Supplementary Figures and Tables

Alphafold-multimer predicts cross-kingdom interactions at the plant-pathogen interface

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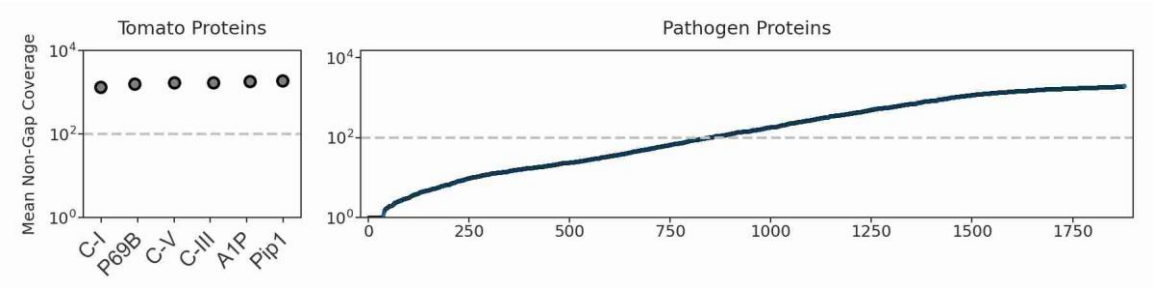
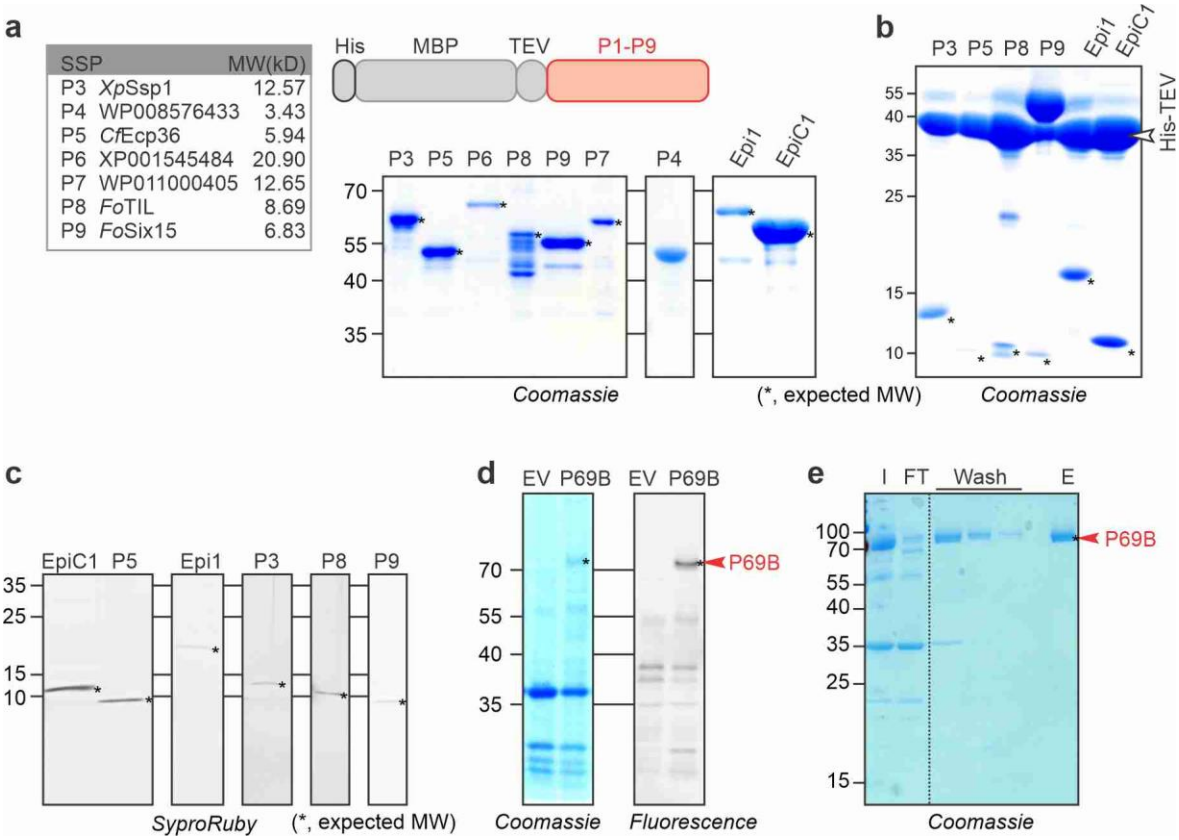


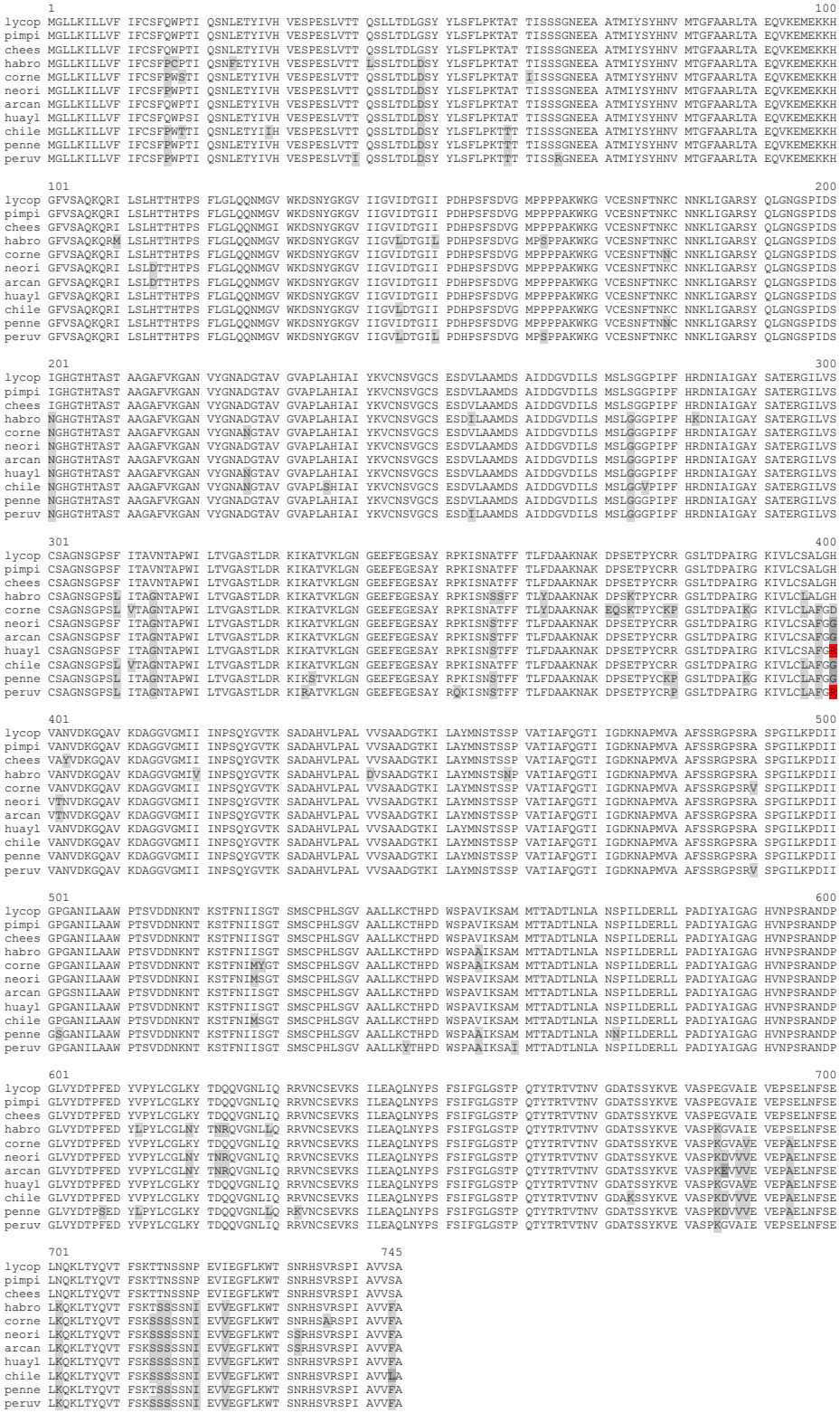
Supplementary Figure 1 MSA depth of SSPs and hydrolases used in Fig. 2.

The mean non-gap multiple sequence alignment (MSA) depth is shown for the tomato hydrolases (left) and the 1,879 SSPs (right), ranked by MSA depth. The dash line indicates the desired minimum of 100 MSA depth.

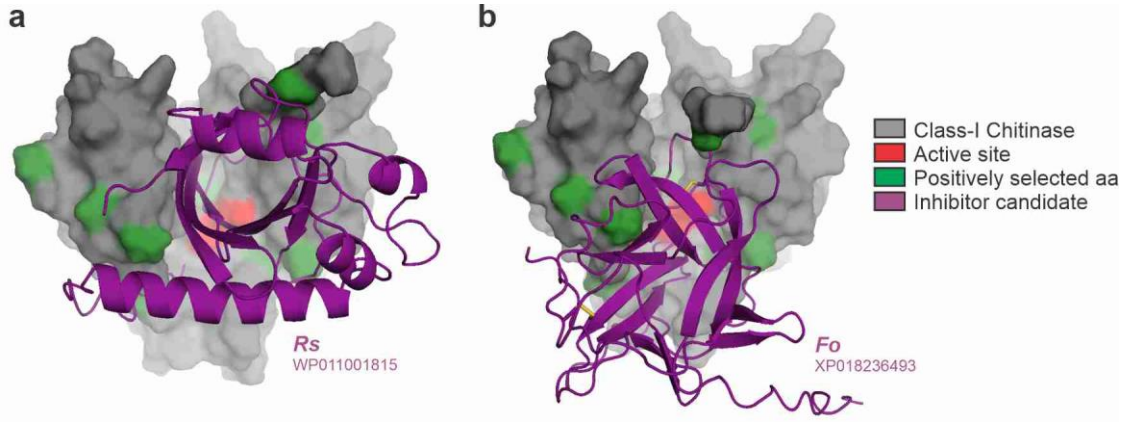


Supplementary Figure 2 Production of candidate inhibitors and P69B for inhibition assays.

a Candidate inhibitors lacking their endogenous signal peptides were codon-optimized for expression in *E. coli* and cloned in-frame with a 6-His purification tag; the maltose binding protein (MBP) and the cleavage site of tobacco etch virus (TEV) protease. Fusion proteins were expressed in *E. coli* and purified on HisPur™ Ni-NTA resin and amylose resin, subsequently. Fusion proteins were detected at their predicted molecular weight (MW, *) by SDS-PAGE and Coomassie staining. Purification of candidate inhibitors was repeated at least once for each candidate independently. **b** Putative inhibitors were released from their purification tags upon incubation with His-TEV protease. This experiment was repeated at least once for each inhibitor independently. **c** Purified inhibitor candidates after removal of their purification tags and TEV proteins, stained with Sypro Ruby. This experiment was repeated at least once for each inhibitor independently. **d** P69B-His is efficiently expressed by agroinfiltration. P69B with a C-terminal His tag and an empty vector (EV) control were transiently expressed by agroinfiltration. Apoplastic fluids were isolated, labeled with FP-TAMRA, separated on SDS-PAGE and scanned for fluorescence (right) and stained with Coomassie (left). Expression of P69B was repeated at least twice to similar effect. **e** Purification of P69B-His on Ni-NTA. I, input sample; FT, flow through; E, eluate. The MW marker is presented in kDa on the left of the gels. Purification of P69B was repeated twice with similar results.

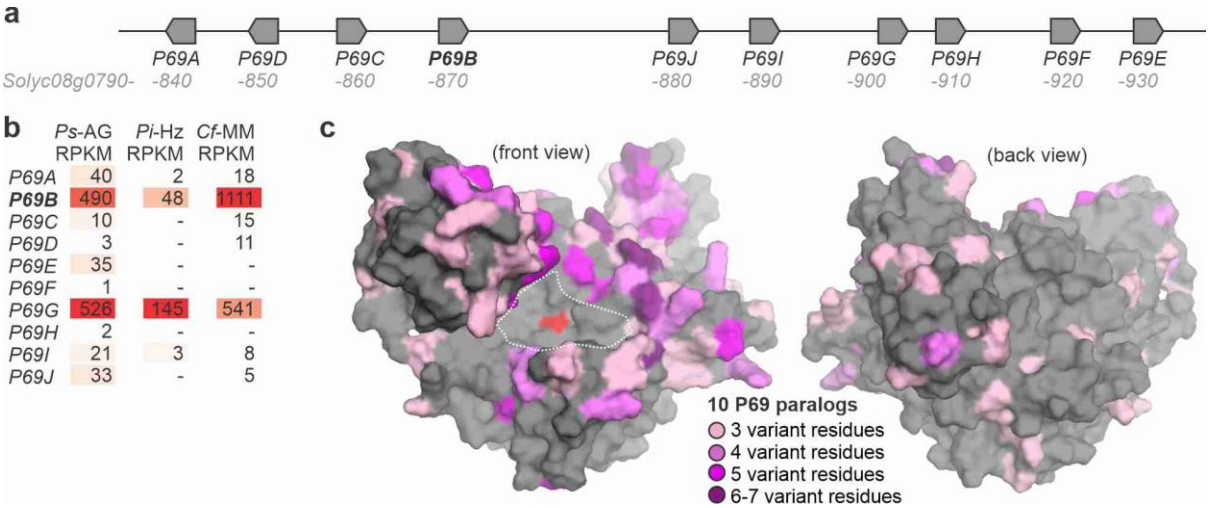


Supplementary Figure 3 Amino acid alignment of P69B orthologs from wild tomato species. P69B orthologs were extracted from genomes from wild tomato species and aligned. Residues that are different from P69B of cultivated tomato are highlighted in light grey, dark grey or red for n = 2, 3 and 4 variant residues, respectively. Note that only position 400 has 4 different residues.



Supplementary Figure 4 Two candidate inhibitors interact with positively selected sites in Class-I chitinases.

Positively selected sites reported previously (Bishop et al., 2000) were plotted onto the AFM-predicted models of tomato Class-I chitinase in complex with inhibitors from *Ralstonia solanacearum* **(a)** and *Fusarium oxysporum f. sp. lycopersici* **(b)**.



Supplementary Figure 5 Expression and variation of the ten P69 paralogs of tomato.

a Genomic P69 cluster contains ten paralogs. Sequence was extracted from the genome of cv. Heinz (Tomato Genome Consortium, 2012). **b** Expression levels in reads per kilobase per million (RPKM) of *P69* genes in three different cultivars infected with *Ps* (cv. Ailsa Graig, Rosli et al., 2013); *Pi* (cv. Heinz, Hwang et al., 2020) and *Cf* (cv. Money Maker, Ilyas et al., 2016). **c** Protein sequences of the ten P69 paralogs of tomato (P60A-I) were aligned and the number of variant residues at each position was plotted on the model of the P69B structure. The variation (purple) is surrounding the active site (red) in the substrate binding groove (dashed line) as a 'ring-of-fire'.

Supplementary Table 1 RMSD and TM scores for control complexes.

AFM model	Structure	Comparison of monomers	RMSD (Å)	TM
Pip1-EpiC2B (compatible)	3IMA	Pip1 - Papain	**0.94**	**0.9517**
		EpiC2B - Tarocystatin	2.37	**0.7827**
		Interface*	**0.85**	**0.89**
P69B-Epi1a (compatible)	1YU6	P69B - Subtilisin	**1.74**	**0.9217**
		Epi1a - OMTKY3	**1.44**	0.5541
		Interface*	**1.12**	**0.83**
Pip1-Epi1a (incompatible)	3IMA	Pip1 - Papain	**0.96**	**0.9509**
	1YU6	Epi1a - OMTKY3	**1.72**	0.5252
P69B-EpiC2B (incompatible)	1YU6	P69B - Subtilisin	**1.77**	**0.9220**
	3IMA	EpiC2B - Tarocystatin	2.47	**0.7687**

*, Calculated from the PDB files by identifying residues that have differential solvent exposure when the complex partner is omitted.

DALI was used to identify experimentally-resolved structures with similarity to AFM-predicted control complexes: tarocystatin-papain (3IMA) for Pip1-EpiC2B and subtilisin-OMTKY3 (1YU6) for P69B-Epi1a. TMalign was used to calculate TM and RMSD values for the monomers in the AFM model compared to the resolved structures. The interface was determined by selecting the residues that show different solvent exposure when the complex partner is omitted. Scores that are above the set threshold are printed in green bold and below the threshold in red.

Supplementary Table 2 Analysed RNAseq samples

SRA run ID	Pathogen	Tomato cultivar	Tissue/time
SRR5467166	*Rs* GMI1000 WT	'Bonny Best'	Petiole/3dpi
SRR5467167	*Rs* GMI1000 WT	'Bonny Best'	Petiole/3dpi
SRR5467168	*Rs* GMI1000 WT	'Bonny Best'	Petiole/3dpi
SRR6924534	*Bc* B05.10 WT	'Marmande'	Leaf/1dpi
SRR6924535	*Bc* B05.10 WT	'Marmande'	Leaf/1dpi
SRR6924536	*Bc* B05.10 WT	'Marmande'	Leaf/1dpi
SRR6050413	*Fol* 4287 WT	'Moneymaker' (S)	Root/1dpi
SRR6050414	*Fol* 4287 WT	'Motelle' (R)	Root/1dpi
SRR1171035	*Cf* race-0WU	'Heinz Cf-0' (S)	Leaf/4dpi
SRR1171040	*Cf* race-0WU	'Heinz Cf-0' (S)	Leaf/8dpi
SRR1171043	*Cf* race-0WU	'Heinz Cf-0' (S)	Leaf/12dpi
SRR1171047	*Cf* IPO1979	'Moneymaker'	Leaf/6dpi

Supplementary Table 3 Transcript levels of six tomato genes in (non)infected plants

Cladosporium fulvum		Day-6, susceptible tomato (n=3) Mean±SD		Day-6, resistant tomato (n=3) Mean±SD	
name	Accession	Mock	*Cf*	Mock	Cf
P69B	Solyc08g079870.3.1	352 ± 371	1111 ± 283	221 ± 56	2628 ± 117
Pip1	Solyc02g077040.4.1	223 ± 263	661±304	118 ± 34	1358 ± 166
A1P	Solyc08g067100.2.1	78 ± 8	88 ± 4	72 ± 9	116 ± 10
C-I	Solyc09g098540.3.1	234 ± 14	195 ± 7	224 ± 12	168 ± 13
C-III	Solyc05g050130.4.1	90 ± 103	232 ± 65	44 ± 18	377 ± 35
C-V	Solyc07g005090.4.1	28 ± 9	51 ± 9	24 ± 7	61 ± 6
Fusarium oxysporum		Day 1, susceptible tomato (n=1)		Day 1, resistant tomato (n=1)	
name	Accession	Mock	*Fo*	Mock	*Fo*
P69B	Solyc08g079870.1.1	3.69	17.09	1.49	5.00
Pip1	Solyc02g077040.2.1	2.14	6.49	3.21	3.62
A1P	Solyc08g067100.2.1	290.53	339.77	285.60	347.14
C-I	Solyc09g098540.2.1	446.14	316.62	363.06	311.31
C-III	Solyc05g050130.2.1	61.33	141.36	60.73	89.85
C-V	Solyc07g005090.2.1	172.49	210.57	168.12	172.49
Phytophthora infestans		Days 1/2/3, susceptible tomato, Pi (n=4) Mean±SD			
name	Accession	Mock	1dpi *Pi*	2dpi *Pi*	3dpi *Pi*
P69B	Solyc08g079870.1.1	37 ± 1	107 ± 3	48 ± 2	46 ± 1
Pip1	Solyc02g077040.2.1	39 ± 1	24 ± 1	19 ± 1	16 ± 1
A1P	Solyc08g067100.2.1	48 ± 1	60 ± 1	40 ± 1	28 ± 1
C-I	Solyc09g098540.2.1	140 ± 3	158 ± 5	76 ± 1	41 ± 1
C-III	Solyc05g050130.2.1	13 ± 1	131 ± 5	92 ± 2	43 ± 2
C-V	Solyc07g005090.2.1	10 ± 1	28 ± 1	32 ± 1	59 ± 1
Botrytis cinerea		Day 1, susceptible tomato, WT *Bc* (n=3)			
name	Accession	Rep1	Rep2	Rep3	Mean±SD
P69B	Solyc08g079870.1.1	5.77	2.74	10.18	6 ± 4
A1P	Solyc08g067100.2.1	19.80	11.35	20.89	17 ± 5
C-I	Solyc09g098540.2.1	10.95	4.75	17.27	11 ± 6
C-III	Solyc05g050130.2.1	0	0	0	0
C-V	Solyc07g005090.2.1	265.26	286.11	451.3	334 ± 102
Ralstonia solanacearum		Day-3, susceptible tomato, *Rs* (n=3)			
name	Accession	Rep1	Rep2	Rep3	Mean±SD
P69B	Solyc08g079870.1.1	503.40	954.43	734.40	731±226
A1P	Solyc08g067100.2.1	97.34	101.76	89.39	96±6
C-I	Solyc09g098540.2.1	905.04	867.27	871.69	881±21
C-III	Solyc05g050130.2.1	661.37	1111.08	865.27	879±225
C-V	Solyc07g005090.2.1	54.25	56.65	45.60	52±6

FPKM values of tomato genes, extracted from Ilyas et al., 2016 (*Cf*); Zhao et al., 2018 (*Fo*); Huang et al., 2020 (*Pi*); Müller et al., 2018 (*Bc*); Khokhani et al., 2017 (*Rs*).

Supplementary Table 4 RNA-seq values of SSPs in infected plants*

Cf	4dpi SRR1171035	6dpi SRR1171047	8dpi SRR1171040	12dpi SRR1171043	Mean(±SD)
KAH3648627 (*Cf*Ecp36)	212.485	436.287	578.257	691.188	479.55 ± 206.34

Fo	MoneyMaker (S) SRR6050413	Motelle (R) SRR6050414	Mean(±SD)
XP018243121 (*Fo*TIL)	180	461	340.50 ± 198.70
APP91304 (*Fo*Six15)	270.034	144.81	207.42 ± 88.55
XP018236493	204.966	227.051	216.01 ± 15.62
XP018248187	5.39765	5.71688	5.56 ± 0.23
XP018241286	1.79816	5.8976	3.85 ± 2.90

Rs	SRR5467166	SRR5467167	SRR5467168	Mean(±SD)
WP011000405	0	6.374	13.972	6.78 ± 6.99
WP011001815	528.431	656.721	612.85	599.33 ± 65.20
WP011002292	2.7102	2.8454	3.11861	2.89 ± 0.21
Bc	SRR6924534	SRR6924535	SRR6924536	Mean(±SD)
XP001545484	2.47535	2.34842	2.50272	2.44 ± 0.82
XP001560184	71.8476	79.0248	27.7998	59.56 ± 27.7

*, all values are in transcripts per million (TPM) reads of the pathogen during infection of tomato. Infection of *Rs* and *Bc* was at 72 and 24 hpi, respectively.

Supplementary Table 5 RMSD and TM scores for the hydrolases in 15 SPP-hydrolase complexes

Hydrolase	SSP	PDB	Protein(s) in PDB	RMSD (Å)	TM
P69B	WP046932418-*Xp*Ssp	1YU6	Subtilisin-OMTKY3	**1.7**	**0.92**
P69B	KAH3648627-*Cf*Ecp36	1YU6	Subtilisin-OMTKY3	**1.7**	**0.92**
P69B	XP018243121-*Fo*TIL	1YU6	Subtilisin-OMTKY3	**1.7**	**0.92**
P69B	APP91304-*Fo*Six15	1YU6	Subtilisin-OMTKY3	**1.7**	**0.92**
P69B	XP001545484	1YU6	Subtilisin-OMTKY3	**1.7**	**0.92**
P69B	WP011000405	1YU6	Subtilisin-OMTKY3	**1.8**	**0.92**
P69B	WP008576433	1YU6	Subtilisin-OMTKY3	**1.8**	**0.92**
C-I	WP011001815	3IWR	Rice class-I chitinase	**1.4**	**0.95**
C-I	XP018236493	3IWR	Rice class-I chitinase	**1.4**	**0.92**
C-III	WP046931881	4TOQ	Class-III chitinase	**0.75**	**0.97**
C-III	XP001560184	4TOQ	Class-III chitinase	**0.76**	**0.97**
C-III	XP018248187	4TOQ	Class-III chitinase	**0.79**	**0.97**
C-III	XP018241286	4TOQ	Class-III chitinase	**0.86**	**0.97**
C-V	WP008572913	3ALG	Class-V chitinase	**1.4**	**0.94**
A1P	WP011002292	4ZL4	Plasmepsin	3.0	0.73

DALI was used to identify the experimentally resolved structure that is closest to that of the hydrolase in the SPP-hydrolase complex and the RMSD and TM scores were calculated for each comparison with TMalign. Scores that are above the set threshold are printed in green bold and below the threshold in red.

Supplementary Table 6 RMSD and TM scores for the SSPs in 15 SPP-hydrolase complexes

SSP	PDB	RMSD (Å)	TM
WP046932418-*Xp*Ssp	x	x	x
KAH3648627-*Cf*Ecp36	6NK9	**1.9**	0.63
XP018243121-*Fo*TIL	x	x	x
APP91304-*Fo*Six15	x	x	x
XP001545484	1WPX	2.6	0.68
WP011000405	x	x	x
WP008576433	x	x	x
WP011001815	5UC0	4.7	0.53
XP018236493	4I1B	3.6	0.62
WP046931881	4MIS	2.2	0.70
XP001560184	3TC2	3.7	0.61
XP018248187	5FJQ	2.7	0.46
XP018241286	4OWL	3.0	0.70
WP008572913	1Y34	2.8	0.66
WP011002292	2HOD	3.0	0.61

DALI was used to identify the resolved structure that is closest to that of the SSP in the SPP-hydrolase complex and the RMSD and TM scores were calculated for each comparison with TMalign. Scores that are above the set threshold are printed in green bold and below the threshold in red. No good structures were identified for several complexes (x).

Supplementary Table 7 Synthesised nucleotide sequences

P69B Fragment-1 GAAGACATAATGGGATTTGTTCTCTTTTCACAATTGCCTTCATTTCTTCTTGTCTCTACACTTCTCTTATTCCT AGTAATATCCCACTCTTGCCGTGCAGGAGGTAATTTAGAGACTTACATCGTCCACGTGGAGAGTCCAGAAT CTTTGGTCACCACTCAATCACTCTTGACAGATTTGGGTAGTTACTATCTTTCCTTTCTGCCCAAAACGGCTAC TACGATCTCCTCAAGTGGCAACGAGGAAGCCGCGACAATGATTTACTCATATCATAACGTAATGACTGGTT TCGCAGCTAGATTAACTGCTGAGCAGGTCAAAGAAATGGAAAAGAAACATGGATTTGTGTCCGCACAGAA GCAAAGAATCTTGAGCCTACATACTACACACACTCCTAGTTTCCTTGGTTTACAGCAAAATATGGGCGTTTG GAAGGACTCAAATTATGGTAAGGGAGTGATCATTGGTGTAATTGATACAGGTATCATTCCCGACCATCCCA GCTTTAGTGATGTTGGCATGCCCCCGCCACCTGCAAAATGGAAAGGTGTTTGCGAGTCTAATTTTACTAATA AGTGTAATAACAAGCTTATAGGTGCCCGATCTTACCAACTAGGTAATGGTTCCCCAATTGATTCTATAGGGC ACGGAACGCACACAGCCAGTACTGCTGCCGGCGCTTTCGTAAAAGGAGCCAACGTGTATGGTAATGCCGAC GGAACAGCCGTAGGGGTGGCACCATTAGCTCATATTGCTATTTATAAGGTCTGCAATTCAGTTGGTTGTTCA GAGTCAGACGTACTTGCAGCCATGGACTCCGCAATAGACGATGGTGTTGATATACTTTCTATGTCTTTGTCT GGAGGTCCGATTCCTTTTCACCGGGACAATATCGCTATAGGGGCCTATAGTGCTACTGAACGTGGAATCCTC GTTTCTTGTTCAGCTGGTAATAGTGGACCTTCCTTTATTACAGCTGTCAATACCGCTCCTTGGATTCTAACTG TCGGAGCTTCCACTTTGGACCGTAAGATTAAGGCAACTGTGAAACTGGGCAACGGTGAGGAATTTGAAGGA GAATCAGCATATCGTCCTAAGATAAGCAATGCTACATTCTTTACACTCTTTGATGCGGCAAAGAACGCTAA AGACCCTAGCGAAACCCCCTATTGTCGCAGGGGAAGTCTAACAGACCCTGCTATCAGGGGTAAAATAGTTC TCTGCAGTGCTCTGGGACATGTTGCAAACGTTGATAAAGGACAGGCGGTAAAGGACGCTGGTGGAGTTGGA ATGATAATCATAAATCCAAGTCAGTATGGAGTAACCAAGTCTGCTGATGCTCATGTGTTGCCTGCTCTCGTA GTGAGCGCCGCTGATGGTATGTCTTC
P69B Fragment-2 GAAGACATTGGTACTAAGATATTGGCATATATGAACTCTACTAGCTCTCCAGTAGCCACAATTGCATTTCAG GGAACGATCATTGGTGACAAGAACGCACCGATGGTTGCGGCATTTAGTTCCCGAGGCCCTTCACGTGCATC CCCTGGTATCCTCAAGCCTGATATCATTGGACCTGGCGCAAACATACTTGCCGCATGGCCTACTTCAGTGGA TGACAATAAGAACACAAAGTCTACTTTTAATATAATTAGTGGTACAAGCATGTCCTGTCCCCACCTGTCTGG AGTAGCTGCACTGCTTAAATGTACGCATCCAGATTGGTCACCAGCTGTTATAAAGAGCGCTATGATGACGA CCGCTGACACCTTGAACCTCGCAAACTCTCCTATTCTTGACGAGCGTTTGCTTCCAGCTGACATCTATGCAA TAGGCGCCGGACATGTGAATCCGAGTAGGGCTAATGACCCAGGGTTGGTGTACGATACTCCTTTCGAAGAT TACGTCCCATATCTCTGTGGACTTAAATATACGGATCAACAGGTTGGTAATTTAATTCAAAGACGTGTAAAC TGTTCCGAAGTTAAGAGCATCTTGGAAGCTCAACTGAATTATCCCAGTTTTTCTATTTTTGGACTAGGAAGT ACTCCTCAGACTTATACAAGAACTGTGACTAATGTCGGAGATGCAACATCTTCCTACAAAGTTGAGGTTGC CAGCCCTGAAGGGGTCGCAATCGAAGTTGAACCTAGCGAGCTTAACTTTTCCGAGCTAAATCAGAAACTTA CGTACCAAGTAACATTTTCAAAGACAACTAACTCTAGTAATCCAGAAGTAATCGAGGGTTTTCTTAAATGG ACTAGTAATCGTCATAGTGTGCGATCTCCCATCGCCGTTGTAAGCGCAGGTGGGCACCATCACCATCACCA CTGAGCTTATGTCTTC
His-MBP-TEV ATGGGCAGCAGCCATCATCATCATCATCATATGAAAATCGAAGAAGGTAAACTGGTAATCTGGATTAACGG CGATAAAGGCTATAACGGTCTCGCTGAAGTCGGTAAGAAATTCGAGAAAGATACCGGAATTAAAGTCACC GTTGAGCATCCGGATAAACTGGAAGAGAAATTCCCACAGGTTGCGGCAACTGGCGATGGCCCTGACATTAT CTTCTGGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGCCTGTTGGCTGAAATCACCCCGGACAAAG CGTTCCAGGACAAGCTGTATCCGTTTACCTGGGATGCCGTACGTTACAACGGCAAGCTGATTGCTTACCCGA TCGCTGTTGAAGCGTTATCGCTGATTTATAACAAAGATCTGCTGCCGAACCCGCCAAAAACCTGGGAAGAG ATCCCGGCGCTGGATAAAGAACTGAAAGCGAAAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCGT ACTTCACCTGGCCGCTGATTGCTGCTGACGGGGGTTATGCGTTCAAGTATGAAAACGGCAAGTACGACATT AAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCGGGTCTGACCTTCCTGGTTGACCTGATTAAAAACAA ACACATGAATGCAGACACCGATTACTCCATCGCAGAAGCTGCCTTTAATAAAGGCGAAACAGCGATGACC ATCAACGGCCCGTGGGCATGGTCCAACATCGACACCAGCAAAGTGAATTATGGTGTAACGGTACTGCCGAC CTTCAAGGGTCAACCATCCAAACCGTTCGTTGGCGTGCTGAGCGCAGGTATTAACGCCGCCAGTCCGAACA AAGAGCTGGCAAAAGAGTTCCTCGAAAACTATCTGCTGACTGATGAAGGTCTGGAAGCGGTTAATAAAGA CAAACCGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGATCCACGTATTGCCGCCA CTATGGAAAACGCCCAGAAAGGTGAAATCATGCCGAACATCCCGCAGATGTCCGCTTTCTGGTATGCCGTG CGTACTGCGGTGATCAACGCCGCCAGCGGTCGTCAGACTGTCGATGAAGCCCTGAAAGACGCGCAGACTA ATTCGAGCTCGAACAACAACAACAATAACAATAACAACAACCTCGGGATCGAGGAAAACCTGTATTTTCAG GGCGAATTCGGATCCTCTAGAGTCGACCTGCAGGCAAGCTT
***Xp*Ssp1-WP046932418.1-P3** GCTCCACCTACAGATACGGCAACTCCCCCCCCAGCGACGGGTTCCACCCGTGGTCCGGCGGCTGGCAAGGC GGTCGTGGTGACCACCACGTGCCGTACCGACGCCGACTGTACCGTGAAGAACGTAGGTAATTGTTGTGGCG CATTTCCGGCGTGCGTGAACGTCAACAGCGCGACCGACCCGAATGGTGTTTTGGCTCAGTGCCAAGCGGGT GGCATGATGAGCGTTTGCGGCTTCCGCGAGATCTCTGCCTGCCAGTGCGTTGCAGGCCAGTGCGCAGCTAA AGATGCCCAAGCGGATACCCTGCGTCCGGCGACTCCGCCGACGGAAACCGTTCACTAG
***Cf*Ecp36-KAH3648627.1-P5** AAAAGGGGGTCAGGTGGAGAATGTAGAACACAATCCGACTGTTGTTACTGCGACCCGGGTTCCGGCTGCAT CCTGAGCTGTCAGGCAGATCGTTCTAGCACCACGGGCTATCGCTGCATTACCAGCCGTCAGTCGGCTTGCA ACGTTGCGGGTTGCAGCTGCTAG

***Fo*TIL-XP_018243121.1-P8** GCTCCCAAGTGTAAAGCAGGAGAACAATTTTTCGAGTGCGGCACCGCTTGCCCGTTGACGTGCGACAAACC GGAACCGCGTCCGTGTACCAAACAATGTGTTCCGGGTTGCTTTTGCAAGGAGGTGCGCATTCTGCGTCAAA GCCAGCAGGTTCTGTCGCCGCTCAAGGCGCTGTTGCTGCCGGTGAGCATCCACAACCGCCCAATCTCTGGT ATTTCCCATAGCCGTCACCTGTAG
***Fo*Six15-APP91304.1-P9** ACAATATATTGTAGGGATGTATCACCACCCCGCGATACCCGTAGCTGGTGTAAAACGAACACCCCGGCGTG GCAAGGTTGCCAGCGTTTTTGCAGCGAGCACTGCCGCTCCACCCCGCGTGACTACCCGGACGGCTGCATGT ATCATCTGCAGGTTGGCGGTGATTACGACTGTTTCTGCAAGTAG
XP001545484.1-P6 TTCACACCACCCGGATTTGAACCTAGTTCAACGAACGATCTGACCGTCGCATACGGCTCGAAACTTGCCAC CAACGGTATTCAAATGCTGCGTGCGGACACCGCGTATGCTCCGATTCTGGGTACAGCGACCAAAATGTCCG GCACCTATGCGGTTATGATGGTTGATCCGGACATCCCGCCGGCAAAGGTGGGTGGTGACACCAGCCAATTT CTGCATTGGATGCAGGCAGACTTGACCAGCTCAAATACTACTACGACCATTGGTGGCCAGAAAATCTACGA GCTGATTAACGTGAAGAATACCTCTGCCTTTGCGACGTACCTGCAGCCGAATCCGCCAGATATCGCTCCGA CCACCCACCGTTATACCCAGTTGCTCTTTAACACCACTGGCATGAATATGAGCTTGGCCAGCCTGCAAACG GCGGGTAAAACCCGCGGTAATTTCAACGCGACGAACGTTGTTAAGTCTGCTAAGTTAACGGTGCTGATGGG TAACTCCTTCGACGTGAGCTTCGGCGATAAAGCGATCAACAACACCGGCGCGTCCACCGGCAGCAGCACCT AG
WP_011000405.1-P7 GCTGATGATGTTCCCGTAGCGGACGCATCACTCCAACCGAGCGTTGAGGCGGCGCGCCCACCGGTTGCTGC GGCGACCGTCGTGCAAGGTTTTGGCCAGGCAGTTGAGGCAAGCGCACTGGAAGGTTATCGTGGTGGTACGC AGCCGCTGTACCAGACCGTCAACGACGCGCGTTTGTCCGGCACGGTGACCGATAATGCCGCGATTAACGTT GCTACTGGCGCTAATATTGTACGTGACGGCAGCTTCGCCAACGCCTCTGGCATCCCGACCGTTATTCAAAAC ACCGGTGCGAACGTGCTGATCCAGAATGCGACCATCGTGAACGTGCAGTTCCGCCCGTAG
WP008576433.1-P4 CTGTATTTTCAGGGCGAATTCGGTTGTAATACAGTAGCTGGAGCAGGGAAAGACATGCAGGGTGCGGGTGA TAAAGTTGAGAAGACCGCTGAAAAGTGCAGCGACGGCAAATGTTAGGAATTCGGATCCTCTAGAGTC

Supplementary Table 8 Used plasmids

Plasmid	Description	Reference
pJK187	Binary vector (pL0V2-2x35S::SC)	This work
pET-32/28	Bacterial expression vector	Novinec et al., 2012
P19	Binary vector carrying p19 silencing inhibitor	Van der Hoorn et al., 2003
pFH20	Binary vector for P69B-His expression	This work
pHJ000	Bacterial expression vector pET-32/28-His-MBP-TEV	This work
pHJ028	Bacterial expression P3(WP046932418.1, *Xp*Ssp1)	This work
pHJ033	Bacterial expression P5(KAH3648627.1, *Cf*Ecp36)	This work
pHJ029	Bacterial expression P6(XP001545484.1,)	This work
pHJ032	Bacterial expression P7(WP011000405.1)	This work
pHJ030	Bacterial expression P8(XP_018243121.1, *Fo*TIL)	This work
pHJ031	Bacterial expression P9(APP91304.1, *Fo*Six15)	This work
pHJ043	Bacterial expression P4(WP008576433.1)	This work
pHJ046	Bacterial expression *Pi*Epi1	This work
pHJ047	Bacterial expression *Pi*EpiC1	This work

Supplementary Table 9 Primer sequences

Primer	Use	Nucleotide sequence (5'-3')
His-MBP-F	Cloning	AAGAAGGAGATATACCATGGGCAGCAGCCATCATCATCAT CATCATATG
His-MBP-R	Cloning	TGGTGGTGGTGGTGCTCGAGAAGCTTGCCTGCAG
Epi1-F	Cloning	CTGTATTTTCAGGGCGAATTCCAAAGCCCGCAAGTCATCAG
Epi1-R	Cloning	GACTCTAGAGGATCCGAATTCTTATCCCTCCTGCGGTGTC
EpiC1-F	Cloning	CTGTATTTTCAGGGCGAATTCCAAGTGGACGGCGGATACTC
EpiC1-R	Cloning	GACTCTAGAGGATCCGAATTCCTACTTAACTGGGGTAATCG
P3-F	Cloning	CTGTATTTTCAGGGCGAATTCGCTCCACCTACAGATACGG
P3-R	Cloning	GACTCTAGAGGATCCGAATTCCTAGTGAACGGTTTCCGTCGG
P4-F	Cloning	CTGTATTTTCAGGGCGAATTC
P4-R	Cloning	GACTCTAGAGGATCCGAATTC
P5-F	Cloning	CTGTATTTTCAGGGCGAATTCAAAAGGGGGTCAGGTGGAGA
P5-R	Cloning	GACTCTAGAGGATCCGAATTCCTAGCAGCTGCAACCCGCAA
P6-F	Cloning	CTGTATTTTCAGGGCGAATTCTTCACACCACCCGGATTTGA
P6-R	Cloning	GACTCTAGAGGATCCGAATTCCTAGGTGCTGCTGCCGGTGG
P7-F	Cloning	CTGTATTTTCAGGGCGAATTCGCTGATGATGTTCCCGTAGC
P7-R	Cloning	GACTCTAGAGGATCCGAATTCCTACGGGCGGAACTGCACGT
P8-F	Cloning	CTGTATTTTCAGGGCGAATTCGCTCCCAAGTGTAAAGCAGG
P8-R	Cloning	GACTCTAGAGGATCCGAATTCCTACAGGTGACGGCTATGGG
P9-F	Cloning	CTGTATTTTCAGGGCGAATTCACAATATATTGTAGGGATGT
P9-R	Cloning	GACTCTAGAGGATCCGAATTCCTACTTGCAGAAACAGTCGT
PJK187-F	Sequencing	CTATCCTTCGCAAGACCCTTC
PJK187-R	Sequencing	CTCAACACATGAGCGAAACC
pet32a-F	Sequencing	TAATACGACTCACTATAGGG
pet32a-R	Sequencing	GCTAGTTATTGCTCAGCGG