKNGAIVI IGGGDTATVA AKYGAEKLS HVSTGGGASL
						401 ELLEGKELPG VAALSSK
						7 - 15 494.3047 986.5948 986.5648 0.0300 0 K.LAITDVDLK.D
						19 - 32 552.6723 1654.9951 1654.9406 0.0544 1 R.VLIRVDFNVPLNEK.K
						23 - 32 587.8250 1173.6354 1173.6030 0.0325 0 R.VDFNVPLNEK.K
						41 - 49 456.3173 910.6200 910.5851 0.0349 0 R.IVGALPTIK.Y
						58 - 71 499.2876 1494.8410 1494.7977 0.0433 0 K.AVVLMSHLGRPDGK.K Oxidation (M)
						76 - 87 467.9474 1400.8204 1400.7915 0.0289 0 K.YSLKPVVPELEK.L
						76 - 87 701.4288 1400.8430 1400.7915 0.0516 0 K.YSLKPVVPELEK.L
						111 - 123 685.4166 1368.8186 1368.7725 0.0462 0 K.ASGGQVILLENLR.F
						153 - 171 669.0314 2004.0724 2004.0065 0.0659 0 K.GLTA LGDIYINDAFGTAHR.A
						172 - 184 462.2453 1383.7141 1383.6817 0.0324 0 R.AHSSMVGVDLPQK.A Oxidation (M)
						172 - 184 692.8756 1383.7366 1383.6817 0.0550 0 R.AHSSMVGVDLPQK.A Oxidation (M)
						193 - 199 450.2427 898.4708 898.4436 0.0272 0 K.ELEYFAK.A
						217 - 230 532.6635 1594.9687 1594.9294 0.0393 1 K.VSDKIQLIDNLLPK.V
						231 - 246 581.6737 1741.9993 1741.9437 0.0556 1 K.VNSLIITGGMAFTFKK.T Oxidation (M)
						253 - 264 619.3207 1236.6268 1236.5986 0.0282 0 K.IGNSLFDEAGSK.T
						265 - 272 437.7579 873.5012 873.4807 0.0205 0 K.TVGDII EK.A
						280 - 291 673.9023 1345.7900 1345.7493 0.0407 0 K.IVLPVDYITADK.F
						280 - 291 673.9078 1345.8010 1345.7493 0.0517 0 K.IVLPVDYITADK.F
						280 - 297 656.0449 1965.1129 1965.0459 0.0670 1 K.IVLPVDYITADKFSADAK.T
						298 - 319 1160.0558 2318.0970 2317.9897 0.1074 0 K.TGYATDEEGIPDGYMGLDVGDK.S Oxidation (M)
						354 - 364 551.8043 1101.5940 1101.5666

						0.0275 0 K.QLDAAVDAAK.N 389 - 406 585.6675 1753.9807 1753.9210 0.0597 0 K.LSHVSTGGGASLELLEGGK.E 407 - 417 536.3262 1070.6378 1070.5972 0.0407 0 K.ELPGVAALSSK.-
20	XP_752379	48459	677	23	5.82	Adenosylhomocysteinase Sequence Coverage: 38% 1 MAAPAQKFKV ADISLAAFGR REIELAEIEM PGLMAIRRKY AEDQPLKGAR 51 IAGCLHMTIQ TAVLIETLTA LGAEVTWTSC NIFSTQDHAA AAIAASGVPV 101 FAWKGETEEE YQWCLEQQLN AFKDGQKLN ILDDGGDLTA LVHSKYPEML 151 KGCYGVSEET TTGVHHLYRM LKEGKLLVPA INVNDSVTKS KFDNLYGCRE 201 SLIDGIKRAT DVMIAQKVAV VAGYGDVGKG CADALRSMGA RVLVTEIDPI 251 NALQAAVQGY QVVTMEEAAP QGQIFVTTTG CRDILVGKHF EVMRNDAIVC 301 NIGHFDIEID VAWLKANAKS VQNIKPQVDR YLMPNGRHII LLAEGRLVNL 351 GCATGHSSFV MSCSFSNQVL AQIALFKAED EAFGKKYVEF GTTGKKPVG 401 YVLPKILDEQ VALLHLEHVN AKLSKLTVPQ AEYLGGLDIAG PFKSDM 8 - 20 465.5890 1393.7452 1393.7718 - 0.0266 1 K.FKVADISLAAFGR.R 8 - 20 697.8864 1393.7582 1393.7718 - 0.0135 1 K.FKVADISLAAFGR.R 10 - 20 560.3039 1118.5932 1118.6084 - 0.0152 0 K.VADISLAAFGR.R 10 - 20 560.3195 1118.6244 1118.6084 0.0160 0 K.VADISLAAFGR.R 22 - 37 923.9560 1845.8974 1845.9216 - 0.0241 0 R.EIELAEIEMPGLMAIR.R 2 Oxidation (M) 22 - 37 923.9574 1845.9002 1845.9216 - 0.0213 0 R.EIELAEIEMPGLMAIR.R 2 Oxidation (M) 128 - 145 632.0074 1893.0004 1893.0207 - 0.0204 0 K.LNLILDDGGDLTALVHSK.Y 176 - 189 741.9138 1481.8130 1481.8453 - 0.0323 0 K.LLVPAINVNDSVTK.S 176 - 189 741.9387 1481.8628 1481.8453 0.0175 0 K.LLVPAINVNDSVTK.S 200 - 208 515.7914 1029.5682 1029.5818 - 0.0136 1 R.ESLIDGIKR.A 208 - 217 539.2856 1076.5566 1076.5648 - 0.0082 1 K.RATDVMIAQK.V Oxidation (M) 209 - 217 461.2349 920.4552 920.4637 -

						0.0085 0 R.ATDVMIA GK.V Oxidation (M) 218 - 229 567.8040 1133.5934 1133.6081 - 0.0146 0 K.VAVVAGYGDVGK.G 289 - 294 417.6919 833.3692 833.3854 - 0.0162 0 K.HFEV MR.N Oxidation (M) 320 - 330 428.5656 1282.6750 1282.6993 - 0.0244 0 K.SVQNIKPQVDR.Y 320 - 330 428.5689 1282.6849 1282.6993 - 0.0145 0 K.SVQNIKPQVDR.Y 338 - 346 511.3010 1020.5874 1020.6080 - 0.0205 0 R.HIILLAEGR.L 386 - 395 565.2932 1128.5718 1128.5815 - 0.0097 1 K.KYVEFGTTGK.K 387 - 395 501.2395 1000.4644 1000.4866 - 0.0221 0 K.YVEFGTTGK.K 396 - 405 550.3407 1098.6668 1098.6801 - 0.0133 0 K.KPVG VYVLPK.I 406 - 422 648.0227 1941.0463 1941.0683 - 0.0221 0 K.ILDEQVALLHLEHVNAK.L 426 - 443 966.5093 1931.0040 1931.0404 - 0.0364 0 K.LTPVQAEYLGLDIAGPFK.S 426 - 443 966.5135 1931.0124 1931.0404 - 0.0280 0 K.LTPVQAEYLGLDIAGPFK.S
21	XP_751658	67070	452	13	6.11	Phosphatidyl synthase Sequence Coverage: 23% 1 MPYMANTRTI PGPTAILPVG PEKGLDAGSA VPGRITMSLV LPIIGNNYSL 51 INTLISFIII LIFAFIHLFS SSPSFLIFSG SRLVNSSSNT DPAHPPPYKS 101 DIIYFSSLIT HSSPSYVSLT LLYVYILSRL SSIATMPRFD DADFGVEPAP 151 AGARSPRDAR GSASGSLPIP NEAGNTVEIP ATRSSISDAA QFMHNL SLSP 201 SMRDRRGSRN SFGTSLPIPR SPRVSR LSSV RKADAASVSR DILASQVQDM 251 SKEKVAAAKN MAFAFDIDGV LAHGNHAIPE AKEALKMLNG DNELGIKIPY 301 ILLTNGGGKT EASRCEQLSE ILEVPISTDQ FIQSHTPMQA LSEYYETVLV 351 LGGEGQKIRE VAENYGFKNV VHPKDILAWD PTISPWR TFT AEDRAEAKPR 401 DFSKIKFDAI LVFADSRDYA TDMQLIIDLL LAEDGKLLTR AKDPVSSRIP 451 IYFSQGDLLM PTDHKGPPRL TQGCFR IAVE AQYKALTGVD LERVVYGKPE 501 RATYTYADEV LKAWMEQIHN ENRLPKNIYM IGDNPQSDIV GGNMYGWNTC 551 LVRTGVFQGG ENDEHN PANF GVFPNVLEAV KAAVRKELGQ EFKFKWNPKV

						601 NPVTHGDGSS AVE 139 - 154 817.8704 1633.7262 1633.7373 - 0.0110 0 R.FDDADFGVEPAPAGAR.S 161 - 183 1119.5671 2237.1196 2237.1288 - 0.0091 0 R.GSASGSLPIPNEAGNTVEIPATR.S 210 - 220 594.8155 1187.6164 1187.6299 - 0.0134 0 R.NSFGTSLPIPR.S 241 - 252 675.8318 1349.6490 1349.6497 - 0.0006 0 R.DILASQVQDMSK.E Oxidation (M) 298 - 309 623.3599 1244.7052 1244.7129 - 0.0076 0 K.IPYILLTNGGGK.T 360 - 368 528.7513 1055.4880 1055.4924 - 0.0043 0 R.EVAENYGFK.N 388 - 394 420.1946 838.3746 838.3821 - 0.0074 0 R.TFTAEDR.A 405 - 417 747.9153 1493.8160 1493.8242 - 0.0082 1 K.IKFDAILVFADSR.D 477 - 484 461.2520 920.4894 920.4967 - 0.0073 0 R.IAVEAQYK.A 485 - 493 487.2698 972.5250 972.5240 0.0010 0 K.ALTGVDLER.V 502 - 512 637.3162 1272.6178 1272.6238 - 0.0059 0 R.ATYTYADEVLK.A 600 - 613 684.8210 1367.6274 1367.6317 - 0.0043 0 K.VNPVTHGDGSSAVE.-
22	EDP5450 6	61335	447	15	5.85	Glucose-6-phosphate isomerase Sequence Coverage: 31% 1 MPGFSQATEL GAWKELQEHH NSLGRNIVLK EYFEKDPQRF EKFSRTFANP 51 VDNTEILFDF SKNFLTEETL ALLVKLAREA GVEELRDAMF KGDPINFTED 101 RAVYHVALRN VTNEPMQVNG KSVVEDVNSV LEHMKEFTEQ VRSGEWKGYT 151 GKKITTIINI GIGGSDLGPV MVTEALKPYG AEDMTLHFVS NIDGSHIAEA 201 LKHSDPETTL FLIASKTFTT AETTNANSA KKWFLESAKD EAHIAKHFVA 251 LSTNEEEVTK FGIDKKNMFG FASWVGGRYS VWSAIGLSVA LYIGFDNFHQ 301 FLAGAHAMDK HFRETPLEQN IPVLGGLLSV WYSDFFGAQT HLVAPFDQYL 351 HRFPAYLQQL SMESNGKAIT RTGEYVKYTT GPILFGEPAT NAQHSFFQLL 401 HQGTKLIPSD FIMAAESHNP VEGGKHQRML ASNFLAQSEA LMVGKTPEQV 451 KTEGAPDNLV PHKTFLGNRP TSILAQKIT PSTLGALIAY YEHLTFTEGA 501 VWNINSFDQW GVELGKVLAK KIQKELETPG AGGDHDASTS GLLLAFKKA

						551 NLA 46 - 62 979.5227 1957.0308 1956.9469 0.0839 0 R.TFANPVDNTEILFDFSK.N 46 - 62 979.5259 1957.0372 1956.9469 0.0903 0 R.TFANPVDNTEILFDFSK.N 63 - 75 745.9560 1489.8974 1489.8392 0.0583 0 K.NFLTEETLALLVK.L 79 - 86 451.7460 901.4774 901.4505 0.0270 0 R.EAGVEELR.D 92 - 101 582.3063 1162.5980 1162.5255 0.0726 0 K.GDPINFTEDR.A 110 - 121 673.8437 1345.6728 1345.6296 0.0432 0 R.NVTNEPMQVNGK.S Oxidation (M) 203 - 216 520.2913 1557.8521 1557.8039 0.0482 0 K.HSDPETTLFLIASK.T 217 - 231 779.4053 1556.7960 1556.7318 0.0642 0 K.TFTTAETTTNANSK.K 217 - 231 779.4058 1556.7970 1556.7318 0.0652 0 K.TFTTAETTTNANSK.K 247 - 260 535.2906 1602.8500 1602.7889 0.0610 0 K.HFVALSTNEEEVTK.F 406 - 425 710.0470 2127.1192 2127.0306 0.0885 0 K.LIPSDFIMAAESHNPVEGGK.H Oxidation (M) 406 - 425 710.0478 2127.1216 2127.0306 0.0909 0 K.LIPSDFIMAAESHNPVEGGK.H Oxidation (M) 452 - 463 426.5680 1276.6822 1276.6412 0.0410 0 K.TEGAPDNLVPHK.T 464 - 478 549.6653 1645.9741 1645.9151 0.0589 0 K.TFLGNRPPTSILAQK.I 525 - 547 762.7462 2285.2168 2285.1176 0.0992 0 K.ELETPGAGGDHDASTSGLLLAFK.K
23	XP_750954	52885	474	18	5.88	ATP citrate lyase subunit (Acl), putatibe Sequence Coverage: 29% 1 MSAKSILEAD GKAILNYHLT RAPVIKPTPL PPSSTHNPPP RLASIYPED 51 AAVKDVLDT EVVYPWLLTP GAKFVAKPDQ LIKRRGKSG LALNKTWPEA 101 REWIEARAGK EIKVETVTGV LRQFLVEPFV PHPQETEEYI NINSVREGDW 151 ILFTHEGGVD VGDVDAKAEK LLIPVNLARNY PSNEEIAAAL LSKVPKGVHN 201 VLVD FISRLY AVYVDCQFTY LEINPLVIP NAEGTSAEVH FLDLAAKLDQ 251 TAEFECGTKW AIARSPANLG LATVPQTDGK VNIDAGPPME FPAPFGRELS 301 KEEKFISDMD AKTGASLKLT VLNANGRIWT LVAGGGASVV YADAIASAGF 351 VSELANYGEY SGAPTETQTY

						NYAKTVLDLM LRAPMHPDGK VLFIGGGIAN 401 FTNVASTFKG VIRAIREVAP VLNEHNVQIW VRRAGPNYQE GLKNIKAVGE 451 ELGLKMHVYG PDMHVSIGVIP LALLGKKTDI KEFGSA 13 - 21 550.8359 1099.6572 1099.6138 0.0434 0 K.AILNYHLTR.A 74 - 83 579.8720 1157.7294 1157.6808 0.0486 0 K.FVAKPDQLIK.R 111 - 122 672.4186 1342.8226 1342.7820 0.0406 1 K.EIKVETVTGVLR.Q 114 - 122 487.3033 972.5920 972.5604 0.0316 0 K.VETVTGVLR.Q 171 - 178 469.3264 936.6382 936.6120 0.0262 0 K.LLIPVNL.R 171 - 178 469.3290 936.6434 936.6120 0.0314 0 K.LLIPVNL.R 179 - 193 810.4426 1618.8706 1618.8202 0.0505 0 R.NYPSNEEIAAALLSK.V 179 - 193 810.4478 1618.8810 1618.8202 0.0609 0 R.NYPSNEEIAAALLSK.V 197 - 208 452.6009 1354.7809 1354.7357 0.0451 0 K.GVHNVLVDFISR.L 197 - 208 678.4030 1354.7914 1354.7357 0.0557 0 K.GVHNVLVDFISR.L 197 - 208 678.4041 1354.7936 1354.7357 0.0579 0 K.GVHNVLVDFISR.L 265 - 280 784.9504 1567.8862 1567.8206 0.0657 0 R.SPANLGLATVPQTDGK.V 265 - 280 784.9531 1567.8916 1567.8206 0.0711 0 R.SPANLGLATVPQTDGK.V 281 - 297 915.9880 1829.9614 1829.8771 0.0844 0 K.VNIDAGPPMEFPAPFGR.E Oxidation (M) 305 - 312 471.7370 941.4594 941.4164 0.0430 0 K.FISDMDAK.T Oxidation (M) 319 - 327 479.2922 956.5698 956.5403 0.0295 0 K.LTVLNANGRI 375 - 382 488.7997 975.5848 975.5423 0.0426 0 K.TVLDLMLR.A Oxidation (M) 391 - 409 978.5823 1955.1500 1955.0517 0.0984 0 K.VLFIGGGIANFTNVASTFK.G
24	Q4WFT3	61393	120	5	5.85	GMP synthase [glutamine- hydrolyzing] Sequence Coverage: 7% 1 MAEEQNPSAT FDTILTLDFG SQYTHLITRR LREIGVYSEM LPCTQKLADL 51 PFKPKGILS GGPYSVYEDG APHADPAVFE LGVPVLGICY GLQEIAIRLG 101 KDNVVAGTAR EYGHADLNAQ RLDNQGHVDK LFAGLEEHVK

						VWMSHGDKLV 151 KLPEGFHTIA TTANSEYAGI AHETKPVYGI QFHPEVTHTP DGAKLLRNFA 201 VDICGANPNW TMSKFVDQEI LRIRKLVGET DHVLGAVSGG VDSTVAAKLM 251 KEAIGDRFHA VLVNNGCMRL NECETVAETL NKHLGINLTV VDASKRFLDG 301 LKGVTDPEKK RMFIGATFID VFEEEAIEKIE ALAENSGAKV KWFLQGTLYP 351 DVIESISFKG PSATIKTHHN VGALPKRMIE GQGMKLEPL RELFKDEVQR 401 LGRELGIAHE LVMRHPFPGP GIAIRVLGEV TPERVDIARK ADHIFISMIR 451 EAGLYDKISQ AYAALDPSKA VGVMGDKRVY AEIHLRAVE TTDCKLTLGI 501 DGDFVLRYY SVMTARAFPF DNEFLSKCAT RIINEVHGVS RVLYDISSKP 551 PATIEME 215 - 222 510.2953 1018.5760 1018.5447 0.0313 0 K.FVDQEILR.I 426 - 434 500.2962 998.5778 998.5397 0.0382 0 R.VLGEVTPER.V 426 - 439 518.6444 1552.9114 1552.8573 0.0541 1 R.VLGEVTPERVDIAR.K 458 - 469 632.3557 1262.6968 1262.6506 0.0462 0 K.ISQAYAALDPSK.A 479 - 487 545.3557 1088.6968 1088.6593 0.0375 0 R.VYAEIHLR.A
25	XP_7506 96	55764	876	19	5.86	6-phosphogluconate dehydrogenase Gnd1 Sequence Coverage: 31% 1 MSTQAVARLA GINVGAPARP LPSADFGILG LAVMGQNLIL NVADHGFTVC 51 AYNRTTSKVD RFLANEAKGK SIVGAHSVEE FCAKLKPRR IMLVMAGKP 101 VDDFIESLLP HLEEGDIID GGNSHFPDSN RRTKYLKEKG IRFVGSGVSG 151 GEEGARYGPS LMPGGNEEAW PFIKDIFQSI AAKSDGEACC DWVGDEGAGH 201 FVKMVHNGIE YGDMQLICEA YDIMKRGLGM PVNEIADVFA KWNKGVLDSF 251 LIEITRDVLY FNDNDGTPLV EKILDKAGQK GTGKWTAINA LDLGMPVTLI 301 GEAVFARCLS AIKDERIRAS SLLDGTPPQF TGDQKAFIDD LEQALYASKI 351 ISYAQGFMLI QEAAREYGWK LNKPSIALMW RGGCIIRSVF LKDITNAYRN 401 NPDLENLLFD DFFKAAIQKA QQGWRNVVSK GALWGIPTPA FSTALSFYDG 451 YRTRDLPANL LQAQRDYFGA

						HTFRVKPECA NENYPEGKDI HVNWTGRGGD 501 VSASTYVV 143 - 156 654.8308 1307.6470 1307.6106 0.0364 0 R.FVGSGVSGGEEGAR.Y 175 - 183 496.7874 991.5602 991.5338 0.0264 0 K.DIFQSIAAK.S 227 - 241 788.9334 1575.8522 1575.7967 0.0556 0 R.GLGMPVNEIADVFAK.W Oxidation (M) 245 - 256 681.9071 1361.7996 1361.7555 0.0442 0 K.GVLDSFLIEITR.D 257 - 272 919.9794 1837.9442 1837.8734 0.0708 0 R.DVLYFNDNDGTPLVEK.I 319 - 334 817.4396 1632.8646 1632.7995 0.0651 0 R.ASSLLDGPTPQFTGDK.Q 319 - 334 817.4401 1632.8656 1632.7995 0.0661 0 R.ASSLLDGPTPQFTGDK.Q 335 - 349 856.4639 1710.9132 1710.8464 0.0668 0 K.QAFIDDLEQALYASK.I 350 - 365 609.6726 1825.9960 1825.9396 0.0564 0 K.IISYAQGFMLIQEAAR.E Oxidation (M) 350 - 365 914.0105 1826.0064 1825.9396 0.0668 0 K.IISYAQGFMLIQEAAR.E Oxidation (M) 350 - 365 914.0181 1826.0216 1825.9396 0.0820 0 K.IISYAQGFMLIQEAAR.E Oxidation (M) 388 - 399 476.2736 1425.7990 1425.7616 0.0374 1 R.SVFLKDITNAYR.N 388 - 399 713.9146 1425.8146 1425.7616 0.0531 1 R.SVFLKDITNAYR.N 393 - 399 426.7232 851.4318 851.4137 0.0181 0 K.DITNAYR.N 400 - 414 920.9688 1839.9230 1839.8679 0.0551 0 R.NNPDLLENLLFDDFFK.A 453 - 465 499.2953 1494.8641 1494.8266 0.0374 1 R.TRDLPANLLQAQR.D 455 - 465 619.8625 1237.7104 1237.6779 0.0326 0 R.DLPANLLQAQR.D 455 - 465 619.8661 1237.7176 1237.6779 0.0398 0 R.DLPANLLQAQR.D 466 - 474 557.2783 1112.5420 1112.5040 0.0381 0 R.DYFGAHTFR.V
26	XP_755071	48784	112	6	5.60	Gamma-glutamyl phosphate reductase Sequence Coverage: 14% 1 MSLTDSSAVE IARAASLASR QLATLPTIDR NDALTALHDA LLRNREILD 51 ANAKDVAIAS QAANNGSLSH SVLKRLDLR PGKYDDMLKG ILSVRDLEDP 101 VGRVTLRTLL DDGLILERVS

						CPIGVLLIIF EARPEVIANI AALSIKSGNA 151 AILKGGKEST ESFIAISKVI SEAISGTRVP VASVQLVKTR DVVSSLLAQD 201 SLIDLVIPRG SNDLVRFVKE NTKIPVLGHA DGLCSAYLHA DADPAIAVKV 251 IVDAKTDYPA ACNSLESLLV HEDALGTIFF AVAEALLAKG VRLRCDIQSK 301 SALLKNISSP PADLLEDAVD SDFDTEFLDL VLAVKTIPST SSPISAVEDA 351 ISHINSHSSK HTDLIVTESK EIAEYFMRGV DSAGVFWNAS TRFADGMRFG 401 FGTEVGISTN KIHTRGPVGL DGLTIYKYLL RGQGHRAGDY FEGEGGKKWK 451 HEHLVI 108 - 118 629.3752 1256.7358 1256.6976 0.0382 0 R.TLLDDGLILER.V 169 - 178 516.7999 1031.5852 1031.5611 0.0241 0 K.VISEAISGTR.V 179 - 188 520.3460 1038.6774 1038.6437 0.0337 0 R.VPVASVQLVK.T 361 - 370 571.8203 1141.6260 1141.5979 0.0281 0 K.HTDLIVTESK.E 399 - 411 678.8641 1355.7136 1355.6722 0.0415 0 R.FGFGTEVGISTNK.I 416 - 427 616.8666 1231.7186 1231.6812 0.0374 0 R.GPVGLDGLTIYK.Y
27	XP_7550 56	52982	59	3	5.47	Glutamate carboxypeptidase Sequence Coverage: 9% 1 MAPQLEPFFK QVDELSNSFI DRLRKAVAIP SISAHDENRK DVFRMAHFLA 51 SELEALGAEV EQRPLGKQPG KEHLDLPPVV IARYGNDKNK RTILVYGHYD 101 VQPALKDDGW ATEPFELTID DQGRMFGRGS TDDKGPVLGW LNVIEAHQKA 151 GVLPVNLLC CFEGMEEYGS EGLEEFIKSE SKKFFKDADA VCISDNYWLG 201 TEKPCLTYGL RGCNYYSVSI SGPAQDLHSG VFGGSTHEPM TDMVNILSKL 251 VDPKGNILIP GIMDLVAPLT EEENSLYSKI SYTMDNLHES LGSKTNIHET 301 KERTLMARWR YPSLSIHGIE GAFSAPGAKT VIPAKVIGKF SIRTVPNMES 351 DAVNKLVDY IKAFAKLNS KNTLDVWLQH DGKWWVASPK HWNFTAASKA 401 VKQVFGVEPD MTREGGSIPV TLSFEQATGK NVLLPMGSS TDAAHSVNEK 451 LDKKNYIEGT KLLGAYLHYV AEPPASEV 11 - 22 711.8683 1421.7220 1421.6787

						0.0434 0 K.QVDELSNSFIDR.L 414 - 430 860.9710 1719.9274 1719.8679 0.0595 0 R.EGGSIPVTLSEFQATGK.N 462 - 478 931.0040 1859.9934 1859.9305 0.0630 0 K.LLGAYLHYVAEEPASEV.-
28	XP_7554 48	52247	349	8	5.33	Secretory pathway gdp dissociation inhibitor Sequence Coverage: 16% 1 MEEIAPEYDV VVLGTGLTEC VLSGVLSVKG NKVLHIDRND HYGGEAASVN 51 IETLFKKYGN VRPGEEPWKK YGRVNDWNID LVPKLLMANG ELTNILVSTD 101 VTRYLEFKQI AGSYVQQGKG PKATVAKVPS DAGEALRSSL MGMFEKRRAK 151 KFLEWVGEFK EDDPATHQGL NVAQCTMKEV YDKFGLEDNT RDFVGHSMAL 201 YPSDDYITTP GMAVETIHRI RLYVNSMARY GKSPYIPLY GLGELPQGFA 251 RLSAIYGGTY MLNTSVDEVL YDESGKVSGI KATMKDRDDN SEAMKFTTKT 301 KKIIADPSYF PGKVRVTGYL LKAICILNHP IEKTDGSDSL QLIPQSQVG 351 RKHDVYIAMV SSAHNVCPKG YYIAIVSTIA ETDANHHLEL EPGFERLGQI 401 EEKFFGPPIP LYEPDLSGEK DNIFISKSYD ATSHFETTTD DVRDLYKRAT 451 GEELVVEGLR EDQRLAED 109 - 119 589.8194 1177.6242 1177.6091 0.0151 0 K.QIAGSYVQQGK.G 128 - 137 507.7666 1013.5186 1013.5142 0.0045 0 K.VPSDAGEALR.S 179 - 191 529.2590 1584.7552 1584.7420 0.0132 1 K.EVYDKFGLEDNTR.D 184 - 191 476.2361 950.4576 950.4458 0.0119 0 K.FGLEDNTR.D 303 - 313 604.3318 1206.6490 1206.6285 0.0206 0 K.IIADPSYFPGK.V 303 - 313 604.3356 1206.6566 1206.6285 0.0282 0 K.IIADPSYFPGK.V 334 - 351 957.5198 1913.0250 1912.9854 0.0396 0 K.TDGSDSLQLIPQSQVGR.K 449 - 460 636.8495 1271.6844 1271.6721 0.0123 0 R.ATGEELVVEGLR.E
29	XP_7478 54	54420	110	4	5.33	Glucokinase GlkA Sequence Coverage: 11% 1 MSSPLVTEAT RIARQFDFSA EQIQSGVKEY IREMCEGLTK EHTTLSQIPT 51 YVTSVPNGTE KGLYLAVDLG GTNFRVCSID LHGDTTFNLT QSKIMIPREL 101 MASGTSKDLF LFLARQIEAF

						LRIHHNEHFE AHLRRRRREP N SEEELFDLGF 151 TFSFPVRQLG INKGTLRWT KGFNIPDAVG HDVCALLQNA IDELDLPVRV 201 AALVNDTVGT LMARSYTSPG DTSTFIGAIF GTGTNGAYVE KLDRTKLQT 251 IEHADYEKST GEMIINAEWG SFDNHLVLP NTKWDKELDE DSNNGIQMF 301 EKRVS GMFLG EILRRALLDM HKDEAFGLFK PNQSSKVVTP ENSPLYRQWG 351 IDTSFLSLVE ADKTDRMEEV KAALKDHLKI ENPSDAECQA VKVLVHAIGK 401 RAARLSAVPL AAILISTGKL ETDDMVDIGV DGSLVEFYFN FEGYIREALR 451 EVPEVGAAGE KKVIRIGISKD GSGVGAALIA LVASRNETGS GPK 15 - 28 792.3962 1582.7778 1582.7627 0.0151 0 R.QDFSAEQIQSGVK.E 337 - 347 637.8438 1273.6730 1273.6666 0.0064 0 K.VVTPENSPLYR.Q 405 - 419 727.4614 1452.9082 1452.8915 0.0167 0 R.LSAVPLAAILISTGK.L 447 - 461 518.9423 1553.8051 1553.8049 0.0002 1 R.EALREVPEVGAAGEK.K
30	XP_7556 57	78713	376	9	5.66	Bifunctional tryptophan synthase TRPB Sequence Coverage: 14% 1 MEGIKSTFAR CQEQRKRAALV AYITAGYPTV EETVDILLGL ENGGAGSLNA 51 NAIRWISTDI IELGIPFTDP IADGPTIQRA NTQALANGVT VTTVLNMVRQ 101 ARSRGLKAPL LLMGYYNPVL RYGEERMLKD CKEAGVNGFI MVDLPPEEAV 151 RFRDLCASNG MSYVPLIAPA TSEARMKLLC KIADSFYVV SRMGVTGATG 201 KLSSNLPELL KRVHQWSGNV PAALGFGVST REHFLSVQEL AEGVVIGSQI 251 ITVLGQAPAG QAAKHAE EYL SSVTGRKLER DAQGILTNEI NVLEAVEKAQ 301 VPAVSQPTAV VTEADTPDGP GLADQIDALN GTGNPAAQPS RFGEFGGQYV 351 PESLMDCLAE LERGFQEAVN DPTFWEEFRS YYPYMGRPSS LHLANRLTEY 401 VGGANIWLKR EDLNHTGSHK INNALGQILI ARRLGKTRII AETGAGQHGV 451 ATATVCAKFG MKCVVYMGA E DVRRQALNVF RMKLLGASVV AVDAGSRTL R 501 DAVNEALRAW VVDLDTTHYI IGSAIGPHPF PTIVRTFQSV IGEETKQMM 551 EAIGKLPAV VACVGGGSNA VGMFYPPAKD TSVKLVGVEA GGDGIDTNRH 601 SATLTGGSKG VLHGVRTYVL

						QDEHGQISET HSIAGLDYP GVGPELSSWK 651 DSDRARFIAA TDAEALIGFR TLAQTEGIIP ALESSHAVWG AMELAKSMKT 701 GDIVLNLSGR GDKDVQSVAD ELPRLGPKIG WDLRF 108 - 121 818.4405 1634.8664 1634.8854 - 0.0190 0 K.APLLLMGYYNPVLR.Y Oxidation (M) 182 - 192 635.3398 1268.6650 1268.6765 - 0.0114 0 K.IADSFYVVS.R 281 - 298 978.5051 1954.9956 1955.0211 - 0.0255 0 R.DAQGILTNEINVLEAVEK.A 421 - 432 648.3893 1294.7640 1294.7721 - 0.0080 0 K.INNALGQILAR.R 475 - 481 424.2388 846.4630 846.4712 - 0.0081 0 R.QALNVFR.M 484 - 497 657.8667 1313.7188 1313.7303 - 0.0115 0 K.LLGASVVAVDAGSR.T 501 - 508 444.2325 886.4504 886.4508 - 0.0004 0 R.DAVNEALR.A 657 - 670 747.8901 1493.7656 1493.7878 - 0.0222 0 R.FIAATDAEALIGFR.T 700 - 710 572.8140 1143.6134 1143.6248 -0.0113 0 K.TGDIVLNLSGR.G
31a	XP_7554 59	84023	181	9	5.62	3-isopropylmalate dehydratase Sequence Coverage: 12% 1 MPGVDDKKPKT LYDKVLDHII VNEQEDGTIL IYIDRHLVHE VTSPQAFEG 51 KNAGRKVRP DCTLATVDHN IPTSSRKNF NVEEFIEETD SRLQCTTLEQ 101 NVKDFGLTYF GMGDKRQGIV HIIGPEQGFT LPGTTVVC GD SHTSTHGAFG 151 ALAFGIGTSE VEHVLATQTL LTRRSKNMRI QVDGELPPGV TSKDVLHII 201 GVIGTAGGTG AVIEFCGSVI RGLSMEARMS MCNMSIEAGA RAGMIAPDET 251 TFEYLKGRPL APKYDSA EWK RAVAFWSSLA SDEGAVYDKT VVLDGKDIIP 301 TVSWGTSPOD VVPITGVVPG PDDFEDENRK VACKRALEYM GLVAGTRI QD 351 IPVDKVFIS CTNARIEDLR AAAKVVRGKK VAANIKRAMV VPGSGLVKQQ 401 AEAEGLD RVF TDAGFEWREA GCSMCLGMNP DILSPQERCA STSNRNFEGR 451 QGAGGRTHLM SPAMAAAAAI TGHADVREH LTASPLLA QPHLDIQEEH 501 EDPTTEDEFD RIMDM PADNE PHANSSAATA AAGSTAGLPK FTTLRGIAAP 551 MDRSNVD TDA IIPKQFLKTI KRTGLGSALF YELRYNPADG SENKSFVLNQ

						601 EPYRNAKILV VTGPNFGCGS SREHAPWALL DFGIKCIAP SFADIFFNNT 651 FKNGLMPVVI SDPAVLATIA AEASAGREEIE VDLVNQEIKD AAGSKLASFE 701 VDAFRKHCLI NGLDDIGLTL QMEDKIRAFE AKRTLETPWL DSGGYLKRGV 751 RGGATMIQAA PVPKTNRGDV KTEPLEW 81 - 92 734.3340 1466.6534 1466.6525 0.0010 0 K.NVEEFIEETDSR.L 180 - 193 720.3961 1438.7776 1438.7668 0.0109 0 R.IQVDGELPPGVTSK.D 399 - 408 558.7718 1115.5290 1115.5207 0.0084 0 K.QQAEAGLDR.V 554 - 564 586.8144 1171.6142 1171.6085 0.0058 0 R.SNVDTDAIPK.Q 573 - 584 663.8622 1325.7098 1325.6979 0.0119 0 R.TGLGSALFYELR.Y 585 - 594 547.7415 1093.4684 1093.4676 0.0009 0 R.YNPADGSENK.S 595 - 604 626.8216 1251.6286 1251.6248 0.0039 0 K.SFVLNQEPYR.N 678 - 689 714.8877 1427.7608 1427.7507 0.0101 0 R.EIEVDLVNQEIK.D 696 - 705 577.7994 1153.5842 1153.5768 0.0075 0 K.LASFEVDAFR.K
31b	XP_7554 59	84023	80	3	5.62	3-isopropylmalate dehydratase Sequence Coverage: 4% 1 MPGVDDKKPKT LYDKVLDHHI VNEQEDGTIL IYIDRHLVHE VTSPQAFEG 51 KNAGRKVRPP DCTLATVDHN IPTSSRKNF NVEEFIEETD SRLQCTTLEQ 101 NVKDFGLTYF GMGDKRQGIV HIIGPEQGFT LPGTTVCCGD SHTSTHGAFG 151 ALAFGIGTSE VEHVLATQTL LTRRSKNMRI QVDGELPPGV TSKDVVLHII 201 GVIGTAGGTG AVIEFCGSVI RGLSMEARMS MCNMSIEAGA RAGMIAPDET 251 TFEYLKGRPL APKYDSA EWK RAVAFWSSLA SDEGAVYDKT VVLDGKDIP 301 TVSWGTSPOD VVPITGVVPG PDDFEDENRK VACKRALEYM GLVAGTRI QD 351 IPVDKVFIGS CTNARIEDLR AAAKVVRGKK VAANIKRAMV VPGSLVKQQ 401 AEAEGLDRVF TDAGFEWREA GCSMCLGMNP DILSPQERCA STSNRNFEGR 451 QGAGGRTHLM SPAMAAAAAI TGHLADVREH LTASPLLAKA QPHLDIQEEH 501 EDPTTEDEFD RIMDMPADNE

						PHANSSAATA AAGSTAGLPK FTTLRGIAAP 551 MDRSNVD TDA IIPKQFLKTI KRTGLGSALF YELRYNPADG SENKSFVLNQ 601 EPYRNAKILV VTGPNFGCGS SREHAPWALL DFGIKCIAP SFADIFFNNT 651 FKNGMLPVVI SDPAVLATIA AEASAGREIE VDLVNQEIKD AAGSKLASFE 701 VDAFRKHCLI NGLDDIGLTL QMEDIKIRAFE AKRTLETPWL DSGGYLKRGN 751 RGGATMIQAA PVPKTNRGDV KTEPLEW 399 - 408 558.7700 1115.5254 1115.5207 0.0048 0 K.QQAEAEGLDR.V 573 - 584 663.8600 1325.7054 1325.6979 0.0075 0 R.TGLGSALFYELR.Y 595 - 604 626.8239 1251.6332 1251.6248 0.0085 0 K.SFVLNQEPYR.N
32	XP_7528 26	92824	86	5	5.46	Phosphoribosyl- AMP cyclohydrolase Sequence Coverage: 5% 1 MATPILISYN PTSASSGLSL SQIAYFGRVL IKVSSLSQAE EFLRQNFRL 51 DVYVDATDIT SSGDIVDILN AGAAKAFISL DQLTSLSQEQ SVPSSRLVVY 101 TSSDSQVDAF QSWVGEDAER KEAGICTESA DVKTVADRLG LNLEAQNLRY 151 TYTTSTVTED AVKETLKQGA VSIVSADALT LDHKNPSGKI AAAALVAARA 201 VADQSNGLYA TSVTDERGVC LGLVWSSDES IAEALRTGTG VYQSRKRGLW 251 YKGQSSGDVQ ELIRLGFDCD SDCLVFVVKQ IGRGFCHLGT ASCFGPYNGL 301 ARLQKTLQAR KADAPAGSYT ARLFNEPKLT QAKIMEEAD LCRATTKEEI 351 AFEAADLLYF ALTRCVAAGV SLEDIERNLD LKSLKVRRK GDAKGPWAEK 401 AGLTASPAET KPAGPAAPAK EAAKKDDSRM EMTRVVTAST PVDKVKEYLK 451 RPSQKSND AI VGLVRPIQD VRDGGDAAVL KYTHKFEKAT SLTSPVIRAP 501 FPPELMKLSP ETQE AIDVSI ANIKKFHSAQ KDSNDVLQVE TMPGVVCSRF 551 SRPIERVGLY VPGGTAVLPS TAMMLGVPAM VAGCQKIVLA SPPRADGSIS 601 PEIVYVAHKV GAESIVLAGG AQAVAAMAYG TESISKVDKI LGPGNQFVTA 651 AKMLVSNDTS AGVSIDMPAG PSEVLVIADK DANPAFVASD LLSQAEHGVD 701 SQVILAIIDL NESQLQAIED EVDAQARALP RMDIVRGLA HSVTFVVRDI 751 DEAMALSNEY APEHLILQVK

						NAESVVEKVV NAGSVFIGQW TPESVGDYSA 801 GVNHSLPTYG YAKQYSGVNL GSFLKHITSS NLTAEGLLGL SRTVEQLAAV 851 EGLDAHKRAV SIRVAAMKKN QA 33 - 44 683.3569 1364.6992 1364.6936 0.0057 0 K.VSSLSQAEEFLR.Q 190 - 199 463.7931 925.5716 925.5709 0.0008 0 K.IAAAALVAAR.A 253 - 264 644.8304 1287.6462 1287.6419 0.0044 0 K.GQSSGDVQELIR.L 489 - 498 522.8088 1043.6030 1043.5975 0.0055 0 K.ATSLTSPVIR.A 587 - 594 426.7669 851.5192 851.5229 - 0.0036 0 K.IVLASPPR.A
33	XP_7538 31	72634	151	4	5.93	Aminopeptidase P Sequence Coverage: 8% 1 MLGFRSPIRL CKLSALGSTR LLPISRPKLF STAVARYAAD METVNTTKRL 51 ARLRQLMQEH KIDVYIVPSE DSHQSEYIAP CDGRREFISG FSGSAGTAIV 101 SMTKAALSTD GRYFNQASKQ LDSNWELLKR GVENVPTWQE WTTEQAQGGK 151 VVGVDPALIT ASGARSLEET LKRNGSSLVG ISQNLVDLVW GKDRPAPPRE 201 KVRVHPDKFS GKTFQEKIAD LRKELEKKKT AGFVISMLDE IAWLFNLRGS 251 DIPYNPVFFA YAIITPTKAE LYIDDDKITP EVVAHLGQDV VIKPYNSIFA 301 DAKALSEARR KEAGETASKF LLSNKASWAL SLSLGEEHV EETRSPiADA 351 KAIKNEVELA GMRACHIRDG AALIEYFAWL ENELVNKKTV LDEVDAADKL 401 EQIRTKHDLF AGLSFDTISS TGPNGAVIHY KPEKGTCsII DPDAIYLCDs 451 GAQYLDGTTD VTRTFHFGKP TELEKKAFTL VLKGLIAIDT AVFPKGTSGF 501 ALDALARQYL WKEGLDYLHG TGHGVGSYLN VHEGPIGIGT RVQYTEVPIA 551 PGNVISDEPG FYEDGKFGIR IENVIMAREV QTTHKFGDKP WLGFHVtMA 601 PIGRNLIEPS LLSDELKwV NDYHAEVWDK THHFFENDEF TRSWLQRETA 651 PITK 151 - 165 713.4113 1424.8080 1424.7987 0.0093 0 K.VVGVDPALITASGAR.S 389 - 404 605.6550 1813.9432 1813.9421 0.0010 1 K.TVLDEVDAADKLEQIR.T 484 - 495 622.8691 1243.7236 1243.7176

						0.0060 0 K.GLIAIDTAVFPK.G 496 - 507 589.8114 1177.6082 1177.6091 - 0.0009 0 K.GTSGFALDALAR.Q
34	XP_7553 28	74420	673	17	6.02	Mitochondrial Hsp70 chaperone (Ssc70) Sequence Coverage: 28% 1 MMPSRLVRV CPSSTGTSSR ARSSGLTLDF LHQLPRTART PAFRVPGASF 51 RRWNSTEGEK VKGQVIGIDL GTTNSAVAVM EGKTPKIIEN AEGARTTPSV 101 VAFAQDGERL VGIAAKRQAV VNPENTLFAT KRLIGRKFTD PEVQRDIKEV 151 PYKIVQHTNG DAWVEARGQK YSPSQIGGFI LQKMKETAEN YLSKPVKNV 201 VTVPAYFNDS QRQATKDAGQ IAGLNVLRV NEPTAAALAY GLEKEADRVV 251 AVYDLGGGTF DISVLEIQKG VFEVKSTNGD THLGGEFDI HLVRHIVQQF 301 KKDSGLDLSN DRMAIQRIRE AAEKAKIELS SSLQTEINLP FITADASGAK 351 HINLKMTRSQ LESLVEPLIN RTVEPVKAL KDANLQASDI QDIILVGGMT 401 RMPKVAESVK SMFGRDPAKS VNPDEAVAIG AAIQGAVLAG EVTDVLLLDV 451 TPLSLGIETL GGVFTRLINR NTTIPTKKSQ TFSTAADFQT AVEIKVFQGE 501 RELVKDNKLL GNFQLVGIPP AHRGVPQIEV TFDIDADSIV HVAADKSTG 551 KDQSITIASG SGLSDAEIQS MVEDAKEYGE QDKERKAAIE AANRADSVLN 601 DTEKALKEFE DRLDKAEAEQ IREKIATLRE FVAKNQSGEG TATAEELKQK 651 TDELQTASLT LFDKMHKAQS EQQQSQGQQ GENKP 87 - 95 486.7551 971.4956 971.5036 - 0.0079 0 K.IIENAEGAR.T 96 - 109 739.3746 1476.7346 1476.7209 0.0138 0 R.TTPSVVAFAQDGER.L 118 - 131 766.4130 1530.8114 1530.8042 0.0072 0 R.QAVVNPENTLFATK.R 118 - 132 563.3167 1686.9283 1686.9053 0.0230 1 R.QAVVNPENTLFATKR.L 138 - 145 496.2477 990.4808 990.4771 0.0038 0 K.FTDPEVQR.D 171 - 183 719.3937 1436.7728 1436.7664 0.0065 0 K.YSPSQIGGFILQK.M) 198 - 212 840.9250 1679.8354 1679.8267 0.0087 0 K.NAVVTVPAYFNDSQR.Q 217 - 228 613.8484 1225.6822 1225.6779 0.0044 0 K.DAGQIAGLNVLR.V 229 - 244 823.4462 1644.8778 1644.8723

						0.0056 0 R.VVNEPTAAALAYGLEK.E 295 - 301 450.2551 898.4956 898.5025 - 0.0068 0 R.HIVQQFK.K 303 - 312 546.2505 1090.4864 1090.4891 - 0.0026 0 K.DSGLDLSNDR.M) 359 - 371 749.4215 1496.8284 1496.8198 0.0086 0 R.SQLESLVEPLINR.T 479 - 495 922.4645 1842.9144 1842.9000 0.0145 0 K.SQTFSTAADFQTAVEIK.V 509 - 523 544.6505 1630.9297 1630.9307 - 0.0011 0 K.LLGNFQLVGIPPAHR.G 635 - 648 717.8427 1433.6708 1433.6634 0.0075 0 K.NQSGEGTATAEELK.Q 635 - 650 564.2789 1689.8149 1689.8169 - 0.0021 1 K.NQSGEGTATAEELKQK.T 651 - 664 791.4071 1580.7996 1580.7934 0.0063 0 K.TDELQ TASLTLFDK.M
35	XP_746746	64991	102	4	5.83	Heat shock protein (Sti1) Sequence Coverage: 9% 1 MLPRSFQRCG TGFTTRKKTNL FVPRNSEKFTQAIELEPSNHILYSNRSVY 51 AAQSDYQKAL DDANKAIEIK PDWSKGYSRK GAACRGLGDL LGAHDAYEEA 101 LKLDPSNDQA KSGLNAVKRA IDGEARADGV NPAAGLGGIFNDPQMFQKLA 151 SNPKTSHLLA DADFMAKLQR LQQNPNSMSPQEIQDPRFLQVMSVLLGIDM 201 SFGAPPEAAG SSRAAAEAE DVPMPDAKPA AAEKKKEPEPAPQPEPEPED 251 EETIAKKKAQ EAGDAEKKIG NDFYKKKQFD EAIEHYTKAW ELNKDITYLN 301 NIGAAKFEKG DLQGAIEICQ KAVEEGRELRA DFKVIAKAFARIGTAYEKL 351 GDFTQAIEYY HKSLTEHRTP DALTKLRNAE KAKVKAEKEA YIDPVEAEKA 401 RELGQKKFQE ADWPGAVEAF TEMTRAPHD PRGFSNRAAA LIKLMAFPQA 451 VQDCDEAIRR DPKFIRAYIR KSQALVAMKE YSKALDACTE AAEQDDGTHT 501 REIDQQQKQC LEAQFSARAG ETEEQTMERIQNDPEIMSILQDPVMSILQ 551 QAKSDPAALQ EHMKNVQVRT KIQKLMAAGV IRLGR 29 - 46 711.3660 2131.0762 2131.0698 0.0064 0 K.FTQAIELEPSNHILYSNR.S 47 - 58 665.8228 1329.6310 1329.6201 0.0110 0 R.SAVYAAQSDYQK.A 295 - 306 646.8488 1291.6830 1291.6772 0.0059 0 K.DITYLNNIGAAK.F

							350 - 362 528.9258 1583.7556 1583.7620 - 0.0064 0 K.LGDFITQAIEYYHK.S
36	XP_747200	66932	478	13	5.30	Hsp70 chaperone (HscA)	Sequence Coverage: 27% 1 MSDEVYEGAI GIDLGTTYSC VANYEGTNVE IIANEQGSYT TPSFVSFTEK 51 ERLIGEAAKN QAAMNPKNTI FDIKRLIGR YEDPIVKDI ESWPFKVVDQ 101 GGNPVVEVEY LGETKTFSPQ EISSMVLMM KEVAETKLGK KVEKAVITVP 151 AYFNDNQRQA TKDAGAIAGL NVLRIINEPT AAAIAYGLGS GKSEKERNVL 201 IYDLGGGTFD VSLNLIQGGV FTVKATAGDT HLGQDFDTN LLEHFKKEFQ 251 KKTGKDLSGD ARALRRLRTA CERAKRTLSN ATQTTVEIDS LFDGEDFNSS 301 ITRARFEDLN AKAFSGTLEP VQQVLKDSGL EKSQVDEIVL VGGSTRIPRI 351 QKLLSDFFDG KKLEKSINPD EAVAYGAAVQ AGILSGKATS AETQDLLLLD 401 VVPLSLGVAM EGNIFAPVVP RGQTVPTIKK RFTTVVDNQ TTVQFPVYQG 451 ERTNCADNTS LGEFTLAPIP PMKAGEAALE VVFEVDVNGI LKVTATEKSS 501 GRSANITISN AVGKLSTTEI EQMINDAAKF KSSDEAFTKK FESRQQLSEY 551 ISRVEEIIISD PTMSLKLKRG NKEKIESALS DAMAQLEIED SAPEDYKKKE 601 LALKRLITKA MATR 80 - 87 510.2887 1018.5628 1018.5447 0.0181 1 R.RYEDPIVK.K 97 - 115 1016.5377 2031.0608 2031.0161 0.0448 0 K.VVDQGGNPVVEVEYLGETK.T 145 - 158 804.4228 1606.8310 1606.8103 0.0207 0 K.AVITVPAYFNDNQR.Q 163 - 174 585.3424 1168.6702 1168.6564 0.0138 0 K.DAGAIAGLNVLR.I 175 - 192 582.6591 1744.9555 1744.9359 0.0196 0 R.IINEPTAAAIAYGLGSGK.S 175 - 192 873.4902 1744.9658 1744.9359 0.0299 0 R.IINEPTAAAIAYGLGSGK.S 313 - 326 758.9335 1515.8524 1515.8297 0.0228 0 K.AFSGTLEPVQQVLK.D 313 - 332 716.0677 2145.1813 2145.1317 0.0495 1 K.AFSGTLEPVQQVLKDSGLEK.S 333 - 346 730.4066 1458.7986 1458.7678 0.0308 0 K.SQVDEIVLVGGSTR.I 353 - 361 521.2710 1040.5274 1040.5179 0.0096 0 K.LLSDFFDGK.K 366 - 387 711.0504 2130.1294 2130.0957

							0.0337 0 K.SINPDEAVAYGAAVQAGILSGK.A 432 - 452 810.7466 2429.2180 2429.1864 0.0316 0 R.TFTTVVDNQTTVQFPVYQGER.T 545 - 553 562.2959 1122.5772 1122.5669 0.0103 0 R.QQLESYISR.V
48	XP_7526 31	79995	293	10	5.08	Hsp70 chaperone Hsp88	Sequence Coverage: 14% 1 MSVVGIDFGA QSTKVGVARN KGIDIITNEV SNRSTPTLVG FGTR SRHIGE 51 GAKTQEMSNL KNTVGNLKR IGR SFNDPDV EIEQ KYTSAA ICDVNGQAGV 101 EVSYLGKKEK FSATQLAAMY LTKIRDITSK ELKLPVSDVT ISVPAWFTDA 151 QRRAMIDAGE IAGLKVLRLI NDTTATALGY GITKLDLPGP EEKPR VMFV 201 DIGHSDYTAS VVEFRKGELN VKATAYDRHF GGRDFDIALT EHFADFKEK 251 FKIDVRSNPK AYARTVAAAE KMKKVLSANP AAPMSIESLM EDVDVRSIVK 301 REELETMVKP LLER VTIPIE EALAEAK LKP EDIDTIEMVG GCTRVPAIKE 351 AISKFFGK TL SFTLNQDEAI ARG CAFSCAI LSPVFRVRDF SVHDIVNYPI 401 EFTWEQSADI PDEDTS�TVF NRGNVMPSTK ILTFYRK QPF DLEAR YAKPD 451 MLPGKINPWI GRFSVKGVKA DANDDFMICK LKARLNLHGI LNVESGYVE 501 DVEVEEPVDE DKMDTDAPEG EQPKKTRKVK KQVRKGDLP I STGTNSVDQT 551 VKETWIEREN AMYMEDKLIA ETDEKKNELE STIYELRDKI DGVYAEFASE 601 EEKDKLRAKL TDMEDWLYEE GEDTTKSVYV AKLDEIR FIA GPIVQR YKEK 651 IEAERQAILK AQEEEEAAKKR AEEEEAKRKAEEAKKAEETK PDEEMKDAPA 701 EGEEAAPAEGE EKQQ 22 - 33 665.8676 1329.7206 1329.6888 0.0318 0 K.GIDIITNEVSNR.S 34 - 44 568.3215 1134.6284 1134.6033 0.0251 0 R.STPTLVGFGTR.S 74 - 85 710.8494 1419.6842 1419.6518 0.0325 0 R.SFNDPDVEIEQK.Y 169 - 184 826.4709 1650.9272 1650.8828 0.0444 0 R.LINDTTATALGYGITK.L 185 - 195 417.5722 1249.6948 1249.6666 0.0281 0 K.LDLPGPEEKPR.R 315 - 327 692.4089 1382.8032 1382.7657 0.0376 0 R.VTIPIEEALAEAK.L 315 - 327 692.4202 1382.8258 1382.7657

						0.0602 0 R.VTIPIEEALAEAK.L 359 - 372 789.9308 1577.8470 1577.8049 0.0421 0 K.TLSFTLNQDEAIAR.G 438 - 445 488.2589 974.5032 974.4821 0.0211 0 K.QPFDLEAR.Y 638 - 646 500.8084 999.6022 999.5865 0.0157 0 R.FIAGPIVQR.Y
38	XP_7479 26	80590	613	13	4.95	Asp f12/Heat shock protein P90/Molecular chaperone and allergen Mod- E/Hsp90/Hsp1 Sequence Coverage: 20% 1 MSSETFEFQA EISQLLSLI NTVYSNKEIF LRELISNASD ALDKIRYQSL 51 SDPTKLDTGK DLRIDIIPDK ENKTLTIRD TIGGMTKADLI NNLGTIARSG 101 TKQFMEALSA GADISMIGQF GVGFYSAYLV ADRVTTVVSKN NDDEQYIWES 151 AAGGTFTLTQ DTEGEQLGRG TKIILHLKDE QTDYLNESRI KEVVRKHSEF 201 ISYPIYLHVL KETEKEVPDE EAEETKEED EEKKAKIEEV DDEEEEEKKK 251 KKKTCTVKES KIEEEELNKT KPIWTRNPAD ITQEEYASFY KSLSNDWEDH 301 LAVKHFSVEG QLEFRAILYV PKRAPFDLFE TKTKNNIKL YVRRVFITDD 351 ATDLIPEWLG FIKGVVDS LPLNLSRETL QQNKIMKVIK KNIVKKTLEL 401 FNEIAEDREQ FDKFYSAFSK NIKLGIHEDA QNRQTLAKLL RYQSTKSGDE 451 ATSLADYVTR MPEHQKQIYY ITGESIKAVA KSPFLDSLKQ KNFEVLFLVD 501 PIDEYAFTQL KEFDGKKLVD ITKDFELEET EEEKAEREKE EKEYENLAKS 551 LKNILGDKVE KVVVSHKLVG SPCAIRTGQF GWSANMERIM KAQALRDTSM 601 SSYMSSKKT F EISPKSSI ELKKKVEADG ENDRTVKSIT QLLFETSLV 651 SGFTIEEPAS FAERIHKLVS LGLNIDEEAE TTEEKATEEA APAEATTGES 701 AMEEVD 33 - 44 638.3338 1274.6530 1274.6354 0.0177 0 R.ELISNASDALDK.I 33 - 46 515.6200 1543.8382 1543.8205 0.0176 1 R.ELISNASDALDKIR.Y 87 - 98 635.8681 1269.7216 1269.7041 0.0176 0 K.ADLINNLGTIAR.S 173 - 189 696.3751 2086.1035 2086.0694 0.0340 1 K.IILHLKDEQTDYLNESR.I 277 - 291 888.4280 1774.8414 1774.8050 0.0365 0 R.NPADITQEEYASFYK.S 323 - 332 612.3378 1222.6610 1222.6346

						0.0264 1 K.RAPFDLFETK.K 324 - 332 534.2825 1066.5504 1066.5335 0.0169 0 R.APFDLFETK.K 364 - 377 757.4090 1512.8034 1512.7784 0.0251 0 K.GVVDSIEDLPLNLSR.E 397 - 408 725.3771 1448.7396 1448.7147 0.0250 0 K.TLELFNEIAEDR.E 424 - 433 576.8013 1151.5880 1151.5683 0.0197 0 K.LGIHEDAQNR.Q 447 - 460 742.8643 1483.7140 1483.6791 0.0350 0 K.SGDEATSLADYVTR.M 467 - 477 657.8640 1313.7134 1313.6867 0.0268 0 K.QIYYITGESIK.A 668 - 685 995.5217 1989.0288 1988.9790 0.0499 0 K.LVSLGLNIDEEAETTEK.A
39a	XP_750490	69618	336	13	5.09	Molecular chaperone Hsp70 Sequence Coverage: 21% 1 MAPAVGIDLG TTYSCVGVFR DDRIEIIAND QGNRTTPSFV AFTDTERLIG 51 DAAKNQVAMN PHNTVFDAGR LIGRRFQDAE VQSDMKHWPV KVVEKGGKPI 101 IEVEFKGETK QFTPEEISSM VLTKMRETAE AYLGGTVNNA VITVPAYFND 151 SQRQATKDAG LIAGLNVLR INEPTAAAI A YGLDKKAEGE RNVLIFDLGG 201 GTFDVSLITI EEGIFEVKAT AGDTHLGGED FDNRLVNHFV NEFKRKHKKD 251 LTTNARALRR LRTACERAKR TLSSAAQTSI EIDSLFEGID FYTSITRARR 301 EELCQDLFRS TMEPVERVLR DAKLDKSSVH EIVLVGGSTR IPKIQRLVAD 351 FFNKEANKSI NPDEAVAYGA AVQAAILSGD TSSKSTNEIL LLDVAPLSLG 401 IETAGGVMTPLIKRNTTIPT KKSETFSTYS DNQPGVLIQV YEGERARTKD 451 NNLLGKFELTGIPPAPRGVP QIEVTFDQDA NGIMNVSAVE KGTGKTNKIT 501 ITNDKGRLSK EEIERMLADA EKYKEEDEAE AARIQAKNGL ESYAYSLKNT 551 ISEGKLNISD ADKEKVSSKV EEIISWLDNN QTATKDEYES QQKELESVAN 601 PIISAAYGGA AGAAPGGAAP GGATRTADEV EERPEELD 5 - 47 736.3688 1470.7230 1470.6991 0.0240 0 R.TTPSFVAFTDTER.L 158 - 169 606.3643 1210.7140 1210.7034 0.0107 0 K.DAGLIAGLNVLR.I) 219 - 234 559.2525 1674.7357 1674.7234 0.0123 0 K.ATAGDTHLGGEDFDNR.L 219 - 234 838.3826 1674.7506 1674.7234

						0.0272 0 K.ATAGDTHLGGEDFDNR.L 235 - 244 623.8430 1245.6714 1245.6506 0.0208 0 R.LVNHFVNEFK.R 235 - 244 416.2338 1245.6796 1245.6506 0.0290 0 R.LVNHFVNEFK.R 347 - 354 477.2595 952.5044 952.5018 0.0026 0 R.LVADFFNK.E 359 - 384 845.7736 2534.2990 2534.2500 0.0490 0 K.SINPDEAVAYGA AVQAAILSGDTSSK.S 457 - 467 599.3448 1196.6750 1196.6553 0.0197 0 K.FELTGIPPAPR.G 508 - 515 502.2818 1002.5490 1002.5345 0.0145 1 R.LSKEEIER.M 523 - 533 437.5370 1309.5892 1309.5786 0.0106 1 K.YKEEDEAEAAAR.I 538 - 548 622.8206 1243.6266 1243.6084 0.0182 0 K.NGLESYAYSLK.N 626 - 638 766.3547 1530.6948 1530.6685 0.0263 0 R.TADEVEERPEELD.-
39b	XP_750490	69618	5.09	21	693	Molecular chaperone Hsp70 Sequence Coverage: 26% 1 MAPAVGIDLG TTYSCVGVFR DDRIEIIAND QGNRTTPSFV AFTDTERLIG 51 DAAKNQVAMN PHNTVFDAKR LIGRRFQDAE VQSDMKHWPV KVVEKGGKPI 101 IEVEFKGETK QFTPEEISSM VLTKMRETAE AYLGGTVNNA VITVPAYFND 151 SQRQATKDAG LIAGLNLRI INEPTAAAI YGLDKKAEGE RNVLIFDLGG 201 GTFDVSLITI EEGIFEVKAT AGDTHLGGED FDNRLVNHFV NEFKRKHKKD 251 LTTNARALRR LRTACERAKR TLSSAAQTSI EIDSLFEGID FYTSITRARF 301 EELCQDLFRS TMEPVERVLV DAKLDKSSVH EIVLVGGSTR IPKIQRLVAD 351 FNKEANKSI NPDEAVAYGA AVQAAILSGD TSSKSTNEIL LLDVAPLSLG 401 IETAGGVMTPLIKRNTTIPT KKSETFSTYS DNQPGVLIQV YEGERARTKD 451 NNLLGKFELT GIPPAPRGVP QIEVTFDVDA NGIMNVSAVE KGTGKTNKIT 501 ITNDKGRLSK EEIERMLADA EKYKEEDEAE AARIQAKNGL ESYAYSLKNT 551 ISEGKLNISD ADKEKVSSKV EEIISWLDNN QTATKDEYES QQKELESVAN 601 PIISAAYGGA AGAAPGGAAP GGATRTADEV EERPEELD 24 - 34 621.8320 1241.6494 1241.6364 0.0131 0 R.IEIIANDQGNR.T

						35 - 47 736.3662 1470.7178 1470.6991 0.0188 0 R.TTPSFVAFDTER.L 158 - 169 606.3650 1210.7154 1210.7034 0.0121 0 K.DAGLIAGLNVLR.I 170 - 185 553.9749 1658.9029 1658.8879 0.0150 0 R.IINEPTAAAIAYGLDK.K 170 - 185 830.4614 1658.9082 1658.8879 0.0204 0 R.IINEPTAAAIAYGLDK.K 170 - 186 596.6722 1786.9948 1786.9828 0.0119 1 R.IINEPTAAAIAYGLDKK.A 219 - 234 559.2504 1674.7294 1674.7234 0.0060 0 K.ATAGDTHLGGEDFDNR.L 219 - 234 838.3850 1674.7554 1674.7234 0.0320 0 K.ATAGDTHLGGEDFDNR.L 235 - 244 623.8408 1245.6670 1245.6506 0.0164 0 R.LVNHFVNEFK.R 235 - 244 623.8414 1245.6682 1245.6506 0.0176 0 R.LVNHFVNEFK.R 235 - 244 416.2370 1245.6892 1245.6506 0.0386 0 R.LVNHFVNEFK.R 327 - 340 480.9323 1439.7751 1439.7733 0.0018 0 K.SSVHEIVLVGGSTR.I 327 - 340 720.9034 1439.7922 1439.7733 0.0190 0 K.SSVHEIVLVGGSTR.I 347 - 354 477.2532 952.4918 952.5018 - 0.0100 0 R.LVADFFNK.E 347 - 354 477.2624 952.5102 952.5018 0.0084 0 R.LVADFFNK.E 359 - 384 845.7729 2534.2969 2534.2500 0.0469 0 K.SINPDEAVAYGAAVQAAILSGDTSSK.S 457 - 467 599.3398 1196.6650 1196.6553 0.0097 0 K.FELTGIPPAPR.G 457 - 467 599.3604 1196.7062 1196.6553 0.0509 0 K.FELTGIPPAPR.G 508 - 515 502.2781 1002.5416 1002.5345 0.0071 1 R.LSKEEIER.M 538 - 548 622.8209 1243.6272 1243.6084 0.0188 0 K.NGLESYAYSLK.N) 626 - 638 766.3547 1530.6948 1530.6685 0.0263 0 R.TADEVEERPEELD.-
40	XP_753589	55586	412	15	5.30	ATP synthase F1, beta subunit Sequence Coverage: 31% 1 MFKSGGLARTF GRAAFARPS VARRAIQPVR YNGLPSLARF ASSEAGSVGK 51 IHQVIGAVVD VKFDGDNLPA ILNAJETENN GQKLVLVLEVSQ HLGENVVRTI 101 AMDGTEGLTR GAPARDTGAP IKIPVGPGTL GRIVNVTGDP IDERGPIKAT 151 KFAPIHAEAP EFTEQSTS AE

						ILVTGIK VVD LLAPYARGGK IGLFGGAGVG 201 KTVFIQELIN NIAKAHGGYS VFTGVGER TR EGNPLYHEMQ ETGVIQLEGE 251 SKVALVFGQM NEPPGARARV ALTGLTIAEY FRDEEGQDVL LFDNIFR FT 301 QAGSEVSALL GRIPSAVGYQ PTLAVDMGGM QERITTTKKG SITSVQAVYV 351 PADDLTD PAP ATTFAHLDAT TVLSR GISEL GIYP AVDPLD SKSRMLDPRI 401 VGEEHYAVAT RVQQMLQEYK SLQDIIAILG MDELSEADKL TVERARKLQR 451 FLSQPFTVAQ VFTGIEGKLV DLKDTIRSFK AIINGEGDDL PEAIFYMVG D 501 FESARAKGEK ILAELEGKA 84 - 98 564.6611 1690.9615 1690.9366 0.0249 0 K.LVLEVSQHLGENVVR.T 116 - 132 550.3268 1647.9586 1647.9308 0.0278 1 R.DTGAPIKIPVGPGLGR.I 133 - 144 664.3539 1326.6932 1326.6779 0.0153 0 R.IVNVTDGPIDER.G 133 - 148 574.9902 1721.9488 1721.9312 0.0176 1 R.IVNVTDGPIDERGPIK.A 178 - 187 558.8283 1115.6420 1115.6339 0.0082 0 K.VVDLLAPYAR.G 191 - 201 488.2902 974.5658 974.5549 0.0109 0 K.IGLFGGAGVGK.T 202 - 214 751.9456 1501.8766 1501.8504 0.0262 0 K.TVFIQELINNIK.A 215 - 228 479.5700 1435.6882 1435.6844 0.0037 0 K.AHGGYSVFTGVGER.T 299 - 312 718.3895 1434.7644 1434.7467 0.0178 0 R.FTQAGSEVSALLGR.I 299 - 312 718.3974 1434.7802 1434.7467 0.0336 0 R.FTQAGSEVSALLGR.I 376 - 392 887.4830 1772.9514 1772.9196 0.0318 0 R.GISELGIYPVDPLDSK.S 400 - 411 448.9020 1343.6842 1343.6834 0.0008 0 R.IVGEEHYAVATR.V 400 - 411 672.8567 1343.6988 1343.6834 0.0155 0 R.IVGEEHYAVATR.V 451 - 468 985.0487 1968.0828 1968.0357 0.0472 0 R.FLSQPFTVAQVFTGIEGK.L 511 - 519 472.2781 942.5416 942.5386 0.0031 1 K.ILAELEGKA.-
41	XP_750312	29183	615	12	9.18	40S ribosomal protein S3 Sequence Coverage: 56% 1 MAAVQGAISK RRRKFVADGVF YAE LNEFFQR ELAEEGYSGV EVRVTPTVTD 51 IIIRATHTQE VLGEQGRIR ELTSLIQKRF

						KFPENSVS LY AAKVQNRGLS
						101 AVAQCESLR Y KLLNGLAVRR ACYGVLR FIM ESGAKGCEVV VSGKLRAARA
						151 KSMKFTDGF M IHSQPAKEF IDSATRHVLL RQGV LGIKVK IMRGSDPEGK
						201 AGPQK TLPDS VTIEPKKEEQ PVLQPM SQDY GAKALAAQQL AEQQRLAEQQ
						251 AAEGQEGAGA EAYAQE
						31 - 43 719.3351 1436.6556 1436.6783 - 0.0227 0 R.ELAEEGYSGVEVR.V
						44 - 54 614.3578 1226.7010 1226.7234 - 0.0224 0 R.VTPTVTDIIR.A
						44 - 54 614.3583 1226.7020 1226.7234 - 0.0214 0 R.VTPTVTDIIR.A
						55 - 67 475.9031 1424.6875 1424.7008 - 0.0133 0 R.ATHTQEV LGEQGR.R
						55 - 68 527.9338 1580.7796 1580.8019 - 0.0223 1 R.ATHTQEV LGEQGRR.I
						80 - 93 800.9128 1599.8110 1599.8297 - 0.0186 1 R.FKFPENSVS LYAAK.V
						98 - 109 645.8162 1289.6178 1289.6398 - 0.0219 0 R.GLSAVAQCESLR.Y Carbamidomethyl (C)
						112 - 119 428.2694 854.5242 854.5338 - 0.0095 0 K.LL NGLAVR.R)
						128 - 135 449.7114 897.4082 897.4266 - 0.0183 0 R.FIMESGAK.G Oxidation (M)
						136 - 144 467.7309 933.4472 933.4590 - 0.0117 0 K.GCEVV VSGK.L Carbamidomethyl (C)
						136 - 144 467.7334 933.4522 933.4590 - 0.0067 0 K.GCEVV VSGK.L Carbamidomethyl (C)
						155 - 168 517.9077 1550.7013 1550.7188 - 0.0175 0 K.FTDGFMIHSGQPAK.E Oxidation (M)
						169 - 176 469.7246 937.4346 937.4505 - 0.0159 0 K.EFIDSATR.H
						169 - 176 469.7295 937.4444 937.4505 - 0.0061 0 K.EFIDSATR.H
						206 - 217 656.8666 1311.7186 1311.7286 - 0.0099 0 K.TLPDSVTIIEPK.E
						206 - 217 656.8704 1311.7262 1311.7286 - 0.0023 0 K.TLPDSVTIIEPK.E
						218 - 233 918.4173 1834.8200 1834.8407 - 0.0207 0 K.EEQPVLQPM SQDYGAK.A Oxidation (M)
						234 - 245 663.8542 1325.6938 1325.7051 - 0.0113 0 K.ALAAQQLAEQQR.L
						234 - 245 663.8573 1325.7000 1325.7051 -

							0.0051 0 K.ALAAQQLAEEQQR.L
42	XP_751171	85475	389	17	6.26	Mitochondrial aconitate hydratase	Sequence Coverage: 21% 1 MISTRRLARAG ALAPKSRLFL GTRAFATVGD SPLDKKVEA NTEKGNVINY 51 KKMSENLDIV RRRLQRPLTY AEKVLVSHLD DPHGQEIERG KSYLKLRPDR 101 VACQDATAQM AILQFMSAGM PSVATPTTVH CDHLIEAQVG GDKDLARANE 151 INKEVYDFLA SATAKYNIGF WKPGSGIIHQ IVLENYAFPG GLMIGTDSHT 201 PNAGGLAMAA IGVGGADAVID VMAGLPWELK APKVIGVKLT GEMSGWTPK 251 DVILKVAGLL TVKGGTGAI EYHGPVTSLSCTGMGTICN MGAEIGATTS 301 MFPFNDRMYD YLKATKRQHI GDFAREYAKE LREDEGAEYD QLEINLSEL 351 EPHINGPFTP DLATPISKFK EAVETNKWPE ELKVGLIGSC TNSSYEDMSR 401 AASIARDALN HGLKAKSLFT VTPGSEQIRA TIERDGLQQT LEEFGGVILA 451 NACGPCIGQW DRRDVKKGEP NSIISSYNRN FTGRNDANPA THAFVASPDL 501 VVAMTIAGTL KFNPLTDKLL DKDGNFLLQ PPTGEGLPK GYDPGRDTYQ 551 APPADRSSVN VAVSPTSDRL QLLAGFEPWD GKDANGIPIL IKCQGKTTTD 601 HISMAGPWLK YRGHLDNISN NMLIGAVNAE NGKANSVKNK FTGEYDAVPA 651 TARDYKARGV KVVVIGDWNV GEGSSREHAA LEPRHLGGLA IITRSFARIH 701 ETNLKKQGML PLTFADPADY DKINPEDTVD LLCTQLEVKG PMTLRVHPKD 751 GSAPFDISLN HTFNESQIEW FKDGSALNTM ARKSGAK 63 - 73 458.9341 1373.7805 1373.7779 0.0026 1 R.RLQRPLTYAEK.V 64 - 73 406.8962 1217.6668 1217.6768 - 0.0100 0 R.LQRPLTYAEK.V 74 - 89 636.6498 1906.9276 1906.9173 0.0102 0 K.VLYSHLDDPHGQEIER.G 148 - 165 662.0120 1983.0142 1982.9949 0.0193 1 R.ANEINKEVYDFLASATAK.Y 154 - 165 657.8387 1313.6628 1313.6503 0.0125 0 K.EVYDFLASATAK.Y 256 - 263 400.7673 799.5200 799.5167 0.0033 0 K.VAGLLTVK.G 417 - 429 717.8925 1433.7704 1433.7514 0.0190 0 K.SLFTVTPGSEQIR.A 512 - 520 538.3137 1074.6128 1074.6073

						0.0055 1 K.FNPLTDKLLK.D 521 - 540 709.3689 2125.0849 2125.0691 0.0157 1 K.DKDGNEFLLQPPTGEGLPAAK.G 523 - 540 941.9929 1881.9712 1881.9472 0.0240 0 K.DGNEFLLQPPTGEGLPAAK.G 541 - 556 593.6111 1777.8115 1777.8020 0.0095 1 K.GYDPGRDITYQAPPADR.S 557 - 569 659.8389 1317.6632 1317.6525 0.0108 0 R.SSVNVAVSPTSDDR.L 583 - 592 527.3240 1052.6334 1052.6230 0.0105 0 K.DANGIPIILK.C) 639 - 653 547.2748 1638.8026 1638.8002 0.0024 1 K.NKFTGEYDAVPATAR.D 641 - 653 699.3455 1396.6764 1396.6623 0.0142 0 K.FTGEYDAVPATAR.D 677 - 684 461.7411 921.4676 921.4668 0.0009 0 R.EHAALPR.H 685 - 694 525.8295 1049.6444 1049.6346 0.0099 0 R.HLGLAITR.S
43	XP_754479	43328	66	2	4.81	Aspartic endopeptidase Pep2 Sequence Coverage: 8% 1 MKSTSLTAS VLLGSASAAV HKLKLNVPL DEQLYTHNID AHVRALGQKY 51 MGIRPNVHQE LLEENSLNDM SRHDLVLDNF LNAQYFSEIS LGTPPQKFKV 101 VLDTGSSNLW VPGSDCSSIA CFLHNKYDSS ASSTYKANGT EFAIKYGSGE 151 LSGFVSQDTL QIGDLKVVKQ DFAEATNEPG LAFAFGRFDG ILGLGYDTIS 201 VNKIVPPFYN MLDQGLLDEP VFAFYLGDTN KEGDNSEASF GGVDKNHYTG 251 ELTKIPLRRK AYWEVDFDAI ALGDNVAELE NTGIILDTGT SLIALPSTLA 301 DLLNKEIGAK KGFTGQYSIE CDKRDSLPLD TFTLAGHNFT IGPYDYTLEV 351 QGSCISSFMG MDFPEPVGPL AILGDAFLRK WYSVYDLGNN AVGLAKAK 170 - 187 970.9763 1939.9380 1939.9064 0.0316 0 K.QDFAEATNEPGLAFAFGR.F 188 - 203 856.4617 1710.9088 1710.8829 0.0260 0 R.FDGILGLGYDTISVKN.I
44	XP_749744	56152	260	7	4.58	Protein disulfide isomerase Pdi1 Sequence Coverage: 16% 1 MRSFAPLVLS LLGASAVASA DATADTTSDV VSLTKDSFKD FMKEHDLVLA 51 EFYAPWCGHC KALAPKYEEA ATELKGNIP LVKVDCTEEE DLCKENGVEG 101 YPTLKIFRGP DSSKPYQGAR QADSIVSYMI KQSLPAVSTV TEENLEEIKT

						151 MDKIVVIGYF ASDDKAANDV FTSFAESQRD NYLFAATSDS AIAKAEGVKQ 201 PSIVLYKDFD EKKAVYDGA EQEAILSWVK TASTPLVGEI GPETYSSYIT 251 AGIPLAYIFA ETKEERDQYA EDFKPVAEKH KGAINIATID AKMFGAHAGN 301 LNLDPQTTPA FAIQDPEKNA KYPYDQSRREF NAKEIGKFIQ DVLDGKVEPS 351 IKSEPIPETQ EGPVTVVVVAH SYQDIVINND KDVLLIFYAP WCGHCKALAP 401 KYEELAALYA GDFKDKVTIA KIDATANDVP DSITGFPTIK LYPAGAKDSP 451 VEYSGSRIVE DLANFIKENG KVKVDALVAA SEKVEEGPDV TASPSATSTE 501 AEAPAAATGDE KGDHDEL 67 - 75 527.2641 1052.5136 1052.5026 0.0111 0 K.YEEAATELK.G 154 - 165 663.8634 1325.7122 1325.6867 0.0255 0 K.IVVIGYFASDDK.A 180 - 194 793.9009 1585.7872 1585.7624 0.0249 0 R.DNYLFAATSDSAIAK.A 282 - 292 543.8177 1085.6208 1085.6080 0.0128 0 K.GAINIATIDAK.M 322 - 328 464.7173 927.4200 927.4086 0.0114 0 K.YPYDQSR.E 422 - 440 988.0107 1974.0068 1973.9946 0.0123 0 K.IDATANDVPDSITGFPTIK.L 458 - 467 575.3217 1148.6288 1148.6077 0.0211 0 R.TVEDLANFIK.E
45	XP_7556 86	93139	58	4	6.51	Translation elongation factor EF-2 subunit Sequence Coverage: 5% 1 MVNFTIEIR SLMDRPTNIR NMSVIAHVDH GKSTLTDSMI QRAGIISAAC 51 AGEGRYMDTR PDEQDRGITI KSTAIPLYAK FPDPEDLKEI PQKVDGAEFL 101 VNLIDSPGHV DFSSEVTAAL RVTDGALVVV DCVEGVVCVQT ETVLRQALTE 151 RIKPVLINK VDRALLELQV SKEDLYQSFS RTVESVNVII ATYHDKALGD 201 VQVYPDRGTV AFGSGLHGWA FTVRQFAVKY AKKFGVDRKK MLERLWGDNY 251 FNPQTKKWTG TGEPEQRAFN MFILDPIFKI FAAVNNDKTE EIHKLVEKLE 301 IKLASDEKDL KGKALLKVIM RKFLPAADAM LEMICHLPS PVTAQKYRAE 351 TLYEGPMDDE CAIGIRDCDP KAPLMYLVSK MVPTSDKGRF YAFGRVFSGI 401 VKSGLKVRIQ GPNYIPGKKD DLFVKAIQRT ILMMGFRFVEP IEDVPAGNIV

						451 GLVGVDQFL KSGTLTTSET AHNLKVMKFS VSPVVQRGVE VKNAQDLPKL 501 VEGLKRLSKS DPCVLTMIN SGQHIVAGAG ELHLEICKD LEEDHAGVPL 551 RISDPVVSYSR ETVGGESSMT ALSKSPNKHNL RLYVTAQPLG EEVSLAIESG 601 KINPRDDFKA RARLLADDYG WDVTDARKIW CFGPDTTGAN LLVDQTKAVQ 651 YLNEIKDSFV SGFQWATREG PIAEPMRSI RFNILDVTLH ADAIHRGGGQ 701 IIPARRVLY AATLLAEP VPEQAMGGIY GVLTRRRGHV 751 YSEEQRPGTP LFNVKAYLPV NESFGFNGDL RQATGGQAFP QSVFDHWSIL 801 PGGSPLDPTT KPGQTVAEMR KRKGLKEQVP GYDNYDDKL 2 - 10 560.8113 1119.6080 1119.5924 0.0156 0 M.VNFTIEIR.S 197 - 207 616.8245 1231.6344 1231.6197 0.0147 0 K.ALGDVQVYPDR.G 462 - 475 487.2554 1458.7444 1458.7314 0.0129 0 K.SGTLTTSETAHNLK.V 479 - 487 509.7906 1017.5666 1017.5607 0.0059 0 K.FSVSPVVQR.G
46	XP_7520 90	86840	89	6	6.33	Cobalamin-independent methionine synthase MetH/D Sequence Coverage: 6% 1 MVQSAVLGFP RMGKLRDLKK ATEAYWGGKI SRDELLSEGG RLRAEHWKIQ 51 KDAGVDIIPS NDAFYDQVL DHIQLFGVVP ERYSKYNLDP LDEYFAMGRG 101 LQKPASEGQP AIDVPSLEMV KWFDSNYHYV KPTLQENQVF KLASNPKPVA 151 QFLEAKEAGI ITRPVILGPV SFLTAKADR GQKIDPIDKI NDLVPVYVDL 201 LAQLKAAGVE DVQIDEPVLV FDLPAKSKAA FKPVEYKIGA LGDKAPRVL 251 ATYFGDIVHN IDVLPALHNL HGIHVDLVRN PEQLDAVIAA LGPKQVLSAG 301 VVDGRNIWKT NFKAIEKVE HAIQKLGKDR VIVSTSSSL HVPHTLESEK 351 NLDPEVREWF SFAVEKTHEV VVIKAVTEG PAAVRDQLEA NAKSVQARAS 401 SARTNDPKVK ERQAAVTEEM HNRKSPFPVR LAEQSKSINL PLFPTTTIGS 451 FPQTKEIRIQ RNKFTKGEIT AEEYEKFIEQ ELAEVVKIQE ELDLDVLVHG 501 EPERNDMVQY FGERLTGYVF TTHAWVQSYG SRCVRPPIIV GDISRPAPMT 551 VKESKYAVSI SKKPMKGMLT GPITCLRWSF PRDDVHQSVM AQQLALALRD

						601 EVIDLEAAGV KVIQVDEPAL REGLPLRAGK EREDYLTWAV RAFRLATSGV 651 SDGTQIHSHF CYSEFQDFH AIAALDADVL SIENSKSDAK LLKVFVEEAY 701 PRHIGPGVYD IHSPRVPSEQ EIKDRIEEML PYLRPDQLWI NPDCGLKTRQ 751 WPETKAALTN MVNAAKFYRQ KYTK 2 - 11 537.3082 1072.6018 1072.6029 - 0.0011 0 M.VQSAVLGFPR.M 2 - 11 537.3125 1072.6104 1072.6029 0.0075 0 M.VQSAVLGFPR.M 376 - 385 485.7758 969.5370 969.5243 0.0127 0 K.AVTEGPAAVR.D 477 - 487 652.8705 1303.7264 1303.7023 0.0241 0 K.FIEQEIAEVVK.I 612 - 621 570.3284 1138.6422 1138.6346 0.0076 0 K.VIQVDEPALR.E 703 - 715 483.2498 1446.7276 1446.7368 - 0.0092 0 R.HIGPGVYDIHSPR.V
47	XP_7526 50	41701	281	7	8.72	Isocitrate dehydrogenase, NAD-dependent Sequence Coverage: 17% 1 MISARNFVAP ARQCLRTRRV SSGFASHLSQ LRGYASAADD RVAKFKGQKG 51 PDGKYTVTLI EGDGIGPEIA QSVKDIFAAA KAPIKWEPVD VTPILKDGTK 101 TIPEEAIKSV QKNYVALKGP LATPVGKGHV SLNLTLRRTF NLFANLRPCR 151 SVAGYKTPYD NVDTVLIREN TEGEYSGIEH VVVDGVVQSI KLITREASER 201 VLRFAFQYAR SVNKKKVRVV HKATIMKMSD GLFLNTAREI AKEFPDIEFD 251 AELLDNSCLK IVTDPTPYND KVLVMPNLYG DILSDMCAGL IGGLGLTPSG 301 NIGDECSIFE AVHGSA PDIA GKGLANPTAL LLSSIMMLQH MGLHEHAARI 351 QKATFDTLAE GKTLTGDLGG KAKTHEYAEA ICKRL 100 - 108 501.2775 1000.5404 1000.5441 - 0.0036 0 K.TTIPEEAIK.S 157 - 168 703.3637 1404.7128 1404.7249 - 0.0121 0 K.TPYDNVDTVLIR.E 204 - 210 451.7187 901.4228 901.4446 - 0.0218 0 R.FAFQYAR.S 228 - 238 620.7956 1239.5766 1239.5918 - 0.0151 0 K.MSDGLFLNTAR.E Oxidation (M) 261 - 271 631.8155 1261.6164 1261.6190 - 0.0026 0 K.IVTDPTPYNDK.V 353 - 362 526.7635 1051.5124 1051.5186 - 0.0061 0 K.ATFDTLAEGK.T 363 - 371 431.2336 860.4526 860.4604 -

						0.0077 0 K.TLTGDLGGK.A
48	XP_752056	64987	63	2	6.39	Phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase Sequence Coverage: 3% 1 MSQQKSAILS VYDKTGLLDL AKGLVKHNVR LLASGGTARM IREAGFPVED 51 VSAITHAPEM LGGRVKTLP AVHGGILARD IESDEKDLAD QNISKVDFVV 101 CNLYPFKETV NKNVNTIAEA VEEIDIGGVT LLRAAAKNHA RVTILSDPQD 151 YPEFLKELEA GEISETSRKQ YALKAFEHTA DYDTAISGFF RKQYAGNGEQ 201 YLPLRYGANP HQKPASAYML HGKLPFKALN GSPGYINLLD ALNAWALVKE 251 LKQALGYPAASFSKHVSPAG AAVGVPSEK ERKVYMVDDI AGIETSGLAQ 301 AYARARGADR MSSFGDLLAL SDVCDVPTAK IISREVSDBGV IAAGYTPEAL 351 EILSKKKGGK YLVLMQMDENY VPASEETR TI YGVQLSQQRN DVVISPKQTF 401 NTIITPKDLK ALPDSALRDL TVATIALKYT QSNSVCYALN GQVIGLGAGQ 451 QSRIHCTRLA GDKADNWWMR FHDRVNLKWKAGTKRADKS NAIDLLCSGQ 501 TPRNEVEKAE YERVFEVPA PFTQEERDSW LSKMGEVAVS SDAFFPFIDN 551 VFRAARSGAK YIAAPSGSQN DGPVFETAEK LGIVFVEQGT RLFHH 379 - 389 646.8580 1291.7014 1291.6884 0.0130 0 R.TYGVQLSQQR.N 581 - 591 609.8524 1217.6902 1217.6768 0.0134 0 K.LGIVFVEQGTR.L
49	XP_754077	48306	94	4	4.43	Nucleosome assembly protein Nap1 Sequence Coverage: 11% 1 MSEPIRNKKA DFPVAPTQPN TPANNAPISS HAQQPGVASI KEESLDHATA 51 ASLFARNPGL VSMIQGKLGS LVGR SSGYIE SLPAPVRRRV AGLKGIQKEH 101 AKLEAQFQEE VLELEKKYFA KFTPLYQRRRA TIVNGAAEPT DDEVQAGKEE 151 EEEEEVDVKA EDERKQEEKD ITTPGIPEFW LSAMKNQISL AEMITDRDEE 201 ALKHLTDVRM EYLD RPPGFRL IFEFAENEFF TNKTISKTTY YKEESGYGGD 251 FIYDHAEGCK IDWKADKDLT VRVESKKQRN KNTKQTRVVK VTPVTESFFN 301 FFSPQPPTD DDDTIATDIE ER LELDYQLG EDIKEKLIPR AIDWFTGEAL 351 QFEELGDDMD ADEFDDDEDDE DEEDEDDEDD DRRSDRDVDD ESEEEVRFSS 401 LYASKYIFAS TPFFTMTAL PQS

						75 - 87 688.3735 1374.7324 1374.7143 0.0181 0 R.SSGYIESLPAPVR.R 103 - 116 852.9508 1703.8870 1703.8617 0.0253 0 K.LEAQFQEEVLELEK.K 122 - 128 462.7514 923.4882 923.4865 0.0018 0 K.FTPLYQR.R 323 - 336 564.9607 1691.8603 1691.8617 - 0.0015 1 R.LELDYQLGEDIKEK.L
50	XP_754843	46200	99	5	4.62	Ran GTPase activating protein 1 (RNA1 protein) Sequence Coverage: 12% 1 MAPPKVFSLE GKGLKLDTAE DIEAHIKPLI ESTDFTEIRL GGNTLGVPAS 51 ERLASVLASQ KSLEVADLAD IFTSRLLSEI PQALTALLNA LLEIKTLHTV 101 NLSDNAFGLN TQAPLVDFLS RHVPLRHLIL NNNGLGPAAG TLIADALTKL 151 AERKEEARKA GEEIPLLDSEI VCGRNRLENG SMEAWARAYK VHAAGIRSVK 201 MTQNGIRQEG ISLLKEGLR HASALEVLDL QDNTFTIMGS TALAGVVAGW 251 PSLRELGVGD CLLSARGGVK VAQALAEKGK QNIQTLRLQY NEITAEGVKL 301 FLHATKTALP SLRRIELNGN KFLEEDPNVT ELQEVLEARK EEHGTDDDPD 351 DMWGVDELDE LEESEEEEE AEEEEEEEEQ EEEERKADKF LKDNVKAEDE 401 KVAQRQDKDV DALAEALGKT AL 40 - 52 635.8472 1269.6798 1269.6677 0.0121 0 R.LGGNTLGVPASER.L 53 - 61 458.7786 915.5426 915.5389 0.0037 0 R.LASVLASQK.S 271 - 279 443.7540 885.4934 885.4920 0.0015 0 K.VAQALAEKGK.N 280 - 287 493.7731 985.5316 985.5305 0.0012 0 K.NQNIQTLR.L 288 - 299 682.8656 1363.7166 1363.6983 0.0183 0 R.LQYNEITAEGVK.L
51	XP_756019	46529	131	4	7.61	Curved DNA-binding protein Sequence Coverage: 11% 1 MEAWYQSHTL ASVRGHNIYF TMAENQAPEV DYTLNPNPDL TKYKTAAQIS 51 HKVLEAVTAL CSEGAKIVEI CQKGDELLEE ELTKVYKGKK ITKGIGHPTT 101 VSPSSYVTPY TPLVSDAQEA ETTLKAGEIV KIQLGAQIDG FGTIVCDMVV 151 VADKESPKDV VTGREADLIH ATHYANELLL RLMVPPGLLA SGTEEEKKKA 201 AAEKPPTQSQ ISALIEKVAK

						AYDCNVVENT TSWLFRNEI EGGKKIILAP 251 GSGVKGEVGP DVGEVWGVEV GLSLGSGKVK TLPHRATLHR RTTTYILKR 301 PSSRQTLSEI VKKFGTFPFS LRQLEDEKSA KVGVEVCVRG GVLRRQYEPAG 351 DADNAPVSRL LTTIAITKNG ITRLAAPNPP DLSKFQTDKK IEDEEILKIL 401 ERPLARNTGN KNKKKKKPTK DSKDEE 74 - 84 638.3303 1274.6460 1274.6241 0.0219 0 K.GDELLEELTK.V 246 - 255 477.8061 953.5976 953.5910 0.0067 0 K.IILAPGSGVK.G 345 - 359 795.3772 1588.7398 1588.7117 0.0281 0 R.QYEPAGDADNAPVSR.L 374 - 384 561.8163 1121.6180 1121.6080 0.0100 0 R.LAAPNPPDLSK.F
52	XP_754690	57418	276	5	5.44	Phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent Sequence Coverage: 11% 1 MTKVDHKVVL IVIDGWGIPG PDSPKGDGAI AAAETPYMSG FAEENSKTAQ 51 GYTELDASSL AVGLPEGLMG NSEVGHLNIG AGRVWQDSV RIDQTLKKGE 101 LNKVDNVVKS FTRAKEGNR LHLLGLVSDG GVHSNITHLV GLLKVAKEME 151 IPQVFIHFFG DGRDTPKSA IKYMQDLLDH TKEIGIGEIA TVVGRYYAMD 201 RDKRWDRVEV AMKGIVSGEG EESDPVKTI KERYEKGEND EFLKPIIVGG 251 KERRVQDNDT LFFFNYSRDR VREITQLLGD YDRSPKPDFP YPKNIQITTM 301 TQYKTDYTFP VAFPPQHMG VLAEWLSKKD IQQCHVAETE KYAHVTFFFN 351 GGIEKQFPGE VRDMIPSPKV PTYDHEPEMS AEA VGKKMAE RIAEGKFEFV 401 MNNFAPPDMV GHTGVYEAAI KGVAATDKAI GEIYQACKKH GYILFITADH 451 GNAEEMLTEK GTPKTSHTTN KVPFVLANAP EGWSLKKEEG VLGDVAPTVL 501 AAMGIEQPEE MSGKSLLVKA 84 - 91 494.7629 987.5112 987.5138 - 0.0025 0 R.VWQDSVR.I 183 - 195 657.3822 1312.7498 1312.7351 0.0148 0 K.EIGIGELATVVGR.Y 214 - 228 745.3665 1488.7184 1488.6944 0.0241 0 K.GIVSGEGEESDPVK.T 255 - 267 839.9080 1677.8014 1677.7787 0.0227 0 R.VQDNDTLFFFNYS.S 273 - 283 661.8368 1321.6590 1321.6514 0.0077 0 R.EITQLLDYDR.S

53	XP_748938	51999	101	4	6.25	Pyruvate dehydrogenase complex, dihydrolipoamide acetyltransferase component	Sequence Coverage: 11% 1 MVASAVRMRI PSAMLSKGGL YVRRPHVIHR FKDAVQPQLP ALSALSRFYA 51 SKSFPPHTII SMPALSPTMS AGNIGAWQKK AGDSLSPGDV LVEIETDKAQ 101 MDFEFQEEGV LAKVLKETGE KDVAVGTPIA VLVEEGTDVA PFESFTLEDA 151 GGDKGTAPPK ESKEEPKAEA APAPSTPEPA PAAQEPETST EKLQPSLDRE 201 PNISPAAKAL ALEKGVPIKA LKGTGRGGQI TKEDVEKYKP SISAAAAAPT 251 YEDIPLTSMR KTIATRLQQS MRENPHFFVS TTLSVTKLLK LRQALNASAE 301 GKYKLSVNDF LVKACAAALM KVPVAVNSSWR EENGQVVIRQ HNTVDISVAV 351 ATPNGLITPV VKNVHSLGLS SISNQIKDLG KRARENKLKP EEYQGGTFTI 401 SNMGMNPAVE RFTAVINPPQ AAILAVGTTR KVAVPVETEE GTSVEWDDQI 451 IVTGSFDHKV VDGAVGAEWI KELKKIVENP LELL 193 - 208 579.3189 1734.9349 1734.9264 0.0085 1 K.LQPSLDREPNISPAAK.A 227 - 237 401.8735 1202.5987 1202.6143 - 0.0156 1 R.GGQITKEDVEK.Y 331 - 339 522.2769 1042.5392 1042.5407 - 0.0015 0 R.EENGQVVIR.Q 412 - 430 970.5660 1939.1174 1939.0891 0.0284 0 R.FTAVINPPQAAILAVGTTR.K
54	XP_664146	41682	64	4	5.54	ACT_BOTCI Actin <i>A. nidulans</i>	Sequence Coverage: 13% 1 MPTEEVAALV IDNGSGMCKA GFAGDDAPRA VFPSIVGRPR HHGIMIGMQ 51 KDSYVGDEAQ SKRGILTTRY PIEHGVVTNW DDMEKIWHHT FYNELRVAPE 101 EHPVLLTEAP INPKSNREKM TQIVFETFNA PAFYVSIQAV LSLYASGRIT 151 GIVLDSGDGV THVVPYIEGF ALPHAISRVD MAGRDLTDYL MKILAERGYT 201 FSTTAEREIV RDIKEKLCYV ALDFEQEIQT ASQSSSLEKS YELPDGQVIT 251 IGNERFRAPE ALFQPSVLGL ESGGIHVTTF NSIMKCDVDV RKDLYGNIVM 301 SGGTTMYPGI SDRMQKEITA LAPSSMKVKI IAPPERKYSV WIGGSILASL 351 STFQQMWISK QEYDESGPSI VHRKCF 20 - 29 488.7349 975.4552 975.4410 0.0142 0 K.AGFAGDDAPR.A 240 - 255 895.9830 1789.9514 1789.8846

						0.0668 0 K.SYELPDGQVITIGNER.F 317 - 327 582.3156 1162.6166 1162.5903 0.0263 0 K.EITALAPSSMK.V Oxidation (M) 361 - 373 506.2470 1515.7192 1515.6954 0.0238 0 K.QEYDESGPSIVHR.K
55	XP_7522 65	40002	88	3	5.85	UPF0160 domain protein MYG1 Sequence Coverage: 8% 1 MADETVAKKL KTSPLLGTH NGHFHADEAL AVYLLRQLPT YASSPLIRTR 51 DPAQLATCHT VVDVGGEYDP ASNRYDHHQR TFSTTFPNHN TRLSAGLVY 101 MHFGRAlIAQ HTSLPLDHED VTLLYEKLYT DFIEAVDAND NGVSVYDPAA 151 LASANIEKRF RDGGITIASV VNDMNNPDPT CPPGEPQDED SLFNRASTFM 201 GHVFTRKLHH AFTSWLPARA TVGAAYQSR EVHPSGRIII LPQGGVPWKE 251 HLYNFEKEAS GAGDINPDEQ VYYVLYPESA TEGSKWRVQC VSVNEGSFES 301 RKPLPESWRG VRDADLDGCL AAEAESGKP KIPEGAVFVH ASGFIGGHKT 351 KEGAFAMAVR SLEL 37 - 48 673.3708 1344.7270 1344.7401 - 0.0131 0 R.QLPTYASSPLIR.T 220 - 229 512.2616 1022.5086 1022.5145 - 0.0058 0 R.ATVGAAAYQSR.R 352 - 360 484.2316 966.4486 966.4593 - 0.0106 0 K.EGAFAMAVR.S Oxidation (M)
56	XP_7517 80	50540	334	10	5.66	Homocitrate synthase Sequence Coverage: 28% 1 MCPGADNEPN GHTNGANGTV PHPGFTAVET RQNPSPASR NPYGHNVGVT 51 DFLSNVSRFK IESTLREGE QFANAFDTE KKIEIAKALD DFGVDYIELT 101 SPCASEQSRK DCEAICKLGL KAKILTHIRC HMDDARVAVE TGVGDGVDVVI 151 GTSSYLREHS HGKDMTYIKN TAIEVIEFVK SKGIEIRFSS EDSFRSDLVD 201 LLSIYSAVDK VGVNRVGIAD TVGCASPRQV YELVRVLRGV VSCDIETHFH 251 NDTGCAIANA YCALEAGATH IDTSVLGIGE RINGITPLGGL MARMMVADPE 301 YVKSKYKLEK LKDIEDLVAA AVEVNIPFNN YITGFCAFTH KAGIHAKAIL 351 NNPSTYEIIN PADFGMTRYV HFASRLTGWN AIKSRAQQLN IEMTDAQYKE 401 CTAKIKALAD IRPIAVDDAD SIIRAYYRNL KSGENKPLLD LTAEEQAQFA 451 AKEKELAGSG VIA 41 - 58 659.3185 1974.9337 1974.9548 -

						0.0211 0 R.NPYGHNVGVTDFLSNVSR.F 68 - 81 816.8560 1631.6974 1631.7104 - 0.0129 0 R.EGEQFANAFDTEK.K 137 - 157 1068.5507 2135.0868 2135.1111 - 0.0242 0 R.VAVETGVDGVDVVGITSSYLRE 170 - 180 631.8462 1261.6778 1261.6918 - 0.0139 0 K.NTAIEVIEFVK.S 188 - 195 487.7136 973.4126 973.4141 - 0.0015 0 R.FSSEDSFR.S 196 - 210 819.4235 1636.8324 1636.8560 - 0.0235 0 R.SDLVDLLSIYSAVDK.V 229 - 235 453.7491 905.4836 905.4971 - 0.0134 0 R.QVYELVR.V 282 - 293 608.3268 1214.6390 1214.6441 - 0.0051 0 R.NGITPLGGLMAR.M Oxidation (M) 294 - 303 607.7679 1213.5212 1213.5359 - 0.0146 0 R.MMVADPEYK.S 2 Oxidation (M) 407 - 424 642.0159 1923.0259 1923.0425 - 0.0166 0 K.ALADIRPIAVDDADSIHR.A
57	XP_755754	64716	284	10	7.55	Dihydroxy acid dehydratase IIv3 Sequence Coverage: 18% 1 MLLSQTRGRL PSTLRSFSRR ALSTTLPRGK DSEETALNKV SRNVTQPISQ 51 GASQAMLYAT GLTEEDMNKA QVGISVWYN GNPCNMHLLD LSNRVREGVQ 101 KAGLVGFQFN TVGVSDAISM GTKGMRYSLQ SRDLIADSIE TVMGGQWYDA 151 NISIPGCDKN MPGVLMAMGR VNRPSLMVYG GTIKPGCART QNNADIDIVS 201 AFQAYGQFLT GEITENQRFD IIRNACPGGG ACGGMYTANT MATAIEVMGM 251 TLPGSSSNPA ESKAKDLECL AAGEAIKRLL KEDIRPSDIL TRQAFENAMI 301 VVNITGGSTN AVLHLIAIAD SVGIKLDIED FQKVSDRTPF LADLKPSGKY 351 VMADLHNIGG TPSLLKFLK EGVIDGSGMT VTGETLAKNL EKVPDFPADQ 401 KIIRPLSNPI KKTGHIQILR GSLAPGGSVG KITGKEGTRF VGKARVFDDE 451 DDFIAALERN EIKKEEKTVV VIRYTGPKGG PGMPEMLKPS SALMGAGLGS 501 SCALITDGRF SGGSHGFLIG HIVPEAAVGG PIGLVKDGDT ITIDAEKRLL 551 DLDVDETELA RRRKEWEALR DAGKLPQTGL TMRGTLGKYA RTVKDASHGC 601 ITDSVE 160 - 170 612.7891 1223.5636 1223.5461 0.0176 0 K.NMPGVLMAMGR.V 3 Oxidation (M)

						279 - 292 556.9983 1667.9731 1667.9570 0.0161 1 R.LLKEDIRPSDILTR.Q 338 - 349 425.2448 1272.7126 1272.7078 0.0048 0 R.TPFLADLKPSGK.Y 371 - 388 890.9545 1779.8944 1779.8561 0.0384 0 K.EGVIDGSGMTVTGETLAK.N Oxidation (M) 421 - 431 465.2571 928.4996 928.4978 0.0018 0 R.GSLAPGGSVGK.I 446 - 459 827.9002 1653.7858 1653.7522 0.0336 0 R.VFDEDDFIAALER.N 537 - 548 445.2258 1332.6556 1332.6521 0.0035 1 K.DGDTITIDAEKR.L 549 - 561 751.4067 1500.7988 1500.7671 0.0317 0 R.LLDLDVDETELAR.R 549 - 562 553.2981 1656.8725 1656.8682 0.0042 1 R.LLDLDVDETELARR.R 575 - 583 516.7834 1031.5522 1031.5434 0.0089 0 K.LPQTGLTMR.G Oxidation (M)
58	XP_749237	58635	204	6	5.82	Myo-inositol-phosphate synthase Sequence Coverage: 11% 1 MAPHATSDAV ANGAVNGSAR TTTAPLFTVN SPNVEYTDNE IKSRYAYHHT 51 DITRTAEGKM VATPKVTNYQ FKVDRKVGKV GMMLVGWGGN NGSTVTAGIL 101 ANRRRLVWET REGERAANY GSLVMSSTVK LGTDSKTGEE INIPFHDMLP 151 MIHPNDLVIG GWDISSMNLA DAMDRAQVLE PTLKQLVRKE MAEMKPLPSI 201 YYPDFIAANQ EDRADNVIEG NKASWAHVER IQQDIRDFKA QNGLDKVIVM 251 WTANTERYAD IIPGVNDTAD NLLNAIKAGH QEVAPSTVFA VACILENVFP 301 INGSPQNTFV PGAIQLAEKH GAFIGGDDFK SGQTKMKSAL VDFLINAGIK 351 LTSIASYNHL GNNDGKNLSS QKQFRSKEIS KSNVDDMV ANHLLYKEGE 401 HPDHTTVIKY MPAVGDNKRA LDEYYAEIFM GGHQTISLFN ICEDSLLASP 451 LIIDLVVIAE MMTRITWKSA DDEEYKGFHS VLSVLSYMLK APLTPPGTPV 501 VNALAKQRSA LTNIACVGV LQPDSEMTLE HKLF 45 - 54 414.2033 1239.5881 1239.5884 - 0.0003 0 R.YAYHTTDITR.T 176 - 184 499.8025 997.5904 997.5808 0.0097 0 R.AQVLEPTLK.Q 214 - 222 480.2441 958.4736 958.4720 0.0017 0 R.ADNVIEGNK.A 320 - 330 582.2874 1162.5602 1162.5407

						0.0195 0 K.HGAFIGGDDFK.S 491 - 506 773.4732 1544.9318 1544.8926 0.0392 0 K.APLTPPGTPVVNALAK.Q 509 - 516 461.2667 920.5188 920.5080 0.0109 0 R.SALTNIFFR.A
59	XP_752164	49337	481	10	5.79	Glutamate/Leucine/Phenylalanine/V aline dehydrogenase Sequence Coverage: 24% 1 MSNLPHEPEF EQAYKELAST LENSTLFEKN PEYRKALAVV SVPERVVQFR 51 VVWEDDNHQQV QINRGYRVQF NSALGPYKGG LRFHPSVNLS ILKFLGFEQI 101 FKNALTGLNM GGGKGGSDFD PKGKSDNEIR RFCVAFMTEL CKHIGADTDV 151 PAGDIGVTGR EIGFLFGQYR KIRNQWEGVL TGKGGSWGGS LIRPEATGYG 201 LVYYVDHMIK YVTKGAESFA GKRVAISGSG NVAQFAALKV IELGGSVVSL 251 SDSKGSLLVN GEGSFTPAEI DIIAQLKVDR KQLSEVATTE AFATKFKYIE 301 GARPWVHVGGK VDVALPSATQ NEVSGEEAQA LIDAGCKFIA EGSNMGCTQA 351 AIDIFEHRQ ANPGAAAIWY APGKAANAGG VAVSGLEMAQ NSARISWTAE 401 EVDSRLKDIM ESCFRNGLDT AVKYATPAEG VLPSLVGTGSN IAGFTKVAEA 451 MKEQGDWW 35 - 45 584.8536 1167.6926 1167.6975 - 0.0049 1 R.KALAVVSVPER.V 36 - 45 520.8068 1039.5990 1039.6026 - 0.0035 0 K.ALAVVSVPER.V 68 - 78 612.3279 1222.6412 1222.6346 0.0066 0 R.VQFNSALGPYK.G 94 - 102 564.8085 1127.6024 1127.6015 0.0009 0 K.FLGFEQIFK.N 143 - 160 584.2945 1749.8617 1749.8646 - 0.0029 0 K.HIGADTDVPAGDIGVTGR.E 161 - 170 615.3186 1228.6226 1228.6241 - 0.0014 0 R.EIGFLFGQYR.K 215 - 223 461.7382 921.4618 921.4668 - 0.0050 1 K.GAESFAGKR.V 224 - 239 766.9347 1531.8548 1531.8358 0.0190 0 R.VAISGSGNVAQFAALK.V 240 - 254 745.4188 1488.8230 1488.8035 0.0195 0 K.VIELGGSVVSLSDSK.G 282 - 295 748.3948 1494.7750 1494.7566 0.0185 0 K.QLSEVATTEAFATK.F
60	XP_750781	114548	283	9	5.03	Assimilatory sulfite reductase Sequence Coverage: 10% 1 MMGSSSPSLS ALGGPTYVTA QTLIQQVAYI LSDKIFSYSP ESFDLDNALR

						51 EWASRQETNA IGESTVVKAM ETRQGAGNIA LGYLFSDQDFD LKKRHVPQGI 101 VASSATLPYM RSALEQLSLL YSVASPVAAH VAAVDYAGEN GLVSDYASAL 151 SLAEELGLGL VSSASVHEAQ HMALLTTLLA SVLPSVHIYD GVRVGRETTR 201 VIDVLDQAGV ARTYEAIKKT LDESRNRHLD TQGVLELFA SLNGELGTDY 251 GLFEYHGHA E PVSVLVAFGT VEASLTAQVA RSLAKDGVRV GVVNVRYRVP 301 FVEEEFLRVL PQSTKTVGVL GQVTDEQDVQ EQGVRSALEY DVLAALTFAS 351 GREHAPTCVD IKYPRSQRWD LINTAAAFQL IFEKPIPAS GESAPLQLID 401 PATVQEYTFW DVDSSVCESA AAVLSEALAA DSASNVTTSK SYDNLIQGGGA 451 LRIDIRKSSK ILDTPYAITA ADTTYVGDIK LLGDIDVAAS IKNKGVIIIN 501 APGVKDDELE KKLPLGFRQA VAQREISLYI VDPSAAGASA PESSVLQSAF 551 LRVALPSQEG VGLKKLSSIT GDSETLETVA KDLDKLLRQV EIPESWRISE 601 EGTEVTQLSK DISINSFVPF DKDEAEAPL LNDWQAAAKG LAFKEAYGTK 651 KALRPETATK TFTVHVKENR RLTPVTYDRN IFHIEFDLGD SGLKYDIGEA 701 LGVHAENDPQ EVSEFITFYG LNPDDVVGVP SREDPAVLEN RTVYQALVQN 751 VDIFGRPPKR FYEALAEFAT DEKEKKDLLT LGGPEGAVEF KRRAEVDTIT 801 FADVLEFPS AHPDFQDLIR IVGPLKRREY SIASCQKVTP NSVALMIVAV 851 NWVDPGRDR FGLATRYLSR LQPGTPVTVS VKSSVMKLPP KSTQPLIMAG 901 LGTGLAPFRA FVQHRALEKA QGKEIGAVLL YMGRHQREE YCYGEEWEAY 951 QEAGVITLLG RAFSRDQPEK IYIQDRMRET LPEIIQAYIR EEGAFYLCGP 1001 TWPVPDVTAV LEEAIA TEAK NTGKKVDTRK EIEKLKDEER YVLEVY 201 - 212 628.3577 1254.7008 1254.6932 0.0076 0 R.VIDVLDQAGVAR.T 441 - 452 653.8477 1305.6808 1305.6677 0.0132 0 K.SYDNLIQGGALR.I 481 - 492 607.8539 1213.6932 1213.6918 0.0015 0 K.LLGDIDVAASIK.N 497 - 511 547.3056 1638.8950 1638.8828 0.0121 1 K.VIINAPGVKDDELEK.K 553 - 565 442.5987 1324.7743 1324.7714
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						0.0028 1 R.VALPSQEGVGLKK.L 598 - 610 710.8676 1419.7206 1419.7093 0.0114 0 R.ISEEGTEVTQLSK.D 672 - 679 482.7568 963.4990 963.5025 - 0.0035 0 R.LTPVTYDR.N 733 - 741 521.7685 1041.5224 1041.5091 0.0134 0 R.EDPAVLENR.T 871 - 882 613.3641 1224.7136 1224.7078 0.0058 0 R.LQPGTPVTVSVK.S
61	XP_754687	51841	131	4	7.64	Serine hydroxymethyltransferase Sequence Coverage: 8% 1 MATYALSQAH REQMEKSLVD SDPEIAQIME KEIQRQRESI LLIASENVTS 51 RAVFDALGSP MSNKYSEGYP GARYYGGNQH IDAIELTCQA RALKAFNLDP 101 EKWGVNVQCL SGSPANLEVY QALMRPHDRL MGLDLPHGGH LSHGYQTPSR 151 KISAVSTYFE TFPYRVNTET GIIDYDTLEA NAELYRPKCL VAGTSAYCRL 201 IDYGRMRKIA DKVGAYLIVD MAHISGLVAA GVIPSPEYA DVVTTTTHKS 251 LRGPRGAMIF FRKGVRSTDP KTGKEIMYDL EGPINFSVFP GHQGGPHNHT 301 ITALAVALKQ AATPEFRQYQ EQVLKNAKAL EVEFKALGHK LVSDGTDSDM 351 VLLDLRPKGL DGARVEAVLE QINIACNKNS IPGDKSALTP CGIRIGTPAM 401 TSRGMSEEDF KRVARIDQV INLCKSIQAD LPKEANKLKD FKAKVASGSV 451 PEILALRKEV AEWASTYPLP V 52 - 64 676.8318 1351.6490 1351.6442 0.0049 0 R.AVFDALGSPMSNK.Y Oxidation (M) 65 - 73 500.2264 998.4382 998.4457 - 0.0075 0 K.YSEGYPGAR.Y 95 - 102 467.2356 932.4566 932.4603 - 0.0037 0 K.AFNLDPEK.W 395 - 403 475.2436 948.4726 948.4699 0.0028 0 R.IGTPAMTSR.G Oxidation (M)
62	XP_748936	35876	559	13	9.08	Malate dehydrogenase, NAD-dependent Sequence Coverage: 38% 1 MFAARQSFNL LQKRAFSASA SQASKVAVLG AAGGIGQPLS LLLKLNPRVS 51 ELALYDIRGG PGVAADLSHI NTNSTVTGYD PTPSGLRDAL KGSEIVLIPA 101 GVPRKPGMTR DDLFNTNASI VRDLAKAAAE ASPEANILVI SNPVNSTVPI 151 VAEVFKSKGV YNPKRLEFGVT TLDVVRASRF ISQIKKTDPA KEAVPVVGGH 201 SGVTIVPLLS QSNHPDIEGE

						TRDTLVNRIQ FGGDEVVKAK DGAGSATLSM 251 AMAGARFAES LLKAAQGEKG VIEPTFVESP LYKDQGVDFV ASRVELGPNG 301 VEKILEVGKV NAYEEKLIQA ALTDLKKNIQ KGRDFVAQNP 49 - 58 589.8170 1177.6194 1177.6343 - 0.0148 0 R.VSELALYDIR.G 88 - 104 579.0051 1733.9935 1734.0040 - 0.0105 1 R.DALKGSEIVLIPAGVPR.K 92 - 104 654.3834 1306.7522 1306.7609 - 0.0086 0 K.GSEIVLIPAGVPR.K 92 - 104 654.3902 1306.7658 1306.7609 0.0050 0 K.GSEIVLIPAGVPR.K 111 - 122 682.8453 1363.6760 1363.6732 0.0029 0 R.DDLFNTNASIVR.D 166 - 176 610.3547 1218.6948 1218.6972 - 0.0024 0 R.LFGVTTLDVVR.A 229 - 238 546.2822 1090.5498 1090.5659 - 0.0160 0 R.IQFGGDEVVK.A 241 - 256 749.8348 1497.6550 1497.6552 - 0.0001 0 K.DGAGSATLSMAMAGAR.F 2 Oxidation (M) 270 - 283 789.9274 1577.8402 1577.8341 0.0061 0 K.GVIEPTFVESPLYK.D 284 - 293 571.2678 1140.5210 1140.5200 0.0010 0 K.DQGVDFFASR.V 294 - 303 521.2324 1040.4502 1040.5502 - 0.1000 0 R.VELGPNGVEK.I 304 - 316 497.9310 1490.7712 1490.7980 - 0.0268 1 K.ILEVGVKNAYEEK.L 332 - 340 502.2418 1002.4690 1002.4883 - 0.0192 1 K.GRDFVAQNP.-
63	XP_754009	37156	381	11	7.55	Alcohol dehydrogenase Sequence Coverage: 31% 1 MTIPDKQWAQ VVLEKGSPPV YKEIPVPKPG PDDILVKLRY SGVCHTDLHA 51 MKGDWPLALK LPLVGGHEGV GVVVAKGELV TGFEIGDHAG IKWLNGSCME 101 CEFCKQSEEP LCPRATMSGY TVDGTFQQYC VAKATHASKI PNGVPLDAAA 151 PILCAGLTVY KGLKESGARP GQTVAIVGAG GGLGSLAQQY AKAMGLRVVA 201 IDGGDEKREM CEKLGAEAYI DFTKSTNVVE DVKAATPGGL GAHAVLLLAV 251 SEKPFQQATD YVRSRGTIVA IGMPAGAYLK APVFNTVVVKM ITIKGSYVGN 301 RQDGVEAIDF FARGLINAPF KKAPLKDLPK IFELMEQGVV AGRYVLEIPE 351

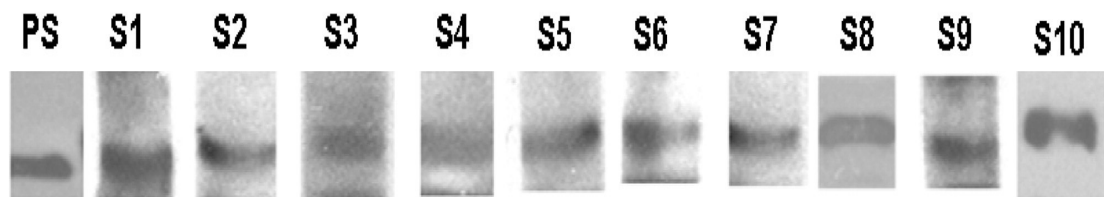
						23 - 37 539.6475 1615.9207 1615.9185 0.0022 0 K.EIPVPKPGPDDILVK.L 61 - 76 510.9688 1529.8846 1529.8930 - 0.0084 0 K.LPLVGGHEGVGVVAK.G 77 - 92 548.2800 1641.8182 1641.8362 - 0.0181 0 K.GELVTGFEIGDHAGIK.W 77 - 92 821.9328 1641.8510 1641.8362 0.0148 0 K.GELVTGFEIGDHAGIK.W 198 - 208 579.8058 1157.5970 1157.6040 - 0.0070 1 R.VVAIDGGDEKR.E 214 - 224 614.3152 1226.6158 1226.6183 - 0.0024 0 K.LGAEAYIDFTK.S 266 - 280 739.4138 1476.8130 1476.8010 0.0120 0 R.GTIVAIGMPAGAYLK.A Oxidation (M) 295 - 313 701.0146 2100.0220 2100.0025 0.0195 1 K.GSYVGNRQDGVEAIDFFAR.G 302 - 313 684.3364 1366.6582 1366.6517 0.0065 0 R.QDGVEAIDFFAR.G 314 - 321 430.2508 858.4870 858.4963 - 0.0093 0 R.GLINAPFK.K 331 - 339 555.7706 1109.5266 1109.5427 - 0.0160 0 R.IFELMEQGK.V Oxidation (M)
64a	XP_748145	36292	341	12	6.96	Glyceraldehyde 3-phosphate dehydrogenase GpdA Sequence Coverage: 28% 1 MATPKVGING FGRIGRIIGL NSLSHGLVDV VAVNDPFIEV HYAAYMLKYD 51 TTHGQFKGTI ETYDQGLIVN GKKIRFYAEK DPSQIPWSET GAAYIVESTG 101 VFTTKEKASA HLKGGAKKVI ISAPSADAPM FVMGVNNTTY TSDIQVLSNA 151 SCTTNCLAPL AKVINDKFGE VEGLMTTVHS YTATQKVVD PSNKDWRGGR 201 TAAQNIIPSS TGAAKAVGKV IPSLNGKLTG MAMRVPTSNV SVVDLTCRLE 251 KGASYDEIKQ AIKAASEEGE LKNILGYTED DVVSSDLNGD ERSSIFDAKA 301 GISLNPNFVK LVAWYDNEWG YSRRVVDLIA YIAKVDSQ 6 - 13 410.2177 818.4208 818.4399 - 0.0190 0 K.VGINGFGR.I 58 - 72 804.4276 1606.8406 1606.8203 0.0204 0 K.GTIETYDQGLIVNGK.K 201 - 215 715.3840 1428.7534 1428.7572 - 0.0038 0 R.TAAQNIIPSTGAAK.A 228 - 234 406.1888 810.3630 810.3728 - 0.0097 0 K.LTGMAMR.V 2 Oxidation (M) 228 - 248 780.4000 2338.1782 2338.1443 0.0338 1 K.LTGMAMRVPTSNVSVVDLTCR.L Carbamidomethyl (C); 2 Oxidation (M)

						235 - 248 773.9117 1545.8088 1545.7821 0.0267 0 R.VPTSNVSVVDLTCR.L Carbamidomethyl (C) 264 - 272 467.2303 932.4460 932.4451 0.0010 0 K.AASEEGELK.N 300 - 310 580.3291 1158.6436 1158.6397 0.0040 0 K.AGISLNPNFVK.L 324 - 334 420.9211 1259.7415 1259.7601 - 0.0187 1 R.RVVDLIAIYIAK.V 324 - 334 630.8852 1259.7558 1259.7601 - 0.0043 1 R.RVVDLIAIYIAK.V 325 - 334 552.8303 1103.6460 1103.6590 - 0.0130 0 R.VVDLIAIYIAK.V 325 - 338 767.4362 1532.8578 1532.8450 0.0128 1 R.VVDLIAIYIAKVDSQ.
64b	XP_748145	36292	162	6	6.96	Glyceraldehyde 3-phosphate dehydrogenase GpdA Sequence Coverage: 23% 1 MATPKVGING FGRIGRIIGL NSLSHGLVDV VAVNDPFIEV HYAAYMLKYD 51 TTHGQFKGTI ETYDQGLIVN GKKIRFYAEK DPSQIPWSET GAAYIVESTG 101 VFTTKEKASA HLKGGAKKVI ISAPSADAPM FVMGVNNTTY TSDIQVLSNA 151 SCTTNCLAPL AKVINDKFGI VEGLMTTVHS YTATQKVVDA PSNKDWRGGR 201 TAAQNIIPSS TGAAKAVGKV IPSLNGKLTG MAMRVPTSNV SVVDLTCRLE 251 KGASYDEIKQ AIKAASEEGE LKNILGYTED DVVSSDLNGD ERSSIFDAKA 301 GISLNPNFVK LVAWYDNEWG YSRRVVDLIAIYIAKVDSQ 58 - 72 804.4311 1606.8476 1606.8203 0.0274 0 K.GTIETYDQGLIVNGK.K 187 - 194 415.2221 828.4296 828.4341 - 0.0045 0 K.VVDAPSNK.D 201 - 215 715.3871 1428.7596 1428.7572 0.0024 0 R.TAAQNIIPSTGAAK.A 264 - 272 467.2277 932.4408 932.4451 - 0.0042 0 K.AASEEGELK.N 300 - 310 580.3285 1158.6424 1158.6397 0.0028 0 K.AGISLNPNFVK.L 325 - 334 552.8398 1103.6650 1103.6590 0.0060 0 R.VVDLIAIYIAK.V
65	XP_747920	52079	258	10	8.69	Citrate synthase (Cit1) Sequence Coverage: 19% 1 MASTMRLGAF ALRSTSITAK PAVQSAAFNG LRCYSTGKAK SLKETFADKL 51 PGEIEKVKKL RKEHGSKVIG EVTLDQAYGG ARGVKCLVWE GSVLDSEEGI 101 RFRGYTIPEC QKLLPKAPGG

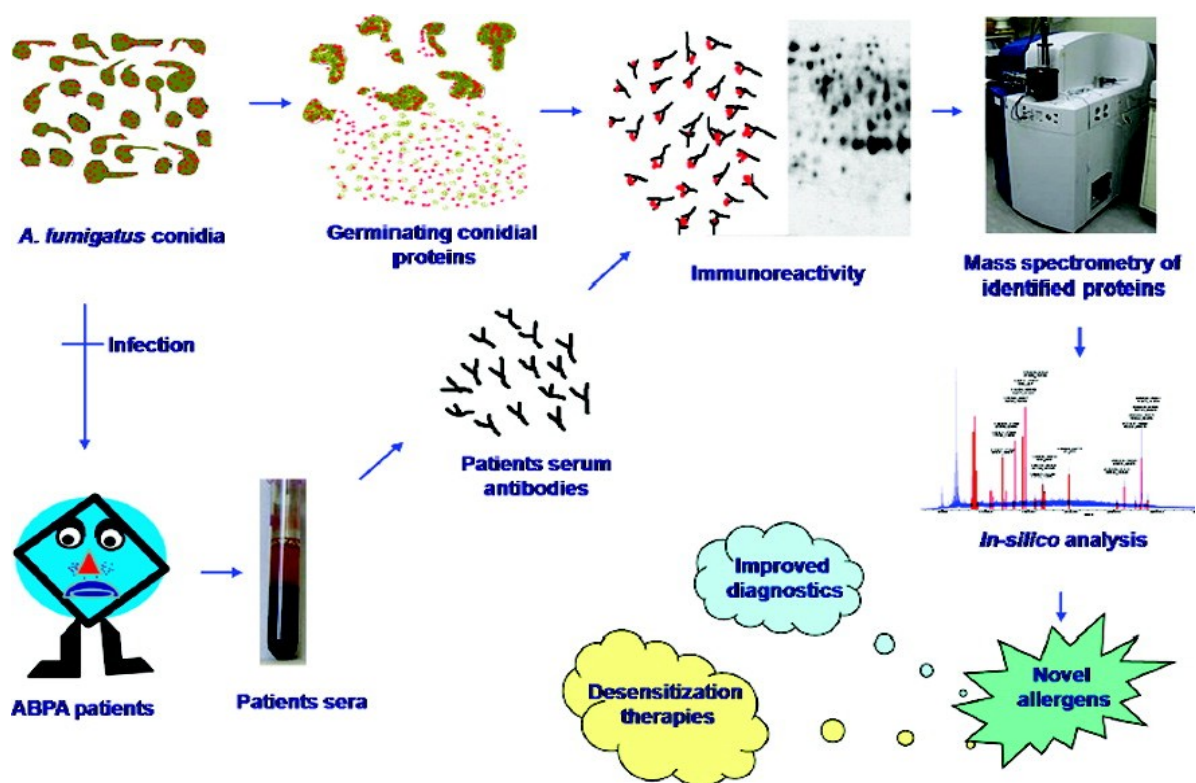
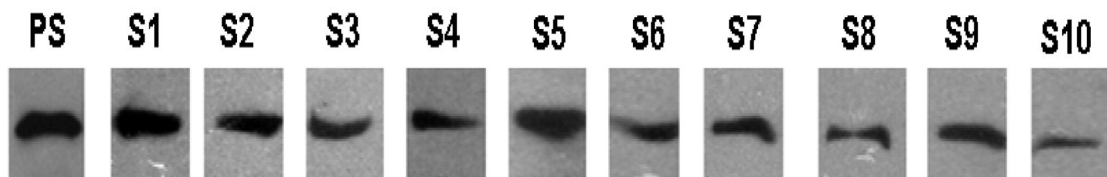
						EEPLPEGLFW LLLTGEIPTE QQVRDLSEAW 151 AARSDLPKFI EELIDRCPST LHPMAQFSLA VTALHEHSAF AKAYAKGINK 201 KDYWNYTYED SMDLIACLPT IAAKIYRNVF KDGGVAPIQK DKDYSFNLN 251 QLGYGDNNDV VELMRLYLTI HSDHEGGNVS AHTTHLVGSA LSSPMLSLAA 301 GLNGLAGPLH GLANQEVNLW LTKMKKSGN DLSDQAIKDY LWSTLNAGQV 351 VPGYGHAVLR KTDPRYVSQR EFALRKLPDD PMFKLVSVQVY KIAPGVLTEH 401 GKTKNPYPNV DAHSGVLLQY YGLTEANYYT VLFQVSRALG VLPQLIIDRA 451 LGAPIERPKS FSTEAYAKLV GAKL 68 - 82 774.9149 1547.8152 1547.7944 0.0209 0 K.VIGEVTLAQYGGAR.G 104 - 112 548.2610 1094.5074 1094.5066 0.0008 0 R.GYTIPECQK.L Carbamidomethyl (C) 159 - 166 517.7797 1033.5448 1033.5444 0.0005 0 K.FIEELIDR.C 159 - 166 517.7823 1033.5500 1033.5444 0.0057 0 K.FIEELIDR.C 228 - 234 404.2158 806.4170 806.4286 - 0.0116 1 R.NVFKDGK.V 376 - 384 553.7829 1105.5512 1105.5478 0.0035 1 R.KLPDDPMFK.L Oxidation (M) 392 - 402 561.3177 1120.6208 1120.6241 - 0.0032 0 K.IAPGVLTEHGK.T 438 - 449 654.4129 1306.8112 1306.7973 0.0140 0 R.ALGVLPQLIIDR.A 450 - 459 526.3135 1050.6124 1050.6185 - 0.0061 0 R.ALGAPIERP.KS 460 - 468 502.2373 1002.4600 1002.4658 - 0.0058 0 K.SFSTEAYAK.L
66	EDP5020 2	36847	286	8	7.01	Zinc-containing alcohol dehydrogenase, putative Sequence Coverage: 20% 1 MKQWVVADKE NGFDSLNFKE GPVPCGENE VLVKLRAASL NYRDLIIPKG 51 MYPPINFPV VPGSDGAGEV VGVGSKVTQF KKGDKVVTLF NQLHQYGPVD 101 TRSTNSGLGG VLDGTLRQYG VFNENGLVRA PRNLNFLESS TLTCALTSW 151 NALYGMNALK PGEIVLVQGT GGVSMFALQF AKAAGATVIA TTSSDTKAKK 201 LKELGADHVI NYKTNPNWGE IARSLTPDNV GVDHIEVGG AGTLSQSLKC 251 IKFEGTISII GFLGGADPKG QPGMLEALNH ICTIRGVYVG SKALMNDMIR 301 AIEVNDIHPV VDEKVFRLDQ

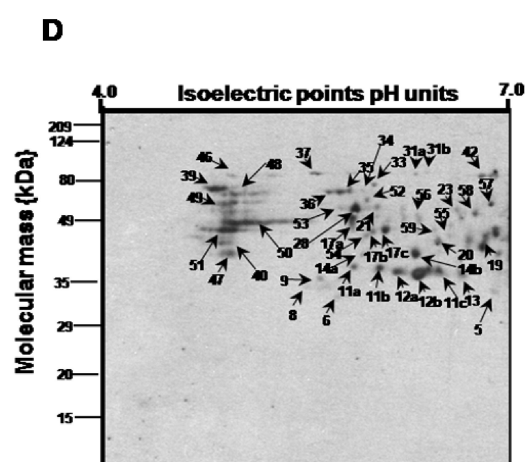
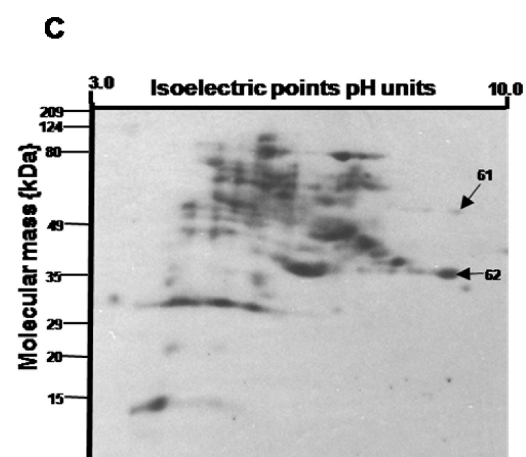
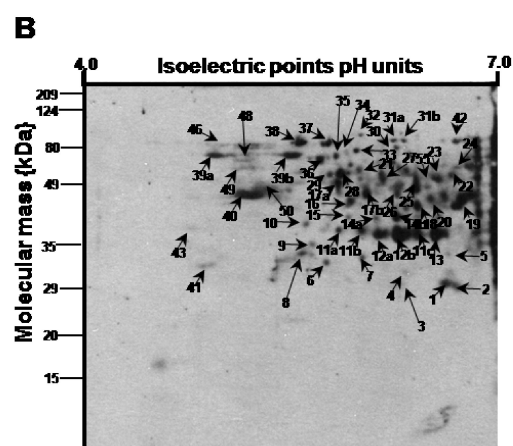
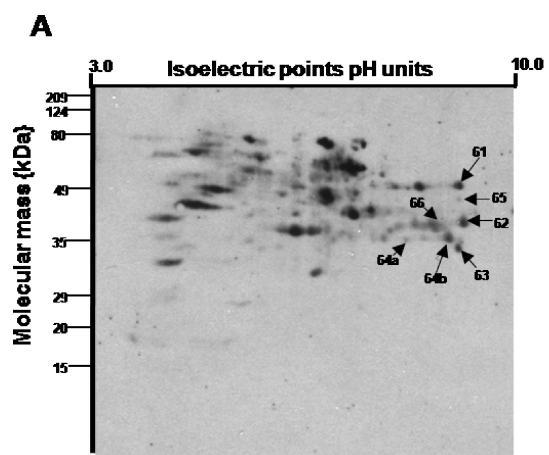
							AKEAYEYMWA QKHLGKLAIE IE 50 - 76 898.4539 2692.3399 2692.3207 0.0191 0 K.GMYPPINFPVVPVPGSDGAGEVVGVGSK.V Oxidation (M) 103 - 117 723.8821 1445.7496 1445.7474 0.0022 0 R.STNSGLGGVLDGTLR.Q 103 - 117 723.8857 1445.7568 1445.7474 0.0094 0 R.STNSGLGGVLDGTLR.Q 103 - 117 723.8862 1445.7578 1445.7474 0.0104 0 R.STNSGLGGVLDGTLR.Q 103 - 117 723.8864 1445.7582 1445.7474 0.0108 0 R.STNSGLGGVLDGTLR.Q 118 - 129 698.3651 1394.7156 1394.6943 0.0214 0 R.QYGVFNENGLVR.A 253 - 269 861.4684 1720.9222 1720.9036 0.0187 0 K.FEGTISIIGFLGGADPK.G 293 - 300 498.2244 994.4342 994.4576 - 0.0233 0 K.ALMNDMIR.A 2 Oxidation (M)
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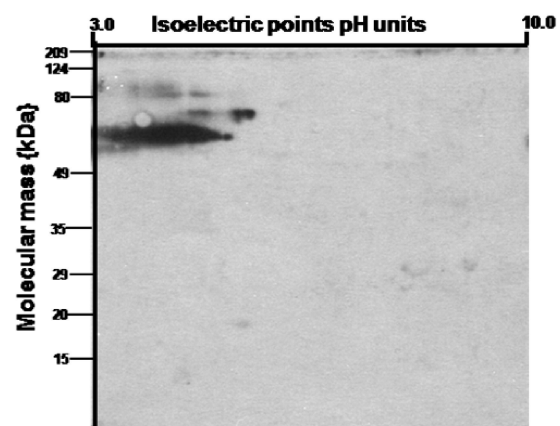
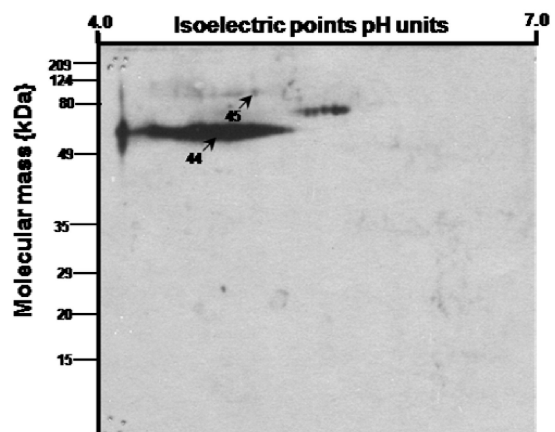
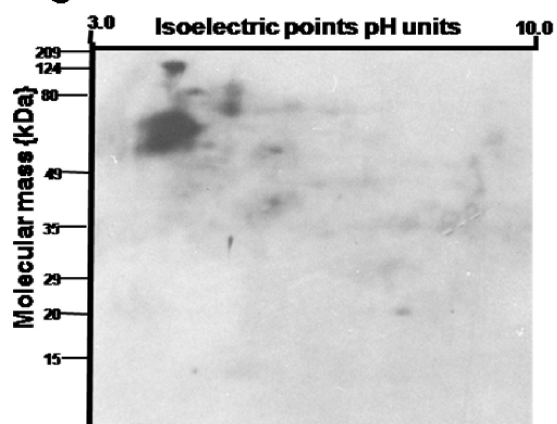
A



B





A**B****C****D**