







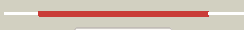















Phyre2

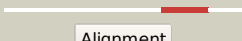

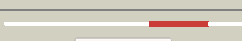
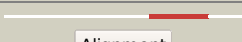
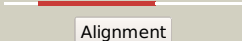
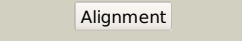
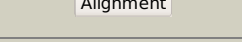



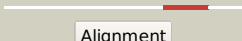


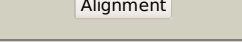
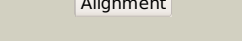
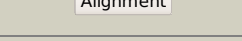
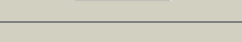
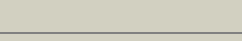


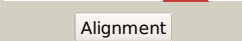

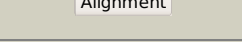


Email	mdejesus@rockefeller.edu
Description	RVBD0125_(pepA)_151146_152213
Date	Tue Jul 23 14:50:16 BST 2019
Unique Job ID	8ffc08a92200c356

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3stjC_	 Alignment		100.0	30	PDB header: hydrolase Chain: C: PDB Molecule: protease degq; PDBTitle: crystal structure of the protease + pdz1 domain of degq from2 escherichia coli
2	c3qo6B_	 Alignment		100.0	27	PDB header: photosynthesis Chain: B: PDB Molecule: protease do-like 1, chloroplastic; PDBTitle: crystal structure analysis of the plant protease deg1
3	c5xdyA_	 Alignment		100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: heat shock protein htra; PDBTitle: crystal structure of htra1 from mycobacterium tuberculosis
4	c4ic6A_	 Alignment		100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: protease do-like 8, chloroplastic; PDBTitle: crystal structure of deg8
5	c1lcyA_	 Alignment		100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: htra2 serine protease; PDBTitle: crystal structure of the mitochondrial serine protease htra2
6	c2zleB_	 Alignment		100.0	30	PDB header: hydrolase Chain: B: PDB Molecule: protease do; PDBTitle: cryo-em structure of degp12/omp
7	c1ky9A_	 Alignment		100.0	29	PDB header: hydrolase Chain: A: PDB Molecule: protease do; PDBTitle: crystal structure of degp (htra)
8	c3gdsA_	 Alignment		100.0	30	PDB header: hydrolase/hydrolase activator Chain: A: PDB Molecule: protease degs; PDBTitle: crystal structure of degs h198p/d320a mutant modified by dfp in2 complex with dnrdgnvyf peptide
9	c4flnB_	 Alignment		100.0	24	PDB header: hydrolase Chain: B: PDB Molecule: protease do-like 2, chloroplastic; PDBTitle: crystal structure of plant protease deg2
10	c3otpF_	 Alignment		100.0	30	PDB header: hydrolase Chain: F: PDB Molecule: protease do; PDBTitle: crystal structure of the degp dodecamer with a model substrate
11	c5il9A_	 Alignment		100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: protease do-like 9; PDBTitle: crystal structure of deg9

12	c4a8a1_	Alignment		100.0	29	PDB header: hydrolase/hydrolase Chain: I: PDB Molecule: periplasmic ph-dependent serine endoprotease degq; PDBTitle: asymmetric cryo-em reconstruction of e. coli degq 12-mer in complex2 with lysozyme
13	c3pv5B_	Alignment		100.0	30	PDB header: hydrolase Chain: B: PDB Molecule: degq; PDBTitle: structure of legionella fallonii degq (n189g/p190g variant)
14	c4ri0A_	Alignment		100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: serine protease htra3; PDBTitle: serine protease htra3, mutationally inactivated
15	c2z9iB_	Alignment		100.0	35	PDB header: hydrolase Chain: B: PDB Molecule: probable serine protease pepd; PDBTitle: crystal structure of rv0983 from mycobacterium tuberculosis-2 proteolytically active form
16	c2r3yC_	Alignment		100.0	33	PDB header: hydrolase/hydrolase activator Chain: C: PDB Molecule: protease degs; PDBTitle: crystal structure of the degs protease in complex with the2 ywf activating peptide
17	c3pv4A_	Alignment		100.0	30	PDB header: hydrolase Chain: A: PDB Molecule: degq; PDBTitle: structure of legionella fallonii degq (delta-pdz2 variant)
18	c5b6iA_	Alignment		100.0	36	PDB header: hydrolase Chain: A: PDB Molecule: putative serine protease hhoa; PDBTitle: structure of deg protease hhoa from synechocystis sp. pcc 6803
19	c5y2dA_	Alignment		100.0	33	PDB header: hydrolase Chain: A: PDB Molecule: periplasmic serine endoprotease degp-like; PDBTitle: crystal structure of h. pylori htra
20	c5jykB_	Alignment		100.0	23	PDB header: hydrolase Chain: B: PDB Molecule: protease do-like 9; PDBTitle: deg9 crystal under 289k
21	c5y09B_	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: B: PDB Molecule: protease do-like 9; PDBTitle: crystal structure of deg9 at 295 k
22	d1ky9a2	Alignment	not modelled	100.0	31	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
23	c2rce1_	Alignment	not modelled	100.0	30	PDB header: hydrolase Chain: I: PDB Molecule: protease degs; PDBTitle: dfp modified degs delta pdz
24	d1l1ja_	Alignment	not modelled	100.0	31	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
25	d2qf3a1	Alignment	not modelled	100.0	33	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
26	c3nziA_	Alignment	not modelled	100.0	25	PDB header: hydrolase/hydrolase substrate Chain: A: PDB Molecule: serine protease htra1; PDBTitle: substrate induced remodeling of the active site regulates htra12 activity
27	d2z9ia2	Alignment	not modelled	100.0	37	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
28	c5y28B_	Alignment	not modelled	100.0	30	PDB header: hydrolase Chain: B: PDB Molecule: periplasmic serine endoprotease degp-like; PDBTitle: crystal structure of h. pylori htra with pdz2 deletion
29	c3stiC_	Alignment	not modelled	100.0	35	PDB header: hydrolase Chain: C: PDB Molecule: protease degq; PDBTitle: crystal structure of the protease domain of degq from escherichia coli

30	c3nwuB	Alignment	not modelled	100.0	26	PDB header: hydrolase Chain: B: PDB Molecule: serine protease htra1; PDBTitle: substrate induced remodeling of the active site regulates htra12 activity
31	c5hmaA	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: trypsin-like serine protease; PDBTitle: crystal structure of mamo protease domain from magnetospirillum2 magneticum (ni bound form)
32	c4ic5B	Alignment	not modelled	100.0	26	PDB header: hydrolase Chain: B: PDB Molecule: protease do-like 5, chloroplastic; PDBTitle: crystal structure of deg5
33	d1lcyA2	Alignment	not modelled	100.0	29	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
34	c3k6zA	Alignment	not modelled	100.0	30	PDB header: hydrolase Chain: A: PDB Molecule: possible membrane-associated serine protease; PDBTitle: crystal structure of rv3671c protease, inactive form
35	c5ilaA	Alignment	not modelled	100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: protease do-like 9; PDBTitle: deg9 protease domain
36	c1zyoA	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: serine protease; PDBTitle: crystal structure of the serine protease domain of sesbania mosaic2 virus polyprotein
37	c3mmgB	Alignment	not modelled	99.9	13	PDB header: viral protein, hydrolase Chain: B: PDB Molecule: nuclear inclusion protein a; PDBTitle: crystal structure of tobacco vein mottling virus protease
38	c2w5eB	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: B: PDB Molecule: putative serine protease; PDBTitle: structural and biochemical analysis of human pathogenic2 astrovirus serine protease at 2.0 angstrom resolution
39	d1q31a	Alignment	not modelled	99.9	11	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral proteases
40	c4inkA	Alignment	not modelled	99.9	25	PDB header: hydrolase Chain: A: PDB Molecule: serine protease spld; PDBTitle: crystal structure of spld protease from staphylococcus aureus at 1.562 a resolution
41	d1lvmb	Alignment	not modelled	99.9	11	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral proteases
42	c2l97A	Alignment	not modelled	99.8	33	PDB header: protein binding Chain: A: PDB Molecule: putative serine protease; PDBTitle: solution structure of htra pdz domain from streptococcus pneumoniae
43	c2vidA	Alignment	not modelled	99.8	21	PDB header: hydrolase Chain: A: PDB Molecule: serine protease splb; PDBTitle: serine protease splb from staphylococcus aureus at 1.8a resolution
44	c5c2zA	Alignment	not modelled	99.8	24	PDB header: toxin Chain: A: PDB Molecule: exfoliative toxin d2; PDBTitle: molecular insights into the specificity of exfoliative toxins from2 staphylococcus aureus
45	d1agja	Alignment	not modelled	99.8	18	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
46	d1qtfa	Alignment	not modelled	99.8	19	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
47	c6e0uB	Alignment	not modelled	99.8	21	PDB header: hydrolase, toxin Chain: B: PDB Molecule: serine protease; PDBTitle: staphylococcus pseudintermedius exfoliative toxin exi
48	c5mm8A	Alignment	not modelled	99.8	24	PDB header: hydrolase Chain: A: PDB Molecule: serine protease sple; PDBTitle: atomic resolution structure of sple protease from staphylococcus2 aureus
49	c6fezB	Alignment	not modelled	99.7	20	PDB header: viral protein Chain: B: PDB Molecule: serine protease domain; PDBTitle: ryegrass mottle virus protease domain
50	c2as9B	Alignment	not modelled	99.7	21	PDB header: hydrolase Chain: B: PDB Molecule: serine protease; PDBTitle: functional and structural characterization of spl proteases from2 staphylococcus aureus
51	c2w7uC	Alignment	not modelled	99.7	23	PDB header: hydrolase Chain: C: PDB Molecule: serine protease spla; PDBTitle: spla serine protease of staphylococcus aureus (2.4a)
52	d2z9ia1	Alignment	not modelled	99.7	41	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: HtrA-like serine proteases
53	d1cqqa	Alignment	not modelled	99.7	16	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral cysteine protease of trypsin fold
54	c5mrtA	Alignment	not modelled	99.6	22	PDB header: hydrolase Chain: A: PDB Molecule: lytic endopeptidase preproenzyme; PDBTitle: crystal structure of I5 protease lysobacter sp. x11
55	c4jcnA	Alignment	not modelled	99.6	23	PDB header: hydrolase Chain: A: PDB Molecule: glutamyl endopeptidase; PDBTitle: structure of esp, serine protease from staphylococcus epidermidis
56	d2qaaa1	Alignment	not modelled	99.6	21	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases

57	c2kl1A	 Alignment	not modelled	99.6	29	PDB header: protein binding Chain: A: PDB Molecule: ylbl protein; PDBTitle: solution structure of gtr34c from geobacillus thermodenitrificans.2 northeast structural genomics consortium target gtr34c
58	c3i18A	 Alignment	not modelled	99.6	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lmo2051 protein; PDBTitle: crystal structure of the pdz domain of the sdrc-like protein (lmo2051)2 from listeria monocytogenes, northeast structural genomics consortium3 target lmr166b
59	c2joaA	 Alignment	not modelled	99.6	20	PDB header: protein binding Chain: A: PDB Molecule: serine protease htra1; PDBTitle: htra1 bound to an optimized peptide: nmr assignment of pdz2 domain and ligand resonances
60	c2p3wB	 Alignment	not modelled	99.6	19	PDB header: protein binding Chain: B: PDB Molecule: probable serine protease htra3; PDBTitle: crystal structure of the htra3 pdz domain bound to a phage-derived2 ligand (fgrwv)
61	d1l1na	 Alignment	not modelled	99.6	13	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral cysteine protease of trypsin fold
62	d2sfaa	 Alignment	not modelled	99.6	20	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
63	d2o8la1	 Alignment	not modelled	99.6	20	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
64	c2o8IA	 Alignment	not modelled	99.6	20	PDB header: hydrolase Chain: A: PDB Molecule: v8 protease; PDBTitle: structure of v8 protease from staphylococcus aureus
65	c2n7pA	 Alignment	not modelled	99.6	16	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: solution structure of pdz domain
66	c1qv6A	 Alignment	not modelled	99.6	20	PDB header: protease Chain: A: PDB Molecule: serine protease; PDBTitle: structue of v8 protease from staphylococcus aureus
67	c1wczA	 Alignment	not modelled	99.6	18	PDB header: hydrolase Chain: A: PDB Molecule: glutamyl endopeptidase; PDBTitle: crystal structure of an alkaline form of v8 protease from2 staphylococcus aureus
68	c2kjpA	 Alignment	not modelled	99.6	28	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein ylbl; PDBTitle: solution structure of protein ylbl (bsu15050) from bacillus2 subtilis, northeast structural genomics consortium target3 sr713a
69	d1lcyA1	 Alignment	not modelled	99.6	23	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: Htra-like serine proteases
70	c4jj0B	 Alignment	not modelled	99.6	16	PDB header: electron transport Chain: B: PDB Molecule: mamp; PDBTitle: crystal structure of mamp
71	c2ouaA	 Alignment	not modelled	99.5	17	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: serine protease; PDBTitle: crystal structure of nocardioopsis protease (napase)
72	c2b0fA	 Alignment	not modelled	99.5	18	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: picornain 3c (protease 3c) (p3c); PDBTitle: nmr structure of the human rhinovirus 3c protease (serotype 14) with2 covalently bound ace-lealfq-ethylpropionate inhibitor
73	d2i4sa1	 Alignment	not modelled	99.5	16	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: EpsC C-terminal domain-like
74	d2h5ca1	 Alignment	not modelled	99.5	21	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
75	c5hj1A	 Alignment	not modelled	99.5	18	PDB header: hydrolase Chain: A: PDB Molecule: pullulanase c protein; PDBTitle: crystal structure of pdz domain of pullulanase c protein of type ii2 secretion system from klebsiella pneumoniae in complex with fatty3 acid
76	d1ky9a1	 Alignment	not modelled	99.5	27	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: Htra-like serine proteases
77	d1sota1	 Alignment	not modelled	99.5	39	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: Htra-like serine proteases
78	d2sgaa	 Alignment	not modelled	99.5	20	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
79	d2hgaa1	 Alignment	not modelled	99.5	32	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: MTH1368 C-terminal domain-like
80	d1hpga	 Alignment	not modelled	99.5	15	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
81	c3wkIA	 Alignment	not modelled	99.4	22	PDB header: hydrolase Chain: A: PDB Molecule: putative zinc metalloprotease aq_1964; PDBTitle: the periplasmic pdz tandem fragment of the rsep homologue from aquifex2 aeolicus
82	d2i6va1	Alianment	not modelled	99.4	19	Fold: PDZ domain-like Superfamily: PDZ domain-like

						Family: EpsC C-terminal domain-like
83	d1fc6a3	Alignment	not modelled	99.4	24	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: Tail specific protease PDZ domain
84	d1arba	Alignment	not modelled	99.4	19	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
85	c2pfeA	Alignment	not modelled	99.4	21	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: alkaline serine protease; PDBTitle: crystal structure of thermobifida fusca protease a (tfpa)
86	c4lk4A	Alignment	not modelled	99.4	19	PDB header: hydrolase Chain: A: PDB Molecule: vesb protease; PDBTitle: structure of vibrio cholerae vesb protease
87	d1p3ca	Alignment	not modelled	99.4	20	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
88	c2ea3A	Alignment	not modelled	99.4	25	PDB header: hydrolase Chain: A: PDB Molecule: chymotrypsin; PDBTitle: crystal structure of cellulomonas bogoriensis chymotrypsin
89	c2zplA	Alignment	not modelled	99.3	20	PDB header: hydrolase Chain: A: PDB Molecule: regulator of sigma e protease; PDBTitle: crystal structure analysis of pdz domain a
90	c4o06A	Alignment	not modelled	99.3	12	PDB header: chaperone Chain: A: PDB Molecule: probable 26s proteasome regulatory subunit p27; PDBTitle: 1.15a resolution structure of the proteasome assembly chaperone nas22 pdz domain
91	c3rleA	Alignment	not modelled	99.3	15	PDB header: membrane protein Chain: A: PDB Molecule: golgi reassembly-stacking protein 2; PDBTitle: crystal structure of grasp55 grasp domain (residues 7-208)
92	d1ky9b2	Alignment	not modelled	99.3	21	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: HtrA-like serine proteases
93	c3cp7B	Alignment	not modelled	99.3	17	PDB header: hydrolase Chain: B: PDB Molecule: alkaline serine protease al20; PDBTitle: crystal structure of a thermostable serine protease al20 from 2 extremophilic microorganism
94	c4reyA	Alignment	not modelled	99.2	16	PDB header: membrane protein Chain: A: PDB Molecule: golgi reassembly-stacking protein 1; PDBTitle: crystal structure of the grasp65-gm130 c-terminal peptide complex
95	c2zpmA	Alignment	not modelled	99.2	20	PDB header: hydrolase Chain: A: PDB Molecule: regulator of sigma e protease; PDBTitle: crystal structure analysis of pdz domain b
96	c3wy8A	Alignment	not modelled	99.2	14	PDB header: hydrolase Chain: A: PDB Molecule: serine protease; PDBTitle: crystal structure of protease anisep from arthrobacter nicotinovorans
97	c6bqmA	Alignment	not modelled	99.2	18	PDB header: hydrolase Chain: A: PDB Molecule: serine protease vesc; PDBTitle: secreted serine protease vesc from vibrio cholerae
98	c6esoA	Alignment	not modelled	99.2	19	PDB header: blood clotting Chain: A: PDB Molecule: plasma kallikrein; PDBTitle: full length human plasma kallikrein with inhibitor
99	c6bxgA	Alignment	not modelled	99.1	15	PDB header: hydrolase/peptide Chain: A: PDB Molecule: tail-specific protease; PDBTitle: 1.45 angstrom resolution crystal structure of pdz domain of carboxy-2 terminal protease from vibrio cholerae in complex with peptide.
100	c3zv8A	Alignment	not modelled	99.1	13	PDB header: hydrolase Chain: A: PDB Molecule: 3c protease; PDBTitle: crystal structure of 3c protease of enterovirus 68
101	c4c2dC	Alignment	not modelled	99.1	14	PDB header: hydrolase/peptide Chain: C: PDB Molecule: carboxy-terminal processing protease ctpb; PDBTitle: crystal structure of the protease ctpb in an active state
102	c3shuB	Alignment	not modelled	99.1	25	PDB header: cell adhesion Chain: B: PDB Molecule: tight junction protein zo-1; PDBTitle: crystal structure of zo-1 pdz3
103	c4durA	Alignment	not modelled	99.1	18	PDB header: hydrolase Chain: A: PDB Molecule: plasminogen; PDBTitle: the x-ray crystal structure of full-length type ii human plasminogen
104	c3diwB	Alignment	not modelled	99.1	22	PDB header: signaling protein/cell adhesion Chain: B: PDB Molecule: tax1-binding protein 3; PDBTitle: c-terminal beta-catenin bound tip-1 structure
105	c2krqA	Alignment	not modelled	99.0	20	PDB header: signaling protein Chain: A: PDB Molecule: na(+)/h(+) exchange regulatory cofactor nhe-rf1; PDBTitle: solution structure of human sodium/ hydrogen exchange2 regulatory factor 1(150-358)
106	c3l4fD	Alignment	not modelled	99.0	13	PDB header: signaling protein/protein binding Chain: D: PDB Molecule: sh3 and multiple ankyrin repeat domains protein 1; PDBTitle: crystal structure of betapix coiled-coil domain and shank pdz complex
107	c2eaqA	Alignment	not modelled	99.0	18	PDB header: metal binding protein Chain: A: PDB Molecule: lim domain only protein 7; PDBTitle: crystal structure of pdz domain of kiaa0858 (lim), ms07932 from homo sapiens PDB header: protein binding

108	c2v90E_	Alignment	not modelled	99.0	21	Chain: E; PDB Molecule: pdz domain-containing protein 3; PDBTitle: crystal structure of the 3rd pdz domain of intestine- and kidney-2 enriched pdz domain ikepp (pdzd3) PDB header: cell adhesion
109	c3shwA_	Alignment	not modelled	99.0	25	Chain: A; PDB Molecule: tight junction protein zo-1; PDBTitle: crystal structure of zo-1 pdz3-sh3-guk supramodule complex with2 connexin-45 peptide PDB header: hydrolase
110	c2f83A_	Alignment	not modelled	99.0	18	Chain: A; PDB Molecule: coagulation factor xi; PDBTitle: crystal structure at 2.9 angstroms resolution of human plasma2 coagulation factor xi zymogen PDB header: hydrolase
111	c2xrcD_	Alignment	not modelled	99.0	19	PDB header: immune system Chain: D; PDB Molecule: human complement factor i; PDBTitle: human complement factor i
112	c1rs0A_	Alignment	not modelled	99.0	16	PDB header: hydrolase Chain: A; PDB Molecule: complement factor b; PDBTitle: crystal structure analysis of the bb segment of factor b2 complexed with di-isopropyl-phosphate (dip)
113	d1x5qa1	Alignment	not modelled	99.0	19	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
114	c5wqlC_	Alignment	not modelled	99.0	25	PDB header: protein binding/signaling protein/hydrol Chain: C; PDB Molecule: tail-specific protease; PDBTitle: structure of a pdz-protease bound to a substrate-binding adaptor
115	d1w9ea1	Alignment	not modelled	99.0	25	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
116	d1rgwa_	Alignment	not modelled	99.0	21	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
117	c3khfA_	Alignment	not modelled	99.0	22	PDB header: transferase Chain: A; PDB Molecule: microtubule-associated serine/threonine-protein kinase 3; PDBTitle: the crystal structure of the pdz domain of human microtubule2 associated serine/threonine kinase 3 (mast3) PDB header: cell adhesion
118	c5wouA_	Alignment	not modelled	99.0	18	Chain: A; PDB Molecule: protein lap4; PDBTitle: crystal structure of drosophila melanogaster scribble pdz1 domain in2 complex with guk-holder PDB header: signaling protein
119	c2kjdA_	Alignment	not modelled	99.0	20	Chain: A; PDB Molecule: sodium/hydrogen exchange regulatory cofactor nhe- PDBTitle: solution structure of extended pdz2 domain from nherf1 (150-2 270)
120	d1wifa_	Alignment	not modelled	99.0	21	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain