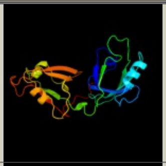
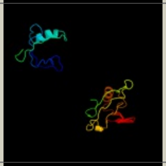
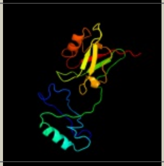
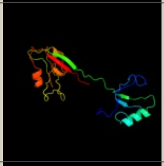
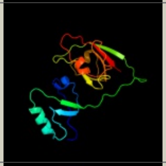
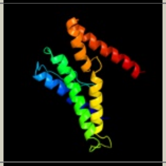
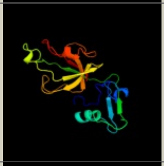
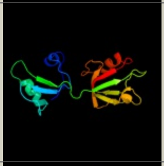
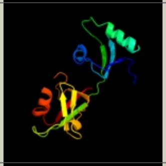
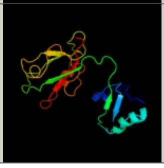
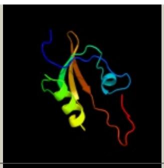
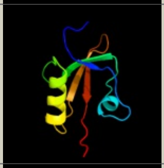
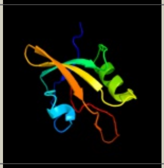
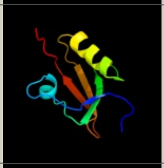
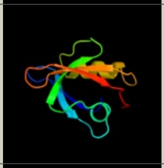
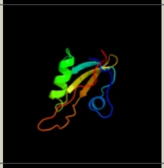
Email	l.a.kelley@imperial.ac.uk
Description	P0AEH1
Date	Thu Jan 5 11:23:20 GMT 2012
Unique Job ID	c74bb06c30929ed5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3rleA_	Alignment		99.9	19	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**golgi reassembly-stacking protein 2; **PDBTitle:** crystal structure of grasp55 grasp domain (residues 7-208)
2	c3pv5B_	Alignment		99.9	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**degq; **PDBTitle:** structure of legionella fallonii degq (n189g/p190g variant)
3	c4a8aI_	Alignment		99.8	18	**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
4	c1p1dA_	Alignment		99.8	17	**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
5	c2ka9A_	Alignment		99.7	14	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**disks large homolog 4; **PDBTitle:** solution structure of psd-95 pdz12 complexed with cypin2 peptide
6	c2qt5A_	Alignment		99.7	22	**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
7	c3b4rB_	Alignment		99.7	43	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative zinc metalloprotease mj0392; **PDBTitle:** site-2 protease from methanocaldococcus jannaschii
8	c3r0hA_	Alignment		99.7	14	**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
9	c1w9qB_	Alignment		99.6	14	**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
10	c1u3bA_	Alignment		99.6	13	**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
11	c2xkxB_	Alignment		99.5	14	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**disks large homolog 4; **PDBTitle:** single particle analysis of psd-95 in negative stain

12	c2p3wB_	Alignment		99.4	31	**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)
13	d1lcya1	Alignment		99.3	29	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
14	c3i18A_	Alignment		99.3	14	**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
15	c1lcyA_	Alignment		99.3	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**htra2 serine protease; **PDBTitle:** crystal structure of the mitochondrial serine protease htra2
16	d2z9ia1	Alignment		99.3	26	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
17	c2kl1A_	Alignment		99.3	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
18	c2zpmA_	Alignment		99.3	89	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**regulator of sigma e protease; **PDBTitle:** crystal structure analysis of pdz domain b
19	c3stjC_	Alignment		99.3	28	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**protease degq; **PDBTitle:** crystal structure of the protease + pdz1 domain of degq from2 escherichia coli
20	c2joaA_	Alignment		99.2	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
21	c3pv4A_	Alignment	not modelled	99.2	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**degq; **PDBTitle:** structure of legionella fallonii degq (delta-pdz2 variant)
22	c2kjpA_	Alignment	not modelled	99.2	21	**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
23	c2zplA_	Alignment	not modelled	99.2	99	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**regulator of sigma e protease; **PDBTitle:** crystal structure analysis of pdz domain a
24	d1fc6a3	Alignment	not modelled	99.1	24	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**Tail specific protease PDZ domain
25	d2hgaa1	Alignment	not modelled	99.1	22	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**MTH1368 C-terminal domain-like
26	d2i4sa1	Alignment	not modelled	99.1	23	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**EpsC C-terminal domain-like
27	c3qo6B_	Alignment	not modelled	99.1	25	**PDB header:**photosynthesis **Chain:** B: **PDB Molecule:**protease do-like 1, chloroplastic; **PDBTitle:** crystal structure analysis of the plant protease deg1
28	d1ky9b2	Alignment	not modelled	99.0	27	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
						Fold:PDZ domain-like

29	d2i6va1	Alignment	not modelled	99.0	20	**Superfamily:**PDZ domain-like **Family:**EpsC C-terminal domain-like
30	c3gdsA_	Alignment	not modelled	99.0	23	**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
31	d1ky9a1	Alignment	not modelled	98.9	31	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
32	c1z87A_	Alignment	not modelled	98.9	22	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**alpha-1-syntrophin; **PDBTitle:** solution structure of the split ph-pdz supramodule of alpha-2 syntrophin
33	c2eaqA_	Alignment	not modelled	98.9	15	**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
34	d1w9ea1	Alignment	not modelled	98.9	23	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
35	c1ky9A_	Alignment	not modelled	98.9	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protease do; **PDBTitle:** crystal structure of degp (htra)
36	d1qaua_	Alignment	not modelled	98.9	18	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
37	d1x5qa1	Alignment	not modelled	98.8	20	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
38	c2krgA_	Alignment	not modelled	98.8	25	**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)
39	c2kjdA_	Alignment	not modelled	98.8	25	**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)
40	c3diwB_	Alignment	not modelled	98.8	24	**PDB header:**signaling protein/cell adhesion **Chain:** B: **PDB Molecule:**tax1-binding protein 3; **PDBTitle:** c-terminal beta-catenin bound tip-1 structure
41	d1sota1	Alignment	not modelled	98.8	26	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
42	d1ozia_	Alignment	not modelled	98.8	21	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
43	d1wh1a_	Alignment	not modelled	98.8	24	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
44	d1m5za_	Alignment	not modelled	98.8	20	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
45	d1wifa_	Alignment	not modelled	98.8	19	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
46	c2vsvB_	Alignment	not modelled	98.8	18	**PDB header:**protein-binding **Chain:** B: **PDB Molecule:**rhophilin-2; **PDBTitle:** crystal structure of the pdz domain of human rhophilin-2
47	c3eggC_	Alignment	not modelled	98.8	30	**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
48	c2vwrA_	Alignment	not modelled	98.8	17	**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
49	c2he4A_	Alignment	not modelled	98.8	20	**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
50	d1wfga_	Alignment	not modelled	98.7	19	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
51	d1p1da2	Alignment	not modelled	98.7	20	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
52	d1q3oa_	Alignment	not modelled	98.7	31	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
53	c3l4fD_	Alignment	not modelled	98.7	25	**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
54	c3shuB_	Alignment	not modelled	98.7	27	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**tight junction protein zo-1; **PDBTitle:** crystal structure of zo-1 pdz3

55	d1pdra_	Alignment	not modelled	98.7	14	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
56	c2eehA_	Alignment	not modelled	98.7	30	**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
57	c2komA_	Alignment	not modelled	98.7	26	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**partitioning defective 3 homolog; **PDBTitle:** solution structure of humar par-3b pdz2 (residues 451-549)
58	d1ueqa_	Alignment	not modelled	98.7	19	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
59	d1rgwa_	Alignment	not modelled	98.7	20	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
60	d1uf1a_	Alignment	not modelled	98.7	26	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
61	c2egkC_	Alignment	not modelled	98.7	23	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**general receptor for phosphoinositides 1- **PDBTitle:** crystal structure of tamalin pdz-intrinsic ligand fusion2 protein
62	c2q3gA_	Alignment	not modelled	98.7	21	**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
63	d1q7xa_	Alignment	not modelled	98.7	22	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
64	d1g9oa_	Alignment	not modelled	98.7	22	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
65	c2iwnA_	Alignment	not modelled	98.7	27	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**multiple pdz domain protein; **PDBTitle:** 3rd pdz domain of multiple pdz domain protein mpdz (casp2 target)
66	d2f5ya1	Alignment	not modelled	98.7	19	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
67	d1d5ga_	Alignment	not modelled	98.7	29	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
68	d2f0aa1	Alignment	not modelled	98.7	18	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
69	d1uhpa_	Alignment	not modelled	98.7	22	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
70	d1tp5a1	Alignment	not modelled	98.7	14	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
71	d1be9a_	Alignment	not modelled	98.7	14	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
72	c2gzvA_	Alignment	not modelled	98.7	23	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**prkca-binding protein; **PDBTitle:** the cystal structure of the pdz domain of human pick1 (casp target)
73	c2jxoA_	Alignment	not modelled	98.7	25	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ezrin-radixin-moesin-binding phosphoprotein 50; **PDBTitle:** structure of the second pdz domain of nherf-1
74	c3khfA_	Alignment	not modelled	98.6	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)
75	c2jilA_	Alignment	not modelled	98.6	27	**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)
76	d1t2ma1	Alignment	not modelled	98.6	28	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
77	c2v90E_	Alignment	not modelled	98.6	21	**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)
78	c3k1rA_	Alignment	not modelled	98.6	20	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**harmonin; **PDBTitle:** structure of harmonin npdz1 in complex with the sam-pbm of2 sans
79	d2fe5a1	Alignment	not modelled	98.6	23	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
80	c2qktB_	Alignment	not modelled	98.6	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
81	c3qikA	Alignment	not modelled	98.6	19	**PDB header:**hydrolase regulator **Chain:** A: **PDB Molecule:**phosphatidylinositol 3,4,5-trisphosphate-

81	c3qikA_	Alignment	not modelled	98.6	19	dependent rac **PDBTitle:** crystal structure of the first pdz domain of prex1
82	c2e7kA_	Alignment	not modelled	98.6	24	**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
83	c2ogpA_	Alignment	not modelled	98.6	25	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**partitioning-defective 3 homolog; **PDBTitle:** solution structure of the second pdz domain of par-3
84	c2k1zA_	Alignment	not modelled	98.6	23	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**partitioning-defective 3 homolog; **PDBTitle:** solution structure of par-3 pdz3
85	c2jikB_	Alignment	not modelled	98.6	26	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**synaptojanin-2 binding protein; **PDBTitle:** crystal structure of pdz domain of synaptojanin-2 binding2 protein
86	d1va8a1	Alignment	not modelled	98.6	20	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
87	c2jreA_	Alignment	not modelled	98.6	30	**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
88	d1ihja_	Alignment	not modelled	98.6	18	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
89	c2d92A_	Alignment	not modelled	98.6	21	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**inad-like protein; **PDBTitle:** solution structure of the fifth pdz domain of inad-like2 protein
90	c2fneB_	Alignment	not modelled	98.6	21	**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
91	c2dkrA_	Alignment	not modelled	98.6	19	**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
92	c2edzA_	Alignment	not modelled	98.6	26	**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
93	d1ry4a_	Alignment	not modelled	98.6	17	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
94	c2o2tB_	Alignment	not modelled	98.6	16	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**multiple pdz domain protein; **PDBTitle:** the crystal structure of the 1st pdz domain of mpdz
95	d1wjla_	Alignment	not modelled	98.6	22	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
96	c2omjA_	Alignment	not modelled	98.6	29	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**rho guanine nucleotide exchange factor 12; **PDBTitle:** solution structure of larg pdz domain
97	c2qg1A_	Alignment	not modelled	98.6	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**multiple pdz domain protein; **PDBTitle:** crystal structure of the 11th pdz domain of mpdz (mupp1)
98	c2d90A_	Alignment	not modelled	98.6	19	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**pdz domain containing protein 1; **PDBTitle:** solution structure of the third pdz domain of pdz domain2 containing protein 1
99	c3qglD_	Alignment	not modelled	98.6	32	**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
100	d1whaa_	Alignment	not modelled	98.6	24	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
101	c2dmzA_	Alignment	not modelled	98.6	33	**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
102	c2dluA_	Alignment	not modelled	98.6	24	**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
103	d2byga1	Alignment	not modelled	98.6	21	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
104	d1kwaa_	Alignment	not modelled	98.6	14	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
105	d2cssa1	Alignment	not modelled	98.6	18	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
106	c3hpmA_	Alignment	not modelled	98.6	23	**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
107	d1p1da1	Alignment	not modelled	98.6	32	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain

108	d1wf8a1	Alignment	not modelled	98.6	32	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
109	d1whda_	Alignment	not modelled	98.6	17	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
110	c2i04B_	Alignment	not modelled	98.6	21	**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
111	c2z17A_	Alignment	not modelled	98.6	24	**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
112	c2v1wB_	Alignment	not modelled	98.6	21	**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
113	d1n7ea_	Alignment	not modelled	98.6	20	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
114	d1um1a_	Alignment	not modelled	98.6	26	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
115	c2dm8A_	Alignment	not modelled	98.6	24	**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
116	d1ujda_	Alignment	not modelled	98.6	22	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
117	d1wf7a_	Alignment	not modelled	98.6	16	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
118	c3shwA_	Alignment	not modelled	98.6	28	**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
119	d1vaea_	Alignment	not modelled	98.6	21	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
120	c3b76A_	Alignment	not modelled	98.6	28	**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