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Multiple roles of Bet v 1 ligands in allergen stabilization and modulation of endosomal protease activity

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Abstract

Background: Over 100 million people worldwide suffer from birch pollen allergy. Bet v 1 has been identified as the major birch pollen allergen. However, the molecular mechanisms of birch allergic sensitization, including the roles of Bet v 1 and other components of the birch pollen extract, remain incompletely understood. Here, we examined how known birch pollen-derived molecules influence the endolysosomal processing of Bet v 1, thereby shaping its allergenicity.

Methods: We analyzed the biochemical and immunological interaction of ligands with Bet v 1. We then investigated the proteolytic processing of Bet v 1 by endosomal extracts in the presence and absence of ligands, followed by a detailed kinetic analysis of Bet v 1 processing by individual endolysosomal proteases as well as the T-cell epitope presentation in BMDCs.

Results: We identified E₁ phytoprostanes as novel Bet v 1 ligands. Pollen-derived ligands enhanced the proteolytic resistance of Bet v 1, affecting degradation kinetics and preferential cleavage sites of the endolysosomal proteases cathepsin S and legumain. E₁ phytoprostanes exhibited a dual role by stabilizing Bet v 1 and inhibiting cathepsin protease activity.

Conclusion: Bet v 1 can serve as a transporter of pollen-derived, bioactive compounds. When carried to the endolysosome, such compounds can modulate the proteolytic activity, including its processing by cysteine cathepsins. We unveil a paradigm shift from an allergen-centered view to a more systemic view that includes the host endolysosomal enzymes.

Abbreviations: AMC, 7-amino-4-methylcoumarin; ANS, 8-anilino-1-naphthalene-sulfonic acid; BMDC, bone marrow-derived dendritic cell; BPE, birch pollen extract; CD, circular dichroism; CMK, chloromethylketones; DC, dendritic cell; DOC, sodium deoxycholate; DTT, dithiothreitol; EDTA, ethylenediaminetetraacetic acid; FACS, fluorescence-activated cell sorting; FcεRI, high-affinity IgE receptor; FTIR, Fourier transform infrared spectroscopy; K_d, equilibrium dissociation constant; Kdo₂, Kdo₂-Lipid A; LPS, lipopolysaccharide; LTA, lipoteichoic acid; moDCs, monocyte-derived dendritic cells; MW, molecular weight; NLR, NOD-like receptor; NMR, nuclear magnetic resonance; PPA₁, PPB₁, PPE₁, PPF₁, phytoprostane A₁, B₁, E₁, and F₁; PPAR-γ, nuclear peroxisome proliferator-activated receptor γ; Q3OS, quercetin 3-O-sophoroside; SAW, surface acoustic wave; SDS-PAGE, sodium dodecyl sulfate-polyacrylamide gel electrophoresis; TCEP, tris(2-carboxyethyl)phosphine; TLR, Toll-like receptor.

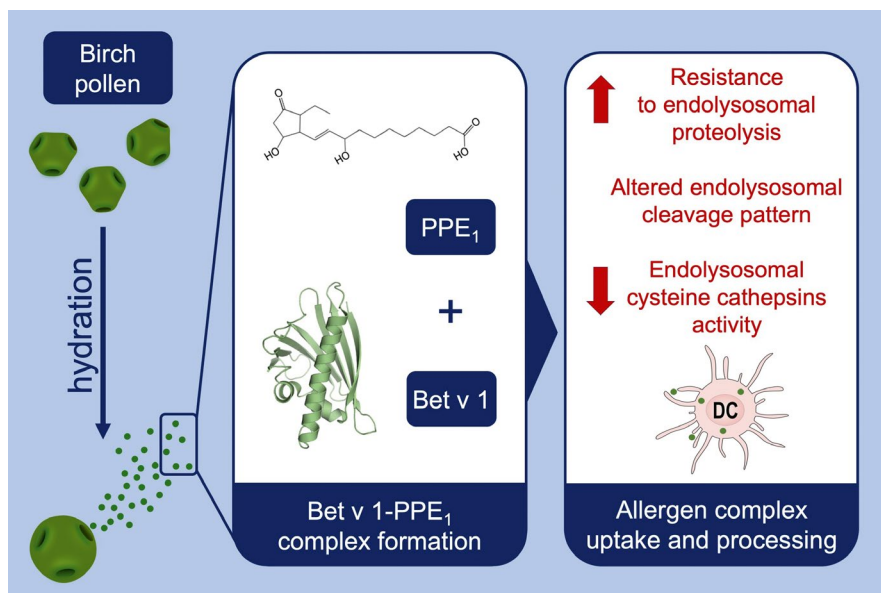
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KEYWORDS

allergenicity, birch pollen extract, E₁ phytoprostanes, ligand interaction, lysosomal protease inhibition



GRAPHICAL ABSTRACT

The newly identified birch pollen-derived ligands, Phytoprostane E₁ (PPE₁), interacts with Bet v 1 affecting its stability and proteolytic processing. Ubiquitous plant phytoprostanes, PPE₁, covalently inhibit lysosomal cysteine cathepsins, with multiple consequences including effects on antigen processing. PPE₁ affected the presentation of Bet v 1 T-cell epitope in BMDC to T-cell.

1 | INTRODUCTION

An allergic response is a two-step process, involving an initial sensitization step characterized by a pronounced Th2 polarization and followed by an acute antibody recognition step.¹ While the latter can be triggered by isolated allergen molecules alone, such as the primary birch pollen allergen Bet v 1, the initial sensitization process is more complex. We recently found that, in the case of birch (*Betula verrucosa*) pollen allergy, Th2 polarization is not driven by its major allergen Bet v 1.² This observation makes the role of Bet v 1 as a major allergen even more intriguing.^{3,4} In this context, Bet v 1's ability to function as a carrier or storage protein for a wide variety of natural hydrophobic ligands has been discussed.⁵ Indeed, several allergens have been investigated concerning their lipid-binding properties as a determinant of allergenicity.⁶

Three major groups of compounds have been proposed to interact or cooperate with Bet v 1, two of which are pollen-derived: (a) flavonoids, (b) phytohormones, and (c) microbe-derived Toll-like receptor (TLR) agonists. In a previous study, the glycosylated flavonoid quercetin 3-O-sophoroside (Q3OS) was found to co-purify with Bet v 1 from pollen and therefore reported as a physiological Bet v 1 ligand.⁷ Phytohormones, including phytoprostanes and brassinosteroids, are low-molecular-weight compounds present in pollen extract. While the ability of Bet v 1 to bind brassinosteroids has been demonstrated,⁸ physical

interactions with Bet v 1 have not yet been reported for phytoprostanes. Phytoprostanes like E₁ (PPE₁) are functionally related to mammalian prostaglandins and possess Th2-skewing activity, making them of potential interest as a sensitization mechanism.⁹ Other ligands of interest include deoxycholate (DOC), a secondary bile acid generated as a microbial metabolic byproduct that is structurally similar to brassinosteroids¹⁰ and serves as an established model ligand for Bet v 1.^{10,11} In addition, immunomodulatory microbial compounds (such as the TLR2 and NLRP6 agonist lipoteichoic acid, LTA, and the endotoxin lipopolysaccharide, LPS) have been proposed to interact with Bet v 1.^{6,12-15}

Bet v 1 ligands have been proposed either to exhibit direct immunomodulatory functions¹⁶ or to stabilize the Bet v 1 conformation indirectly, which could change its immunogenicity and allergenicity by influencing its processing in the endolysosome.^{17,18} Among endolysosomal proteases, the large family of cathepsins, most of which are cysteine proteases belonging to the papain family, plays an important role in proteolytic activity.¹⁹ Only a few other proteases have been shown to be relevant in antigen processing, including the cysteine protease legumain.²⁰ As such, the endosomal degradation of Bet v 1 can be modeled by microsomal extracts and reproduced using purified extracts, particularly cathepsin S and legumain.²¹

In this study, we biochemically and immunologically dissected the interactions of recombinant Bet v 1.0101 (termed Bet v 1 in the following), the most abundant isoform of Bet v 1 present at approximately

50%-70%,²² with several ligands, including Q3OS, PPE₁, and DOC. Remarkably, PPE₁ was not only retained by Bet_v_1, but also inhibited the cysteine cathepsins in the endolysosome. We discuss the implications of these new findings for our understanding of pollen-derived allergy.

2 | MATERIALS AND METHODS

A detailed description of the methods is provided in the Appendix S1.

2.1 | Expression, purification, and physicochemical characterization of recombinant Bet_v_1

Production of recombinant Bet_v_1.0101 and monitoring of endotoxin contamination (<0.3 ng/mL) were performed as previously described.^{3,11}

2.2 | Investigated compounds and Bet_v_1 ligands

DOC, 8-anilidonaphthalene-1-sulfonic acid (ANS), naringenin, LTA from *Staphylococcus aureus*, and LPS from *Escherichia coli* O111:B4 were purchased from Sigma-Aldrich, Inc; Kdo₂-Lipid A (Kdo₂) from Adipogen, Inc or Avanti Polar Lipids, Inc; and quercetin 3-O-sophorose (Q3OS) from Haihang Industry Co., Ltd. PPE₁, B₁-phytoprostanes (PPB₁), F₁-phytoprostanes (PPF₁), and an isomeric mixture consisting of B₁-, E₁-, and F₁-phytoprostanes (PP_{mix}) were produced by autooxidation of α -linolenic acid, as described elsewhere.²³ Type I or/and type II phytoprostanes were used, as indicated in Figure 4C. Unless otherwise stated, Bet_v_1 was mixed with each of the six ligands in a 1:10 molar ratio and incubated either overnight at 4°C or for 2 hours at room temperature. A₁-phytoprostanes (PPA₁) were purchased from Cayman Chemicals and dried and dissolved in DMSO.

2.3 | Protein-ligand interaction

Surface acoustic wave (SAW) technology and NMR spectroscopy were used to observe the interaction of Bet_v_1 with the selected compounds, including determination of the dissociation constant (K_d). The influence of ligand binding on the secondary structure elements and the thermal stability of Bet_v_1 was monitored using circular dichroism (CD, JASCO J-815 spectropolarimeter, Jasco) and Fourier transform infrared (FTIR) spectroscopy (Tensor II FTIR system, Bruker Optics Inc). A detailed description of these methods is available (Appendix S1).

2.4 | Immunological assays

The ability of ligand-loaded Bet_v_1 to induce IgE-antigen cross-linking and basophil degranulation was assessed by mediator-release assays using rat basophil (RBL-2H3) cells, transfected with the human high-affinity IgE receptor (Fc ϵ RI), as previously described.^{2,24} In vitro uptake of labeled Bet_v_1 was performed using CD11c⁺ murine bone marrow-derived dendritic cells (BMDCs). The maturation of human monocyte-derived dendritic cells (moDCs) was analyzed as previously described.² T-cell proliferation assays

using CD4⁺ T-cell hybridomas were performed as previously described.¹⁷ A detailed description of the in vitro assays is available (Appendix S1).

2.5 | In vitro simulation of endolysosomal degradation using microsomes and individual endolysosomal proteases

The endolysosomal degradation assay was performed with ligand-bound (either DOC, PPE₁, or Q3OS in 10 $\times$ molar excess) and Bet_v_1 without ligands (apo-Bet_v_1) as previously described.²¹ Recombinant human cathepsin S and human legumain were used in proteolytic degradation assays. Experimental details are described in the Appendix S1.

2.6 | Enzymatic activity assays

To evaluate the influence of Bet_v_1 ligands on cathepsin S and legumain activities, 10 nmol/L of protease was incubated with 100 μ mol/L of ligand (unless otherwise stated) and 50 μ mol/L of fluorogenic substrate in digestion buffer (0.1 mol/L sodium acetate pH 5.0, 0.1 mol/L sodium chloride, 5 mmol/L EDTA, and 2 mmol/L DTT), as described in the Appendix S1. The effect of birch pollen extract (BPE) (20-200 μ g/mL) on the cathepsin S and legumain activities was assessed in parallel. The inhibitory effect of PPE₁ was assessed by replacing DTT with 0.5 mmol/L TCEP. Activities of recombinant rat cathepsin B (provided by Dr Lukas Mach) and papain (Merck) at 10 nmol/L were assayed using Z-FR-AMC (Bachem) as a fluorogenic substrate.

3 | RESULTS

3.1 | Bet_v_1 interacts with high affinity with pollen-derived PPE₁ and Q3OS and with the brassinosteroid-like compound DOC, but not with LTA or LPS

To assess the interactions between Bet_v_1 and Q3OS, DOC, PPE₁, LTA, or LPS, we determined the dissociation constants (K_d) using SAW binding assays (Table 1, Figure S1), a more quantitative approach than previously described qualitative assays.^{11,25} In addition, the LPS-substructure Kdo₂-Lipid A (Kdo₂) was used for binding studies, due to its more homogenous structure but similar immune stimulatory activity when compared to native LPS.

As a reference ligand, the binding of ANS to Bet_v_1 was determined (K_d of 32.7 μ mol/L) which is similar to previously published K_d values (18.5 μ mol/L).²⁶ The two pollen-derived components, Q3OS and PPE₁, exhibited high binding affinities with K_d = 1.5 and 0.5 μ mol/L, respectively. The bacterial TLR agonists, LTA (199.8 μ mol/L) and LPS (185.0 μ mol/L), and the model substances, DOC (58.8 μ mol/L) and Kdo₂ (379.8 μ mol/L), demonstrated higher K_d values, indicating lower binding affinities. For the phytoprostane derivatives, PPB₁ and PPF₁, as well as for a physiologically

relevant isomeric mixture consisting of B₁-, E₁-, and F₁-phytoprostanes (PP_{mix}), we observed dissociation constants of 1.0, 2.4, and 1.2 μmol/L, respectively.

To validate the interactions determined by SAW, we used NMR spectroscopy to test the specific binding of PPE₁, LTA, LPS, and Kdo₂ to Bet_v_1 (Table 1, Figure S2). Substantial differences between the ¹H-¹⁵N HSQC spectra of ¹⁵N-labeled Bet_v_1 in the absence and presence of PPE₁ confirmed that the allergen specifically binds PPE₁. The *K_d* was consistent with a low to sub-μmol/L affinity, but intermediate exchange and a poor signal-to-noise ratio prevented direct measurement. The commercially available PPA₁ was used as a substitute for PPE₁ to identify the phytoprostane binding site(s). No significant interactions were observed for LTA, LPS, or Kdo₂, indicating that these bacterial compounds do not specifically bind to Bet_v_1, consistent with LPS pull-down assays using Bet_v_1 and biotinylated LPS immobilized on Strep-Tactin Sepharose beads (Figure S3).

Moreover, using CD and FTIR spectroscopy we observed an increased melting point (*T_m*) of approximately 4°C and nearly 7°C for Bet_v_1 bound to DOC and PPE₁, respectively (Table 2). Bet_v_1 binding of DOC, Q3OS or PPE₁ to Bet_v_1 did not significantly alter its secondary structure content (Figure S4).

3.2 | Ligand binding to Bet_v_1 does not affect basophil degranulation or the activation of dendritic cells

We next set out to test for effects on Bet_v_1-complexes on different stages of the allergic immune response. Antigen uptake was assessed by uptake of pHrodo™ Red-labeled Bet_v_1, with or without ligands (Figure S5A), and subsequent FACS analysis. Sensitizing potential was assessed on the level of dendritic cells by flow cytometric analysis of maturation marker expression and by determination of Th polarization-associated cytokines in cell culture supernatants (Figure S5B and C). IgE cross-linking by Bet_v_1-complexes was assessed by RBL assay (Figure S6). None of the above described readouts was influenced by the presence of plant-derived Bet_v_1 ligands (Q3OS, PPE₁, and DOC).

3.3 | Ligand interactions with Bet_v_1 influence its lysosomal processing

Given the relevance of conformational stability and proteolytic resistance for MHCII presentation,²⁷ we prepared endosomal extracts to assess the resistance of Bet_v_1 in complex with the model ligands toward endolysosomal proteases over 48 hours. Densitometric analysis of SDS-PAGE (Figure 1A and B) revealed an enhanced proteolytic stability of Bet_v_1 in the presence of PPE₁ and DOC. By contrast, Q3OS had only a weakly stabilizing effect over the first 12 hours. This observation correlated with our thermal stability data.

As the lysosomal resistance of allergens correlates with the quality and quantity of the ensuing immune response,¹⁷ we analyzed the peptides generated after 12-hours incubation with

endolysosomal proteases (Figure 1C). The binding of Q3OS resulted in a 2-fold higher diversity of peptides within the different peptide clusters than with the apo form of Bet_v_1, whereas the resulting Bet_v_1 peptide diversity was reduced upon binding of PPE₁ and DOC (to 53.9% and 69.7%, respectively). In a semi-quantitative approach, the generated peptides were grouped into seven main core clusters with their relative abundances shown (Figure 1D). The rate of core peptide production and/or elimination was affected by the presence of ligands. In the presence of PPE₁ or DOC, Bet_v_1 processing preferentially accumulated the two N-terminal cluster peptides. Bet_v_1 in complex with Q3OS or DOC showed an altered pattern of proteolytic processing, which resulted in a more efficient generation of the immunodominant T-cell epitope, as indicated by the number of identified peptides (gray box in Figure 1C). Bet_v_1 Together, these data show that both the quantity and the quality of the peptide pool available for MHCII presentation are affected by the ligands.

3.4 | Modeling the microsomal processing of Bet_v_1 by cathepsin S and legumain reveals the mechanistic basis of attenuated degradation

Since an endosomal extract is a complex mixture of various hydrolases, we aimed to break down the complexity of the assay by identifying key proteases of the microsomal extracts and further analyzing the influence of ligand binding to Bet_v_1 on their processing capability. Based on previously described enzymatic data,^{21,28} we tested the microsomal fraction for enzymatic activity toward substrates of cathepsin and legumain, two prominent endolysosomal cysteine protease families with complementary substrate preferences and orthogonal catalytic mechanisms.²⁹ Consistent with the literature,³⁰ we detected both cathepsin-like and legumain-like enzymatic activities in microsomal extracts, and these activities were specifically inhibited by cathepsin S/B and legumain inhibitors (Figure S7).

Consequently, we tested whether cathepsin S or legumain qualitatively reproduced the endolysosomal degradation kinetics of apo and ligand-bound Bet_v_1. Indeed, processing by the individual proteases was strongly retarded by DOC, and, in the case of cathepsin S, also by PPE₁. Other reported Bet_v_1 ligands¹¹ had either a minor (Naringenin) or no detectable (PPB₁, ANS) effect on its proteolytic resistance. SDS, which also binds Bet_v_1,³¹ significantly accelerated its degradation by both proteases (Figure 3A and B). By contrast, SDS reduced the cleavage of fluorogenic substrates by cathepsin S (Figure 3A). These observations can be reconciled by assuming that the binding of SDS to Bet_v_1 exposes additional vulnerable sites to the protease.

The majority of the peptide clusters were generated using cathepsin S alone; however, several cleavage sites after asparagine were only reproduced using legumain, as no other known protease exhibits an asparaginyl-peptidase activity,³² particularly relevant for the production of C-terminal peptide clusters (Figure 1C, Figure S8). To understand how the pattern and the kinetics of Bet_v_1

TABLE 1 Binding affinity (K_d) of Bet_v_1 to the selected compounds as determined by SAW interaction studies and binding confirmation by NMR spectroscopy

	Compound	MW [Da]	K_d [μ mol/L]	SD [μ mol/L]	NMR [μ mol/L]
Pollen-derived compounds	Q3OS	626.5	1.5	± 0.1	[7]
	PP _{mix}		1.2	± 0.1	n.d.
	PPB ₁	308.4	1.0	± 0.4	n.d.
	PPF ₁	328.4	2.4	± 0.5	n.d.
	PPE ₁	356.5	0.5	± 0.1	0.1-1
	PPA ₁	308.4	n.d.	n.d.	0.1-1
Model compounds mimicking essential binding groups	DOC	414.6	58.8	± 24.3	[11]
	ANS	299.34	32.7	± 0.3	[11]
Bacteria-derived compounds	LTA	4000-8000	199.8	± 55.7	No significant interactions
	LPS	10 000-20 000	185.0	± 123.1	No significant interactions
	Kdo ₂	2306.8	379.8	± 62.8	No significant interactions

Ligand	T_m CD	SD CD	T_m FTIR	SD FTIR	Δ CD	Δ FTIR
-	63.68	± 0.06	63.38	± 2.24		
Q3OS	64.04	± 0.10	65.26	± 1.77	+0.36	+1.88
DOC	67.44	± 0.58	66.6	± 4.36	+3.81	+3.22
PPE1	70.62	± 0.15	69.31	± 0.05	+6.94	+5.93

TABLE 2 Influence of ligand interaction on thermal stability of Bet_v_1 (values in °C)

Abbreviations: CD, circular dichroism; FTIR, Fourier transform infrared spectroscopy; T_m , melting point; SD, Standard deviation.

processing were affected by the presence of ligands, we analyzed the relative abundance of the resulting peptides. The presence of ligands mostly affected the frequency of cleavages at certain sites within Bet_v_1, but rarely generated new cleavage sites not present in the apo form. PPE₁ induced prominent changes in relative preference of the Bet_v_1 cleavage sites. Although other ligands affected the cleavage pattern as well, PPE₁ was used to illustrate the effect of ligand binding on the generation of cleavage sites: Upon incubation with cathepsin S, preferential cleavage was observed after Phe20, Lys21, and in the C-terminal region; upon incubation with legumain, cleavage frequency after Asn120 and Asp157 strongly increased (Figure 2C). Overall, this analysis shows that the relative abundance of peptides available for MHC presentation is strongly affected by the presence of ligands.

3.5 | Birch pollen extract reduces cathepsin activity in a dose-dependent manner

We wondered whether the observed (de)stabilizing effects of the ligands were caused exclusively by the interaction with Bet_v_1. Therefore, we tested whether the ligands affected protease activity toward small peptidic substrates. Surprisingly, PPE₁ specifically inhibited cathepsin S, but not legumain (Figure 3A).

Since approximately 0.5 μ g of PPE₁ is present in 1 mg of birch pollen-extracted protein,⁹ we can expect about 150 pmol PPE₁ in 100 μ g of pollen-extracted protein per mL, that is, 150 nM PPE₁, in agreement with the reported concentration range.³³ Although the

extraction will come with significant losses, and only type II of PPE₁ is an active inhibitor, we hypothesized that BPE at corresponding concentrations should also attenuate proteolytic activity. Therefore, we investigated the influence of BPE on cathepsin S and legumain activity (Figure 3B). In contrast to the marginal effects on legumain activity, a dose-dependent inhibition of cathepsin S was observed. Bet_v_1 at the highest concentration (200 μ g/mL) was used to exclude possible substrate competition effects. These data suggest that the BPE-mediated cathepsin S inhibition may be partially caused by PPE₁.

3.6 | PPE₁ inhibits lysosomal cathepsins by blocking their catalytic cysteine

To further investigate the mechanism of PPE₁-mediated inhibition, we analyzed other proteases and found PPE₁-mediated inhibition of the papain-like protease family, such as cysteine cathepsins. By contrast, legumain, which belongs to a different protease class, was not inhibited (Figure 4A). Importantly, the structurally similar PPB₁ and PPF₁ did not inhibit cathepsin S activity (Figure 4B and C). We wanted to examine whether PPE₁ exerts its effect by reacting with the nucleophilic cysteine thiol in the active site, a characteristic for this protease class. Therefore, we compared the effect of two reducing agents, (a) the thiol-containing DTT and (b) tris(2-carboxyethyl) phosphine (TCEP), which lacks any thiol groups. Cathepsin S activity was completely abolished by PPE₁ in the presence of TCEP, but not in the presence of DTT (Figure 4D, Figure S9). This differential effect can be understood by DTT thiols competing for the reactive site on

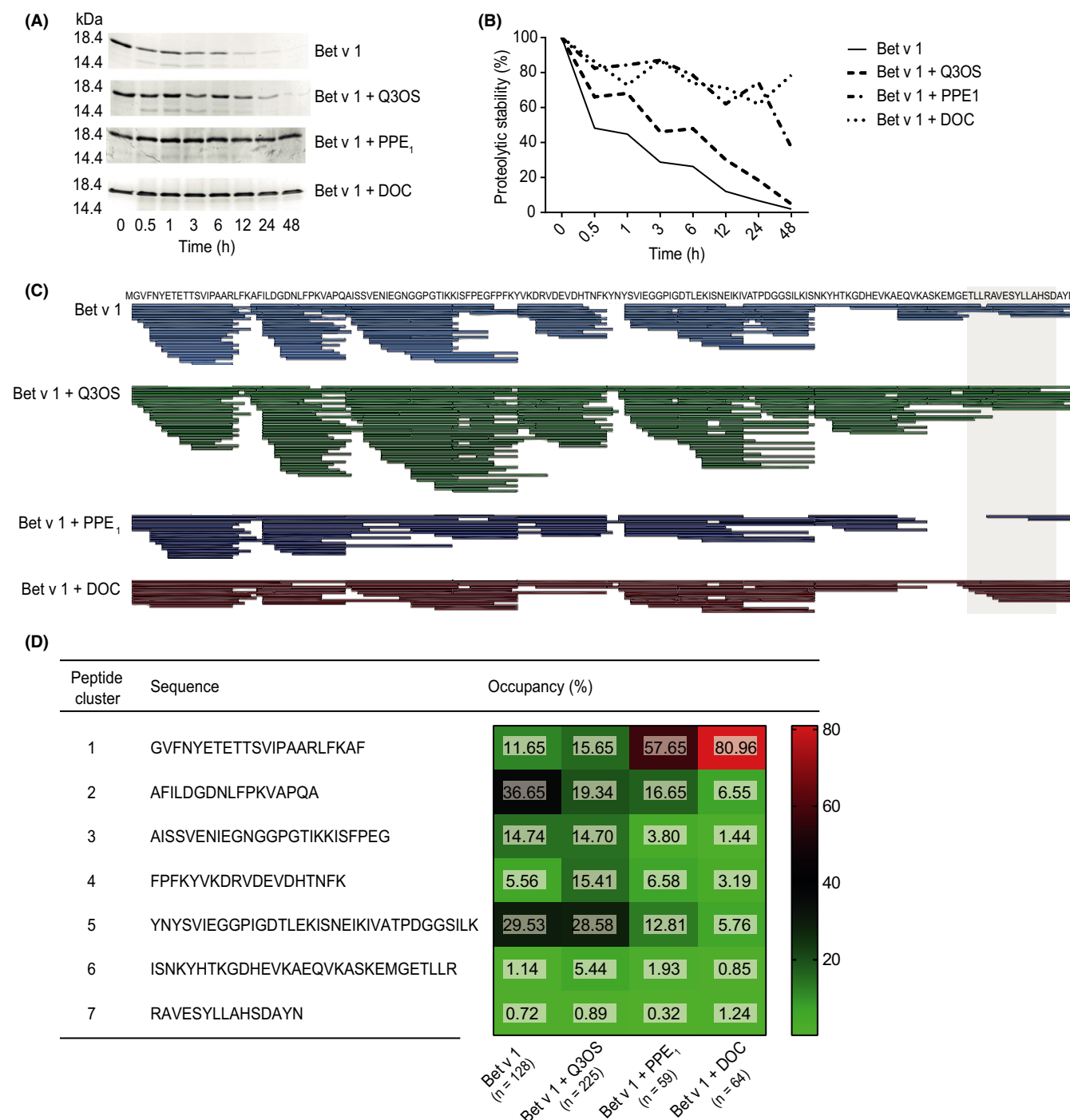


FIGURE 1 Ligand interaction alters the proteolytic susceptibility of Bet_v 1. A, SDS-PAGE analysis of in vitro endolysosomal degradation of Bet_v 1 with and without ligand recorded at different time points from 0 to 48 h and B, densitometric analysis thereof, interpreted with Image Lab 4.0.1 Software (Bio-Rad). C, Generated peptide clusters obtained after 12 h of proteolytic degradation analyzed by mass spectrometry. D, The peptide sequences were grouped into seven degradation clusters with their relative abundance, as derived from MS intensities. The number of unique peptide sequences is shown in brackets

the PPE₁ inhibitor. By contrast, no inhibitory effect on legumain by PPE₁ was found. In the absence of PPE₁, we found high cathepsin S activity toward a fluorogenic substrate in the presence of both TCEP and DTT (Figure 4D, Figure S9). The slightly stronger activity-enhancing effect of TCEP vs DTT is due to its stronger reducing capacity at acidic pH.³⁴

3.7 | PPE₁ and DOC affect Bet_v 1 processing and presentation in DCs

In order to test the relevance of the identified Bet_v 1 ligands in processing and presentation by DCs in a time-dependent manner, we incubated BMDCs with Bet_v 1 in complex with different

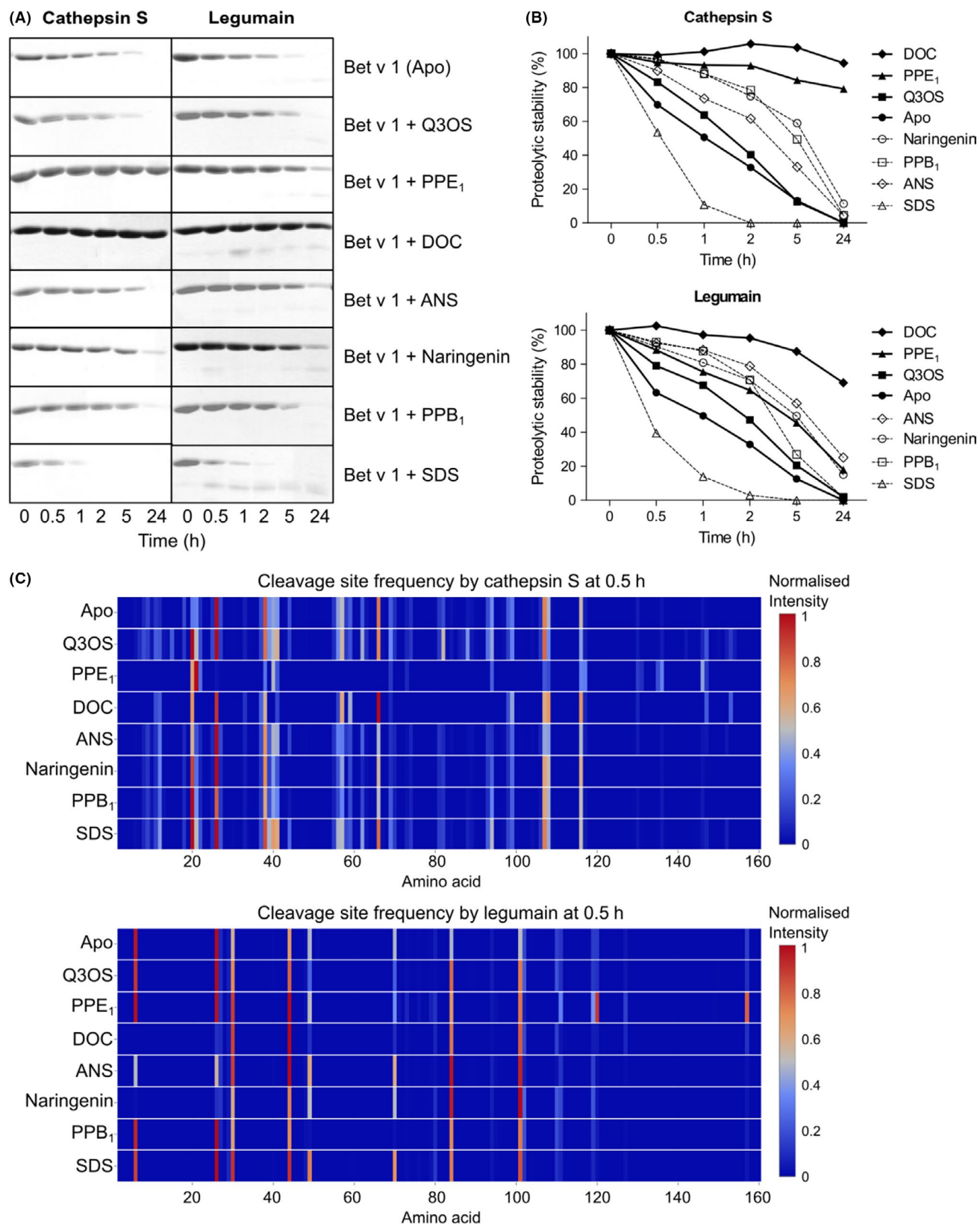


FIGURE 2 Effect of ligands on Bet_v_1 degradation in vitro. A, Bet_v_1 degradation assay by cathepsin S and legumain in the absence or presence of various ligands. The degradation profile was analyzed by Coomassie Blue-stained SDS-PAGE and B, densitometric analysis. C, Bet_v_1 cleavage site frequency analyses of the degradation assay in (A). The analyses were based on the relative abundance of peptides measured by mass spectrometry, and the peptide intensity was normalized to the most abundant peptide found for the respective ligand. This is not a direct representation of the available cleavage sites, but rather emphasizes the varying kinetic accessibility of individual sites for one given ligand. The peptide profiles are presented in Figure S8

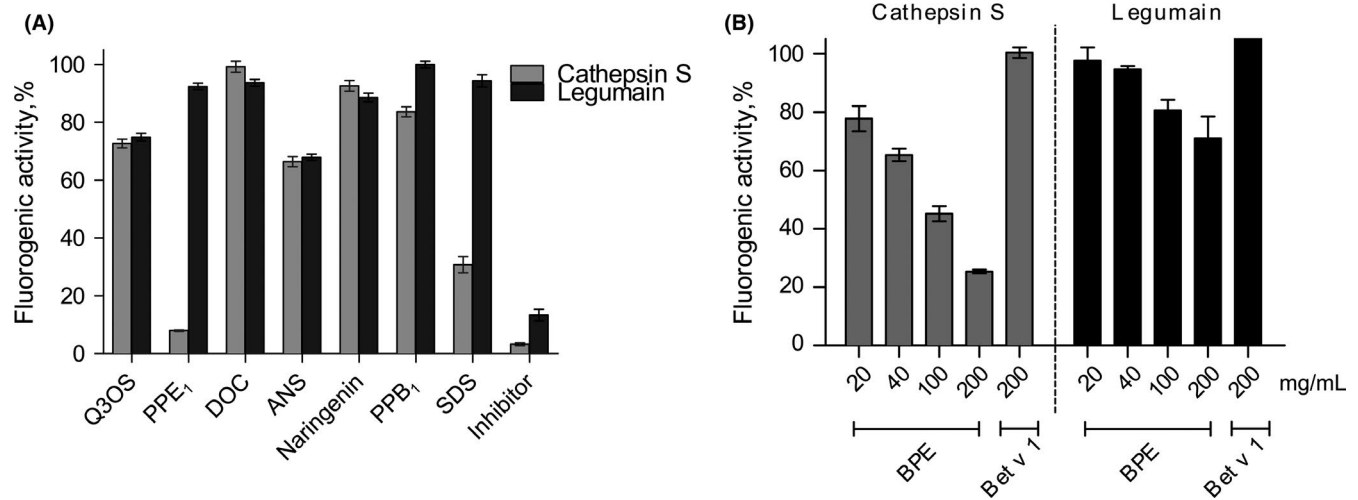


FIGURE 3 Effect of ligands and birch pollen extract (BPE) on cathepsin S and legumain activities. A, Effect of ligands on fluorogenic activity of lysosomal proteases. B, Effect of BPE on lysosomal protease activity. BPE was incubated with the respective protease, and the fluorogenic activity was measured after 15 min. Recombinant Bet_v_1 was used as control for a possible substrate competition effect. The percent fluorogenic activity was calculated over buffer control. Error bars indicate standard deviations

ligands and detected the presentation of Bet_v_1 by using CD4⁺ T-cell hybridoma cells specific for the immune-dominant T-cell epitope (Thr142-Ala153). T-cell proliferation was monitored indirectly by IL-2 secretion (Figure 5). Interestingly, Bet_v_1 in complex with PPE₁ consistently affected the MHCII presentation of Bet_v_1 epitope on DCs (Figure 5B-F), whereas in complex with DOC epitope presentation was affected only after 48 hours (Figure 5F). In contrast, Q3OS and PPB₁ did not affect the presentation of Bet_v_1.

4 | DISCUSSION

Th2 polarization cannot be explained by allergenic proteins exclusively; instead, components of the pollen extract significantly contribute to the process of allergic sensitization.² In this context, pollen-derived compounds able to bind allergens represent promising candidates in the search for additional factors complementing Bet_v_1 allergenicity.^{11,35-39} Structurally, this property is encoded by Bet_v_1's hydrophobic binding pocket, which can harbor compounds of up to 1400 Da.^{40,41} Here, for the first time, we observed that Bet_v_1 binds phytoprostanes, but not the TLR agonists LTA and LPS. The pollen-derived ligands Q3OS and PPE₁, as well as DOC, have micromolar affinities to Bet_v_1, comparable to previously published values for Q3OS and DOC.^{22,26}

PPE₁ inhibits the production of IL-12p70 in LPS-stimulated human DCs via blocking of NF- κ B and activation of PPAR- γ , thus favoring a Th2-dominated immune response.^{23,33} By contrast, we found that stimulation of moDCs by PPE₁ in complex with Bet_v_1 without additional LPS-co-stimulation did not upregulate maturation markers nor alter cytokine expression, neither did Bet_v_1 alone nor Bet_v_1 in complex with Q3OS or DOC. These discrepancies can be explained by the additional treatment with LPS, which via activation of TLR4 can induce expression of maturation markers.⁴²

It has been suggested that diminished proteolytic processing of antigens results in low loading and density of class II MHC-peptide complexes, thus favoring Th2 polarization.¹⁸ Our results revealed that ligand binding resulted in an overall protein-stabilizing effect. Increased thermal stability tended to correlate with proteolytic stability, which in turn affects immunogenicity/allergenicity.¹⁷ Indeed, the susceptibility of Bet_v_1 to degradation by endolysosomal extracts was substantially reduced by the ligands DOC and PPE₁. Due to its complexity, the reaction conditions of the endolysosomal fraction cannot be easily controlled, but its degradation pattern can largely be mimicked by cathepsin S, allowing us to establish an in vitro degradation system.²¹ Here, we revealed significant legumain activity as a component of the endolysosomal fraction, albeit with lower fluorescence signal. Consequently, legumain was included in the in vitro degradation system. Importantly, legumain is not a member of the papain-like protease clan and therefore possesses mechanistic properties, substrate profiles, and inhibition profiles that are fundamentally different from cathepsins.²⁹

Investigation using the in vitro degradation system revealed that Bet_v_1 ligands can tune Bet_v_1 endolysosomal processing in two mechanistically different ways. Firstly, ligands affected the allergen processing primarily with respect to the relative abundance of generated peptides available for MHC presentation. Secondly, the newly identified Bet_v_1 ligand PPE₁ selectively inhibited cathepsin S and other papain-like cysteine proteases, but not legumain. Why PPE₁, but not the two structurally related phytoprostanes PPB₁ and PPF₁, possesses this inhibitory function can be explained by the chemical structure of PPE₁, which differs from PPB₁ and PPF₁ at the five-membered ring⁴³ (Figure 4C). The mechanistic explanation for the cathepsin S-inhibitory effect is that, under acidic conditions, PPE₁ can spontaneously undergo dehydration,⁴³ converting the five-membered ring into an electrophilic

Michael acceptor. The cyclopentenone favors the addition of the nucleophilic thiolate of the catalytic cysteine, thereby covalently blocking the protease active site (Figure 4E). The access to the active site of legumain is sterically more stringently controlled than the active site of papain-like proteases,³² explaining why

legumain neither reacts with nor is inhibited by PPE₁. The reactive 3-hydroxy-cyclopentanone is commonly found in plants⁴⁴ and, in particular, was identified in birch pollen.^{9,45} PPE₁ was found in plants at concentrations ranging from 4.5 to 61 ng per gram of dry weight.⁴⁴

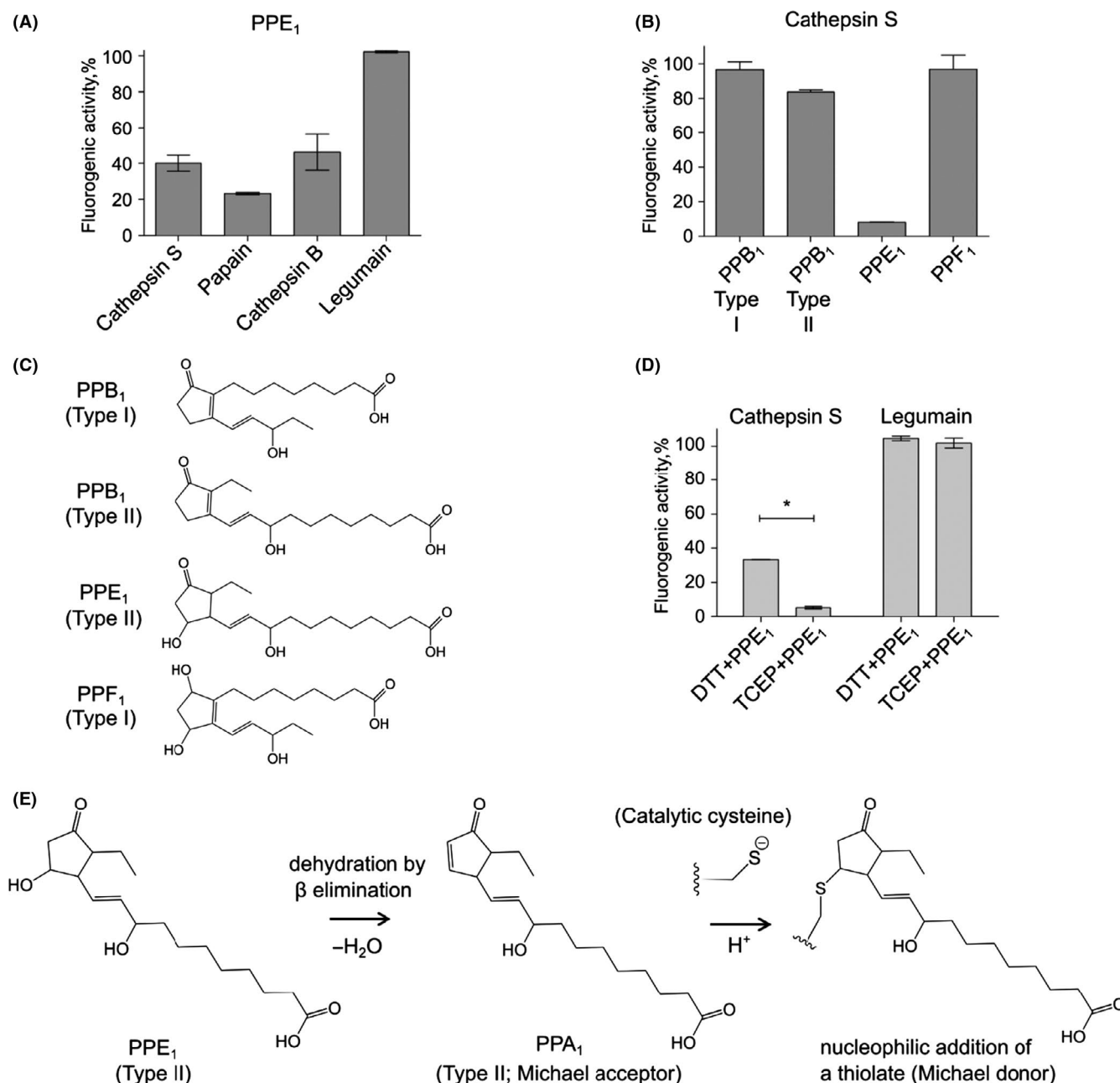
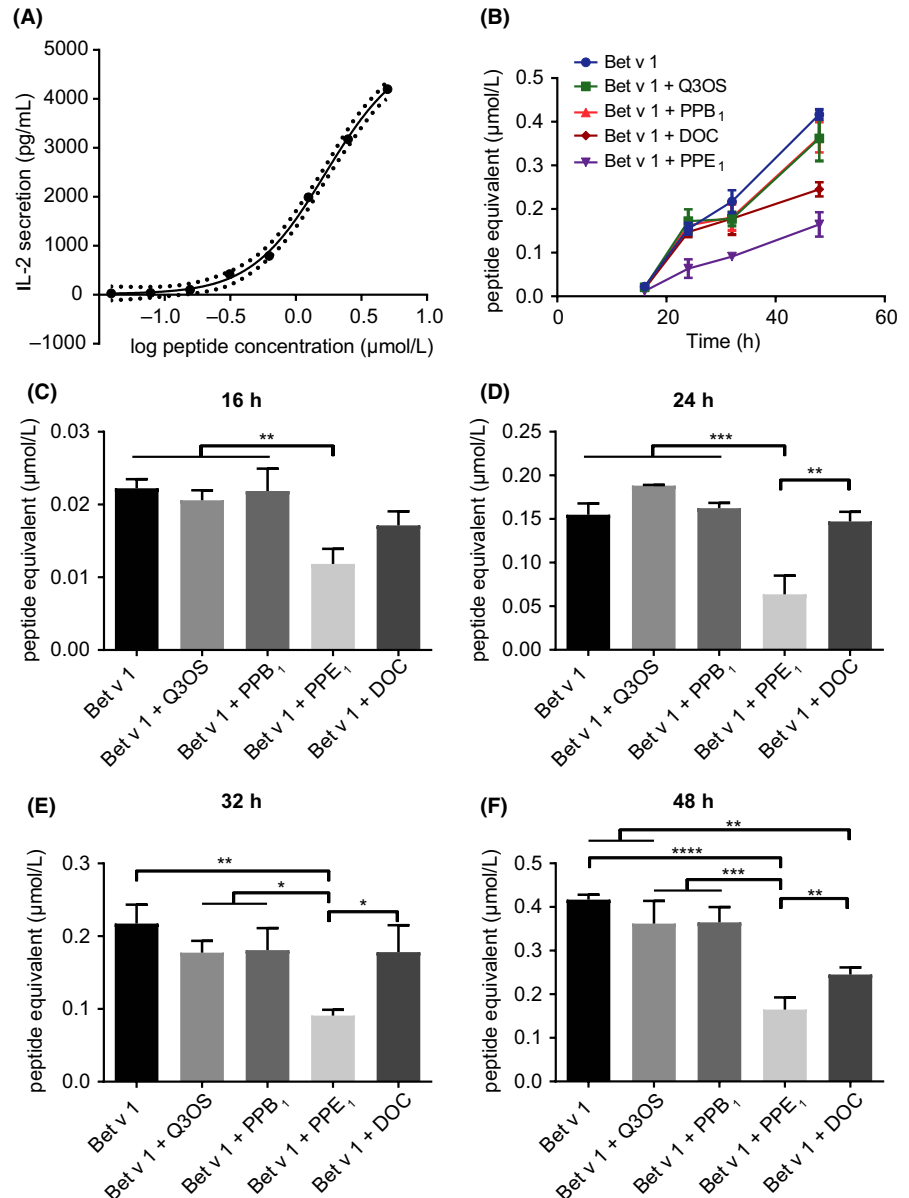


FIGURE 4 Inhibition mechanism of PPE₁. A, PPE₁ inhibits papain-like cysteine proteases, but not legumain. Papain-like cysteine proteases (rat cathepsin B, cathepsin S, and papain) and legumain were incubated with PPE₁ (5 μmol/L), and fluorogenic activities were recorded after 15 min. B, Effect of phytohormones (0.1 mmol/L) structurally related to PPE₁ on cathepsin S activity. Fluorogenic activity was recorded after 15 min. C, Chemical structure of phytohormones used in (B). D, Effect of reducing agents on PPE₁ inhibition of cathepsin S and legumain. The ability of proteases to cleave the fluorogenic substrates with and without PPE₁ (5 μmol/L) in the presence of DTT and TCEP. Fluorogenic substrates used for cathepsin S and legumain were Z-VVR-AMC and Z-AAN-AMC, respectively. Error bars indicate standard deviations. Asterisk indicates statistical significance with $P < 0.05$. E, Proposed mechanism of cathepsin S inhibition by PPE₁. PPE₁ undergoes spontaneous dehydration by β-elimination, resulting in PPA₁.⁴³ This reaction does not occur with PPB₁, which lacks a hydroxyl group in the ring, and is disfavored in PPF₁ due to the missing ketone group. The resulting PPA₁ is an electrophile (Michael acceptor) and can be readily attacked by the nucleophilic cysteine of cathepsin S (Michael donor) at the β carbon to form a covalent adduct,⁴⁸ thus inhibiting cathepsin S activity

FIGURE 5 Effect of ligand binding on the Bet_v_1-specific presentation of BMDCs to CD4⁺ T cells. A, Dose-response curve relating the IL-2 secretion of T-cell hybridoma cells (in pg/mL) to the logarithmic concentration of the corresponding immune-dominant peptide (Thr142-Ala153) upon presentation by BMDCs. B, kinetics of Bet_v_1 T-cell epitope presentation by BMDCs from 16 to 48 h. C-F, comparison of the presented Bet_v_1 T-cell epitope in dependency of involved ligand at each individual time point (16, 24, 32, and 48 h). P-values were calculated with one-way ANOVA and a Tukey's multiple comparisons test. All statistical calculations were performed using GraphPad Prism 7 software; Ns, $P > 0.05$; * $P \leq 0.05$; ** $P \leq 0.01$; *** $P \leq 0.001$; **** $P \leq 0.0001$



The immunological relevance of these unexpected findings was even demonstrated in a T-cell proliferation assay, showing a unique reduction in the presentation of the T-cell epitopes when Bet_v_1 was complexed with PPE₁. This drastic effect can mostly be explained by PPE₁'s cysteine cathepsin-inhibition function, and hardly to its stabilizing properties since such an effect was not observed for PPB₁.

So far, it is unknown whether Bet_v_1 homologues from other pollen or food sources are able to bind ligands, which enables them to further increase their allergenicity in terms of proteolytic stability, processing, T-cell proliferations, or IgE binding. Especially, in the light of the pollen-food syndrome, future studies investigating ligand binding of clinically relevant Bet_v_1 homologues, such as Cor a 1, are required.⁴⁶

To summarize, we identified an unexpected mechanism by which Bet_v_1 serves as a carrier of an endosomal inhibitor, which interferes with the main class of antigen-processing proteases. Increased proteolytic resistance of Bet_v_1 drastically affects its allergenicity

and immunogenicity.¹⁷ Furthermore, such broad-spectrum inhibition is likely to change not only the presented immunopeptidome but also the proteolytic activation of endosomal and intracellular immune receptors like TLRs and NLRs. Additionally, there may be a direct interaction of Bet_v_1 ligands with these receptors.⁴⁷ The relevance of such direct or indirect activation by pollen-derived non-proteinogenic molecules can help to reconcile the intriguing finding that the sensitization process by birch pollen extracts is independent from Bet_v_1.²

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CONFLICTS OF INTEREST

F. Ferreira is a member of Scientific Advisory Boards (HAL Allergy, NL; SIAF, Davos, CH; AllergenOnline, USA). The remaining authors declare that they have no relevant conflicts of interest.

AUTHOR CONTRIBUTIONS

WTS, LA, SH, SG, TS, PT, PB, and GM performed the experiments. WTS, LA, GM, SG, R.L, C.T-H., CC, HB, and FF devised the experiments and interpreted the data. WTS, LA, HB, and F.F wrote the manuscript.

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SUPPORTING INFORMATION

Additional supporting information may be found online in the Supporting Information section at the end of the article.

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Fig. S1

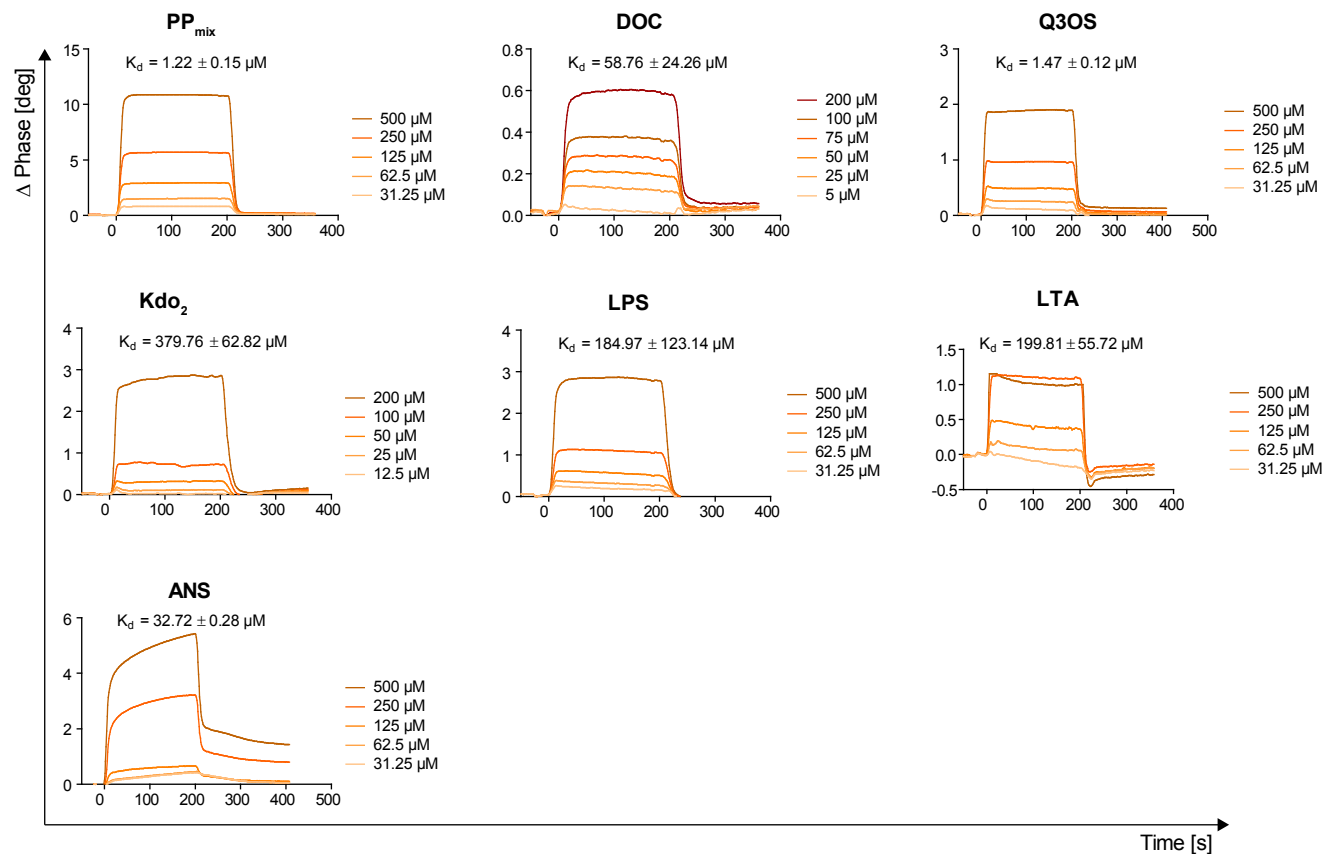


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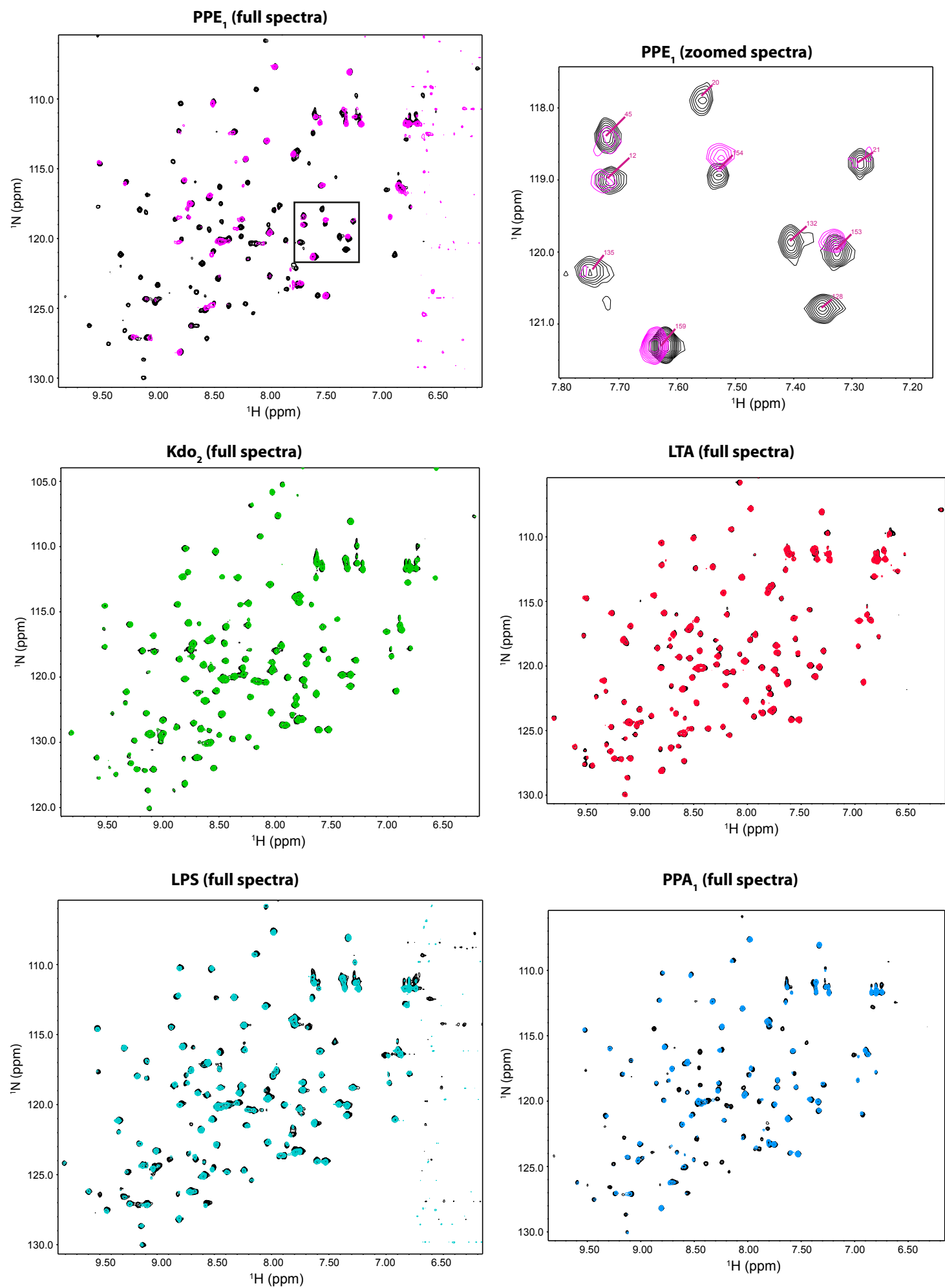


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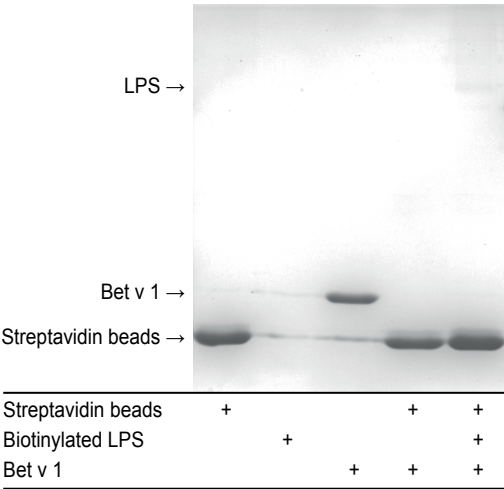


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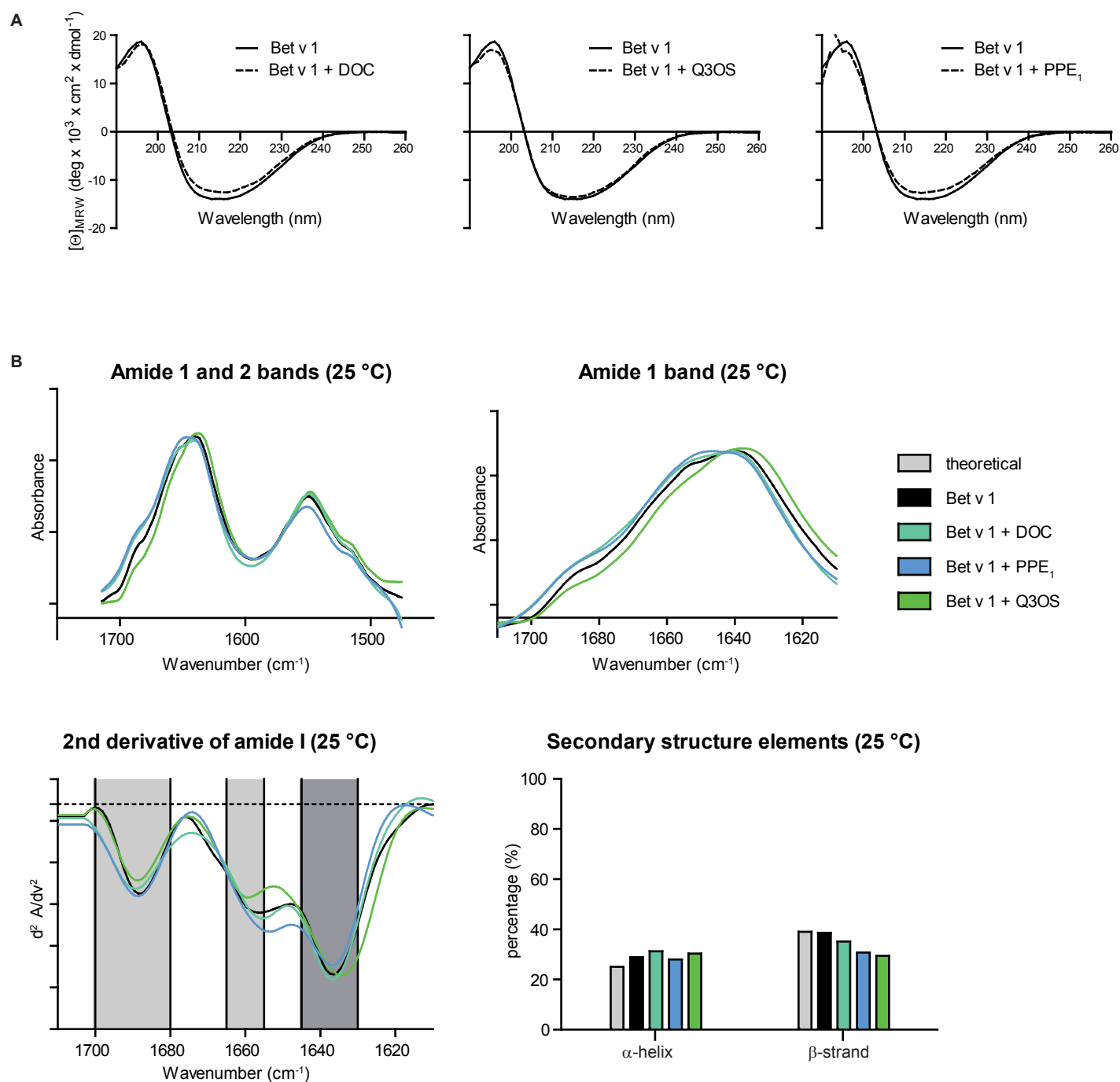
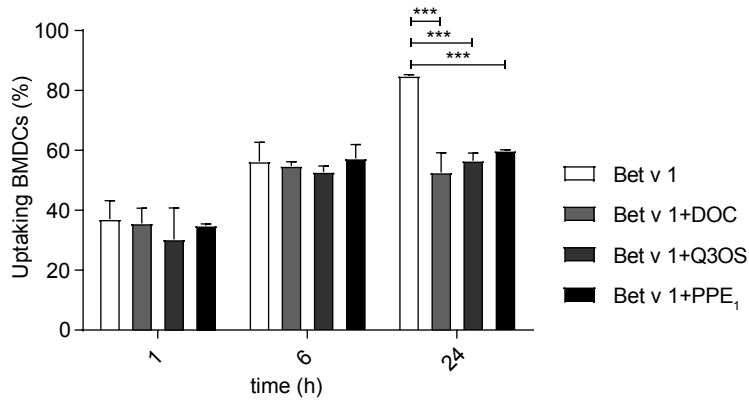
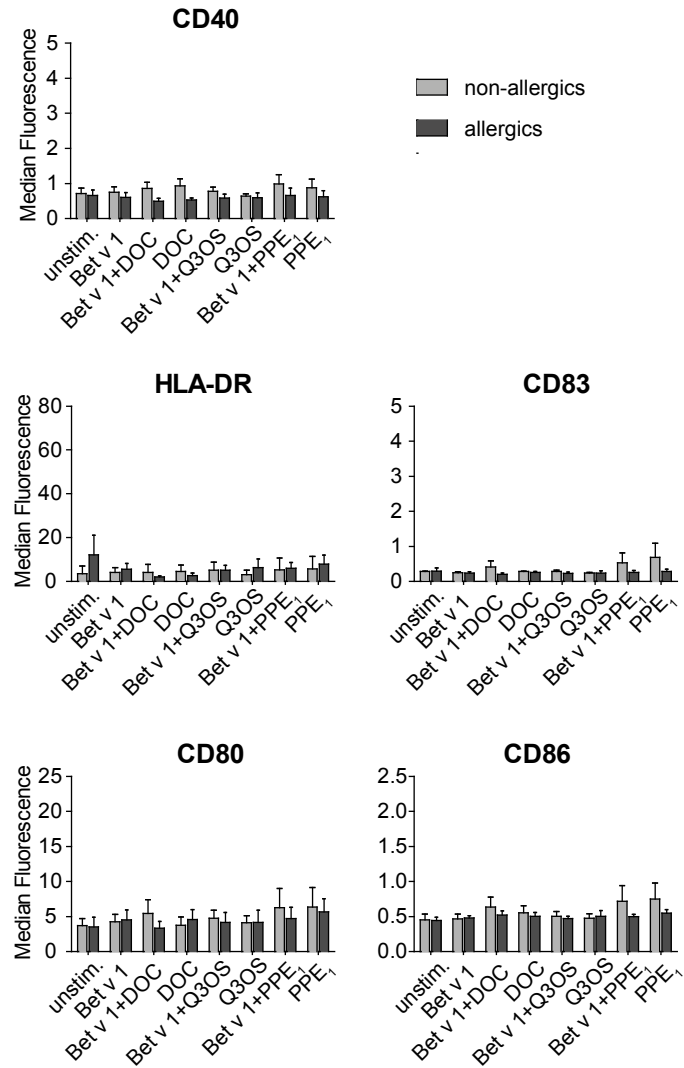


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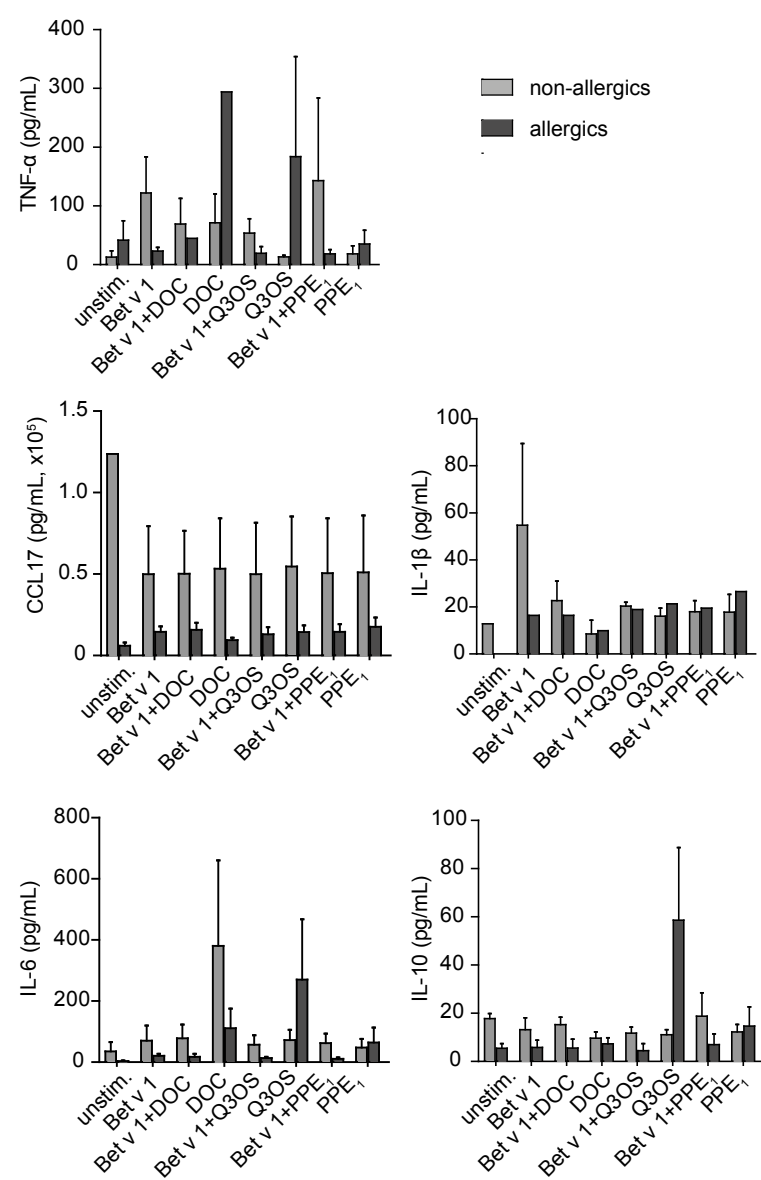
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B



C



A

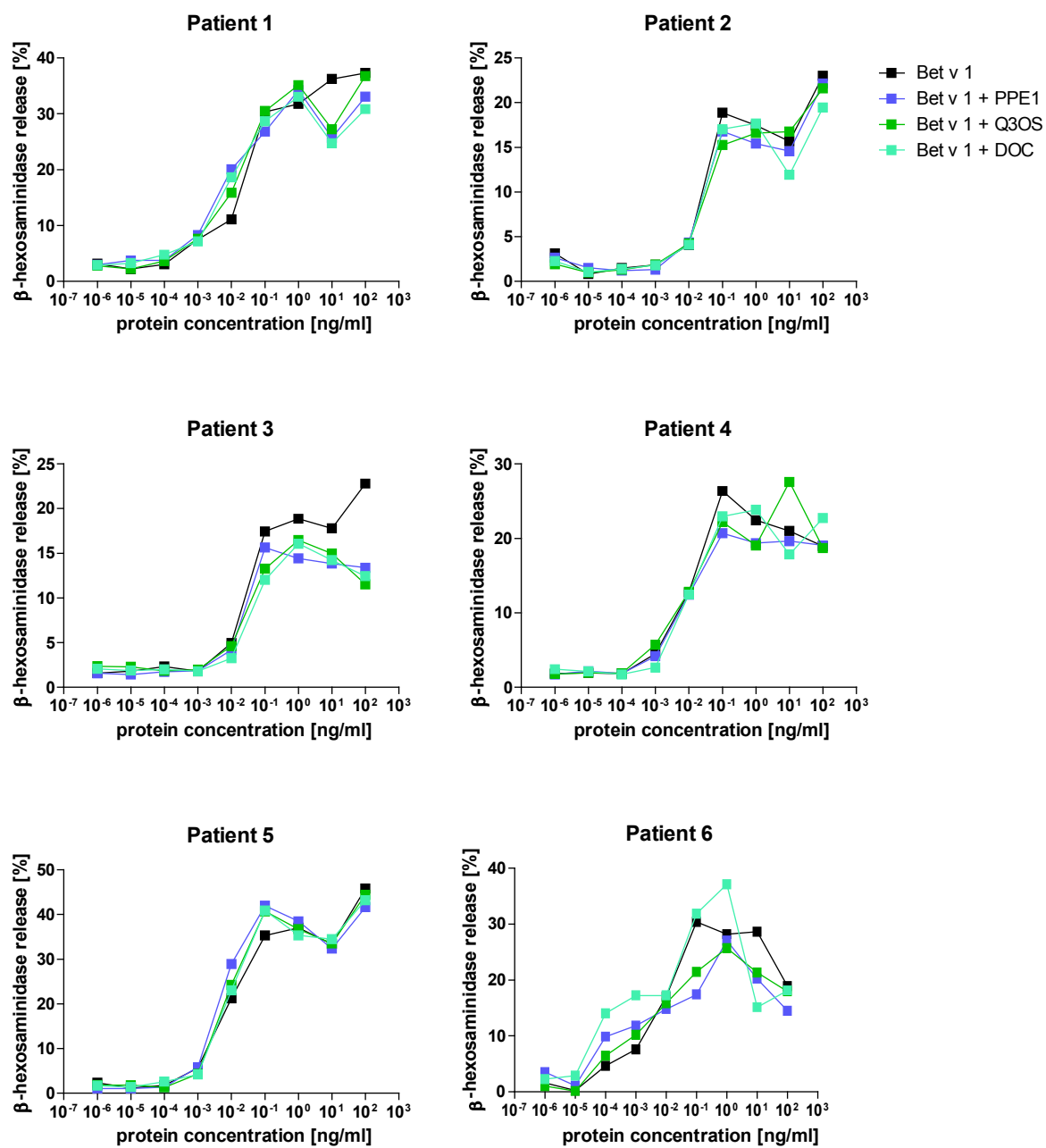


Fig. S6

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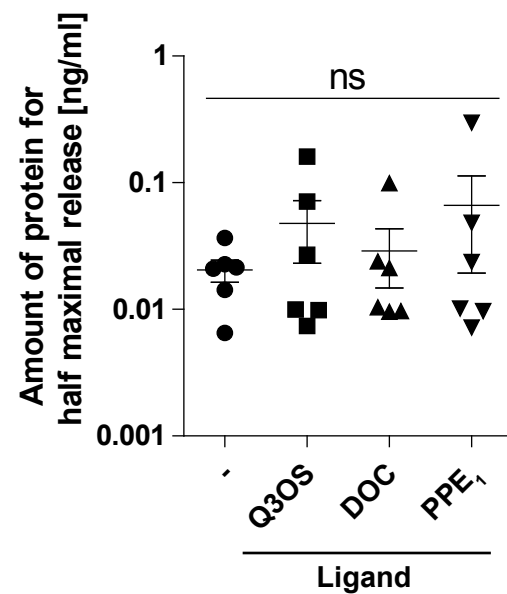


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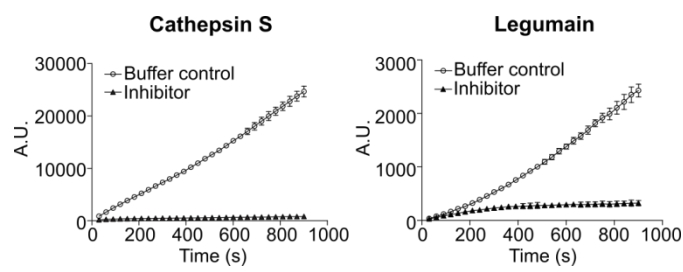


Fig. S8

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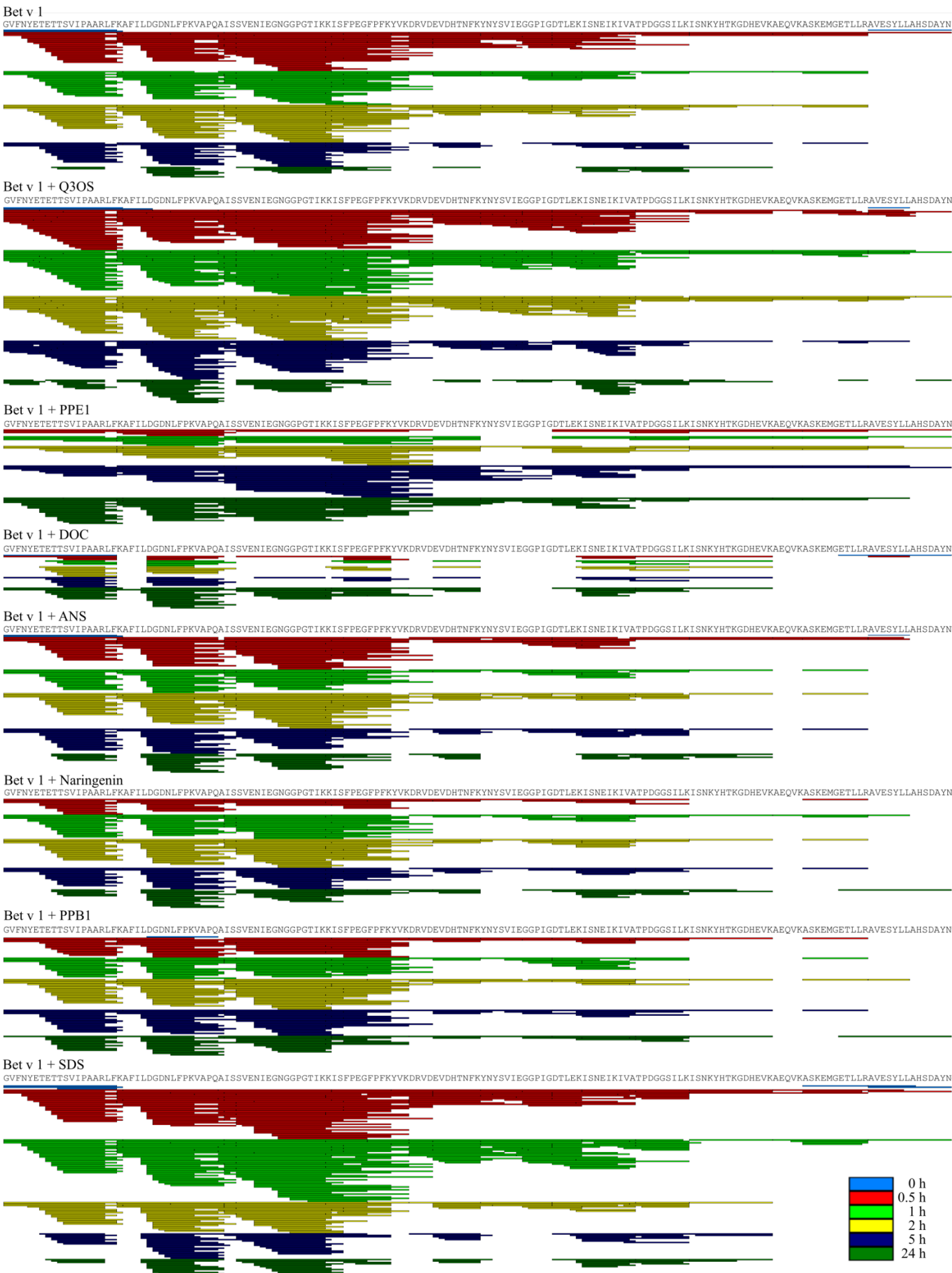
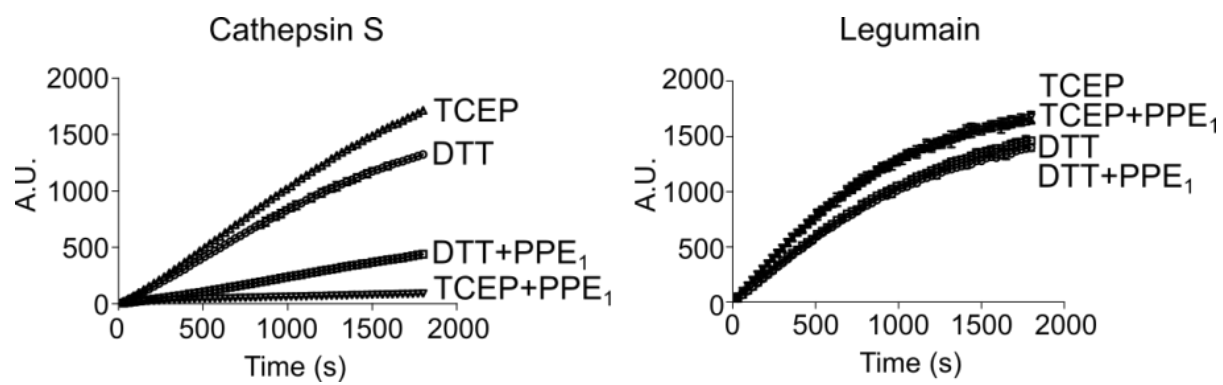


Fig. S8



Fig. S9



SUPPORTING INFORMATION

Title: MULTIPLE ROLES OF BET V 1 LIGANDS IN ALLERGEN STABILIZATION AND MODULATION OF ENDOSOMAL PROTEASE ACTIVITY

Running Title: MULTIPLE ROLES OF BET V 1 LIGANDS

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Supplementary Materials and Methods

Allergic Patients

The sera for mediator-release assays were collected from birch pollen-allergic patients ($n = 6$) and selected based on case history, positive skin prick test and allergen-specific IgE reactivity. Detection of total and allergen-specific IgE levels was performed using Immuno-CAP (Thermo Fisher Scientific, Uppsala, Sweden). The study was approved by the ethics committee of the medical faculty of Technical University of Munich (19/15 S).

Surface acoustic wave (SAW) interaction studies and determination of the affinity constant K_d

For the determination of the affinity constant K_d , we used surface acoustic wave (SAW) technology. The interaction of the six ligands with Bet v 1 was investigated using a sam® 5BLUE biosensor instrument (Nanotemper, Munich, Germany). Bet v 1 was immobilized in PBS on the surface of a SAW CM-Dextran 3D sensor chip. The surface of the chip was activated with a freshly prepared mixture of NHS (100 mM) and EDC (400 mM), and free activated sites were subsequently blocked with ethanolamine, pH 8.5 (1 M). For calculating the affinity constant K_d , different concentrations of the ligands dissolved in a 5 mM sodium phosphate buffer, pH 7.4, were applied to the Bet v 1-coupled chip. Depending on the ligand, the concentration range of the injected ligand varied between 5 μ M and 500 μ M. For the removal of residual ligand between the sample injections, the chip was washed with regeneration buffer (10 mM citric acid buffer, pH 2.8). The recorded SAW phase changes were analyzed using the software TraceDrawer 1.7 (Ridgeview Instruments, Uppsala, Sweden). The affinity constant K_d was calculated by kinetic evaluation and affinity/EC50 estimation. For kinetic evaluation, an OneToOne curve fit was chosen to match the raw data.

Experiments were performed with two coated chips in duplicate, and the coupling efficiency was evaluated using a mouse monoclonal anti-Bet v 1 antibody.

Expression and Purification of ^{15}N - ^1H labeled Bet v 1

^{15}N - ^1H labeled Bet v 1 was expressed following variation of a previously described method.¹ Two liters of bacteria were grown overnight in LB medium, centrifuged and resuspended in 0.5 L of M9 salts lacking any carbon or nitrogen source and equilibrated for 35 min. Cells, fed with glucose, ^{15}N ammonium chloride, and ^{15}N Celltone (1/25 g) (Cambridge Isotope Labs), were incubated for 35 min and then induced with IPTG. The protein suspension was purified as described above. In addition, an extra Superdex 75 size-exclusion column (GE Healthcare Biosciences, Little Chalfont, UK) step was used.

NMR spectroscopy

The NMR data were acquired with either a 600 or 800 MHz Agilent DD2 spectrometer with a cryogenically cooled probe using the pulse sequence gNhsqc. Bet v 1 assignments were taken from.² The experiments were performed under the following conditions: LTA: 45 μM Bet v 1 and 300 μM LTA in PBS, 10% $^2\text{H}_2\text{O}$, 60 μM DSS; PPE₁: 25 μM Bet v 1 and 2 μM PPE₁ in PBS, 5% ^2H -(d6) DMSO, 10% $^2\text{H}_2\text{O}$, 60 μM DSS; PPA₁: 100 μM Bet v 1 and 302 μM PPA₁ (Cayman Chemical, MI, USA) in PBS, 8.7% ^2H -(d6) DMSO, 10% $^2\text{H}_2\text{O}$, 60 μM DSS; LPS: 100 μM Bet v 1 and 400 μM LPS in PBS pH 7.4, 10% $^2\text{H}_2\text{O}$, 60 μM DSS. Kdo2: 100 μM Bet v 1 and 422 μM Kdo2 in PBS pH 7.0, 10% $^2\text{H}_2\text{O}$, 8.6% ^2H -(d6) DMSO, 60 μM DSS.

LPS pull-down assay

To investigate whether Bet v 1 binds LPS, a pull-down assay using biotinylated ultrapure *E. coli* O111:B4 LPS (InvivoGen, San Diego, CA, USA) was performed as previously described.³ In short, biotinylated LPS was immobilized on Strep-Tactin Sepharose beads (IBA Lifesciences, Göttingen, Germany) and incubated with Bet v 1 for 20 min at room temperature. Unbound protein was washed off and beads were analyzed by SDS-PAGE. As control, the individual components (Bet v 1, biotinylated LPS and Strep-Tactin Sepharose beads), and Bet v 1+beads to exclude unspecific binding, were analyzed.

Determination of secondary structure elements and thermal stability

The influence of ligand binding on the secondary structure elements and the thermal stability of Bet v 1 was addressed by circular dichroism (CD) and Fourier transform infrared (FTIR) spectroscopy. CD spectroscopy was performed with a JASCO J-815 spectropolarimeter fitted with a PTC-423S Peltier-type single position cell holder (Jasco, Tokyo, Japan) over the wavelength range 190 to 260 nm. For measurement, Bet v 1 with and without ligand was diluted in a 10 mM potassium phosphate buffer to a concentration of 0.1 mg/ml. The thermal stability analysis was recorded at 222 nm. The protein was denatured with a temperature slope of 1°C/min from 20 to 95°C.

FTIR amide 1 and amide 2 spectra of Bet v 1 at concentrations of 1.0-2.0 mg/ml with and without ligand were recorded with an AquaSpec transmission cell adapted to a Tensor II FTIR system (Bruker Optics Inc., Billerica, MA, USA). Measurement was performed at a constant temperature (25°C), controlled by a Haake F8 thermostat (Thermo Electron, Germany) with internal temperature control. For data analysis, OPUS spectroscopy software 6.0 (Bruker Optics Inc., Billerica, MA, USA) was used. The Savitzky-Golay algorithm was applied on

vector-normalized amide I spectra (25 smoothing points) to obtain the second derivative. For the quantification of secondary structure elements, a Quant2 method of the OPUS software was used. For thermal stability analysis, spectra were recorded with a BioATR II unit (Bruker Optics Inc., Billerica, MA, USA) at 25 to 95°C (dT=2.5K). The determined relative signal change in the amide I band by creating a difference spectrum for each temperature point was used to calculate the melting point (T_m).

Mediator release assay

A mediator-release assay was performed to assess the capacity of ligand-loaded Bet v 1 to induce IgE-antigen-crosslinking and basophil degranulation. In this respect, rat basophil (RBL-2H3) cells, transfected with the human high-affinity IgE receptor (FcεRI) were passively sensitized with sera of six subjects allergic to birch pollen (1:10), and used as previously described.⁴ For cell-stimulation, Bet v 1 was used at 10-fold dilutions from 1 µg/ml to 0.01 pg/ml. Toxicity of ligands on RBL-2H3 was determined by cell viability assay using MTT (3-(4,5-Dimethylthiazol-2-yl)-2,5-Diphenyltetrazolium Bromide) from Sigma-Aldrich, Inc. (St. Louis, MO, USA). Results were expressed as percentage of total enzyme release of cells lysed with Triton X-100, and the half maximal release (in ng) was determined. Statistics were calculated with a repeated ANOVA followed by a Dunnett post-hoc test of logarithmically transformed half maximal release values (not significant, ns $P > 0.05$, * $P < 0.05$, ** $P < 0.01$, and *** $P < 0.001$).

***In vitro* antigen uptake of murine bone marrow-derived dendritic cells (BMDCs)**

BMDCs from C57BL/6 mouse bone marrow were isolated as described previously.⁵ cultured in BMDC medium (RPMI 1640, 5% fetal calf serum, 2 mM L-glutamine, 1% penicillin-streptomycin, 20% granulocyte-macrophage colony-stimulating factor supernatant and 200 μ M β -mercaptoethanol) (BMDC medium) for 10 days, and stored frozen in liquid nitrogen. BMDCs were treated over a certain period of time (24, 6 or 1 hours) with 0.5 μ g of Bet v 1 per 2×10^5 cells. Bet v 1 was labeled with pHrodo™ Red succinimidyl ester (Thermo Fisher Scientific, Waltham, MA, USA) and pre-incubated with one of the ligands (DOC, Q3OS or PPE₁). CD11c⁺ cells were analyzed via flow cytometry (allophycocyanin-conjugated anti-mouse CD11c antibody, clone N418; eBioscience, Inc., San Diego, CA, USA) on a FACSCanto II instrument (BD Biosciences, San Jose, CA, USA). For the live/dead staining a fixable viability stain 450 (BD Biosciences) was used. Granulocytes and monocytes were excluded via the V450 Rat anti-Mouse LY-6G and LY-6C (BD Biosciences) antibody. Data were recorded and analyzed using the BD FACSDiva software (BD Biosciences). Statistical analysis was performed using ANOVA with a Bonferroni post-test to compare all groups. The data represent the mean of duplicate experiments and are derived from at least 2 independent experiments.

Activation and cytokine secretion of human monocyte-derived dendritic cells (moDCs)

Immature moDCs from PBMCs of either healthy/non-atopic donors (n=5) or atopic patients (n=7) were isolated and cultured as described elsewhere.⁶ Cell viability using the Aqua® dye (Invitrogen, Carlsbad, CA, USA), expression of CD1a (eBioscience, Inc., San Diego, CA, USA) and loss of CD14 (BD Biosciences) expression were analyzed by flow cytometry on a Navios flow cytometer (Beckman Coulter, Brea, CA, USA). Cells (1×10^6 cells/ml) were

stimulated for 24 hours with 1 µg/ml of Bet v 1 either alone or in complex with one of the three ligands (DOC, PPE₁ or Q3OS). As a control, unstimulated moDCs and the individual ligands without Bet v 1 were used at the same concentrations. The cell supernatant was frozen for the analysis of cytokine secretion. Of note, no LPS co-stimulation was induced. The following maturation markers were investigated: CD40 (eBioscience), HLA-DR, CD80, CD83 and CD86 (BD Biosciences). Cytokine expression of CCL17, IL-1β, IL-10 (BD Biosciences), TNFα and IL-6 (eBioscience) was determined by ELISA. Statistical analysis was performed using one-way ANOVA with a Bonferroni post-test to compare all groups. The study was approved by the ethics committee of the medical faculty of Technical University of Munich (54/17 S).

***In vitro* simulation of endolysosomal degradation**

The endolysosomal degradation assay was performed with ligand-bound (either DOC, PPE₁, or Q3OS in 10× molar excess) and Bet v 1 without ligands (apo-Bet v 1) as previously described.⁷ The protein (5 µg) was incubated with 7 µg of microsomes in 100 mM citrate buffer pH 4.8 and 2 mM dithiothreitol (DTT) for 0, 0.5, 1, 3, 6, 12, 24, and 48 h at 37°C. The different digestion preparations were analyzed by SDS-PAGE and quantitatively interpreted using Image Lab 4.0.1 Software (Bio-Rad). The generated peptides obtained after 12 h of digestion were analyzed using mass spectrometry with a Q-Exactive Orbitrap Mass Spectrometer (Thermo Fisher Scientific, Waltham, MA, USA), nanoelectrospray, and nano-HPLC (Dionex Ultimate 3000, Thermo Fisher Scientific).

Data analysis of *in vitro* simulation of endolysosomal degradation

For data analysis, the web-based application MSTools was used.⁸ For the semi-quantitative analysis of the abundance of the generated peptides at 12 hours of degradation, the obtained peptide sequences were clustered into 7 groups according to their amino acid sequence (cluster 1, GVF-NYE-TET-TSV-IPA-ARL-FKA-F; cluster 2, AIL-DGD-NLF-PKV-APQ-A;

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Bet v 1 *in vitro* proteolytic degradation assay using individual endolysosomal proteases

Recombinant human cathepsin S and human legumain were heterologously expressed and purified as described previously.^{9,10} Bet v 1 (20 μ M) was incubated with ligand (100 μ M) in digestion buffer (0.1 M sodium acetate, pH 5.0, 0.1 M sodium chloride, 5 mM EDTA, and 2 mM DTT) at room temperature prior to the addition of cathepsin S (1 μ M) or legumain (2 μ M). The reactions were incubated at 37°C for 0, 0.5, 1, 2, 5, and 24 h. At each time point, the reaction was halted by the addition of E64 (for cathepsin S) or YVAD-CMK (for legumain) at a final concentration of 50 μ M, and analyzed by SDS-PAGE. Control reactions without the addition of protease were performed. The generated peptides were analyzed using mass spectrometry.

Enzymatic activity assays

For the detection of cathepsin or legumain activities in the microsomal fraction, 8 μ g of microsomal extract was incubated with 50 μ M fluorogenic substrate with or without inhibitor in assay buffer (100 mM citrate pH 4.8 and 2 mM DTT). The enzymatic reactions were carried out in a 50 μ L reaction volume in a 96-half-well black flat bottom assay plate (Corning Inc., Corning, NY, USA) at 37°C. The fluorescence signal was recorded using a Tecan Infinite-200 plate reader (Tecan, Männedorf, Switzerland) at an excitation wavelength

of 380 nm and emission wavelength of 460 nm for 15 min of continuous measurement with a 30-s interval reading. The fluorogenic substrates used for cathepsin S and legumain were Z-VVR-AMC and Z-AAN-AMC (Bachem, Bubendorf, Switzerland), respectively. The inhibitors used for cathepsin S and legumain were Z-FL-COCHO (Sigma-Aldrich, CA, USA) and Ac-YVAD-CMK (Bachem), respectively¹¹.

Preparation of aqueous birch pollen extract (BPE)

Pollen extract was prepared by incubating 250 mg of Birch pollens (Batch: 012517101, Allergon AB, Ängelholm, Sweden) in 1 mL of extraction buffer (10 mM Tris pH 7.5, 150 mM NaCl) at 4°C under vigorous shaking conditions for 22 hours. Extract was recovered by centrifugation at 12000 g, 4°C for 30 minutes and subsequently filtered through a 0.22 µm filter (Pall, Dreieich, Germany) which was prewashed with extraction buffer twice. Protein concentration was estimated using Bradford protein assay (Bio-Rad, Vienna, USA) using BSA (bovine serum albumin) as standard.

Mass spectrometry

Samples were desalted using PierceC18 Tips (Thermo Fisher Scientific, Bremen, Germany) and injected into an UltiMate 3000 RSLCnano HPLC system (Thermo Fisher Scientific, Waltham, MA, USA) by using a 1.0 µL-Pickup injection. At a flow rate of 350 nL/min, peptides were separated using an in-house packed 200 x 0.1 mm i.d. Hypersil GOLD™ aQ C18 capillary column with 3.0 µm particles. Water (A) and acetonitrile (B) with 0.10 % (v/v) formic acid (FA, Sigma Aldrich) were used as eluents. For the separation, the column temperature was set to 50.0°C and a linear gradient of 5.0-40.0% B in 100.0 min was used. The HPLC-system was hyphenated to a Q Exactive™ Hybrid Quadrupole-Orbitrap™ mass spectrometer (Thermo Scientific) by using a nano-electrospray ionization source. The source

was operated in positive ion mode with a spray voltage of 1.5 kV. Ionized peptides were measured using data dependent acquisition based on the Top 15 most abundant precursor ions with a full MS resolution of 70,000, AGC target of 1e6, maximum injection time of 120 ms with a scan range of 370 to 2000 m/z. Fragment spectra were recorded with a resolution of 35,000 applying a normalized collision energy (NCE) of 29. The AGC target was set to 2e5 with a maximum injection time of 100 ms and an isolation window of 2.0 m/z. The dynamic exclusion was set to 45.0 s.

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T-cell proliferation assay

Bet v 1 was incubated over night with a 10-fold molar excess of either Q3OS, PPB₁, PPE₁, or DOC before incubation with murine BMDCs at a concentration of 10 µg/mL in BMDC medium (online supporting information). After 16, 24, 32, and 48h, DCs were washed and CD4⁺ T-cell hybridomas specific for the immune-dominant epitope 142-153 of Bet v 1 were added to the culture at a ratio of 1:10 (DC:T-cell) for 24h¹⁷. Supernatants were harvested and IL-2 levels were determined by ELISA (Invitrogen, Thermo Fisher Scientific, Waltham, MA, USA). As a reference, BMDCs were pulsed at each time point with different concentrations of peptide 142-153 and co-cultured with CD4⁺ T-cell hybridomas. By interpolating in a standard curve, a µM peptide equivalent from the measured IL-2 was calculated from DCs pulsed with different peptide concentrations. The assays were carried out in triplicates.

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SUPPORTING INFORMATION

Title: MULTIPLE ROLES OF BET V 1 LIGANDS IN ALLERGEN STABILIZATION AND MODULATION OF ENDOSOMAL PROTEASE ACTIVITY

Running Title: MULTIPLE ROLES OF BET V 1 LIGANDS

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Supplementary Materials and Methods

Allergic Patients

The sera for mediator-release assays were collected from birch pollen-allergic patients ($n = 6$) and selected based on case history, positive skin prick test and allergen-specific IgE reactivity. Detection of total and allergen-specific IgE levels was performed using Immuno-CAP (Thermo Fisher Scientific, Uppsala, Sweden). The study was approved by the ethics committee of the medical faculty of Technical University of Munich (19/15 S).

Surface acoustic wave (SAW) interaction studies and determination of the affinity constant K_d

For the determination of the affinity constant K_d , we used surface acoustic wave (SAW) technology. The interaction of the six ligands with Bet v 1 was investigated using a sam® 5BLUE biosensor instrument (Nanotemper, Munich, Germany). Bet v 1 was immobilized in PBS on the surface of a SAW CM-Dextran 3D sensor chip. The surface of the chip was activated with a freshly prepared mixture of NHS (100 mM) and EDC (400 mM), and free activated sites were subsequently blocked with ethanolamine, pH 8.5 (1 M). For calculating the affinity constant K_d , different concentrations of the ligands dissolved in a 5 mM sodium phosphate buffer, pH 7.4, were applied to the Bet v 1-coupled chip. Depending on the ligand, the concentration range of the injected ligand varied between 5 μ M and 500 μ M. For the removal of residual ligand between the sample injections, the chip was washed with regeneration buffer (10 mM citric acid buffer, pH 2.8). The recorded SAW phase changes were analyzed using the software TraceDrawer 1.7 (Ridgeview Instruments, Uppsala, Sweden). The affinity constant K_d was calculated by kinetic evaluation and affinity/EC50 estimation. For kinetic evaluation, an OneToOne curve fit was chosen to match the raw data.

Experiments were performed with two coated chips in duplicate, and the coupling efficiency was evaluated using a mouse monoclonal anti-Bet v 1 antibody.

Expression and Purification of ^{15}N - ^1H labeled Bet v 1

^{15}N - ^1H labeled Bet v 1 was expressed following variation of a previously described method.¹ Two liters of bacteria were grown overnight in LB medium, centrifuged and resuspended in 0.5 L of M9 salts lacking any carbon or nitrogen source and equilibrated for 35 min. Cells, fed with glucose, ^{15}N ammonium chloride, and ^{15}N Celltone (1/25 g) (Cambridge Isotope Labs), were incubated for 35 min and then induced with IPTG. The protein suspension was purified as described above. In addition, an extra Superdex 75 size-exclusion column (GE Healthcare Biosciences, Little Chalfont, UK) step was used.

NMR spectroscopy

The NMR data were acquired with either a 600 or 800 MHz Agilent DD2 spectrometer with a cryogenically cooled probe using the pulse sequence gNhsqc. Bet v 1 assignments were taken from.² The experiments were performed under the following conditions: LTA: 45 μM Bet v 1 and 300 μM LTA in PBS, 10% $^2\text{H}_2\text{O}$, 60 μM DSS; PPE₁: 25 μM Bet v 1 and 2 μM PPE₁ in PBS, 5% ^2H -(d6) DMSO, 10% $^2\text{H}_2\text{O}$, 60 μM DSS; PPA₁: 100 μM Bet v 1 and 302 μM PPA₁ (Cayman Chemical, MI, USA) in PBS, 8.7% ^2H -(d6) DMSO, 10% $^2\text{H}_2\text{O}$, 60 μM DSS; LPS: 100 μM Bet v 1 and 400 μM LPS in PBS pH 7.4, 10% $^2\text{H}_2\text{O}$, 60 μM DSS. Kdo2: 100 μM Bet v 1 and 422 μM Kdo2 in PBS pH 7.0, 10% $^2\text{H}_2\text{O}$, 8.6% ^2H -(d6) DMSO, 60 μM DSS.

LPS pull-down assay

To investigate whether Bet v 1 binds LPS, a pull-down assay using biotinylated ultrapure *E. coli* O111:B4 LPS (InvivoGen, San Diego, CA, USA) was performed as previously described.³ In short, biotinylated LPS was immobilized on Strep-Tactin Sepharose beads (IBA Lifesciences, Göttingen, Germany) and incubated with Bet v 1 for 20 min at room temperature. Unbound protein was washed off and beads were analyzed by SDS-PAGE. As control, the individual components (Bet v 1, biotinylated LPS and Strep-Tactin Sepharose beads), and Bet v 1+beads to exclude unspecific binding, were analyzed.

Determination of secondary structure elements and thermal stability

The influence of ligand binding on the secondary structure elements and the thermal stability of Bet v 1 was addressed by circular dichroism (CD) and Fourier transform infrared (FTIR) spectroscopy. CD spectroscopy was performed with a JASCO J-815 spectropolarimeter fitted with a PTC-423S Peltier-type single position cell holder (Jasco, Tokyo, Japan) over the wavelength range 190 to 260 nm. For measurement, Bet v 1 with and without ligand was diluted in a 10 mM potassium phosphate buffer to a concentration of 0.1 mg/ml. The thermal stability analysis was recorded at 222 nm. The protein was denatured with a temperature slope of 1°C/min from 20 to 95°C.

FTIR amide 1 and amide 2 spectra of Bet v 1 at concentrations of 1.0-2.0 mg/ml with and without ligand were recorded with an AquaSpec transmission cell adapted to a Tensor II FTIR system (Bruker Optics Inc., Billerica, MA, USA). Measurement was performed at a constant temperature (25°C), controlled by a Haake F8 thermostat (Thermo Electron, Germany) with internal temperature control. For data analysis, OPUS spectroscopy software 6.0 (Bruker Optics Inc., Billerica, MA, USA) was used. The Savitzky-Golay algorithm was applied on

vector-normalized amide I spectra (25 smoothing points) to obtain the second derivative. For the quantification of secondary structure elements, a Quant2 method of the OPUS software was used. For thermal stability analysis, spectra were recorded with a BioATR II unit (Bruker Optics Inc., Billerica, MA, USA) at 25 to 95°C (dT=2.5K). The determined relative signal change in the amide I band by creating a difference spectrum for each temperature point was used to calculate the melting point (T_m).

Mediator release assay

A mediator-release assay was performed to assess the capacity of ligand-loaded Bet v 1 to induce IgE-antigen-crosslinking and basophil degranulation. In this respect, rat basophil (RBL-2H3) cells, transfected with the human high-affinity IgE receptor (FcεRI) were passively sensitized with sera of six subjects allergic to birch pollen (1:10), and used as previously described.⁴ For cell-stimulation, Bet v 1 was used at 10-fold dilutions from 1 µg/ml to 0.01 pg/ml. Toxicity of ligands on RBL-2H3 was determined by cell viability assay using MTT (3-(4,5-Dimethylthiazol-2-yl)-2,5-Diphenyltetrazolium Bromide) from Sigma-Aldrich, Inc. (St. Louis, MO, USA). Results were expressed as percentage of total enzyme release of cells lysed with Triton X-100, and the half maximal release (in ng) was determined. Statistics were calculated with a repeated ANOVA followed by a Dunnett post-hoc test of logarithmically transformed half maximal release values (not significant, ns $P > 0.05$, * $P < 0.05$, ** $P < 0.01$, and *** $P < 0.001$).

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SUPPORTING INFORMATION

Title: MULTIPLE ROLES OF BET V 1 LIGANDS IN ALLERGEN STABILIZATION AND MODULATION OF ENDOSOMAL PROTEASE ACTIVITY

Running Title: MULTIPLE ROLES OF BET V 1 LIGANDS

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Supplementary Materials and Methods

Allergic Patients

The sera for mediator-release assays were collected from birch pollen-allergic patients ($n = 6$) and selected based on case history, positive skin prick test and allergen-specific IgE reactivity. Detection of total and allergen-specific IgE levels was performed using Immuno-CAP (Thermo Fisher Scientific, Uppsala, Sweden). The study was approved by the ethics committee of the medical faculty of Technical University of Munich (19/15 S).

Surface acoustic wave (SAW) interaction studies and determination of the affinity constant K_d

For the determination of the affinity constant K_d , we used surface acoustic wave (SAW) technology. The interaction of the six ligands with Bet v 1 was investigated using a sam® 5BLUE biosensor instrument (Nanotemper, Munich, Germany). Bet v 1 was immobilized in PBS on the surface of a SAW CM-Dextran 3D sensor chip. The surface of the chip was activated with a freshly prepared mixture of NHS (100 mM) and EDC (400 mM), and free activated sites were subsequently blocked with ethanolamine, pH 8.5 (1 M). For calculating the affinity constant K_d , different concentrations of the ligands dissolved in a 5 mM sodium phosphate buffer, pH 7.4, were applied to the Bet v 1-coupled chip. Depending on the ligand, the concentration range of the injected ligand varied between 5 μ M and 500 μ M. For the removal of residual ligand between the sample injections, the chip was washed with regeneration buffer (10 mM citric acid buffer, pH 2.8). The recorded SAW phase changes were analyzed using the software TraceDrawer 1.7 (Ridgeview Instruments, Uppsala, Sweden). The affinity constant K_d was calculated by kinetic evaluation and affinity/EC50 estimation. For kinetic evaluation, an OneToOne curve fit was chosen to match the raw data.

Experiments were performed with two coated chips in duplicate, and the coupling efficiency was evaluated using a mouse monoclonal anti-Bet v 1 antibody.

Expression and Purification of ^{15}N - ^1H labeled Bet v 1

^{15}N - ^1H labeled Bet v 1 was expressed following variation of a previously described method.¹ Two liters of bacteria were grown overnight in LB medium, centrifuged and resuspended in 0.5 L of M9 salts lacking any carbon or nitrogen source and equilibrated for 35 min. Cells, fed with glucose, ^{15}N ammonium chloride, and ^{15}N Celltone (1/25 g) (Cambridge Isotope Labs), were incubated for 35 min and then induced with IPTG. The protein suspension was purified as described above. In addition, an extra Superdex 75 size-exclusion column (GE Healthcare Biosciences, Little Chalfont, UK) step was used.

NMR spectroscopy

The NMR data were acquired with either a 600 or 800 MHz Agilent DD2 spectrometer with a cryogenically cooled probe using the pulse sequence gNhsqc. Bet v 1 assignments were taken from.² The experiments were performed under the following conditions: LTA: 45 μM Bet v 1 and 300 μM LTA in PBS, 10% $^2\text{H}_2\text{O}$, 60 μM DSS; PPE₁: 25 μM Bet v 1 and 2 μM PPE₁ in PBS, 5% ^2H -(d6) DMSO, 10% $^2\text{H}_2\text{O}$, 60 μM DSS; PPA₁: 100 μM Bet v 1 and 302 μM PPA₁ (Cayman Chemical, MI, USA) in PBS, 8.7% ^2H -(d6) DMSO, 10% $^2\text{H}_2\text{O}$, 60 μM DSS; LPS: 100 μM Bet v 1 and 400 μM LPS in PBS pH 7.4, 10% $^2\text{H}_2\text{O}$, 60 μM DSS. Kdo2: 100 μM Bet v 1 and 422 μM Kdo2 in PBS pH 7.0, 10% $^2\text{H}_2\text{O}$, 8.6% ^2H -(d6) DMSO, 60 μM DSS.

LPS pull-down assay

To investigate whether Bet v 1 binds LPS, a pull-down assay using biotinylated ultrapure *E. coli* O111:B4 LPS (InvivoGen, San Diego, CA, USA) was performed as previously described.³ In short, biotinylated LPS was immobilized on Strep-Tactin Sepharose beads (IBA Lifesciences, Göttingen, Germany) and incubated with Bet v 1 for 20 min at room temperature. Unbound protein was washed off and beads were analyzed by SDS-PAGE. As control, the individual components (Bet v 1, biotinylated LPS and Strep-Tactin Sepharose beads), and Bet v 1+beads to exclude unspecific binding, were analyzed.

Determination of secondary structure elements and thermal stability

The influence of ligand binding on the secondary structure elements and the thermal stability of Bet v 1 was addressed by circular dichroism (CD) and Fourier transform infrared (FTIR) spectroscopy. CD spectroscopy was performed with a JASCO J-815 spectropolarimeter fitted with a PTC-423S Peltier-type single position cell holder (Jasco, Tokyo, Japan) over the wavelength range 190 to 260 nm. For measurement, Bet v 1 with and without ligand was diluted in a 10 mM potassium phosphate buffer to a concentration of 0.1 mg/ml. The thermal stability analysis was recorded at 222 nm. The protein was denatured with a temperature slope of 1°C/min from 20 to 95°C.

FTIR amide 1 and amide 2 spectra of Bet v 1 at concentrations of 1.0-2.0 mg/ml with and without ligand were recorded with an AquaSpec transmission cell adapted to a Tensor II FTIR system (Bruker Optics Inc., Billerica, MA, USA). Measurement was performed at a constant temperature (25°C), controlled by a Haake F8 thermostat (Thermo Electron, Germany) with internal temperature control. For data analysis, OPUS spectroscopy software 6.0 (Bruker Optics Inc., Billerica, MA, USA) was used. The Savitzky-Golay algorithm was applied on

vector-normalized amide I spectra (25 smoothing points) to obtain the second derivative. For the quantification of secondary structure elements, a Quant2 method of the OPUS software was used. For thermal stability analysis, spectra were recorded with a BioATR II unit (Bruker Optics Inc., Billerica, MA, USA) at 25 to 95°C (dT=2.5K). The determined relative signal change in the amide I band by creating a difference spectrum for each temperature point was used to calculate the melting point (T_m).

Mediator release assay

A mediator-release assay was performed to assess the capacity of ligand-loaded Bet v 1 to induce IgE-antigen-crosslinking and basophil degranulation. In this respect, rat basophil (RBL-2H3) cells, transfected with the human high-affinity IgE receptor (FcεRI) were passively sensitized with sera of six subjects allergic to birch pollen (1:10), and used as previously described.⁴ For cell-stimulation, Bet v 1 was used at 10-fold dilutions from 1 µg/ml to 0.01 pg/ml. Toxicity of ligands on RBL-2H3 was determined by cell viability assay using MTT (3-(4,5-Dimethylthiazol-2-yl)-2,5-Diphenyltetrazolium Bromide) from Sigma-Aldrich, Inc. (St. Louis, MO, USA). Results were expressed as percentage of total enzyme release of cells lysed with Triton X-100, and the half maximal release (in ng) was determined. Statistics were calculated with a repeated ANOVA followed by a Dunnett post-hoc test of logarithmically transformed half maximal release values (not significant, ns $P > 0.05$, * $P < 0.05$, ** $P < 0.01$, and *** $P < 0.001$).

***In vitro* antigen uptake of murine bone marrow-derived dendritic cells (BMDCs)**

BMDCs from C57BL/6 mouse bone marrow were isolated as described previously.⁵ cultured in BMDC medium (RPMI 1640, 5% fetal calf serum, 2 mM L-glutamine, 1% penicillin-streptomycin, 20% granulocyte-macrophage colony-stimulating factor supernatant and 200 μ M β -mercaptoethanol) (BMDC medium) for 10 days, and stored frozen in liquid nitrogen. BMDCs were treated over a certain period of time (24, 6 or 1 hours) with 0.5 μ g of Bet v 1 per 2×10^5 cells. Bet v 1 was labeled with pHrodo™ Red succinimidyl ester (Thermo Fisher Scientific, Waltham, MA, USA) and pre-incubated with one of the ligands (DOC, Q3OS or PPE₁). CD11c⁺ cells were analyzed via flow cytometry (allophycocyanin-conjugated anti-mouse CD11c antibody, clone N418; eBioscience, Inc., San Diego, CA, USA) on a FACSCanto II instrument (BD Biosciences, San Jose, CA, USA). For the live/dead staining a fixable viability stain 450 (BD Biosciences) was used. Granulocytes and monocytes were excluded via the V450 Rat anti-Mouse LY-6G and LY-6C (BD Biosciences) antibody. Data were recorded and analyzed using the BD FACSDiva software (BD Biosciences). Statistical analysis was performed using ANOVA with a Bonferroni post-test to compare all groups. The data represent the mean of duplicate experiments and are derived from at least 2 independent experiments.

Activation and cytokine secretion of human monocyte-derived dendritic cells (moDCs)

Immature moDCs from PBMCs of either healthy/non-atopic donors (n=5) or atopic patients (n=7) were isolated and cultured as described elsewhere.⁶ Cell viability using the Aqua® dye (Invitrogen, Carlsbad, CA, USA), expression of CD1a (eBioscience, Inc., San Diego, CA, USA) and loss of CD14 (BD Biosciences) expression were analyzed by flow cytometry on a Navios flow cytometer (Beckman Coulter, Brea, CA, USA). Cells (1×10^6 cells/ml) were

stimulated for 24 hours with 1 µg/ml of Bet v 1 either alone or in complex with one of the three ligands (DOC, PPE₁ or Q3OS). As a control, unstimulated moDCs and the individual ligands without Bet v 1 were used at the same concentrations. The cell supernatant was frozen for the analysis of cytokine secretion. Of note, no LPS co-stimulation was induced. The following maturation markers were investigated: CD40 (eBioscience), HLA-DR, CD80, CD83 and CD86 (BD Biosciences). Cytokine expression of CCL17, IL-1β, IL-10 (BD Biosciences), TNFα and IL-6 (eBioscience) was determined by ELISA. Statistical analysis was performed using one-way ANOVA with a Bonferroni post-test to compare all groups. The study was approved by the ethics committee of the medical faculty of Technical University of Munich (54/17 S).

***In vitro* simulation of endolysosomal degradation**

The endolysosomal degradation assay was performed with ligand-bound (either DOC, PPE₁, or Q3OS in 10× molar excess) and Bet v 1 without ligands (apo-Bet v 1) as previously described.⁷ The protein (5 µg) was incubated with 7 µg of microsomes in 100 mM citrate buffer pH 4.8 and 2 mM dithiothreitol (DTT) for 0, 0.5, 1, 3, 6, 12, 24, and 48 h at 37°C. The different digestion preparations were analyzed by SDS-PAGE and quantitatively interpreted using Image Lab 4.0.1 Software (Bio-Rad). The generated peptides obtained after 12 h of digestion were analyzed using mass spectrometry with a Q-Exactive Orbitrap Mass Spectrometer (Thermo Fisher Scientific, Waltham, MA, USA), nanoelectrospray, and nano-HPLC (Dionex Ultimate 3000, Thermo Fisher Scientific).

Data analysis of *in vitro* simulation of endolysosomal degradation

For data analysis, the web-based application MSTools was used.⁸ For the semi-quantitative analysis of the abundance of the generated peptides at 12 hours of degradation, the obtained peptide sequences were clustered into 7 groups according to their amino acid sequence (cluster 1, GVF-NYE-TET-TSV-IPA-ARL-FKA-F; cluster 2, AIL-DGD-NLF-PKV-APQ-A;

cluster 3, AIS-SVE-NIE-GNG-GPG-TIK-KIS-FPE-G; cluster 4, FPF-KYV-KDR-VDE-VDH-TNF-K; cluster 5, YNY-SVI-EGG-PIG-DTL-EKI-SNE-IKI-VAT-PDG-GSI-LK; cluster 6, ISN-KYH-TKG-DHE-VKA-EQV-KAS-KEM-GET-LLR; and cluster 7, RAV-ESY-LLA-HSD-AYN), and the total sum of peak areas of all sequences per cluster was calculated (in percentage).

Bet v 1 *in vitro* proteolytic degradation assay using individual endolysosomal proteases

Recombinant human cathepsin S and human legumain were heterologously expressed and purified as described previously.^{9,10} Bet v 1 (20 μ M) was incubated with ligand (100 μ M) in digestion buffer (0.1 M sodium acetate, pH 5.0, 0.1 M sodium chloride, 5 mM EDTA, and 2 mM DTT) at room temperature prior to the addition of cathepsin S (1 μ M) or legumain (2 μ M). The reactions were incubated at 37°C for 0, 0.5, 1, 2, 5, and 24 h. At each time point, the reaction was halted by the addition of E64 (for cathepsin S) or YVAD-CMK (for legumain) at a final concentration of 50 μ M, and analyzed by SDS-PAGE. Control reactions without the addition of protease were performed. The generated peptides were analyzed using mass spectrometry.

Enzymatic activity assays

For the detection of cathepsin or legumain activities in the microsomal fraction, 8 μ g of microsomal extract was incubated with 50 μ M fluorogenic substrate with or without inhibitor in assay buffer (100 mM citrate pH 4.8 and 2 mM DTT). The enzymatic reactions were carried out in a 50 μ L reaction volume in a 96-half-well black flat bottom assay plate (Corning Inc., Corning, NY, USA) at 37°C. The fluorescence signal was recorded using a Tecan Infinite-200 plate reader (Tecan, Männedorf, Switzerland) at an excitation wavelength

of 380 nm and emission wavelength of 460 nm for 15 min of continuous measurement with a 30-s interval reading. The fluorogenic substrates used for cathepsin S and legumain were Z-VVR-AMC and Z-AAN-AMC (Bachem, Bubendorf, Switzerland), respectively. The inhibitors used for cathepsin S and legumain were Z-FL-COCHO (Sigma-Aldrich, CA, USA) and Ac-YVAD-CMK (Bachem), respectively¹¹.

Preparation of aqueous birch pollen extract (BPE)

Pollen extract was prepared by incubating 250 mg of Birch pollens (Batch: 012517101, Allergon AB, Ängelholm, Sweden) in 1 mL of extraction buffer (10 mM Tris pH 7.5, 150 mM NaCl) at 4°C under vigorous shaking conditions for 22 hours. Extract was recovered by centrifugation at 12000 g, 4°C for 30 minutes and subsequently filtered through a 0.22 µm filter (Pall, Dreieich, Germany) which was prewashed with extraction buffer twice. Protein concentration was estimated using Bradford protein assay (Bio-Rad, Vienna, USA) using BSA (bovine serum albumin) as standard.

Mass spectrometry

Samples were desalted using PierceC18 Tips (Thermo Fisher Scientific, Bremen, Germany) and injected into an UltiMate 3000 RSLCnano HPLC system (Thermo Fisher Scientific, Waltham, MA, USA) by using a 1.0 µL-Pickup injection. At a flow rate of 350 nL/min, peptides were separated using an in-house packed 200 x 0.1 mm i.d. Hypersil GOLD™ aQ C18 capillary column with 3.0 µm particles. Water (A) and acetonitrile (B) with 0.10 % (v/v) formic acid (FA, Sigma Aldrich) were used as eluents. For the separation, the column temperature was set to 50.0°C and a linear gradient of 5.0-40.0% B in 100.0 min was used. The HPLC-system was hyphenated to a Q Exactive™ Hybrid Quadrupole-Orbitrap™ mass spectrometer (Thermo Scientific) by using a nano-electrospray ionization source. The source

was operated in positive ion mode with a spray voltage of 1.5 kV. Ionized peptides were measured using data dependent acquisition based on the Top 15 most abundant precursor ions with a full MS resolution of 70,000, AGC target of 1e6, maximum injection time of 120 ms with a scan range of 370 to 2000 m/z. Fragment spectra were recorded with a resolution of 35,000 applying a normalized collision energy (NCE) of 29. The AGC target was set to 2e5 with a maximum injection time of 100 ms and an isolation window of 2.0 m/z. The dynamic exclusion was set to 45.0 s.

Survey and fragment spectra were analyzed with PEAKS Studio 8 (Bioinformatics Solutions, Waterloo, ON, Canada). Searches were done with a Bet v 1 database. Only peptides with a high confidence score ($-10\lg P \geq 35$) were considered for further analysis.

T-cell proliferation assay

Bet v 1 was incubated over night with a 10-fold molar excess of either Q3OS, PPB₁, PPE₁, or DOC before incubation with murine BMDCs at a concentration of 10 µg/mL in BMDC medium (online supporting information). After 16, 24, 32, and 48h, DCs were washed and CD4⁺ T-cell hybridomas specific for the immune-dominant epitope 142-153 of Bet v 1 were added to the culture at a ratio of 1:10 (DC:T-cell) for 24h¹⁷. Supernatants were harvested and IL-2 levels were determined by ELISA (Invitrogen, Thermo Fisher Scientific, Waltham, MA, USA). As a reference, BMDCs were pulsed at each time point with different concentrations of peptide 142-153 and co-cultured with CD4⁺ T-cell hybridomas. By interpolating in a standard curve, a µM peptide equivalent from the measured IL-2 was calculated from DCs pulsed with different peptide concentrations. The assays were carried out in triplicates.

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