Phyre2

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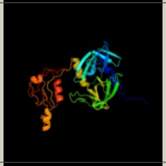
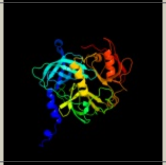
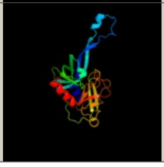
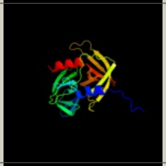
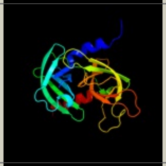
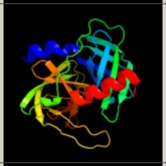
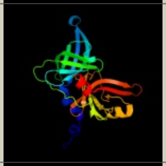
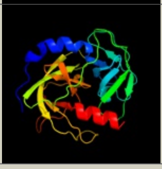
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4a8al_	Alignment		100.0	98	**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
2	c3pv5B_	Alignment		100.0	45	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**degq; **PDBTitle:** structure of legionella fallonii degq (n189g/p190g variant)
3	c3stjC_	Alignment		100.0	100	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**protease degq; **PDBTitle:** crystal structure of the protease + pdz1 domain of degq from2 escherichia coli
4	c1ky9A_	Alignment		100.0	63	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protease do; **PDBTitle:** crystal structure of degp (htra)
5	c3pv4A_	Alignment		100.0	51	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**degq; **PDBTitle:** structure of legionella fallonii degq (delta-pdz2 variant)
6	c3gdsA_	Alignment		100.0	42	**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
7	c3qo6B_	Alignment		100.0	37	**PDB header:**photosynthesis **Chain:** B: **PDB Molecule:**protease do-like 1, chloroplastic; **PDBTitle:** crystal structure analysis of the plant protease deg1
8	c2z9iB_	Alignment		100.0	42	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable serine protease pepd; **PDBTitle:** crystal structure of rv0983 from mycobacterium tuberculosis-2 proteolytically active form
9	c1lcyA_	Alignment		100.0	34	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**htra2 serine protease; **PDBTitle:** crystal structure of the mitochondrial serine protease htra2
10	c2r3yC_	Alignment		100.0	46	**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
11	d1ky9a2	Alignment		100.0	64	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases

12	d1l1ja_	Alignment		100.0	42	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
13	c2rceI_	Alignment		100.0	47	**PDB header:**hydrolase **Chain:** I: **PDB Molecule:**protease degs; **PDBTitle:** dfp modified degs delta pdz
14	c3stiC_	Alignment		100.0	100	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**protease degq; **PDBTitle:** crystal structure of the protease domain of degq from escherichia coli
15	d2qf3a1	Alignment		100.0	52	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
16	c3nziA_	Alignment		100.0	43	**PDB header:**hydrolase/hydrolase substrate **Chain:** A: **PDB Molecule:**serine protease htra1; **PDBTitle:** substrate induced remodeling of the active site regulates htra12 activity
17	d2z9ia2	Alignment		100.0	47	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
18	d1lcya2	Alignment		100.0	39	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
19	c3nwuB_	Alignment		100.0	45	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**serine protease htra1; **PDBTitle:** substrate induced remodeling of the active site regulates htra12 activity
20	c3k6zA_	Alignment		100.0	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**possible membrane-associated serine protease; **PDBTitle:** crystal structure of rv3671c protease, inactive form
21	c3mmgB_	Alignment	not modelled	99.9	16	**PDB header:**viral protein, hydrolase **Chain:** B: **PDB Molecule:**nuclear inclusion protein a; **PDBTitle:** crystal structure of tobacco vein mottling virus protease
22	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
23	d1q31a_	Alignment	not modelled	99.9	16	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral proteases
24	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
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	26	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
27	c2qt5A_	Alignment	not modelled	99.9	18	**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
28	c1p1dA_	Alignment	not modelled	99.9	18	**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
						Fold: Trypsin-like serine proteases

29	d1agja_	Alignment	not modelled	99.9	23	**Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
30	c2ka9A_	Alignment	not modelled	99.9	20	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**disks large homolog 4; **PDBTitle:** solution structure of psd-95 pdz12 complexed with cypin2 peptide
31	c3rleA_	Alignment	not modelled	99.9	21	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**golgi reassembly-stacking protein 2; **PDBTitle:** crystal structure of grasp55 grasp domain (residues 7-208)
32	c3r0hA_	Alignment	not modelled	99.8	16	**PDB header:**peptide binding protein **Chain:** A: **PDB Molecule:**inactivation-no-after-potential d protein; **PDBTitle:** structure of inad pdz45 in complex with ng2 peptide
33	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 1.8a2 resolution
34	c2xkxB_	Alignment	not modelled	99.8	20	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**disks large homolog 4; **PDBTitle:** single particle analysis of psd-95 in negative stain
35	c1w9qB_	Alignment	not modelled	99.8	23	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**syntenin 1; **PDBTitle:** crystal structure of the pdz tandem of human syntenin in2 complex with tnefaf peptide
36	c1u3bA_	Alignment	not modelled	99.8	19	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**amyloid beta a4 precursor protein-binding, **PDBTitle:** auto-inhibition mechanism of x11s/mints family scaffold2 proteins revealed by the closed conformation of the tandem3 pdz domains
37	c2w7uC_	Alignment	not modelled	99.8	20	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**serine protease spla; **PDBTitle:** spla serine protease of staphylococcus aureus (2.4a)
38	d1cqqa_	Alignment	not modelled	99.8	17	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral cysteine protease of trypsin fold
39	c2b0fA_	Alignment	not modelled	99.8	20	**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
40	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
41	d1l1na_	Alignment	not modelled	99.7	18	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral cysteine protease of trypsin fold
42	d2qaaa1	Alignment	not modelled	99.7	20	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
43	c2ouaA_	Alignment	not modelled	99.7	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**serine protease; **PDBTitle:** crystal structure of nocardiopsis protease (napase)
44	d2h5ca1	Alignment	not modelled	99.7	17	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
45	d1ky9a1	Alignment	not modelled	99.7	60	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
46	c2joaA_	Alignment	not modelled	99.6	21	**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
47	c2o8lA_	Alignment	not modelled	99.6	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**v8 protease; **PDBTitle:** structure of v8 protease from staphylococcus aureus
48	d2o8la1	Alignment	not modelled	99.6	22	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
49	c2p3wB_	Alignment	not modelled	99.6	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)
50	d2sfaa_	Alignment	not modelled	99.6	20	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
51	c1qy6A_	Alignment	not modelled	99.6	22	**PDB header:**protease **Chain:** A: **PDB Molecule:**serine protease; **PDBTitle:** structue of v8 protease from staphylococcus aureus
52	d1lcya1	Alignment	not modelled	99.6	22	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
53	c2pfeA_	Alignment	not modelled	99.6	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alkaline serine protease; **PDBTitle:** crystal structure of thermobifida fusca protease a (tfpa)
54	d2sgaa_	Alignment	not modelled	99.6	20	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
55	c1wczA_	Alignment	not modelled	99.6	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glutamyl endopeptidase;

						PDBTitle: crystal structure of an alkaline form of v8 protease from2 staphylococcus aureus
56	d2z9ia1	Alignment	not modelled	99.5	34	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
57	c1z87A_	Alignment	not modelled	99.5	15	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**alpha-1-syntrophin; **PDBTitle:** solution structure of the split ph-pdz supramodule of alpha-2 syntrophin
58	c2ea3A_	Alignment	not modelled	99.5	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chymotrypsin; **PDBTitle:** crystal structure of cellulomonas bogoriensis chymotrypsin
59	d1hpga_	Alignment	not modelled	99.5	18	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
60	d1p3ca_	Alignment	not modelled	99.4	17	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
61	c2krgA_	Alignment	not modelled	99.4	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)
62	d1arba_	Alignment	not modelled	99.4	14	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
63	c2kl1A_	Alignment	not modelled	99.4	26	**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
64	d1ky9b2	Alignment	not modelled	99.4	48	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
65	c3i18A_	Alignment	not modelled	99.3	24	**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
66	d1p1da2	Alignment	not modelled	99.3	20	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
67	c2kjdA_	Alignment	not modelled	99.3	22	**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)
68	c3eggC_	Alignment	not modelled	99.3	22	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**spinophilin; **PDBTitle:** crystal structure of a complex between protein phosphatase 1 alpha2 (pp1) and the pp1 binding and pdz domains of spinophilin
69	d1ozia_	Alignment	not modelled	99.3	19	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
70	d1rgwa_	Alignment	not modelled	99.3	15	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
71	c2iwnA_	Alignment	not modelled	99.3	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**multiple pdz domain protein; **PDBTitle:** 3rd pdz domain of multiple pdz domain protein mpdz (casp2 target)
72	d1sota1	Alignment	not modelled	99.3	35	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
73	c3l4fD_	Alignment	not modelled	99.3	16	**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
74	d1q3oa_	Alignment	not modelled	99.3	16	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
75	d2i4sa1	Alignment	not modelled	99.3	17	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**EpsC C-terminal domain-like
76	c2eehA_	Alignment	not modelled	99.3	22	**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
77	c2q3gA_	Alignment	not modelled	99.3	18	**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
78	c2kjpA_	Alignment	not modelled	99.2	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
79	d1fc6a3	Alignment	not modelled	99.2	20	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**Tail specific protease PDZ domain
						PDB header:structural protein

80	c3k1rA_	Alignment	not modelled	99.2	19	**Chain:** A: **PDB Molecule:**harmonin; **PDBTitle:** structure of harmonin npdz1 in complex with the sam-pbm of2 sans
81	d1t2ma1	Alignment	not modelled	99.2	17	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
82	c2o2tB_	Alignment	not modelled	99.2	24	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**multiple pdz domain protein; **PDBTitle:** the crystal structure of the 1st pdz domain of mpdz
83	d1uf1a_	Alignment	not modelled	99.2	22	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
84	d1m5za_	Alignment	not modelled	99.2	17	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
85	c2dkrA_	Alignment	not modelled	99.2	25	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**lin-7 homolog b; **PDBTitle:** solution structure of the pdz domain from human lin-72 homolog b
86	c2jikB_	Alignment	not modelled	99.2	23	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**synaptojanin-2 binding protein; **PDBTitle:** crystal structure of pdz domain of synaptojanin-2 binding2 protein
87	d1wfga_	Alignment	not modelled	99.2	18	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
88	d1x5qa1	Alignment	not modelled	99.2	25	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
89	d1qava_	Alignment	not modelled	99.2	19	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
90	c2pkuA_	Alignment	not modelled	99.2	19	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**prkca-binding protein; **PDBTitle:** solution structure of pick1 pdz in complex with the2 carboxyl tail peptide of glur2
91	d1n7ea_	Alignment	not modelled	99.2	16	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
92	d1wf7a_	Alignment	not modelled	99.2	16	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
93	c2v1wB_	Alignment	not modelled	99.2	18	**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
94	d1wjla_	Alignment	not modelled	99.2	18	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
95	c2vwrA_	Alignment	not modelled	99.2	21	**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
96	d1ueqa_	Alignment	not modelled	99.2	23	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
97	c2v90E_	Alignment	not modelled	99.2	26	**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)
98	c2iwqA_	Alignment	not modelled	99.2	18	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**multiple pdz domain protein; **PDBTitle:** 7th pdz domain of multiple pdz domain protein mpdz
99	d2fe5a1	Alignment	not modelled	99.2	26	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
100	c3hpmA_	Alignment	not modelled	99.2	21	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**protein interacting with prkca 1; **PDBTitle:** oxidized dimeric pick1 pdz c46g mutant in complex with the carboxyl2 tail peptide of glur2
101	d1d5ga_	Alignment	not modelled	99.2	18	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
102	d1uhpa_	Alignment	not modelled	99.2	27	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
103	d1be9a_	Alignment	not modelled	99.2	23	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
104	d1vb7a_	Alignment	not modelled	99.2	19	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
105	d1g9oa_	Alignment	not modelled	99.2	24	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
106	c2jilA_	Alignment	not modelled	99.2	25	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**glutamate receptor interacting protein-1; **PDBTitle:** crystal structure of 2nd pdz domain of glutamate receptor2 interacting protein-1 (grip1)
						Fold:PDZ domain-like

107	d1pdra_	Alignment	not modelled	99.2	22	**Superfamily:**PDZ domain-like **Family:**PDZ domain
108	d1whaa_	Alignment	not modelled	99.2	27	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
109	c2he4A_	Alignment	not modelled	99.2	25	**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
110	d1um1a_	Alignment	not modelled	99.2	25	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
111	d1ry4a_	Alignment	not modelled	99.2	25	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
112	d2f0aa1	Alignment	not modelled	99.2	27	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
113	d1wh1a_	Alignment	not modelled	99.2	27	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
114	d2f5ya1	Alignment	not modelled	99.2	25	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
115	c2dazA_	Alignment	not modelled	99.2	19	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**inad-like protein; **PDBTitle:** solution structure of the 7th pdz domain of inad-like2 protein
116	c2qg1A_	Alignment	not modelled	99.2	22	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**multiple pdz domain protein; **PDBTitle:** crystal structure of the 11th pdz domain of mpdz (mupp1)
117	d2hgaa1	Alignment	not modelled	99.2	22	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**MTH1368 C-terminal domain-like
118	c2jxoA_	Alignment	not modelled	99.2	22	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ezrin-radixin-moesin-binding phosphoprotein 50; **PDBTitle:** structure of the second pdz domain of nherf-1
119	d2byga1	Alignment	not modelled	99.2	24	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
120	c3diwB_	Alignment	not modelled	99.1	26	**PDB header:**signaling protein/cell adhesion **Chain:** B: **PDB Molecule:**tax1-binding protein 3; **PDBTitle:** c-terminal beta-catenin bound tip-1 structure