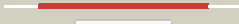























Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2869c_(-)_3180558_3181772
Date	Wed Aug 7 12:50:54 BST 2019
Unique Job ID	9b1ee069eb862764

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3b4rA_	 Alignment		99.8	37	PDB header: hydrolase Chain: A: PDB Molecule: putative zinc metalloprotease mj0392; PDBTitle: site-2 protease from methanocaldococcus jannaschii
2	c3b4rB_	 Alignment		99.8	37	PDB header: hydrolase Chain: B: PDB Molecule: putative zinc metalloprotease mj0392; PDBTitle: site-2 protease from methanocaldococcus jannaschii
3	c5xdyA_	 Alignment		99.4	32	PDB header: hydrolase Chain: A: PDB Molecule: heat shock protein htra; PDBTitle: crystal structure of htra1 from mycobacterium tuberculosis
4	d1lcyA1	 Alignment		99.4	26	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: HtrA-like serine proteases
5	c2p3wB_	 Alignment		99.3	21	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)
6	c1lcyA_	 Alignment		99.3	23	PDB header: hydrolase Chain: A: PDB Molecule: htra2 serine protease; PDBTitle: crystal structure of the mitochondrial serine protease htra2
7	c2zpmA_	 Alignment		99.3	28	PDB header: hydrolase Chain: A: PDB Molecule: regulator of sigma e protease; PDBTitle: crystal structure analysis of pdz domain b
8	c2joaA_	 Alignment		99.3	20	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
9	c3i18A_	 Alignment		99.3	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lmo2051 protein; PDBTitle: crystal structure of the pdz domain of the sdrc-like protein (lmo2051)2 from listeria monocytogenes, northeast structural genomics consortium3 target lmr166b
10	d2z9ia1	 Alignment		99.3	32	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: HtrA-like serine proteases
11	c3wkIA_	 Alignment		99.3	19	PDB header: hydrolase Chain: A: PDB Molecule: putative zinc metalloprotease aq_1964; PDBTitle: the periplasmic pdz tandem fragment of the rsep homologue from aquifex2 aeolicus

12	c2k1A_	Alignment		99.3	16	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
13	c5b6A_	Alignment		99.3	26	PDB header: hydrolase Chain: A; PDB Molecule: putative serine protease hhoa; PDBTitle: structure of deg protease hhoa from synechocystis sp. pcc 6803
14	c2l97A_	Alignment		99.3	21	PDB header: protein binding Chain: A; PDB Molecule: putative serine protease; PDBTitle: solution structure of htra pdz domain from streptococcus pneumoniae
15	c4ri0A_	Alignment		99.2	23	PDB header: hydrolase Chain: A; PDB Molecule: serine protease htra3; PDBTitle: serine protease htra3, mutationally inactivated
16	c3stjC_	Alignment		99.2	19	PDB header: hydrolase Chain: C; PDB Molecule: protease degq; PDBTitle: crystal structure of the protease + pdz1 domain of degq from2 escherichia coli
17	c2n7pA_	Alignment		99.2	26	PDB header: transferase Chain: A; PDB Molecule: putative uncharacterized protein; PDBTitle: solution structure of pdz domain
18	d1ky9b2	Alignment		99.2	17	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: HtraA-like serine proteases
19	c2zplA_	Alignment		99.2	17	PDB header: hydrolase Chain: A; PDB Molecule: regulator of sigma e protease; PDBTitle: crystal structure analysis of pdz domain a
20	c2kjpA_	Alignment		99.2	17	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	c3pv4A_	Alignment	not modelled	99.2	24	PDB header: hydrolase Chain: A; PDB Molecule: degq; PDBTitle: structure of legionella fallonii degq (delta-pdz2 variant)
22	c4a8aI_	Alignment	not modelled	99.1	22	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
23	d2i4sa1	Alignment	not modelled	99.1	17	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: EpsC C-terminal domain-like
24	c5hj1A_	Alignment	not modelled	99.1	12	PDB header: hydrolase Chain: A; PDB Molecule: pullulanase c protein; PDBTitle: crystal structure of pdz domain of pullulanase c protein of type ii2 secretion system from klebsiella pneumoniae in complex with fatty3 acid
25	c4o06A_	Alignment	not modelled	99.1	14	PDB header: chaperone Chain: A; PDB Molecule: probable 26s proteasome regulatory subunit p27; PDBTitle: 1.15a resolution structure of the proteasome assembly chaperone nas22 pdz domain
26	c4jj0B_	Alignment	not modelled	99.1	21	PDB header: electron transport Chain: B; PDB Molecule: mamp; PDBTitle: crystal structure of mamp
27	c3pv5B_	Alignment	not modelled	99.1	17	PDB header: hydrolase Chain: B; PDB Molecule: degq; PDBTitle: structure of legionella fallonii degq (n189g/p190g variant)
28	d2hgaa1	Alignment	not modelled	99.1	14	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: MTH1368 C-terminal domain-like

29	c4ic6A_	Alignment	not modelled	99.1	23	PDB header: hydrolase Chain: A: PDB Molecule: protease do-like 8, chloroplastic; PDBTitle: crystal structure of deg8
30	c2zleB_	Alignment	not modelled	99.0	17	PDB header: hydrolase Chain: B: PDB Molecule: protease do; PDBTitle: cryo-em structure of degp12/omp
31	d2i6va1	Alignment	not modelled	99.0	18	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: EpsC C-terminal domain-like
32	c3qo6B_	Alignment	not modelled	99.0	27	PDB header: photosynthesis Chain: B: PDB Molecule: protease do-like 1, chloroplastic; PDBTitle: crystal structure analysis of the plant protease deg1
33	d1fc6a3	Alignment	not modelled	99.0	23	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: Tail specific protease PDZ domain
34	c3gdsA_	Alignment	not modelled	99.0	29	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 dnrdgnvyvf peptide
35	c4revA_	Alignment	not modelled	99.0	20	PDB header: membrane protein Chain: A: PDB Molecule: golgi reassembly-stacking protein 1; PDBTitle: crystal structure of the grasp65-gm130 c-terminal peptide complex
36	c3rleA_	Alignment	not modelled	99.0	13	PDB header: membrane protein Chain: A: PDB Molecule: golgi reassembly-stacking protein 2; PDBTitle: crystal structure of grasp55 grasp domain (residues 7-208)
37	d1ky9a1	Alignment	not modelled	99.0	28	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: HtrA-like serine proteases
38	c1ky9A_	Alignment	not modelled	98.9	26	PDB header: hydrolase Chain: A: PDB Molecule: protease do; PDBTitle: crystal structure of degp (htra)
39	c3otpF_	Alignment	not modelled	98.9	16	PDB header: hydrolase Chain: F: PDB Molecule: protease do; PDBTitle: crystal structure of the degp dodecamer with a model substrate
40	c5y09B_	Alignment	not modelled	98.8	11	PDB header: hydrolase Chain: B: PDB Molecule: protease do-like 9; PDBTitle: crystal structure of deg9 at 295 k
41	d1sota1	Alignment	not modelled	98.8	28	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: HtrA-like serine proteases
42	c4l8nA_	Alignment	not modelled	98.8	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: pdz domain protein; PDBTitle: crystal structure of a pdz domain protein (bdi_1242) from2 parabacteroides distasonis atcc 8503 at 2.50 a resolution
43	c5jykb_	Alignment	not modelled	98.8	12	PDB header: hydrolase Chain: B: PDB Molecule: protease do-like 9; PDBTitle: deg9 crystal under 289k
44	d1x5qa1	Alignment	not modelled	98.7	24	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
45	d1rgwa_	Alignment	not modelled	98.7	14	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
46	c3l4fD_	Alignment	not modelled	98.7	21	PDB header: signaling protein/protein binding Chain: D: PDB Molecule: sh3 and multiple ankyrin repeat domains protein 1; PDBTitle: crystal structure of betapix coiled-coil domain and shank pdz complex
47	c5il9A_	Alignment	not modelled	98.7	12	PDB header: hydrolase Chain: A: PDB Molecule: protease do-like 9; PDBTitle: crystal structure of deg9
48	c5y2dA_	Alignment	not modelled	98.7	17	PDB header: hydrolase Chain: A: PDB Molecule: periplasmic serine endoprotease degp-like; PDBTitle: crystal structure of h. pylori htra
49	c3khfA_	Alignment	not modelled	98.7	17	PDB header: transferase Chain: A: PDB Molecule: microtubule-associated serine/threonine-protein kinase 3; PDBTitle: the crystal structure of the pdz domain of human microtubule2 associated serine/threonine kinase 3 (mast3)
50	c5wouA_	Alignment	not modelled	98.7	28	PDB header: cell adhesion Chain: A: PDB Molecule: protein lap4; PDBTitle: crystal structure of drosophila melanogaster scribble pdz1 domain in2 complex with guk-holder
51	c1p1dA_	Alignment	not modelled	98.7	10	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
52	c4flnB_	Alignment	not modelled	98.7	19	PDB header: hydrolase Chain: B: PDB Molecule: protease do-like 2, chloroplastic; PDBTitle: crystal structure of plant protease deg2
53	c2z9iB_	Alignment	not modelled	98.7	37	PDB header: hydrolase Chain: B: PDB Molecule: probable serine protease pepd; PDBTitle: crystal structure of rv0983 from mycobacterium tuberculosis-2 proteolytically active form
54	c2eaqA_	Alignment	not modelled	98.7	21	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
						PDB header: structural genomics Chain: A: PDB Molecule: unknown function protein 7

55	c2q3gA_	Alignment	not modelled	98.7	24	Chain: A: PDB Molecule: pdz and iim domain protein 7; PDBTitle: structure of the pdz domain of human pdlim7 bound to a c-2 terminal extension from human beta-tropomyosin
56	d1q3oa_	Alignment	not modelled	98.7	21	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
57	d2f5ya1	Alignment	not modelled	98.7	25	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
58	d1p1da2	Alignment	not modelled	98.6	14	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
59	d1wf7a_	Alignment	not modelled	98.6	21	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
60	c2krqA_	Alignment	not modelled	98.6	16	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)
61	d2fe5a1	Alignment	not modelled	98.6	19	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
62	c2kv8A_	Alignment	not modelled	98.6	20	PDB header: signaling protein Chain: A: PDB Molecule: regulator of g-protein signaling 12; PDBTitle: solution structure of rgs12 pdz domain
63	c2he4A_	Alignment	not modelled	98.6	19	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
64	c2yuyA_	Alignment	not modelled	98.6	18	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
65	c2v90E_	Alignment	not modelled	98.6	22	PDB header: protein binding Chain: E: PDB Molecule: pdz domain-containing protein 3; PDBTitle: crystal structure of the 3rd pdz domain of intestine- and kidney-2 enriched pdz domain ikepp (pdzd3)
66	c2qt5A_	Alignment	not modelled	98.6	20	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
67	c2kjdA_	Alignment	not modelled	98.6	17	PDB header: signaling protein Chain: A: PDB Molecule: sodium/hydrogen exchange regulatory cofactor nhe- PDBTitle: solution structure of extended pdz2 domain from nherf1 (150-2 270)
68	c2osgB_	Alignment	not modelled	98.6	30	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
69	d1m5za_	Alignment	not modelled	98.6	16	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
70	c6irdC_	Alignment	not modelled	98.6	20	PDB header: hydrolase/protein binding Chain: C: PDB Molecule: inad-like protein; PDBTitle: complex structure of inad1 pdz89 and plcb4 c-terminal cc-pbm
71	c2vvrA_	Alignment	not modelled	98.6	19	PDB header: protein binding Chain: A: PDB Molecule: ligand of numb protein x 2; PDBTitle: crystal structure of the second pdz domain of numb-binding protein 2
72	c2iwnA_	Alignment	not modelled	98.6	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)
73	c2egkC_	Alignment	not modelled	98.6	19	PDB header: protein binding Chain: C: PDB Molecule: general receptor for phosphoinositides 1-associated PDBTitle: crystal structure of tamalin pdz-intrinsic ligand fusion protein
74	d1t2ma1	Alignment	not modelled	98.6	19	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
75	c2ka9A_	Alignment	not modelled	98.6	14	PDB header: cell adhesion Chain: A: PDB Molecule: disks large homolog 4; PDBTitle: solution structure of psd-95 pdz12 complexed with cypin2 peptide
76	d2byga1	Alignment	not modelled	98.6	17	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
77	d1ozia_	Alignment	not modelled	98.6	18	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
78	c3qgD_	Alignment	not modelled	98.6	20	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
79	d1lhja_	Alignment	not modelled	98.6	15	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
80	d1whda_	Alignment	not modelled	98.6	25	Fold: PDZ domain-like Superfamily: PDZ domain-like

						Family:PDZ domain
81	c2enoA	Alignment	not modelled	98.6	19	PDB header: endocytosis Chain: A: PDB Molecule: synaptojanin-2-binding protein; PDBTitle: solution structure of the pdz domain from human2 synaptojanin 2 binding protein
82	c2dm8A	Alignment	not modelled	98.5	29	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
83	c2vspA	Alignment	not modelled	98.5	22	PDB header: transport protein Chain: A: PDB Molecule: pdz domain-containing protein 1; PDBTitle: crystal structure of the fourth pdz domain of pdz domain-containing2 protein 1
84	c2v1wB	Alignment	not modelled	98.5	17	PDB header: structural protein Chain: B: PDB Molecule: pdz and lim domain protein 4; PDBTitle: crystal structure of human lim protein ril (pdlim4) pdz domain bound2 to the c-terminal peptide of human alpha-actinin-1
85	d1uhpa	Alignment	not modelled	98.5	21	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
86	c2gzvA	Alignment	not modelled	98.5	24	PDB header: signaling protein Chain: A: PDB Molecule: prkca-binding protein; PDBTitle: the cystal structure of the pdz domain of human pick1
87	c3diwB	Alignment	not modelled	98.5	22	PDB header: signaling protein/cell adhesion Chain: B: PDB Molecule: tax1-binding protein 3; PDBTitle: c-terminal beta-catenin bound tip-1 structure
88	d1q7xa	Alignment	not modelled	98.5	19	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
89	c2eehA	Alignment	not modelled	98.5	19	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
90	c3cyyA	Alignment	not modelled	98.5	29	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
91	d1ry4a	Alignment	not modelled	98.5	17	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
92	c3eggC	Alignment	not modelled	98.5	27	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
93	c5gljB	Alignment	not modelled	98.5	20	PDB header: hydrolase Chain: B: PDB Molecule: tyrosine-protein phosphatase non-receptor type 13; PDBTitle: crystal structure of pdz1 domain of human protein tyrosine phosphatase2 ptp-bas
94	c2z17A	Alignment	not modelled	98.5	16	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
95	c2o2tB	Alignment	not modelled	98.5	13	PDB header: structural protein Chain: B: PDB Molecule: multiple pdz domain protein; PDBTitle: the crystal structure of the 1st pdz domain of mpdz
96	c1r6jA	Alignment	not modelled	98.5	19	PDB header: membrane protein Chain: A: PDB Molecule: syntenin 1; PDBTitle: ultrahigh resolution crystal structure of syntenin pdz2
97	d1r6ja	Alignment	not modelled	98.5	19	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
98	c1nteA	Alignment	not modelled	98.5	19	PDB header: signaling protein Chain: A: PDB Molecule: syntenin 1; PDBTitle: crystal structure analysis of the second pdz domain of syntenin
99	c2jxoA	Alignment	not modelled	98.5	17	PDB header: protein binding Chain: A: PDB Molecule: ezrin-radixin-moesin-binding phosphoprotein 50; PDBTitle: structure of the second pdz domain of nherf-1
100	c2vsvB	Alignment	not modelled	98.5	17	PDB header: protein binding Chain: B: PDB Molecule: rhophilin-2; PDBTitle: crystal structure of the pdz domain of human rhophilin-2
101	d1g9oa	Alignment	not modelled	98.5	21	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
102	d1vb7a	Alignment	not modelled	98.5	21	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
103	d1y7na1	Alignment	not modelled	98.5	15	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
104	c3shuB	Alignment	not modelled	98.5	15	PDB header: cell adhesion Chain: B: PDB Molecule: tight junction protein zo-1; PDBTitle: crystal structure of zo-1 pdz3
105	d1wf8a1	Alignment	not modelled	98.5	25	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
106	d1d5ga	Alignment	not modelled	98.5	20	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain

107	c6bxgA_	Alignment	not modelled	98.5	23	PDB header: hydrolase/peptide Chain: A: PDB Molecule: tail-specific protease; PDBTitle: 1.45 angstrom resolution crystal structure of pdz domain of carboxy-2 terminal protease from vibrio cholerae in complex with peptide.
108	c2xkxB_	Alignment	not modelled	98.5	15	PDB header: structural protein Chain: B: PDB Molecule: disks large homolog 4; PDBTitle: single particle analysis of psd-95 in negative stain
109	c2d90A_	Alignment	not modelled	98.5	23	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
110	c4c2dC_	Alignment	not modelled	98.5	19	PDB header: hydrolase/peptide Chain: C: PDB Molecule: carboxy-terminal processing protease ctpb; PDBTitle: crystal structure of the protease ctpb in an active state
111	c2jikB_	Alignment	not modelled	98.5	21	PDB header: membrane protein Chain: B: PDB Molecule: synaptojanin-2 binding protein; PDBTitle: crystal structure of pdz domain of synaptojanin-2 binding2 protein
112	c2jilA_	Alignment	not modelled	98.5	18	PDB header: membrane protein Chain: A: PDB Molecule: glutamate receptor interacting protein-1; PDBTitle: crystal structure of 2nd pdz domain of glutamate receptor interacting2 protein-1 (grip1)
113	d1pdra_	Alignment	not modelled	98.5	27	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
114	c2iwoA_	Alignment	not modelled	98.5	22	PDB header: signaling protein Chain: A: PDB Molecule: multiple pdz domain protein; PDBTitle: 12th pdz domain of multiple pdz domain protein mpdz (casp2 target)
115	c2m0tA_	Alignment	not modelled	98.5	20	PDB header: protein binding Chain: A: PDB Molecule: na(+)/h(+) exchange regulatory cofactor nhe-rf1; PDBTitle: structural characterization of the extended pdz1 domain from nherf1
116	d1whaa_	Alignment	not modelled	98.5	18	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
117	d1u3ba2	Alignment	not modelled	98.5	15	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
118	d1wjla_	Alignment	not modelled	98.5	14	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
119	c1obxA_	Alignment	not modelled	98.5	19	PDB header: cell adhesion Chain: A: PDB Molecule: syntenin 1; PDBTitle: crystal structure of the complex of pdz2 of syntenin with an2 interleukin 5 receptor alpha peptide.
120	d1obxA_	Alignment	not modelled	98.5	19	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain