Phyre^{2}

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Description	P0AEE3
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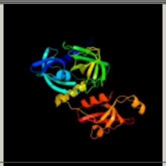
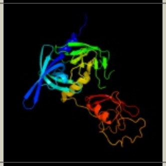
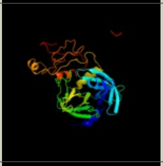
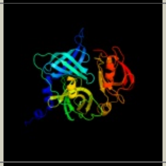
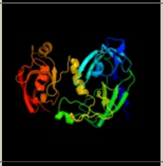
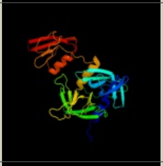
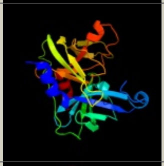
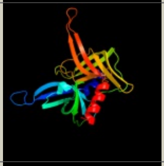
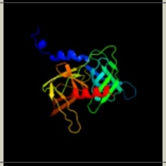
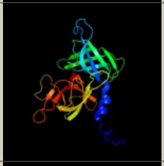
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3stjC_	Alignment		100.0	43	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**protease degq; **PDBTitle:** crystal structure of the protease + pdz1 domain of degq from2 escherichia coli
2	c1ky9A_	Alignment		100.0	40	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protease do; **PDBTitle:** crystal structure of degp (htra)
3	c3gdsA_	Alignment		100.0	95	**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 dnrdgnvyyf peptide
4	c4a8aI_	Alignment		100.0	42	**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
5	c3pv5B_	Alignment		100.0	44	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**degq; **PDBTitle:** structure of legionella fallonii degq (n189g/p190g variant)
6	c3qo6B_	Alignment		100.0	35	**PDB header:**photosynthesis **Chain:** B: **PDB Molecule:**protease do-like 1, chloroplastic; **PDBTitle:** crystal structure analysis of the plant protease deg1
7	c1lcyA_	Alignment		100.0	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**htra2 serine protease; **PDBTitle:** crystal structure of the mitochondrial serine protease htra2
8	c3pv4A_	Alignment		100.0	44	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**degq; **PDBTitle:** structure of legionella fallonii degq (delta-pdz2 variant)
9	c2r3yC_	Alignment		100.0	100	**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
10	c2z9iB_	Alignment		100.0	36	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable serine protease pepd; **PDBTitle:** crystal structure of rv0983 from mycobacterium tuberculosis-2 proteolytically active form
11	d1ky9a2	Alignment		100.0	43	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases

12	c2rcel_	Alignment		100.0	97	**PDB header:**hydrolase **Chain:** I: **PDB Molecule:**protease degs; **PDBTitle:** dfp modified degs delta pdz
13	d1l1ja_	Alignment		100.0	39	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
14	d2qf3a1	Alignment		100.0	97	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
15	c3nziA_	Alignment		100.0	35	**PDB header:**hydrolase/hydrolase substrate **Chain:** A: **PDB Molecule:**serine protease htra1; **PDBTitle:** substrate induced remodeling of the active site regulates htra12 activity
16	c3stiC_	Alignment		100.0	52	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**protease degq; **PDBTitle:** crystal structure of the protease domain of degq from escherichia coli
17	d2z9ia2	Alignment		100.0	39	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
18	c3nwuB_	Alignment		100.0	39	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**serine protease htra1; **PDBTitle:** substrate induced remodeling of the active site regulates htra12 activity
19	d1lcya2	Alignment		100.0	34	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
20	c3k6zA_	Alignment		100.0	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**possible membrane-associated serine protease; **PDBTitle:** crystal structure of rv3671c protease, inactive form
21	c1zyoA_	Alignment	not modelled	100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**serine protease; **PDBTitle:** crystal structure of the serine protease domain of sesbania mosaic2 virus polyprotein
22	c3mmgB_	Alignment	not modelled	99.9	19	**PDB header:**viral protein, hydrolase **Chain:** B: **PDB Molecule:**nuclear inclusion protein a; **PDBTitle:** crystal structure of tobacco vein mottling virus protease
23	c2w5eB_	Alignment	not modelled	99.9	18	**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
24	d1q31a_	Alignment	not modelled	99.9	18	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral proteases
25	d1lvmb_	Alignment	not modelled	99.9	17	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral proteases
26	d1qtfa_	Alignment	not modelled	99.9	28	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
27	d1agja_	Alignment	not modelled	99.9	23	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
28	c2vidA_	Alignment	not modelled	99.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**serine protease splb; **PDBTitle:** serine protease splb from staphylococcus aureus at 1.8a2 resolution
						PDB header:hydrolase

29	c2w7uC_	Alignment	not modelled	99.8	26	**Chain:** C: **PDB Molecule:**serine protease spla; **PDBTitle:** spla serine protease of staphylococcus aureus (2.4a)
30	d1cqqa_	Alignment	not modelled	99.8	15	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral cysteine protease of trypsin fold
31	c2p3wB_	Alignment	not modelled	99.8	28	**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)
32	d1lcya1	Alignment	not modelled	99.8	27	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
33	c2as9B_	Alignment	not modelled	99.8	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**serine protease; **PDBTitle:** functional and structural characterization of spl proteases2 from staphylococcus aureus
34	d1ky9a1	Alignment	not modelled	99.8	34	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
35	c2b0fA_	Alignment	not modelled	99.8	19	**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
36	c2joaA_	Alignment	not modelled	99.8	30	**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
37	d2qaaa1	Alignment	not modelled	99.8	17	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
38	d1l1na_	Alignment	not modelled	99.8	15	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral cysteine protease of trypsin fold
39	d2o8la1	Alignment	not modelled	99.7	18	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
40	c2o8lA_	Alignment	not modelled	99.7	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**v8 protease; **PDBTitle:** structure of v8 protease from staphylococcus aureus
41	c1qy6A_	Alignment	not modelled	99.7	19	**PDB header:**protease **Chain:** A: **PDB Molecule:**serine protease; **PDBTitle:** structue of v8 protease from staphylococcus aureus
42	d2z9ia1	Alignment	not modelled	99.7	27	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
43	c1wczA_	Alignment	not modelled	99.7	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glutamyl endopeptidase; **PDBTitle:** crystal structure of an alkaline form of v8 protease from2 staphylococcus aureus
44	c2ouaA_	Alignment	not modelled	99.7	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**serine protease; **PDBTitle:** crystal structure of nocardiopsis protease (napase)
45	c2kl1A_	Alignment	not modelled	99.7	25	**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
46	d2h5ca1	Alignment	not modelled	99.7	18	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
47	d2sfaa_	Alignment	not modelled	99.6	17	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
48	d2sgaa_	Alignment	not modelled	99.6	17	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
49	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 protein2 (lmo2051) from listeria monocytogenes, northeast structural3 genomics consortium target lmr166b
50	c2kjpA_	Alignment	not modelled	99.6	29	**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
51	d2i4sa1	Alignment	not modelled	99.6	14	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**EpsC C-terminal domain-like
52	d1p3ca_	Alignment	not modelled	99.6	15	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
53	c2pfeA_	Alignment	not modelled	99.6	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alkaline serine protease; **PDBTitle:** crystal structure of thermobifida fusca protease a (tfpa)
54	d1hpga_	Alignment	not modelled	99.6	19	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
						Fold:PDZ domain-like

55	d1sota1	Alignment	not modelled	99.6	97	**Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
56	c2ea3A_	Alignment	not modelled	99.6	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chymotrypsin; **PDBTitle:** crystal structure of cellulomonas bogoriensis chymotrypsin
57	d1arba_	Alignment	not modelled	99.5	14	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
58	d2i6va1	Alignment	not modelled	99.5	13	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**EpsC C-terminal domain-like
59	d2hgaa1	Alignment	not modelled	99.5	21	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**MTH1368 C-terminal domain-like
60	d1ky9b2	Alignment	not modelled	99.4	28	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
61	d1fc6a3	Alignment	not modelled	99.4	24	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**Tail specific protease PDZ domain
62	c2zplA_	Alignment	not modelled	99.4	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**regulator of sigma e protease; **PDBTitle:** crystal structure analysis of pdz domain a
63	c3rleA_	Alignment	not modelled	99.3	13	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**golgi reassembly-stacking protein 2; **PDBTitle:** crystal structure of grasp55 grasp domain (residues 7-208)
64	c2zpmA_	Alignment	not modelled	99.3	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**regulator of sigma e protease; **PDBTitle:** crystal structure analysis of pdz domain b
65	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 al202 from extremophilic microoganism
66	c2eaqA_	Alignment	not modelled	99.1	26	**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
67	c3diwB_	Alignment	not modelled	99.1	29	**PDB header:**signaling protein/cell adhesion **Chain:** B: **PDB Molecule:**tax1-binding protein 3; **PDBTitle:** c-terminal beta-catenin bound tip-1 structure
68	d1uf1a_	Alignment	not modelled	99.1	24	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
69	c2eehA_	Alignment	not modelled	99.1	28	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**pdz domain-containing protein 7; **PDBTitle:** solution structure of first pdz domain of pdz domain2 containing protein 7
70	d1x5qa1	Alignment	not modelled	99.1	28	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
71	c3shuB_	Alignment	not modelled	99.0	25	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**tight junction protein zo-1; **PDBTitle:** crystal structure of zo-1 pdz3
72	d1rgwa_	Alignment	not modelled	99.0	14	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
73	c2q3gA_	Alignment	not modelled	99.0	26	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**pdz and lim domain protein 7; **PDBTitle:** structure of the pdz domain of human pdlim7 bound to a c-2 terminal extension from human beta-tropomyosin
74	c3l4fD_	Alignment	not modelled	99.0	17	**PDB header:**signaling protein/protein binding **Chain:** D: **PDB Molecule:**sh3 and multiple ankyrin repeat domains protein **PDBTitle:** crystal structure of betapix coiled-coil domain and shank2 pdz complex
75	c2v90E_	Alignment	not modelled	99.0	24	**PDB header:**protein-binding **Chain:** E: **PDB Molecule:**pdz domain-containing protein 3; **PDBTitle:** crystal structure of the 3rd pdz domain of intestine- and2 kidney-enriched pdz domain ikepp (pdzd3)
76	d2f5ya1	Alignment	not modelled	99.0	23	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
77	d1wfga_	Alignment	not modelled	99.0	17	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
78	c2v1wB_	Alignment	not modelled	99.0	20	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**pdz and lim domain protein 4; **PDBTitle:** crystal structure of human lim protein ril (pdlim4) pdz2 domain bound to the c-terminal peptide of human alpha-3 actinin-1
79	c2komA_	Alignment	not modelled	99.0	20	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**partitioning defective 3 homolog; **PDBTitle:** solution structure of humar par-3b pdz2 (residues 451-549)
80	d1m5za_	Alignment	not modelled	99.0	18	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
81	c2krgA_	Alignment	not modelled	99.0	21	**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)
82	c2yuyA_	Alignment	not modelled	99.0	22	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**rho gtpase activating protein 21; **PDBTitle:** solution structure of pdz domain of rho gtpase activating2 protein 21
83	d1ueqa_	Alignment	not modelled	99.0	23	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
84	d1q3oa_	Alignment	not modelled	99.0	18	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
85	d1p1da2	Alignment	not modelled	99.0	13	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
86	d1wifa_	Alignment	not modelled	99.0	23	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
87	c2iwnA_	Alignment	not modelled	99.0	26	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**multiple pdz domain protein; **PDBTitle:** 3rd pdz domain of multiple pdz domain protein mpdz (casp2 target)
88	c3f1sB_	Alignment	not modelled	99.0	15	**PDB header:**hydrolase inhibitor/hydrolase **Chain:** B: **PDB Molecule:**vitamin k-dependent protein z; **PDBTitle:** crystal structure of protein z complexed with protein z-dependent2 inhibitor
89	c2f83A_	Alignment	not modelled	99.0	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**coagulation factor xi; **PDBTitle:** crystal structure at 2.9 angstroms resolution of human plasma2 coagulation factor xi zymogen
90	c2kjdA_	Alignment	not modelled	99.0	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**sodium/hydrogen exchange regulatory cofactor nhe- **PDBTitle:** solution structure of extended pdz2 domain from nherf1 (150-2 270)
91	d1wf7a_	Alignment	not modelled	99.0	19	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
92	c3shwA_	Alignment	not modelled	98.9	26	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**tight junction protein zo-1; **PDBTitle:** crystal structure of zo-1 pdz3-sh3-guk supramodule complex with2 connexin-45 peptide
93	d1ozia_	Alignment	not modelled	98.9	20	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
94	d1w9ea1	Alignment	not modelled	98.9	17	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
95	d2fe5a1	Alignment	not modelled	98.9	16	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
96	c2he4A_	Alignment	not modelled	98.9	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**na(+)/h(+) exchange regulatory cofactor nhe-rf2; **PDBTitle:** the crystal structure of the second pdz domain of human2 nherf-2 (slc9a3r2) interacting with a mode 1 pdz binding3 motif
97	c2egkC_	Alignment	not modelled	98.9	23	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**general receptor for phosphoinositides 1- **PDBTitle:** crystal structure of tamalin pdz-intrinsic ligand fusion2 protein
98	c3cyyA_	Alignment	not modelled	98.9	27	**PDB header:**peptide binding protein **Chain:** A: **PDB Molecule:**tight junction protein zo-1; **PDBTitle:** the crystal structure of zo-1 pdz2 in complex with the cx43 peptide
99	c3osyA_	Alignment	not modelled	98.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**3c protease; **PDBTitle:** human enterovirus 71 3c protease
100	c2xrcD_	Alignment	not modelled	98.9	16	**PDB header:**immune system **Chain:** D: **PDB Molecule:**human complement factor i; **PDBTitle:** human complement factor i
101	c3k1rA_	Alignment	not modelled	98.9	21	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**harmonin; **PDBTitle:** structure of harmonin npdz1 in complex with the sam-pbm of2 sans
102	c2vsvB_	Alignment	not modelled	98.9	21	**PDB header:**protein-binding **Chain:** B: **PDB Molecule:**rhophilin-2; **PDBTitle:** crystal structure of the pdz domain of human rhophilin-2
103	d1rzxa_	Alignment	not modelled	98.9	20	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
104	d1g9oa_	Alignment	not modelled	98.9	16	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
105	c2vwrA_	Alignment	not modelled	98.9	16	**PDB header:**protein-binding **Chain:** A: **PDB Molecule:**ligand of numb protein x 2; **PDBTitle:** crystal structure of the second pdz domain of numb-binding2 protein 2
106	d1t2ma1	Alignment	not modelled	98.9	24	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
107	c2o2tB_	Alignment	not modelled	98.9	19	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**multiple pdz domain protein; **PDBTitle:** the crystal structure of the 1st pdz domain of mpdz

108	d1ry4a_	Alignment	not modelled	98.9	20	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
109	c2i04B_	Alignment	not modelled	98.9	24	**PDB header:**peptide binding protein **Chain:** B: **PDB Molecule:**membrane-associated guanylate kinase, ww and pdz **PDBTitle:** x-ray crystal structure of magi-1 pdz1 bound to the c-2 terminal peptide of hpv18 e6
110	c1p1dA_	Alignment	not modelled	98.9	11	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**glutamate receptor interacting protein; **PDBTitle:** structural insights into the inter-domain chaperoning of2 tandem pdz domains in glutamate receptor interacting3 proteins
111	d2byga1	Alignment	not modelled	98.9	21	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
112	c1rs0A_	Alignment	not modelled	98.9	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	c2ok5A_	Alignment	not modelled	98.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**complement factor b; **PDBTitle:** human complement factor b
114	c2omjA_	Alignment	not modelled	98.9	29	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**rho guanine nucleotide exchange factor 12; **PDBTitle:** solution structure of larg pdz domain
115	c2qt5A_	Alignment	not modelled	98.9	23	**PDB header:**peptide binding protein **Chain:** A: **PDB Molecule:**glutamate receptor-interacting protein 1; **PDBTitle:** crystal structure of grip1 pdz12 in complex with the fras12 peptide
116	c3khfA_	Alignment	not modelled	98.9	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**microtubule-associated serine/threonine-protein **PDBTitle:** the crystal structure of the pdz domain of human microtubule2 associated serine/threonine kinase 3 (mast3)
117	c2jxoA_	Alignment	not modelled	98.9	21	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ezrin-radixin-moesin-binding phosphoprotein 50; **PDBTitle:** structure of the second pdz domain of nherf-1
118	d1ueza_	Alignment	not modelled	98.9	26	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
119	c2ogpA_	Alignment	not modelled	98.9	23	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**partitioning-defective 3 homolog; **PDBTitle:** solution structure of the second pdz domain of par-3
120	c3qglD_	Alignment	not modelled	98.9	20	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**sorting nexin-27; **PDBTitle:** crystal structure of pdz domain of sorting nexin 27 (snx27) in complex2 with the eseskv peptide corresponding to the c-terminal tail of girk3