Phyre2

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Description	P45757
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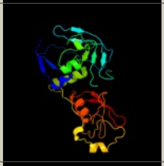
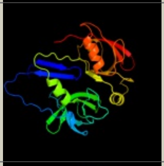
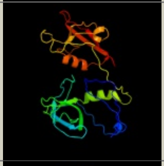
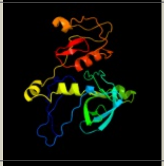
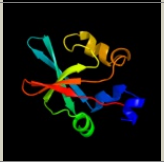
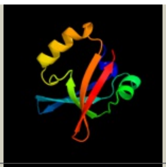
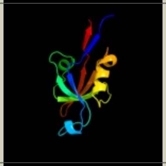
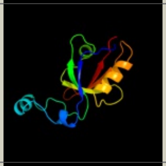
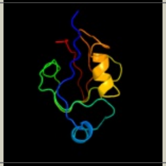
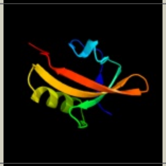
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3stjC_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**protease degq; **PDBTitle:** crystal structure of the protease + pdz1 domain of degq from2 escherichia coli
2	c4a8al_	Alignment		100.0	15	**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
3	c3pv5B_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**degq; **PDBTitle:** structure of legionella fallonii degq (n189g/p190g variant)
4	c1ky9A_	Alignment		100.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protease do; **PDBTitle:** crystal structure of degp (htra)
5	c1lcyA_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**htra2 serine protease; **PDBTitle:** crystal structure of the mitochondrial serine protease htra2
6	c3gdsA_	Alignment		100.0	11	**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	c3pv4A_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**degq; **PDBTitle:** structure of legionella fallonii degq (delta-pdz2 variant)
8	c3qo6B_	Alignment		100.0	12	**PDB header:**photosynthesis **Chain:** B: **PDB Molecule:**protease do-like 1, chloroplastic; **PDBTitle:** crystal structure analysis of the plant protease deg1
9	c2z9iB_	Alignment		100.0	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable serine protease pepd; **PDBTitle:** crystal structure of rv0983 from mycobacterium tuberculosis-2 proteolytically active form
10	c2r3yC_	Alignment		99.9	13	**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	d2i4sa1	Alignment		99.8	20	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**EpsC C-terminal domain-like

12	d2i6va1	Alignment		99.7	22	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**EpsC C-terminal domain-like
13	c2p3wB_	Alignment		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)
14	c2joaA_	Alignment		99.6	18	**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
15	d1lcya1	Alignment		99.6	17	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
16	d2z9ia1	Alignment		99.5	13	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
17	d1ky9a1	Alignment		99.5	11	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
18	c2kl1A_	Alignment		99.5	9	**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
19	c3i18A_	Alignment		99.5	10	**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
20	c2kjpA_	Alignment		99.4	8	**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
21	d1ky9a2	Alignment	not modelled	99.4	14	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
22	c2rcel_	Alignment	not modelled	99.3	13	**PDB header:**hydrolase **Chain:** I: **PDB Molecule:**protease degs; **PDBTitle:** dfp modified degs delta pdz
23	c3ossC_	Alignment	not modelled	99.3	30	**PDB header:**protein transport **Chain:** C: **PDB Molecule:**type 2 secretion system, gspc; **PDBTitle:** the crystal structure of enterotoxigenic escherichia coli gspc-gspd2 complex from the type ii secretion system
24	d1sota1	Alignment	not modelled	99.3	12	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
25	d2hgaa1	Alignment	not modelled	99.3	16	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**MTH1368 C-terminal domain-like
26	d1ky9b2	Alignment	not modelled	99.2	16	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
27	c3mmgB_	Alignment	not modelled	99.2	9	**PDB header:**viral protein, hydrolase **Chain:** B: **PDB Molecule:**nuclear inclusion protein a; **PDBTitle:** crystal structure of tobacco vein mottling virus protease
28	d1fc6a3	Alignment	not modelled	99.2	11	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**Tail specific protease PDZ domain
29	c3rleA	Alignment	not modelled	99.1	17	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**golgi reassembly-stacking protein 2;

29	c3rleA_	Alignment	not modelled	99.1	17	**PDBTitle:** crystal structure of grasp55 grasp domain (residues 7-208)
30	c2zplA_	Alignment	not modelled	99.1	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**regulator of sigma e protease; **PDBTitle:** crystal structure analysis of pdz domain a
31	d1l1ja_	Alignment	not modelled	99.1	15	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
32	c2zpmA_	Alignment	not modelled	99.1	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**regulator of sigma e protease; **PDBTitle:** crystal structure analysis of pdz domain b
33	d1q31a_	Alignment	not modelled	99.1	11	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral proteases
34	d2qf3a1	Alignment	not modelled	99.0	14	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
35	d2z9ia2	Alignment	not modelled	98.9	12	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
36	d1lvmb_	Alignment	not modelled	98.9	11	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral proteases
37	c3nwuB_	Alignment	not modelled	98.8	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**serine protease htra1; **PDBTitle:** substrate induced remodeling of the active site regulates htra12 activity
38	c3nziA_	Alignment	not modelled	98.8	13	**PDB header:**hydrolase/hydrolase substrate **Chain:** A: **PDB Molecule:**serine protease htra1; **PDBTitle:** substrate induced remodeling of the active site regulates htra12 activity
39	c2yuyA_	Alignment	not modelled	98.8	16	**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
40	c3stiC_	Alignment	not modelled	98.8	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**protease degq; **PDBTitle:** crystal structure of the protease domain of degq from escherichia coli
41	c2eaqA_	Alignment	not modelled	98.8	22	**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
42	d1qtfa_	Alignment	not modelled	98.7	10	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
43	d1wifa_	Alignment	not modelled	98.7	20	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
44	d1x5qa1	Alignment	not modelled	98.7	18	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
45	c3shuB_	Alignment	not modelled	98.6	20	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**tight junction protein zo-1; **PDBTitle:** crystal structure of zo-1 pdz3
46	d1wfga_	Alignment	not modelled	98.6	22	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
47	c2b0fA_	Alignment	not modelled	98.6	3	**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
48	c3diwB_	Alignment	not modelled	98.6	16	**PDB header:**signaling protein/cell adhesion **Chain:** B: **PDB Molecule:**tax1-binding protein 3; **PDBTitle:** c-terminal beta-catenin bound tip-1 structure
49	c3l4fD_	Alignment	not modelled	98.6	10	**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
50	c2krgA_	Alignment	not modelled	98.6	13	**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)
51	c2komA_	Alignment	not modelled	98.6	15	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**partitioning defective 3 homolog; **PDBTitle:** solution structure of humar par-3b pdz2 (residues 451-549)
52	d1ueqa_	Alignment	not modelled	98.6	16	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
53	c2q3gA_	Alignment	not modelled	98.6	10	**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
54	d1q3oa_	Alignment	not modelled	98.6	11	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
55	d1rgwa_	Alignment	not modelled	98.6	12	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like

						Family:PDZ domain
56	d1m5za_	Alignment	not modelled	98.6	17	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
57	c2eehA_	Alignment	not modelled	98.6	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
58	d2f5ya1	Alignment	not modelled	98.5	17	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
59	d1ozia_	Alignment	not modelled	98.5	18	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
60	c2kjdA_	Alignment	not modelled	98.5	12	**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)
61	d1uf1a_	Alignment	not modelled	98.5	22	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
62	d1lcya2	Alignment	not modelled	98.5	14	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
63	c3khfA_	Alignment	not modelled	98.5	13	**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)
64	c3shwA_	Alignment	not modelled	98.5	21	**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
65	d1p1da2	Alignment	not modelled	98.5	23	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
66	c2vwrA_	Alignment	not modelled	98.5	24	**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
67	c2v90E_	Alignment	not modelled	98.5	13	**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)
68	c2w5eB_	Alignment	not modelled	98.5	9	**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
69	c2qt5A_	Alignment	not modelled	98.5	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
70	d1t2ma1	Alignment	not modelled	98.5	18	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
71	d2fe5a1	Alignment	not modelled	98.5	22	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
72	c3k6zA_	Alignment	not modelled	98.5	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**possible membrane-associated serine protease; **PDBTitle:** crystal structure of rv3671c protease, inactive form
73	d1ihja_	Alignment	not modelled	98.5	13	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
74	c2egkC_	Alignment	not modelled	98.5	12	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**general receptor for phosphoinositides 1- **PDBTitle:** crystal structure of tamalin pdz-intrinsic ligand fusion2 protein
75	c1p1dA_	Alignment	not modelled	98.5	22	**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
76	c2v1wB_	Alignment	not modelled	98.5	14	**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
77	d1wf7a_	Alignment	not modelled	98.5	16	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
78	d2cssa1	Alignment	not modelled	98.5	18	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
79	d1w9ea1	Alignment	not modelled	98.4	21	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
80	c1u38A_	Alignment	not modelled	98.4	21	**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

81	c3qglD_	Alignment	not modelled	98.4	13	**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
82	d1q7xa_	Alignment	not modelled	98.4	20	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
83	c2dm8A_	Alignment	not modelled	98.4	21	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**inad-like protein; **PDBTitle:** solution structure of the eighth pdz domain of human inad-2 like protein
84	c2o2tB_	Alignment	not modelled	98.4	22	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**multiple pdz domain protein; **PDBTitle:** the crystal structure of the 1st pdz domain of mpdz
85	d1p1da1	Alignment	not modelled	98.4	16	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
86	c1u37A_	Alignment	not modelled	98.4	21	**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
87	d1wf8a1	Alignment	not modelled	98.4	20	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
88	d2byga1	Alignment	not modelled	98.4	22	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
89	c3eggC_	Alignment	not modelled	98.4	20	**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
90	c2ogpA_	Alignment	not modelled	98.4	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**partitioning-defective 3 homolog; **PDBTitle:** solution structure of the second pdz domain of par-3
91	c2iwnA_	Alignment	not modelled	98.4	18	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**multiple pdz domain protein; **PDBTitle:** 3rd pdz domain of multiple pdz domain protein mpdz (casp2 target)
92	c2he4A_	Alignment	not modelled	98.4	12	**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
93	c2gzvA_	Alignment	not modelled	98.4	11	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**prkca-binding protein; **PDBTitle:** the cystal structure of the pdz domain of human pick1 (casp target)
94	c2omjA_	Alignment	not modelled	98.4	18	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**rho guanine nucleotide exchange factor 12; **PDBTitle:** solution structure of larg pdz domain
95	c3cyyA_	Alignment	not modelled	98.4	13	**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
96	d1uhpa_	Alignment	not modelled	98.4	17	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
97	c2i04B_	Alignment	not modelled	98.4	13	**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
98	c2osgB_	Alignment	not modelled	98.4	18	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**tight junction protein zo-2; **PDBTitle:** solution structure and binding property of the domain-2 swapped dimer of zo2pdz2
99	c2jilA_	Alignment	not modelled	98.4	15	**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)
100	d1ry4a_	Alignment	not modelled	98.4	14	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
101	d1d5ga_	Alignment	not modelled	98.4	20	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
102	c2ka9A_	Alignment	not modelled	98.4	19	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**disks large homolog 4; **PDBTitle:** solution structure of psd-95 pdz12 complexed with cypin2 peptide
103	c2z17A_	Alignment	not modelled	98.4	13	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**pleckstrin homology sec7 and coiled-coil domains- **PDBTitle:** crystal sturcture of pdz domain from human pleckstrin2 homology, sec7
104	d1g9oa_	Alignment	not modelled	98.4	9	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
105	c2jreA_	Alignment	not modelled	98.4	15	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**c60-1 pdz domain peptide; **PDBTitle:** c60-1, a pdz domain designed using statistical

						coupling2 analysis
106	c2iwoA_	Alignment	not modelled	98.4	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**multiple pdz domain protein; **PDBTitle:** 12th pdz domain of multiple pdz domain protein mpdz (casp2 target)
107	c2vsvB_	Alignment	not modelled	98.3	11	**PDB header:**protein-binding **Chain:** B: **PDB Molecule:**rhophilin-2; **PDBTitle:** crystal structure of the pdz domain of human rhophilin-2
108	c3r0hA_	Alignment	not modelled	98.3	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
109	c2k1zA_	Alignment	not modelled	98.3	19	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**partitioning-defective 3 homolog; **PDBTitle:** solution structure of par-3 pdz3
110	d1qaua_	Alignment	not modelled	98.3	18	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
111	d1b8qa_	Alignment	not modelled	98.3	21	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
112	c2jxoA_	Alignment	not modelled	98.3	9	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ezrin-radixin-moesin-binding phosphoprotein 50; **PDBTitle:** structure of the second pdz domain of nherf-1
113	d1um1a_	Alignment	not modelled	98.3	18	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
114	d1uepa_	Alignment	not modelled	98.3	15	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
115	c3k1rA_	Alignment	not modelled	98.3	23	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**harmonin; **PDBTitle:** structure of harmonin npdz1 in complex with the sam-pbm of2 sans
116	c2jikB_	Alignment	not modelled	98.3	17	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**synaptojanin-2 binding protein; **PDBTitle:** crystal structure of pdz domain of synaptojanin-2 binding2 protein
117	d1whda_	Alignment	not modelled	98.3	16	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
118	d1wh1a_	Alignment	not modelled	98.3	16	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
119	c3ggeA_	Alignment	not modelled	98.3	13	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**pdz domain-containing protein gipc2; **PDBTitle:** crystal structure of the pdz domain of pdz domain-containing protein2 gipc2
120	d1x5ra1	Alignment	not modelled	98.3	17	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain