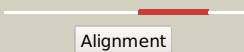

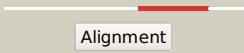

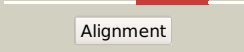

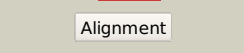



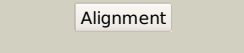

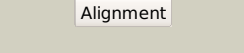



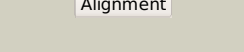

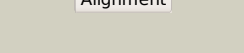

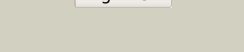
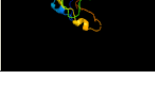


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3194c (-) _3563261_3564283
Date	Thu Aug 8 16:20:38 BST 2019
Unique Job ID	90fd4bfb5b0be23b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1z0eF_</a>	 Alignment		99.8	23	<b>PDB header:</b> hydrolase <b>Chain:</b> F; <b>PDB Molecule:</b> putative protease Ia homolog type; <b>PDBTitle:</b> crystal structure of a. fulgidus lon proteolytic domain
2	<a href="#">c3k1jA_</a>	 Alignment		99.7	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> atp-dependent protease lon; <b>PDBTitle:</b> crystal structure of lon protease from thermococcus onnurineus na1
3	<a href="#">c4fw9A_</a>	 Alignment		99.7	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> ttc1975 peptidase; <b>PDBTitle:</b> crystal structure of the lon-like protease mtalonc
4	<a href="#">c3i18A_</a>	 Alignment		99.7	27	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> lmo2051 protein; <b>PDBTitle:</b> crystal structure of the pdz domain of the sdrc-like protein (lmo2051)2 from listeria monocytogenes, northeast structural genomics consortium3 target lmr166b
5	<a href="#">c2x36F_</a>	 Alignment		99.7	27	<b>PDB header:</b> hydrolase <b>Chain:</b> F; <b>PDB Molecule:</b> lon protease homolog, mitochondrial; <b>PDBTitle:</b> structure of the proteolytic domain of the human2 mitochondrial lon protease
6	<a href="#">d1xhka_</a>	 Alignment		99.7	25	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> ATP-dependent protease Lon (La), catalytic domain
7	<a href="#">c5e7sG_</a>	 Alignment		99.7	26	<b>PDB header:</b> hydrolase <b>Chain:</b> G; <b>PDB Molecule:</b> lon protease; <b>PDBTitle:</b> hexameric structure of a lona protease domain in active state
8	<a href="#">c2kl1A_</a>	 Alignment		99.7	26	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> ylb1 protein; <b>PDBTitle:</b> solution structure of gtr34c from geobacillus thermodenitrificans.2 northeast structural genomics consortium target gtr34c
9	<a href="#">c5jykB_</a>	 Alignment		99.7	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> protease do-like 9; <b>PDBTitle:</b> deg9 crystal under 289k
10	<a href="#">c3wk1A_</a>	 Alignment		99.7	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> putative zinc metalloprotease aq_1964; <b>PDBTitle:</b> the periplasmic pdz tandem fragment of the rsep homologue from aquifex2 aeolicus
11	<a href="#">d2hgaa1</a>	 Alignment		99.7	21	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> MTH1368 C-terminal domain-like

12	<a href="#">c4flnB_</a>	Alignment		99.7	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> protease do-like 2, chloroplastic; <b>PDBTitle:</b> crystal structure of plant protease deg2
13	<a href="#">c2kjpA_</a>	Alignment		99.7	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ylbl; <b>PDBTitle:</b> solution structure of protein ylbl (bsu15050) from bacillus2 subtilis, northeast structural genomics consortium target3 sr713a
14	<a href="#">c5y09B_</a>	Alignment		99.7	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> protease do-like 9; <b>PDBTitle:</b> crystal structure of deg9 at 295 k
15	<a href="#">d1rrea_</a>	Alignment		99.7	26	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> ATP-dependent protease Lon (La), catalytic domain
16	<a href="#">c5il9A_</a>	Alignment		99.6	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protease do-like 9; <b>PDBTitle:</b> crystal structure of deg9
17	<a href="#">c6on2A_</a>	Alignment		99.6	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent protease la; <b>PDBTitle:</b> lon protease from yersinia pestis with y2853 substrate
18	<a href="#">c3pv5B_</a>	Alignment		99.6	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> degq; <b>PDBTitle:</b> structure of legionella fallonii degq (n189g/p190g variant)
19	<a href="#">c2i97A_</a>	Alignment		99.6	20	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> putative serine protease; <b>PDBTitle:</b> solution structure of htra pdz domain from streptococcus pneumoniae
20	<a href="#">c5xdyA_</a>	Alignment		99.6	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> heat shock protein htra; <b>PDBTitle:</b> crystal structure of htra1 from mycobacterium tuberculosis
21	<a href="#">c3m6aC_</a>	Alignment	not modelled	99.6	28	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> atp-dependent protease la 1; <b>PDBTitle:</b> crystal structure of bacillus subtilis lon c-terminal domain
22	<a href="#">c5b6iA_</a>	Alignment	not modelled	99.5	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative serine protease hhoa; <b>PDBTitle:</b> structure of deg protease hhoa from synechocystis sp. pcc 6803
23	<a href="#">c3stjC_</a>	Alignment	not modelled	99.5	22	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> protease degq; <b>PDBTitle:</b> crystal structure of the protease + pdz1 domain of degq from2 escherichia coli
24	<a href="#">c2zpmA_</a>	Alignment	not modelled	99.5	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> regulator of sigma e protease; <b>PDBTitle:</b> crystal structure analysis of pdz domain b
25	<a href="#">d2z9ia1</a>	Alignment	not modelled	99.5	17	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> HtrA-like serine proteases
26	<a href="#">c3otpF_</a>	Alignment	not modelled	99.5	16	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> protease do; <b>PDBTitle:</b> crystal structure of the degp dodecamer with a model substrate
27	<a href="#">c5lkmB_</a>	Alignment	not modelled	99.5	14	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> dna repair protein rada; <b>PDBTitle:</b> rada bound to dtdp
28	<a href="#">c3pv4A_</a>	Alignment	not modelled	99.5	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> degq; <b>PDBTitle:</b> structure of legionella fallonii degq (delta-pdz2 variant)
						<b>PDB header:</b> hydrolase/hydrolase <b>Chain:</b> I: <b>PDB Molecule:</b> periplasmic ph-dependent serine

29	<a href="#">c4a8aL_</a>	Alignment	not modelled	99.5	17	endoprotease degq; <b>PDBTitle:</b> asymmetric cryo-em reconstruction of e. coli degq 12-mer in complex2 with lysozyme
30	<a href="#">c4yplE_</a>	Alignment	not modelled	99.4	27	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> lon protease; <b>PDBTitle:</b> crystal structure of a hexameric lona protease bound to three adps
31	<a href="#">d2i4sa1</a>	Alignment	not modelled	99.4	17	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> EpsC C-terminal domain-like
32	<a href="#">c1lcyA_</a>	Alignment	not modelled	99.4	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> htra2 serine protease; <b>PDBTitle:</b> crystal structure of the mitochondrial serine protease htra2
33	<a href="#">c2zleB_</a>	Alignment	not modelled	99.4	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> protease do; <b>PDBTitle:</b> cryo-em structure of degp12/omp
34	<a href="#">d1lcyA1</a>	Alignment	not modelled	99.4	18	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> HtraA-like serine proteases
35	<a href="#">c2p3wB_</a>	Alignment	not modelled	99.4	21	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> probable serine protease htra3; <b>PDBTitle:</b> crystal structure of the htra3 pdz domain bound to a phage-derived2 ligand (fgrwv)
36	<a href="#">c4ic6A_</a>	Alignment	not modelled	99.4	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protease do-like 8, chloroplastic; <b>PDBTitle:</b> crystal structure of deg8
37	<a href="#">c2joaA_</a>	Alignment	not modelled	99.4	18	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> serine protease htra1; <b>PDBTitle:</b> htra1 bound to an optimized peptide: nmr assignment of pdz2 domain and ligand resonances
38	<a href="#">c4reyA_</a>	Alignment	not modelled	99.4	12	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> golgi reassembly-stacking protein 1; <b>PDBTitle:</b> crystal structure of the grasp65-gm130 c-terminal peptide complex
39	<a href="#">c4ij0B_</a>	Alignment	not modelled	99.4	16	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> mamp; <b>PDBTitle:</b> crystal structure of mamp
40	<a href="#">c5hj1A_</a>	Alignment	not modelled	99.4	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pullulanase c protein; <b>PDBTitle:</b> crystal structure of pdz domain of pullulanase c protein of type ii2 secretion system from klebsiella pneumoniae in complex with fatty3 acid
41	<a href="#">c4ri0A_</a>	Alignment	not modelled	99.4	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> serine protease htra3; <b>PDBTitle:</b> serine protease htra3, mutationally inactivated
42	<a href="#">c4o06A_</a>	Alignment	not modelled	99.3	12	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> probable 26s proteasome regulatory subunit p27; <b>PDBTitle:</b> 1.15a resolution structure of the proteasome assembly chaperone nas22 pdz domain
43	<a href="#">c2n7pA_</a>	Alignment	not modelled	99.3	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> solution structure of pdz domain
44	<a href="#">c3qo6B_</a>	Alignment	not modelled	99.3	31	<b>PDB header:</b> photosynthesis <b>Chain:</b> B: <b>PDB Molecule:</b> protease do-like 1, chloroplastic; <b>PDBTitle:</b> crystal structure analysis of the plant protease deg1
45	<a href="#">c3qdsA_</a>	Alignment	not modelled	99.3	19	<b>PDB header:</b> hydrolase/hydrolase activator <b>Chain:</b> A: <b>PDB Molecule:</b> protease degs; <b>PDBTitle:</b> crystal structure of degs h198p/d320a mutant modified by dfp in2 complex with dnrdgnvyvf peptide
46	<a href="#">d1ky9a1</a>	Alignment	not modelled	99.3	17	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> HtraA-like serine proteases
47	<a href="#">c1p1dA_</a>	Alignment	not modelled	99.3	12	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate receptor interacting protein; <b>PDBTitle:</b> structural insights into the inter-domain chaperoning of2 tandem pdz domains in glutamate receptor interacting3 proteins
48	<a href="#">d2i6va1</a>	Alignment	not modelled	99.3	18	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> EpsC C-terminal domain-like
49	<a href="#">c5wqlC_</a>	Alignment	not modelled	99.3	18	<b>PDB header:</b> protein binding/signaling protein/hydrol <b>Chain:</b> C: <b>PDB Molecule:</b> tail-specific protease; <b>PDBTitle:</b> structure of a pdz-protease bound to a substrate-binding adaptor
50	<a href="#">c2zplA_</a>	Alignment	not modelled	99.3	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> regulator of sigma e protease; <b>PDBTitle:</b> crystal structure analysis of pdz domain a
51	<a href="#">d1fc6a3</a>	Alignment	not modelled	99.2	28	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> Tail specific protease PDZ domain
52	<a href="#">c1ky9A_</a>	Alignment	not modelled	99.2	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protease do; <b>PDBTitle:</b> crystal structure of degp (htra)
53	<a href="#">c4c2dC_</a>	Alignment	not modelled	99.2	13	<b>PDB header:</b> hydrolase/peptide <b>Chain:</b> C: <b>PDB Molecule:</b> carboxy-terminal processing protease ctpb; <b>PDBTitle:</b> crystal structure of the protease ctpb in an active state
54	<a href="#">c3rleA_</a>	Alignment	not modelled	99.2	16	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> golgi reassembly-stacking protein 2; <b>PDBTitle:</b> crystal structure of grasp55 grasp domain (residues 7-208)
						<b>Fold:</b> PDZ domain-like

55	<a href="#">d1ky9b2</a>	Alignment	not modelled	99.2	20	<b>Superfamily:</b> PDZ domain-like <b>Family:</b> HtrA-like serine proteases
56	<a href="#">c2ka9A_</a>	Alignment	not modelled	99.2	17	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> disks large homolog 4; <b>PDBTitle:</b> solution structure of psd-95 pdz12 complexed with cypin2 peptide
57	<a href="#">c2qt5A_</a>	Alignment	not modelled	99.1	16	<b>PDB header:</b> peptide binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate receptor-interacting protein 1; <b>PDBTitle:</b> crystal structure of grip1 pdz12 in complex with the fras12 peptide
58	<a href="#">d1sota1</a>	Alignment	not modelled	99.1	20	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> HtrA-like serine proteases
59	<a href="#">c6irdC_</a>	Alignment	not modelled	99.1	17	<b>PDB header:</b> hydrolase/protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> inad-like protein; <b>PDBTitle:</b> complex structure of inad pdz89 and plcb4 c-terminal cc-pbm
60	<a href="#">c3r0hA_</a>	Alignment	not modelled	99.1	20	<b>PDB header:</b> peptide binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> inactivation-no-after-potential d protein; <b>PDBTitle:</b> structure of inad pdz45 in complex with ng2 peptide
61	<a href="#">c2z9iB_</a>	Alignment	not modelled	99.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> probable serine protease pepd; <b>PDBTitle:</b> crystal structure of rv0983 from mycobacterium tuberculosis-2 proteolytically active form
62	<a href="#">c5y2dA_</a>	Alignment	not modelled	99.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic serine endoprotease degp-like; <b>PDBTitle:</b> crystal structure of h. pylori htra
63	<a href="#">c6bxgA_</a>	Alignment	not modelled	99.0	20	<b>PDB header:</b> hydrolase/peptide <b>Chain:</b> A: <b>PDB Molecule:</b> tail-specific protease; <b>PDBTitle:</b> 1.45 angstrom resolution crystal structure of pdz domain of carboxy-2 terminal protease from vibrio cholerae in complex with peptide.
64	<a href="#">c4wyuA_</a>	Alignment	not modelled	99.0	25	<b>PDB header:</b> structural protein/peptide <b>Chain:</b> A: <b>PDB Molecule:</b> protein scribble homolog; <b>PDBTitle:</b> crystal structure of scribble pdz34 tandem in complex with its target2 peptide
65	<a href="#">c2eagA_</a>	Alignment	not modelled	98.9	20	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> lim domain only protein 7; <b>PDBTitle:</b> crystal structure of pdz domain of kiaa0858 (lim), ms07932 from homo sapiens
66	<a href="#">d1wifa_</a>	Alignment	not modelled	98.9	25	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain
67	<a href="#">c3diwB_</a>	Alignment	not modelled	98.8	27	<b>PDB header:</b> signaling protein/cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> tax1-binding protein 3; <b>PDBTitle:</b> c-terminal beta-catenin bound tip-1 structure
68	<a href="#">c1u3bA_</a>	Alignment	not modelled	98.8	16	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> amyloid beta a4 precursor protein-binding; <b>PDBTitle:</b> auto-inhibition mechanism of x11s/mints family scaffold2 proteins revealed by the closed conformation of the tandem3 pdz domains
69	<a href="#">c3l4fD_</a>	Alignment	not modelled	98.8	19	<b>PDB header:</b> signaling protein/protein binding <b>Chain:</b> D: <b>PDB Molecule:</b> sh3 and multiple ankyrin repeat domains protein 1; <b>PDBTitle:</b> crystal structure of betapix coiled-coil domain and shank pdz complex
70	<a href="#">c3shuB_</a>	Alignment	not modelled	98.8	28	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> tight junction protein zo-1; <b>PDBTitle:</b> crystal structure of zo-1 pdz3
71	<a href="#">c5wouA_</a>	Alignment	not modelled	98.8	23	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> protein lap4; <b>PDBTitle:</b> crystal structure of drosophila melanogaster scribble pdz1 domain in2 complex with guk-holder
72	<a href="#">d1x5qa1</a>	Alignment	not modelled	98.8	20	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain
73	<a href="#">c2krqA_</a>	Alignment	not modelled	98.8	19	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> na(+)/h(+) exchange regulatory cofactor nhe-rf1; <b>PDBTitle:</b> solution structure of human sodium/ hydrogen exchange2 regulatory factor 1(150-358)
74	<a href="#">d1ueqa_</a>	Alignment	not modelled	98.8	25	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain
75	<a href="#">c2komA_</a>	Alignment	not modelled	98.8	25	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> partitioning defective 3 homolog; <b>PDBTitle:</b> solution structure of humar par-3b pdz2 (residues 451-549)
76	<a href="#">d1mfga_</a>	Alignment	not modelled	98.8	29	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain
77	<a href="#">d1w9ea1</a>	Alignment	not modelled	98.8	23	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain
78	<a href="#">c5oakA_</a>	Alignment	not modelled	98.8	18	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> bazooka, isoform c,ld29223p; <b>PDBTitle:</b> structure of the dmpar3 pdz1 domain in complex with the dmpar6 pbm
79	<a href="#">d1m5za_</a>	Alignment	not modelled	98.8	17	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain
80	<a href="#">d1wfga_</a>	Alignment	not modelled	98.7	17	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain

81	<a href="#">d2h3la1</a>	Alignment	not modelled	98.7	27	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain
82	<a href="#">c3bpuA</a>	Alignment	not modelled	98.7	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> membrane-associated guanylate kinase, ww and pdz domain- <b>PDBTitle:</b> crystal structure of the 3rd pdz domain of human membrane associated2 guanylate kinase, c677s and c709s double mutant
83	<a href="#">d1q3oa</a>	Alignment	not modelled	98.7	21	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain
84	<a href="#">c2kjdA</a>	Alignment	not modelled	98.7	21	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> sodium/hydrogen exchange regulatory cofactor nhe- <b>PDBTitle:</b> solution structure of extended pdz2 domain from nherf1 (150-2 270)
85	<a href="#">c5v6bA</a>	Alignment	not modelled	98.7	17	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> pdz domain-containing protein gipc1; <b>PDBTitle:</b> crystal structure of gipc1
86	<a href="#">c2q3gA</a>	Alignment	not modelled	98.7	13	<b>PDB header:</b> structural genomics <b>Chain:</b> A: <b>PDB Molecule:</b> pdz and lim domain protein 7; <b>PDBTitle:</b> structure of the pdz domain of human pdlim7 bound to a c-2 terminal extension from human beta-tropomyosin
87	<a href="#">c5n7gA</a>	Alignment	not modelled	98.7	25	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> membrane-associated guanylate kinase, ww and pdz domain- <b>PDBTitle:</b> magi-1 complexed with a synthetic prsk1 peptide
88	<a href="#">c2edvA</a>	Alignment	not modelled	98.7	24	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> ferm and pdz domain-containing protein 1; <b>PDBTitle:</b> solution structure of the pdz domain from human ferm and2 pdz domain containing 1
89	<a href="#">d1qaua</a>	Alignment	not modelled	98.7	18	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain
90	<a href="#">d2csja1</a>	Alignment	not modelled	98.7	23	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain
91	<a href="#">c1w9qB</a>	Alignment	not modelled	98.7	18	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> syntenin 1; <b>PDBTitle:</b> crystal structure of the pdz tandem of human syntenin in complex with2 tnefaf peptide
92	<a href="#">c2iwnA</a>	Alignment	not modelled	98.7	33	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> multiple pdz domain protein; <b>PDBTitle:</b> 3rd pdz domain of multiple pdz domain protein mpdz (casp2 target)
93	<a href="#">d1wh1a</a>	Alignment	not modelled	98.7	16	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain
94	<a href="#">c3khfA</a>	Alignment	not modelled	98.7	31	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> microtubule-associated serine/threonine-protein kinase 3; <b>PDBTitle:</b> the crystal structure of the pdz domain of human microtubule2 associated serine/threonine kinase 3 (mast3)
95	<a href="#">c5h45A</a>	Alignment	not modelled	98.7	25	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna repair protein rada; <b>PDBTitle:</b> crystal structure of the c-terminal lon protease-like domain of2 thermus thermophilus rada/sms
96	<a href="#">c3eggC</a>	Alignment	not modelled	98.7	25	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> spinophilin; <b>PDBTitle:</b> crystal structure of a complex between protein phosphatase 1 alpha2 (pp1) and the pp1 binding and pdz domains of spinophilin
97	<a href="#">c2i04B</a>	Alignment	not modelled	98.7	25	<b>PDB header:</b> peptide binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> membrane-associated guanylate kinase, ww and pdz <b>PDBTitle:</b> x-ray crystal structure of magi-1 pdz1 bound to the c-2 terminal peptide of hpv18 e6
98	<a href="#">d1rgwa</a>	Alignment	not modelled	98.7	14	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain
99	<a href="#">c2ogpA</a>	Alignment	not modelled	98.7	26	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> partitioning-defective 3 homolog; <b>PDBTitle:</b> solution structure of the second pdz domain of par-3
100	<a href="#">c2xkxB</a>	Alignment	not modelled	98.7	16	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> disks large homolog 4; <b>PDBTitle:</b> single particle analysis of psd-95 in negative stain
101	<a href="#">d1ozia</a>	Alignment	not modelled	98.7	23	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain
102	<a href="#">d2fe5a1</a>	Alignment	not modelled	98.6	25	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain
103	<a href="#">c3qglD</a>	Alignment	not modelled	98.6	23	<b>PDB header:</b> protein binding <b>Chain:</b> D: <b>PDB Molecule:</b> sorting nexin-27; <b>PDBTitle:</b> crystal structure of pdz domain of sorting nexin 27 (snx27) in complex2 with the esesk peptide corresponding to the c-terminal tail of girk3
104	<a href="#">d2f5ya1</a>	Alignment	not modelled	98.6	21	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain
105	<a href="#">d1p1da1</a>	Alignment	not modelled	98.6	20	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain

106	<a href="#">d1p1da2</a>	Alignment	not modelled	98.6	15	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain
107	<a href="#">c2egkC</a>	Alignment	not modelled	98.6	23	<b>PDB header:</b> protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> general receptor for phosphoinositides 1-associated <b>PDBTitle:</b> crystal structure of tamalin pdz-intrinsic ligand fusion protein
108	<a href="#">d1t2ma1</a>	Alignment	not modelled	98.6	28	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain
109	<a href="#">c2he4A</a>	Alignment	not modelled	98.6	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> na(+)/h(+) exchange regulatory cofactor nhe-rf2; <b>PDBTitle:</b> the crystal structure of the second pdz domain of human2 nherf-2 (slc9a3r2) interacting with a mode 1 pdz binding3 motif
110	<a href="#">c2eehA</a>	Alignment	not modelled	98.6	18	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> pdz domain-containing protein 7; <b>PDBTitle:</b> solution structure of first pdz domain of pdz domain2 containing protein 7
111	<a href="#">c2vsvB</a>	Alignment	not modelled	98.6	21	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> rhophilin-2; <b>PDBTitle:</b> crystal structure of the pdz domain of human rhophilin-2
112	<a href="#">c2v90E</a>	Alignment	not modelled	98.6	22	<b>PDB header:</b> protein binding <b>Chain:</b> E: <b>PDB Molecule:</b> pdz domain-containing protein 3; <b>PDBTitle:</b> crystal structure of the 3rd pdz domain of intestine- and kidney-2 enriched pdz domain ikepp (pdzd3)
113	<a href="#">c2vwrA</a>	Alignment	not modelled	98.6	18	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> ligand of numb protein x 2; <b>PDBTitle:</b> crystal structure of the second pdz domain of numb-binding protein 2
114	<a href="#">d1q7xa</a>	Alignment	not modelled	98.6	23	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain
115	<a href="#">d1wf7a</a>	Alignment	not modelled	98.6	20	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain
116	<a href="#">c2gzvA</a>	Alignment	not modelled	98.6	25	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> prka-binding protein; <b>PDBTitle:</b> the cystal structure of the pdz domain of human pick1
117	<a href="#">c3shwA</a>	Alignment	not modelled	98.6	26	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> tight junction protein zo-1; <b>PDBTitle:</b> crystal structure of zo-1 pdz3-sh3-guk supramodule complex with2 connexin-45 peptide
118	<a href="#">d2cssa1</a>	Alignment	not modelled	98.6	23	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain
119	<a href="#">c2r3yC</a>	Alignment	not modelled	98.6	24	<b>PDB header:</b> hydrolase/hydrolase activator <b>Chain:</b> C: <b>PDB Molecule:</b> protease degs; <b>PDBTitle:</b> crystal structure of the degs protease in complex with the2 ywf activating peptide
120	<a href="#">d1ry4a</a>	Alignment	not modelled	98.6	22	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain