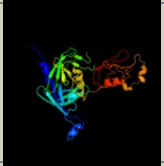
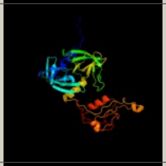
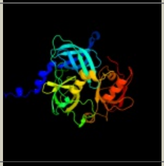
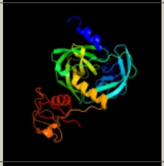
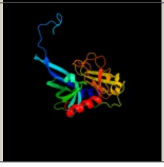
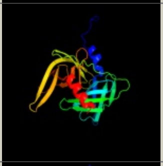
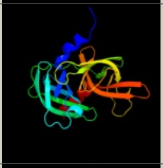
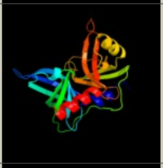
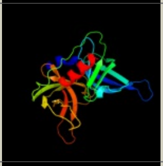
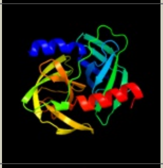
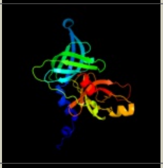
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P0C0V0
Date	Thu Jan 5 11:30:02 GMT 2012
Unique Job ID	39500de3398df43d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4a8aI_	Alignment		100.0	62	**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	46	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**degq; **PDBTitle:** structure of legionella fallonii degq (n189g/p190g variant)
3	c3stjC_	Alignment		100.0	70	**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	94	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protease do; **PDBTitle:** crystal structure of degp (htra)
5	c3pv4A_	Alignment		100.0	52	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**degq; **PDBTitle:** structure of legionella fallonii degq (delta-pdz2 variant)
6	c3gdsA_	Alignment		100.0	41	**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	36	**PDB header:**photosynthesis **Chain:** B: **PDB Molecule:**protease do-like 1, chloroplastic; **PDBTitle:** crystal structure analysis of the plant protease deg1
8	c1lcyA_	Alignment		100.0	34	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**htra2 serine protease; **PDBTitle:** crystal structure of the mitochondrial serine protease htra2
9	c2z9iB_	Alignment		100.0	45	**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		100.0	44	**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	98	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases

12	d1l1ja_	Alignment		100.0	44	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
13	c2rceI_	Alignment		100.0	44	**PDB header:**hydrolase **Chain:** I: **PDB Molecule:**protease degs; **PDBTitle:** dfp modified degs delta pdz
14	c3stiC_	Alignment		100.0	75	**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	51	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
16	c3nziA_	Alignment		100.0	46	**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	42	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
19	c3nwuB_	Alignment		100.0	48	**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	100.0	20	**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	15	**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	21	**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	21	**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	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
						PDB header:protein binding

29	c1p1dA_	Alignment	not modelled	99.9	17	**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
30	d1agja_	Alignment	not modelled	99.9	26	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
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	99.9	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	99.9	20	**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	99.9	20	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**disks large homolog 4; **PDBTitle:** single particle analysis of psd-95 in negative stain
35	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
36	c1w9qB_	Alignment	not modelled	99.8	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
37	c2w7uC_	Alignment	not modelled	99.8	21	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**serine protease spla; **PDBTitle:** spla serine protease of staphylococcus aureus (2.4a)
38	c2as9B_	Alignment	not modelled	99.8	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**serine protease; **PDBTitle:** functional and structural characterization of spl proteases2 from staphylococcus aureus
39	c2b0fA_	Alignment	not modelled	99.8	21	**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	d1cqqa_	Alignment	not modelled	99.8	15	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral cysteine protease of trypsin fold
41	d2qaaa1	Alignment	not modelled	99.8	17	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
42	d1l1na_	Alignment	not modelled	99.8	16	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral cysteine protease of trypsin fold
43	d2h5ca1	Alignment	not modelled	99.7	17	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
44	c2ouaA_	Alignment	not modelled	99.7	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**serine protease; **PDBTitle:** crystal structure of nocardiopsis protease (napase)
45	c2p3wB_	Alignment	not modelled	99.7	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)
46	d1ky9a1	Alignment	not modelled	99.7	97	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
47	c2joaA_	Alignment	not modelled	99.7	25	**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
48	d1lcya1	Alignment	not modelled	99.7	22	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
49	c2o8lA_	Alignment	not modelled	99.7	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**v8 protease; **PDBTitle:** structure of v8 protease from staphylococcus aureus
50	d2o8la1	Alignment	not modelled	99.7	21	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
51	c1qy6A_	Alignment	not modelled	99.7	21	**PDB header:**protease **Chain:** A: **PDB Molecule:**serine protease; **PDBTitle:** structue of v8 protease from staphylococcus aureus
52	d2sfaa_	Alignment	not modelled	99.7	17	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
53	d2sgaa_	Alignment	not modelled	99.6	17	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
54	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)
55	c1wczA	Alignment	not modelled	99.6	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glutamyl endopeptidase;

55	c1wczA_	Alignment	not modelled	99.6	22	**PDBTitle:** crystal structure of an alkaline form of v8 protease from2 staphylococcus aureus
56	d2z9ia1	Alignment	not modelled	99.6	32	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
57	c2ea3A_	Alignment	not modelled	99.5	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chymotrypsin; **PDBTitle:** crystal structure of cellulomonas bogoriensis chymotrypsin
58	d1hpga_	Alignment	not modelled	99.5	17	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
59	c1z87A_	Alignment	not modelled	99.5	14	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**alpha-1-syntrophin; **PDBTitle:** solution structure of the split ph-pdz supramodule of alpha-2 syntrophin
60	d1p3ca_	Alignment	not modelled	99.5	15	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
61	d1ky9b2	Alignment	not modelled	99.5	99	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
62	c2kl1A_	Alignment	not modelled	99.4	28	**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
63	d1arba_	Alignment	not modelled	99.4	12	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Prokaryotic proteases
64	d1ozia_	Alignment	not modelled	99.4	17	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
65	c2krgA_	Alignment	not modelled	99.4	18	**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)
66	c3i18A_	Alignment	not modelled	99.4	22	**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
67	c3eggC_	Alignment	not modelled	99.4	18	**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
68	d2i4sa1	Alignment	not modelled	99.4	18	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**EpsC C-terminal domain-like
69	d1p1da2	Alignment	not modelled	99.4	19	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
70	d1sota1	Alignment	not modelled	99.3	34	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
71	c2kjpA_	Alignment	not modelled	99.3	32	**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
72	d1fc6a3	Alignment	not modelled	99.3	22	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**Tail specific protease PDZ domain
73	c2kjdA_	Alignment	not modelled	99.3	18	**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)
74	c2jikB_	Alignment	not modelled	99.3	21	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**synaptojanin-2 binding protein; **PDBTitle:** crystal structure of pdz domain of synaptojanin-2 binding2 protein
75	c3diwB_	Alignment	not modelled	99.3	24	**PDB header:**signaling protein/cell adhesion **Chain:** B: **PDB Molecule:**tax1-binding protein 3; **PDBTitle:** c-terminal beta-catenin bound tip-1 structure
76	c2jilA_	Alignment	not modelled	99.3	21	**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)
77	c3l4fD_	Alignment	not modelled	99.3	19	**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
78	d1x5qa1	Alignment	not modelled	99.3	27	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
79	c2v90E_	Alignment	not modelled	99.3	18	**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)
						Fold:PDZ domain-like

80	d1um1a_	Alignment	not modelled	99.3	20	**Superfamily:**PDZ domain-like **Family:**PDZ domain
81	d2fe5a1	Alignment	not modelled	99.3	16	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
82	d1uhpa_	Alignment	not modelled	99.3	25	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
83	d1rgwa_	Alignment	not modelled	99.3	18	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
84	d1d5ga_	Alignment	not modelled	99.3	17	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
85	d1wfga_	Alignment	not modelled	99.3	15	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
86	d1wh1a_	Alignment	not modelled	99.3	26	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
87	c2iwnA_	Alignment	not modelled	99.3	19	**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	d1t2ma1	Alignment	not modelled	99.3	19	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
89	d2byga1	Alignment	not modelled	99.3	18	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
90	d1q7xa_	Alignment	not modelled	99.3	16	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
91	d1m5za_	Alignment	not modelled	99.3	22	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
92	c2db5A_	Alignment	not modelled	99.3	20	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**inad-like protein; **PDBTitle:** solution structure of the first pdz domain of inad-like2 protein
93	c3qglD_	Alignment	not modelled	99.3	23	**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
94	d2f0aa1	Alignment	not modelled	99.3	24	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
95	c2o2tB_	Alignment	not modelled	99.3	28	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**multiple pdz domain protein; **PDBTitle:** the crystal structure of the 1st pdz domain of mpdz
96	d1ujda_	Alignment	not modelled	99.3	15	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
97	d1ry4a_	Alignment	not modelled	99.3	20	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
98	c2vwrA_	Alignment	not modelled	99.3	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
99	d1ihja_	Alignment	not modelled	99.3	21	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
100	c2djtA_	Alignment	not modelled	99.2	19	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**unnamed protein product; **PDBTitle:** solution structures of the pdz domain of human unnamed2 protein product
101	d1wf8a1	Alignment	not modelled	99.2	17	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
102	c2ogpA_	Alignment	not modelled	99.2	26	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**partitioning-defective 3 homolog; **PDBTitle:** solution structure of the second pdz domain of par-3
103	c2q3gA_	Alignment	not modelled	99.2	17	**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
104	d2hgaa1	Alignment	not modelled	99.2	26	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**MTH1368 C-terminal domain-like
105	d1whaa_	Alignment	not modelled	99.2	22	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
106	c2komA_	Alignment	not modelled	99.2	24	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**partitioning defective 3 homolog; **PDBTitle:** solution structure of humar par-3b pdz2 (residues 451-549)
						Fold:PDZ domain-like

107	d1q3oa_	Alignment	not modelled	99.2	21	**Superfamily:**PDZ domain-like **Family:**PDZ domain
108	c2gzvA_	Alignment	not modelled	99.2	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)
109	c3k1rA_	Alignment	not modelled	99.2	16	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**harmonin; **PDBTitle:** structure of harmonin npdz1 in complex with the sam-pbm of2 sans
110	d1rzxa_	Alignment	not modelled	99.2	18	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
111	d2f5ya1	Alignment	not modelled	99.2	28	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
112	c2k1zA_	Alignment	not modelled	99.2	22	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**partitioning-defective 3 homolog; **PDBTitle:** solution structure of par-3 pdz3
113	c2fneB_	Alignment	not modelled	99.2	22	**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
114	c2v1wB_	Alignment	not modelled	99.2	16	**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
115	c2iwoA_	Alignment	not modelled	99.2	18	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**multiple pdz domain protein; **PDBTitle:** 12th pdz domain of multiple pdz domain protein mpdz (casp2 target)
116	c2dm8A_	Alignment	not modelled	99.2	20	**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
117	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
118	c2jreA_	Alignment	not modelled	99.2	23	**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
119	d1nf3c_	Alignment	not modelled	99.2	17	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
120	c2iwqA_	Alignment	not modelled	99.2	15	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**multiple pdz domain protein; **PDBTitle:** 7th pdz domain of multiple pdz domain protein mpdz