Phyre²

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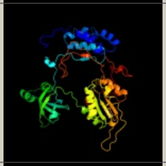
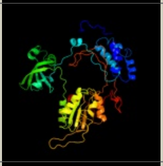
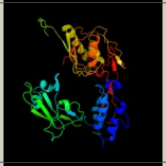
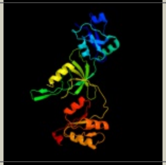
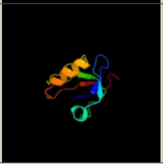
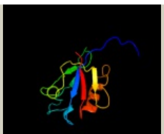
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1fc9A_	Alignment		100.0	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**photosystem ii d1 protease; **PDBTitle:** photosystem ii d1 c-terminal processing protease
2	c3k50A_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative s41 protease; **PDBTitle:** crystal structure of putative s41 protease (yp_211611.1) from2 bacteroides fragilis nctc 9343 at 2.00 a resolution
3	c1k32E_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**tricorn protease; **PDBTitle:** crystal structure of the tricorn protease
4	c1n6dE_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**tricorn protease; **PDBTitle:** tricorn protease in complex with tetrapeptide chloromethyl2 ketone derivative
5	d1fc6a4	Alignment		100.0	28	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Tail specific protease, catalytic domain
6	c3djaA_	Alignment		100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein ct_858; **PDBTitle:** crystal structure of cpaf solved with mad
7	d1j7xa_	Alignment		100.0	24	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Tail specific protease, catalytic domain
8	d1k32a4	Alignment		100.0	18	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Tail specific protease, catalytic domain
9	c3shwA_	Alignment		99.7	12	**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
10	d1fc6a3	Alignment		99.6	35	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**Tail specific protease PDZ domain
11	d1wifa_	Alignment		99.3	24	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain

12	c2edzA_	Alignment		99.1	25	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**pdz domain-containing protein 1; **PDBTitle:** solution structures of the pdz domain of mus musculus pdz2 domain-containing protein 1
13	c2krgA_	Alignment		99.1	31	**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)
14	d1w9ea1	Alignment		99.1	21	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
15	c3k1rA_	Alignment		99.1	25	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**harmonin; **PDBTitle:** structure of harmonin npdz1 in complex with the sam-pbm of2 sans
16	d2z9ia1	Alignment		99.1	27	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
17	c2qktB_	Alignment		99.1	20	**PDB header:**peptide binding protein **Chain:** B: **PDB Molecule:**inactivation-no-after-potential d protein; **PDBTitle:** crystal structure of the 5th pdz domain of inad
18	d1qaua_	Alignment		99.0	22	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
19	c2komA_	Alignment		99.0	19	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**partitioning defective 3 homolog; **PDBTitle:** solution structure of humar par-3b pdz2 (residues 451-549)
20	d1ueqa_	Alignment		99.0	33	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
21	c3eggC_	Alignment	not modelled	99.0	26	**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
22	c2kjdA_	Alignment	not modelled	99.0	31	**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)
23	c3diwB_	Alignment	not modelled	99.0	25	**PDB header:**signaling protein/cell adhesion **Chain:** B: **PDB Molecule:**tax1-binding protein 3; **PDBTitle:** c-terminal beta-catenin bound tip-1 structure
24	c2e7kA_	Alignment	not modelled	99.0	28	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**maguk p55 subfamily member 2; **PDBTitle:** solution structure of the pdz domain from human maguk p552 subfamily member 2
25	c2vsvB_	Alignment	not modelled	99.0	21	**PDB header:**protein-binding **Chain:** B: **PDB Molecule:**rhophilin-2; **PDBTitle:** crystal structure of the pdz domain of human rhophilin-2
26	c2eaqA_	Alignment	not modelled	99.0	17	**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
27	d1wg6a_	Alignment	not modelled	98.9	23	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
28	d1d5ga_	Alignment	not modelled	98.9	19	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain

29	d1t2ma1	Alignment	not modelled	98.9	24	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
30	d2fe5a1	Alignment	not modelled	98.9	26	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
31	c3l4fD_	Alignment	not modelled	98.9	21	**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
32	c3ggeA_	Alignment	not modelled	98.9	25	**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
33	c2v90E_	Alignment	not modelled	98.9	29	**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)
34	d1va8a1	Alignment	not modelled	98.9	23	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
35	c1w9qB_	Alignment	not modelled	98.9	22	**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	c2jikB_	Alignment	not modelled	98.9	26	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**synaptojanin-2 binding protein; **PDBTitle:** crystal structure of pdz domain of synaptojanin-2 binding2 protein
37	c2he4A_	Alignment	not modelled	98.9	32	**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
38	c2jilA_	Alignment	not modelled	98.9	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)
39	d2byga1	Alignment	not modelled	98.9	24	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
40	c2xkxB_	Alignment	not modelled	98.9	29	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**disks large homolog 4; **PDBTitle:** single particle analysis of psd-95 in negative stain
41	c2d92A_	Alignment	not modelled	98.9	25	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**inad-like protein; **PDBTitle:** solution structure of the fifth pdz domain of inad-like2 protein
42	c2omjA_	Alignment	not modelled	98.9	30	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**rho guanine nucleotide exchange factor 12; **PDBTitle:** solution structure of larg pdz domain
43	d1x5qa1	Alignment	not modelled	98.9	29	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
44	d1ry4a_	Alignment	not modelled	98.9	23	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
45	d1nf3c_	Alignment	not modelled	98.9	21	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
46	c2vwrA_	Alignment	not modelled	98.9	26	**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
47	d1wf8a1	Alignment	not modelled	98.9	23	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
48	d1g9oa_	Alignment	not modelled	98.9	26	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
49	c2ogpA_	Alignment	not modelled	98.9	22	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**partitioning-defective 3 homolog; **PDBTitle:** solution structure of the second pdz domain of par-3
50	d1ozia_	Alignment	not modelled	98.9	19	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
51	d2fcfa1	Alignment	not modelled	98.9	22	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
52	c2iwnA_	Alignment	not modelled	98.9	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)
53	c2i04B_	Alignment	not modelled	98.9	34	**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
54	c3khfA_	Alignment	not modelled	98.9	29	**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)
55	d1um1a_	Alignment	not modelled	98.9	28	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
56	c2dm8A_	Alignment	not modelled	98.9	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
57	c2ejyA_	Alignment	not modelled	98.9	22	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**55 kda erythrocyte membrane protein; **PDBTitle:** solution structure of the p55 pdz t85c domain complexed2 with the glycophorin c f127c peptide
58	c3qikA_	Alignment	not modelled	98.9	22	**PDB header:**hydrolase regulator **Chain:** A: **PDB Molecule:**phosphatidylinositol 3,4,5-trisphosphate-dependent rac **PDBTitle:** crystal structure of the first pdz domain of prex1
59	c2dluA_	Alignment	not modelled	98.9	26	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**inad-like protein; **PDBTitle:** solution structure of the second pdz domain of human inad-2 like protein
60	c2dmzA_	Alignment	not modelled	98.9	21	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**inad-like protein; **PDBTitle:** solution structure of the third pdz domain of human inad-2 like protein
61	c2k1zA_	Alignment	not modelled	98.9	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**partitioning-defective 3 homolog; **PDBTitle:** solution structure of par-3 pdz3
62	c2iwoA_	Alignment	not modelled	98.9	24	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**multiple pdz domain protein; **PDBTitle:** 12th pdz domain of multiple pdz domain protein mpdz (casp2 target)
63	d1whaa_	Alignment	not modelled	98.9	22	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
64	c1z87A_	Alignment	not modelled	98.8	27	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**alpha-1-syntrophin; **PDBTitle:** solution structure of the split ph-pdz supramodule of alpha-2 syntrophin
65	c3shuB_	Alignment	not modelled	98.8	26	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**tight junction protein zo-1; **PDBTitle:** crystal structure of zo-1 pdz3
66	d1uhpa_	Alignment	not modelled	98.8	19	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
67	d1n7ea_	Alignment	not modelled	98.8	25	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
68	c2jreA_	Alignment	not modelled	98.8	29	**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
69	c2jxoA_	Alignment	not modelled	98.8	29	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ezrin-radixin-moesin-binding phosphoprotein 50; **PDBTitle:** structure of the second pdz domain of nherf-1
70	d1qlca_	Alignment	not modelled	98.8	28	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
71	d2f5ya1	Alignment	not modelled	98.8	19	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
72	c2yt7A_	Alignment	not modelled	98.8	28	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**amyloid beta a4 precursor protein-binding family **PDBTitle:** solution structure of the pdz domain of amyloid beta a42 precursor protein-binding family a member 3
73	c2djtA_	Alignment	not modelled	98.8	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**unnamed protein product; **PDBTitle:** solution structures of the pdz domain of human unnamed2 protein product
74	c2dazA_	Alignment	not modelled	98.8	25	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**inad-like protein; **PDBTitle:** solution structure of the 7th pdz domain of inad-like2 protein
75	d1be9a_	Alignment	not modelled	98.8	26	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
76	d1ihja_	Alignment	not modelled	98.8	31	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
77	d1kwaa_	Alignment	not modelled	98.8	18	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
78	c2egkC_	Alignment	not modelled	98.8	27	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**general receptor for phosphoinositides 1- **PDBTitle:** crystal structure of tamalin pdz-intrinsic ligand fusion2 protein
79	c1u38A_	Alignment	not modelled	98.8	32	**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
						Fold:PDZ domain-like

80	d1pdra_	Alignment	not modelled	98.8	29	**Superfamily:**PDZ domain-like **Family:**PDZ domain
81	d2f0aa1	Alignment	not modelled	98.8	23	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
82	d1p1da2	Alignment	not modelled	98.8	20	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
83	d1whda_	Alignment	not modelled	98.8	18	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
84	d1rzxa_	Alignment	not modelled	98.8	23	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
85	c1u37A_	Alignment	not modelled	98.8	32	**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
86	c2gzvA_	Alignment	not modelled	98.8	24	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**prkca-binding protein; **PDBTitle:** the cystal structure of the pdz domain of human pick1 (casp target)
87	d1uf1a_	Alignment	not modelled	98.8	23	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
88	c2opgB_	Alignment	not modelled	98.8	21	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**multiple pdz domain protein; **PDBTitle:** the crystal structure of the 10th pdz domain of mpdz
89	d1tp5a1	Alignment	not modelled	98.8	28	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
90	d1m5za_	Alignment	not modelled	98.8	20	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
91	d1wi4a1	Alignment	not modelled	98.8	19	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
92	c2dkrA_	Alignment	not modelled	98.8	23	**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
93	d1v6ba_	Alignment	not modelled	98.8	19	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
94	c3hpmA_	Alignment	not modelled	98.8	20	**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
95	c2q3gA_	Alignment	not modelled	98.8	22	**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
96	d1v62a_	Alignment	not modelled	98.8	23	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
97	c2eehA_	Alignment	not modelled	98.8	17	**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
98	d1rgra_	Alignment	not modelled	98.8	32	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
99	c2v1wB_	Alignment	not modelled	98.8	22	**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
100	d1qava_	Alignment	not modelled	98.8	28	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
101	d1i16a_	Alignment	not modelled	98.8	24	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**Interleukin 16
102	d2cssa1	Alignment	not modelled	98.8	17	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
103	c2fneB_	Alignment	not modelled	98.8	26	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**multiple pdz domain protein; **PDBTitle:** the crystal structure of the 13th pdz domain of mpdz
104	d1ujda_	Alignment	not modelled	98.8	13	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
105	c3o46A_	Alignment	not modelled	98.8	20	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**maguk p55 subfamily member 7; **PDBTitle:** crystal structure of the pdz domain of mpp7
106	d1q3oa_	Alignment	not modelled	98.8	20	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain

107	d1q7xa_	Alignment	not modelled	98.8	20	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
108	d1vaea_	Alignment	not modelled	98.8	22	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
109	c3qglD_	Alignment	not modelled	98.7	26	**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
110	d1wfga_	Alignment	not modelled	98.7	19	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
111	c3b76A_	Alignment	not modelled	98.7	25	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase lnx; **PDBTitle:** crystal structure of the third pdz domain of human ligand-of-numb2 protein-x (lnx1) in complex with the c-terminal peptide from the3 coxsackievirus and adenovirus receptor
112	d1zoka1	Alignment	not modelled	98.7	31	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
113	c2ehrA_	Alignment	not modelled	98.7	26	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**inad-like protein; **PDBTitle:** solution structure of the sixth pdz domain of human inad-2 like protein
114	c2qg1A_	Alignment	not modelled	98.7	28	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**multiple pdz domain protein; **PDBTitle:** crystal structure of the 11th pdz domain of mpdz (mupp1)
115	c2p3wB_	Alignment	not modelled	98.7	22	**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)
116	d1rgwa_	Alignment	not modelled	98.7	20	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
117	c2ka9A_	Alignment	not modelled	98.7	25	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**disks large homolog 4; **PDBTitle:** solution structure of psd-95 pdz12 complexed with cypin2 peptide
118	d1lcya1	Alignment	not modelled	98.7	28	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
119	d1p1da1	Alignment	not modelled	98.7	24	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
120	d1u3ba2	Alignment	not modelled	98.7	23	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain