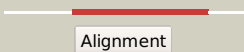

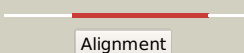

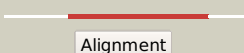

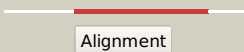
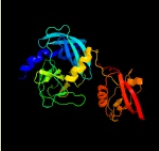
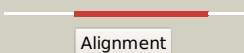

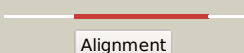

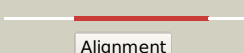
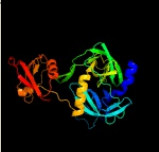



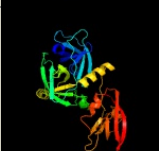
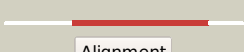

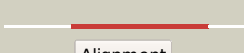





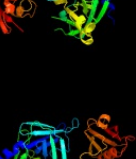



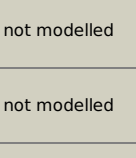


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0983_(pepD)_1099070_1100464
Date	Wed Jul 31 22:05:05 BST 2019
Unique Job ID	81a20fdb228e4812

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5xdyA_</a>	 Alignment		100.0	47	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> heat shock protein htra; <b>PDBTitle:</b> crystal structure of htra1 from mycobacterium tuberculosis
2	<a href="#">c3stjC_</a>	 Alignment		100.0	42	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> protease degg; <b>PDBTitle:</b> crystal structure of the protease + pdz1 domain of degg from2 escherichia coli
3	<a href="#">c4ic6A_</a>	 Alignment		100.0	32	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protease do-like 8, chloroplastic; <b>PDBTitle:</b> crystal structure of deg8
4	<a href="#">c2zleB_</a>	 Alignment		100.0	42	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> protease do; <b>PDBTitle:</b> cryo-em structure of degp12/omp
5	<a href="#">c3otpF_</a>	 Alignment		100.0	41	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> protease do; <b>PDBTitle:</b> crystal structure of the degp dodecamer with a model substrate
6	<a href="#">c3pv5B_</a>	 Alignment		100.0	37	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> degq; <b>PDBTitle:</b> structure of legionella fallonii degq (n189g/p190g variant)
7	<a href="#">c3qo6B_</a>	 Alignment		100.0	38	<b>PDB header:</b> photosynthesis <b>Chain:</b> B: <b>PDB Molecule:</b> protease do-like 1, chloroplastic; <b>PDBTitle:</b> crystal structure analysis of the plant protease deg1
8	<a href="#">c1ky9A_</a>	 Alignment		100.0	41	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protease do; <b>PDBTitle:</b> crystal structure of degp (htra)
9	<a href="#">c5il9A_</a>	 Alignment		100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protease do-like 9; <b>PDBTitle:</b> crystal structure of deg9
10	<a href="#">c4a8aI_</a>	 Alignment		100.0	41	<b>PDB header:</b> hydrolase/hydrolase <b>Chain:</b> I: <b>PDB Molecule:</b> periplasmic ph-dependent serine endoprotease degg; <b>PDBTitle:</b> asymmetric cryo-em reconstruction of e. coli degq 12-mer in complex2 with lysozyme
11	<a href="#">c3gdsA_</a>	 Alignment		100.0	33	<b>PDB header:</b> hydrolase/hydrolase activator <b>Chain:</b> A: <b>PDB Molecule:</b> protease degs; <b>PDBTitle:</b> crystal structure of degs h198p/d320a mutant modified by dfp in2 complex with dnrdgnvyvf peptide

12	<a href="#">c4flnB_</a>	Alignment		100.0	28	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> protease do-like 2, chloroplastic; <b>PDBTitle:</b> crystal structure of plant protease deg2
13	<a href="#">c2z9iB_</a>	Alignment		100.0	92	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> probable serine protease pepd; <b>PDBTitle:</b> crystal structure of rv0983 from mycobacterium tuberculosis-2 proteolytically active form
14	<a href="#">c5b6iA_</a>	Alignment		100.0	42	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative serine protease hhoa; <b>PDBTitle:</b> structure of deg protease hhoa from synechocystis sp. pcc 6803
15	<a href="#">c1lcyA_</a>	Alignment		100.0	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> htra2 serine protease; <b>PDBTitle:</b> crystal structure of the mitochondrial serine protease htra2
16	<a href="#">c3pv4A_</a>	Alignment		100.0	36	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> degq; <b>PDBTitle:</b> structure of legionella fallonii degq (delta-pdz2 variant)
17	<a href="#">c4ri0A_</a>	Alignment		100.0	34	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> serine protease htra3; <b>PDBTitle:</b> serine protease htra3, mutationally inactivated
18	<a href="#">c2r3yC_</a>	Alignment		100.0	35	<b>PDB header:</b> hydrolase/hydrolase activator <b>Chain:</b> C: <b>PDB Molecule:</b> protease degs; <b>PDBTitle:</b> crystal structure of the degs protease in complex with the2 ywf activating peptide
19	<a href="#">c5y2dA_</a>	Alignment		100.0	40	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic serine endoprotease degp-like; <b>PDBTitle:</b> crystal structure of h. pylori htra
20	<a href="#">c5jykB_</a>	Alignment		100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> protease do-like 9; <b>PDBTitle:</b> deg9 crystal under 289k
21	<a href="#">d1ky9a2</a>	Alignment	not modelled	100.0	46	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Prokaryotic proteases
22	<a href="#">c5y09B_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> protease do-like 9; <b>PDBTitle:</b> crystal structure of deg9 at 295 k
23	<a href="#">c2rceI_</a>	Alignment	not modelled	100.0	38	<b>PDB header:</b> hydrolase <b>Chain:</b> I: <b>PDB Molecule:</b> protease degs; <b>PDBTitle:</b> dfp modified degs delta pdz
24	<a href="#">d1l1ja_</a>	Alignment	not modelled	100.0	38	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Prokaryotic proteases
25	<a href="#">d2qf3a1</a>	Alignment	not modelled	100.0	41	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Prokaryotic proteases
26	<a href="#">c5y28B_</a>	Alignment	not modelled	100.0	44	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> periplasmic serine endoprotease degp-like; <b>PDBTitle:</b> crystal structure of h. pylori htra with pdz2 deletion
27	<a href="#">d2z9ia2</a>	Alignment	not modelled	100.0	97	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Prokaryotic proteases
28	<a href="#">c4ic5B_</a>	Alignment	not modelled	100.0	40	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> protease do-like 5, chloroplastic; <b>PDBTitle:</b> crystal structure of deg5
29	<a href="#">c3etiC_</a>	Alignment	not modelled	100.0	50	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> protease degq;

29	<a href="#">c3stc_</a>	Alignment	not modelled	100.0	30	<b>PDBTitle:</b> crystal structure of the protease domain of degq from escherichia coli <b>PDB header:</b> hydrolase
30	<a href="#">c5hmaA_</a>	Alignment	not modelled	100.0	24	<b>Chain:</b> A; <b>PDB Molecule:</b> trypsin-like serine protease; <b>PDBTitle:</b> crystal structure of mamo protease domain from magnetospirillum2 magneticum (ni bound form)
31	<a href="#">c3nziA_</a>	Alignment	not modelled	100.0	41	<b>PDB header:</b> hydrolase/hydrolase substrate <b>Chain:</b> A; <b>PDB Molecule:</b> serine protease htra1; <b>PDBTitle:</b> substrate induced remodeling of the active site regulates htra12 activity
32	<a href="#">c3nwuB_</a>	Alignment	not modelled	100.0	43	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> serine protease htra1; <b>PDBTitle:</b> substrate induced remodeling of the active site regulates htra12 activity
33	<a href="#">d1lcyA2</a>	Alignment	not modelled	100.0	40	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Prokaryotic proteases
34	<a href="#">c3k6zA_</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> possible membrane-associated serine protease; <b>PDBTitle:</b> crystal structure of rv3671c protease, inactive form
35	<a href="#">c5ilaA_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> protease do-like 9; <b>PDBTitle:</b> deg9 protease domain
36	<a href="#">c3mmgB_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> viral protein, hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> nuclear inclusion protein a; <b>PDBTitle:</b> crystal structure of tobacco vein mottling virus protease
37	<a href="#">c1zyoA_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> serine protease; <b>PDBTitle:</b> crystal structure of the serine protease domain of sesbania mosaic2 virus polyprotein
38	<a href="#">d1q31a_</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Viral proteases
39	<a href="#">c4inkA_</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> serine protease spld; <b>PDBTitle:</b> crystal structure of spld protease from staphylococcus aureus at 1.562 a resolution
40	<a href="#">c2w5eB_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> putative serine protease; <b>PDBTitle:</b> structural and biochemical analysis of human pathogenic2 astrovirus serine protease at 2.0 angstrom resolution
41	<a href="#">d1lvmB_</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Viral proteases
42	<a href="#">c2l97A_</a>	Alignment	not modelled	99.9	37	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> putative serine protease; <b>PDBTitle:</b> solution structure of htra pdz domain from streptococcus pneumoniae
43	<a href="#">d1qtfa_</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Prokaryotic proteases
44	<a href="#">c6e0uB_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> hydrolase, toxin <b>Chain:</b> B; <b>PDB Molecule:</b> serine protease; <b>PDBTitle:</b> staphylococcus pseudintermedius exfoliative toxin exi
45	<a href="#">c5c2zA_</a>	Alignment	not modelled	99.9	24	<b>PDB header:</b> toxin <b>Chain:</b> A; <b>PDB Molecule:</b> exfoliative toxin d2; <b>PDBTitle:</b> molecular insights into the specificity of exfoliative toxins from2 staphylococcus aureus
46	<a href="#">d1agja_</a>	Alignment	not modelled	99.9	23	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Prokaryotic proteases
47	<a href="#">c5mm8A_</a>	Alignment	not modelled	99.8	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> serine protease sple; <b>PDBTitle:</b> atomic resolution structure of sple protease from staphylococcus2 aureus
48	<a href="#">c2vidA_</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> serine protease splb; <b>PDBTitle:</b> serine protease splb from staphylococcus aureus at 1.8a resolution
49	<a href="#">c6fezB_</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> viral protein <b>Chain:</b> B; <b>PDB Molecule:</b> serine protease domain; <b>PDBTitle:</b> ryegrass mottle virus protease domain
50	<a href="#">c2w7uC_</a>	Alignment	not modelled	99.8	23	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> serine protease spla; <b>PDBTitle:</b> spla serine protease of staphylococcus aureus (2.4a)
51	<a href="#">d2z9ia1</a>	Alignment	not modelled	99.8	99	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> HtraA-like serine proteases
52	<a href="#">c2as9B_</a>	Alignment	not modelled	99.8	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> serine protease; <b>PDBTitle:</b> functional and structural characterization of spl proteases from2 staphylococcus aureus
53	<a href="#">d1cqqa_</a>	Alignment	not modelled	99.7	13	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Viral cysteine protease of trypsin fold
54	<a href="#">c2b0fA_</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A; <b>PDB Molecule:</b> picornain 3c (protease 3c) (p3c); <b>PDBTitle:</b> nmr structure of the human rhinovirus 3c protease (serotype 14) with2 covalently bound ace-lealfq-ethylpropionate inhibitor
55	<a href="#">c5mrtA_</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> lytic endopeptidase preproenzyme; <b>PDBTitle:</b> crystal structure of I5 protease lysobacter sp. x11

56	<a href="#">d2o8la1</a>	Alignment	not modelled	99.7	18	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Prokaryotic proteases
57	<a href="#">c2o8A_</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> v8 protease; <b>PDBTitle:</b> structure of v8 protease from staphylococcus aureus
58	<a href="#">c2n7pA_</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> solution structure of pdz domain
59	<a href="#">c1qy6A_</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> protease <b>Chain:</b> A: <b>PDB Molecule:</b> serine protease; <b>PDBTitle:</b> structue of v8 protease from staphylococcus aureus
60	<a href="#">d2qaaa1</a>	Alignment	not modelled	99.7	24	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Prokaryotic proteases
61	<a href="#">c4jcnA_</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl endopeptidase; <b>PDBTitle:</b> structure of esp, serine protease from staphylococcus epidermidis
62	<a href="#">c2p3wB_</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> probable serine protease htra3; <b>PDBTitle:</b> crystal structure of the htra3 pdz domain bound to a phage-derived2 ligand (fgrwv)
63	<a href="#">d1lcyA1</a>	Alignment	not modelled	99.7	24	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> HtraA-like serine proteases
64	<a href="#">c2joaA_</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> serine protease htra1; <b>PDBTitle:</b> htra1 bound to an optimized peptide: nmr assignment of pdz2 domain and ligand resonances
65	<a href="#">d2h5ca1</a>	Alignment	not modelled	99.6	21	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Prokaryotic proteases
66	<a href="#">d1l1na_</a>	Alignment	not modelled	99.6	15	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Viral cysteine protease of trypsin fold
67	<a href="#">c2ouaA_</a>	Alignment	not modelled	99.6	25	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> serine protease; <b>PDBTitle:</b> crystal structure of nocardiosis protease (napase)
68	<a href="#">c4jj0B_</a>	Alignment	not modelled	99.6	20	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> mamp; <b>PDBTitle:</b> crystal structure of mamp
69	<a href="#">d2sfaa_</a>	Alignment	not modelled	99.6	20	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Prokaryotic proteases
70	<a href="#">c1wczA_</a>	Alignment	not modelled	99.6	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl endopeptidase; <b>PDBTitle:</b> crystal structure of an alkaline form of v8 protease from2 staphylococcus aureus
71	<a href="#">d1ky9a1</a>	Alignment	not modelled	99.6	30	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> HtraA-like serine proteases
72	<a href="#">c5hj1A_</a>	Alignment	not modelled	99.5	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pullulanase c protein; <b>PDBTitle:</b> crystal structure of pdz domain of pullulanase c protein of type ii2 secretion system from klebsiella pneumoniae in complex with fatty3 acid
73	<a href="#">d2i4sa1</a>	Alignment	not modelled	99.5	12	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> EpsC C-terminal domain-like
74	<a href="#">c3i18A_</a>	Alignment	not modelled	99.5	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> lmo2051 protein; <b>PDBTitle:</b> crystal structure of the pdz domain of the sdrc-like protein (lmo2051)2 from listeria monocytogenes, northeast structural genomics consortium3 target lmr166b
75	<a href="#">c2pfeA_</a>	Alignment	not modelled	99.5	24	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> alkaline serine protease; <b>PDBTitle:</b> crystal structure of thermobifida fusca protease a (tfpa)
76	<a href="#">d2sgaa_</a>	Alignment	not modelled	99.5	27	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Prokaryotic proteases
77	<a href="#">c2kl1A_</a>	Alignment	not modelled	99.5	23	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> ylbl protein; <b>PDBTitle:</b> solution structure of gtr34c from geobacillus thermodenitrificans.2 northeast structural genomics consortium target gtr34c
78	<a href="#">c2kjpA_</a>	Alignment	not modelled	99.5	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ylbl; <b>PDBTitle:</b> solution structure of protein ylbl (bsu15050) from bacillus2 subtilis, northeast structural genomics consortium target3 sr713a
79	<a href="#">d1p3ca_</a>	Alignment	not modelled	99.5	16	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Prokaryotic proteases
80	<a href="#">c2ea3A_</a>	Alignment	not modelled	99.5	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> chymotrypsin; <b>PDBTitle:</b> crystal structure of cellulomonas bogoriensis chymotrypsin
81	<a href="#">d1arba_</a>	Alignment	not modelled	99.4	14	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Prokaryotic proteases

82	<a href="#">d1sota1</a>	Alignment	not modelled	99.4	31	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> HtrA-like serine proteases
83	<a href="#">d1hpga</a>	Alignment	not modelled	99.4	18	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Prokaryotic proteases
84	<a href="#">d1fc6a3</a>	Alignment	not modelled	99.4	23	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> Tail specific protease PDZ domain
85	<a href="#">d2i6va1</a>	Alignment	not modelled	99.4	12	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> EpsC C-terminal domain-like
86	<a href="#">c3zv8A</a>	Alignment	not modelled	99.3	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 3c protease; <b>PDBTitle:</b> crystal structure of 3c protease of enterovirus 68
87	<a href="#">d2hgaa1</a>	Alignment	not modelled	99.3	19	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> MTH1368 C-terminal domain-like
88	<a href="#">c3wkIA</a>	Alignment	not modelled	99.3	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative zinc metalloprotease aq_1964; <b>PDBTitle:</b> the periplasmic pdz tandem fragment of the rsep homologue from aquifex2 aeolicus
89	<a href="#">c2zplA</a>	Alignment	not modelled	99.3	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> regulator of sigma e protease; <b>PDBTitle:</b> crystal structure analysis of pdz domain a
90	<a href="#">c4lk4A</a>	Alignment	not modelled	99.2	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> vesb protease; <b>PDBTitle:</b> structure of vibrio cholerae vesb protease
91	<a href="#">c4o06A</a>	Alignment	not modelled	99.2	15	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> probable 26s proteasome regulatory subunit p27; <b>PDBTitle:</b> 1.15a resolution structure of the proteasome assembly chaperone nas22 pdz domain
92	<a href="#">c3wy8A</a>	Alignment	not modelled	99.2	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> serine protease; <b>PDBTitle:</b> crystal structure of protease anisep from arthrobacter nicotinovorans
93	<a href="#">c3cp7B</a>	Alignment	not modelled	99.2	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> alkaline serine protease al20; <b>PDBTitle:</b> crystal structure of a thermostable serine protease al20 from 2 extremophilic microorganism
94	<a href="#">c3rleA</a>	Alignment	not modelled	99.2	10	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> golgi reassembly-stacking protein 2; <b>PDBTitle:</b> crystal structure of grasp55 grasp domain (residues 7-208)
95	<a href="#">d1ky9b2</a>	Alignment	not modelled	99.2	22	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> HtrA-like serine proteases
96	<a href="#">c6bqmA</a>	Alignment	not modelled	99.2	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> serine protease vesc; <b>PDBTitle:</b> secreted serine protease vesc from vibrio cholerae
97	<a href="#">c2krqA</a>	Alignment	not modelled	99.2	24	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> na(+)/h(+) exchange regulatory cofactor nhe-rf1; <b>PDBTitle:</b> solution structure of human sodium/ hydrogen exchange2 regulatory factor 1(150-358)
98	<a href="#">c4reyA</a>	Alignment	not modelled	99.2	15	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> golgi reassembly-stacking protein 1; <b>PDBTitle:</b> crystal structure of the grasp65-gm130 c-terminal peptide complex
99	<a href="#">c2zpmA</a>	Alignment	not modelled	99.1	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> regulator of sigma e protease; <b>PDBTitle:</b> crystal structure analysis of pdz domain b
100	<a href="#">c2kjdA</a>	Alignment	not modelled	99.1	24	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> sodium/hydrogen exchange regulatory cofactor nhe- <b>PDBTitle:</b> solution structure of extended pdz2 domain from nherf1 (150-2 270)
101	<a href="#">c6esoA</a>	Alignment	not modelled	99.1	19	<b>PDB header:</b> blood clotting <b>Chain:</b> A: <b>PDB Molecule:</b> plasma kallikrein; <b>PDBTitle:</b> full length human plasma kallikrein with inhibitor
102	<a href="#">c6bxgA</a>	Alignment	not modelled	99.1	20	<b>PDB header:</b> hydrolase/peptide <b>Chain:</b> A: <b>PDB Molecule:</b> tail-specific protease; <b>PDBTitle:</b> 1.45 angstrom resolution crystal structure of pdz domain of carboxy-2 terminal protease from vibrio cholerae in complex with peptide.
103	<a href="#">d1g9oa</a>	Alignment	not modelled	99.1	24	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain
104	<a href="#">c2m0tA</a>	Alignment	not modelled	99.1	25	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> na(+)/h(+) exchange regulatory cofactor nhe-rf1; <b>PDBTitle:</b> structural characterization of the extended pdz1 domain from nherf1
105	<a href="#">c5wouA</a>	Alignment	not modelled	99.0	31	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> protein lap4; <b>PDBTitle:</b> crystal structure of drosophila melanogaster scribble pdz1 domain in2 complex with guk-holder
106	<a href="#">d1ueqa</a>	Alignment	not modelled	99.0	20	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain
107	<a href="#">c2eaqA</a>	Alignment	not modelled	99.0	14	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> lim domain only protein 7; <b>PDBTitle:</b> crystal structure of pdz domain of kiaa0858 (lim),

						ms07932 from homo sapiens
108	<a href="#">c3shuB_</a>	Alignment	not modelled	99.0	21	<b>PDB header:</b> cell adhesion <b>Chain:</b> B; <b>PDB Molecule:</b> tight junction protein zo-1; <b>PDBTitle:</b> crystal structure of zo-1 pdz3
109	<a href="#">d1m5za_</a>	Alignment	not modelled	99.0	13	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain
110	<a href="#">c4c2dC_</a>	Alignment	not modelled	99.0	16	<b>PDB header:</b> hydrolase/peptide <b>Chain:</b> C; <b>PDB Molecule:</b> carboxy-terminal processing protease ctpb; <b>PDBTitle:</b> crystal structure of the protease ctpb in an active state
111	<a href="#">c3l4fD_</a>	Alignment	not modelled	99.0	21	<b>PDB header:</b> signaling protein/protein binding <b>Chain:</b> D; <b>PDB Molecule:</b> sh3 and multiple ankyrin repeat domains protein 1; <b>PDBTitle:</b> crystal structure of betapix coiled-coil domain and shank pdz complex
112	<a href="#">c2he4A_</a>	Alignment	not modelled	99.0	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> na(+)/h(+) exchange regulatory cofactor nhe-rf2; <b>PDBTitle:</b> the crystal structure of the second pdz domain of human2 nherf-2 (slc9a3r2) interacting with a mode 1 pdz binding3 motif
113	<a href="#">c2vwrA_</a>	Alignment	not modelled	99.0	23	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> ligand of numb protein x 2; <b>PDBTitle:</b> crystal structure of the second pdz domain of numb-binding protein 2
114	<a href="#">c2komA_</a>	Alignment	not modelled	99.0	23	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> partitioning defective 3 homolog; <b>PDBTitle:</b> solution structure of humar par-3b pdz2 (residues 451-549)
115	<a href="#">c5oakA_</a>	Alignment	not modelled	99.0	13	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> bazooka, isoform c,ld29223p; <b>PDBTitle:</b> structure of the dmpar3 pdz1 domain in complex with the dmpar6 pbm
116	<a href="#">d1qaua_</a>	Alignment	not modelled	99.0	27	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain
117	<a href="#">c4durA_</a>	Alignment	not modelled	99.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> plasminogen; <b>PDBTitle:</b> the x-ray crystal structure of full-length type ii human plasminogen
118	<a href="#">c3diwB_</a>	Alignment	not modelled	99.0	26	<b>PDB header:</b> signaling protein/cell adhesion <b>Chain:</b> B; <b>PDB Molecule:</b> tax1-binding protein 3; <b>PDBTitle:</b> c-terminal beta-catenin bound tip-1 structure
119	<a href="#">d1x5qa1</a>	Alignment	not modelled	99.0	30	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain
120	<a href="#">d1wfga_</a>	Alignment	not modelled	99.0	24	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain