


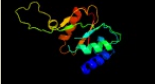




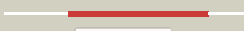




















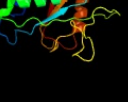



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3242c_(-)_3621567_3622208
Date	Thu Aug 8 16:20:44 BST 2019
Unique Job ID	a5ef3d9b6d0bfcd1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ecfa1	 Alignment		99.8	20	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
2	c1ecjB_	 Alignment		99.7	19	PDB header: transferase Chain: B: PDB Molecule: glutamine phosphoribosylpyrophosphate PDBTitle: escherichia coli glutamine phosphoribosylpyrophosphate2 (prpp) amidotransferase complexed with 2 amp per tetramer
3	d1gph11	 Alignment		99.6	22	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
4	c1gph1_	 Alignment		99.5	24	PDB header: transferase Chain: 1: PDB Molecule: glutamine phosphoribosyl-pyrophosphate amidotransferase; PDBTitle: structure of the allosteric regulatory enzyme of purine biosynthesis
5	d1wd5a_	 Alignment		99.5	26	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
6	c5zgoB_	 Alignment		99.5	20	PDB header: transferase Chain: B: PDB Molecule: adenine phosphoribosyltransferase; PDBTitle: crystal structure of apt2 from thermus thermophilus hb8
7	d1g2qa_	 Alignment		99.5	17	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
8	d1zn7a1	 Alignment		99.4	15	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
9	d1vcha1	 Alignment		99.3	20	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
10	c2dy0A_	 Alignment		99.2	16	PDB header: transferase Chain: A: PDB Molecule: adenine phosphoribosyltransferase; PDBTitle: crystal structure of project jw0458 from escherichia coli
11	c4rhyC_	 Alignment		99.2	14	PDB header: transferase/transferase inhibitor Chain: C: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: crystal structures of mycobacterium tuberculosis 6-oxopurine2 phosphoribosyltransferase which is a potential target for drug3 development against this disease

12	c5ipfA	Alignment		99.2	15	PDB header: transferase Chain: A: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase (hgprt); PDBTitle: crystal structure of hypoxanthine-guanine phosphoribosyltransferase2 from schistosoma mansoni in complex with imp
13	d1a3ca	Alignment		99.2	19	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
14	d1vdma1	Alignment		99.2	20	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
15	c4m0kD	Alignment		99.2	21	PDB header: transferase Chain: D: PDB Molecule: adenine phosphoribosyltransferase; PDBTitle: crystal structure of adenine phosphoribosyltransferase from2 rhodothermus marinus dsm 4252, nysgrc target 029775.
16	d1j7ja	Alignment		99.2	18	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
17	d1mzva	Alignment		99.2	19	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
18	c3kb8A	Alignment		99.2	11	PDB header: transferase Chain: A: PDB Molecule: hypoxanthine phosphoribosyltransferase; PDBTitle: 2.09 angstrom resolution structure of a hypoxanthine-guanine2 phosphoribosyltransferase (hpt-1) from bacillus anthracis str. 'ames3 ancestor' in complex with gmp
19	d1w30a	Alignment		99.2	20	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
20	c4z1oB	Alignment		99.1	15	PDB header: transferase Chain: B: PDB Molecule: phosphoribosyltransferase; PDBTitle: hypoxanthine-guanine-xanthine phosphoribosyltransferase (hgxprt) from2 sulfobolus solfataricus in complex with alpha-3 phosphoribosylpyrophosphoric acid (prpp) and magnesium
21	d1o57a2	Alignment	not modelled	99.1	16	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
22	c4lzaB	Alignment	not modelled	99.1	17	PDB header: transferase Chain: B: PDB Molecule: adenine phosphoribosyltransferase; PDBTitle: crystal structure of adenine phosphoribosyltransferase from2 thermoanaerobacter pseudethanolicus atcc 33223, nysgrc target 029700.
23	c5eswB	Alignment	not modelled	99.1	15	PDB header: transferase Chain: B: PDB Molecule: purine/pyrimidine phosphoribosyltransferase; PDBTitle: crystal structure of apo hypoxanthine-guanine2 phosphoribosyltransferase from legionella pneumophila
24	c6apsA	Alignment	not modelled	99.1	12	PDB header: transferase Chain: A: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: trypanosoma brucei hypoxanthine guanine phosphoribosyltransferase in2 complex with [(2-((guanine-9h-yl)methyl)propane-1,3 diyl)bis(oxy)3]bis(methylene)diphosphonic acid
25	d1tc1a	Alignment	not modelled	99.1	12	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
26	c5yw2D	Alignment	not modelled	99.1	18	PDB header: transferase Chain: D: PDB Molecule: adenine phosphoribosyltransferase; PDBTitle: crystal structure of adenine phosphoribosyltransferase from2 francisella tularensis.
27	d2igba1	Alignment	not modelled	99.1	18	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)

28	d1y0ba1	Alignment	not modelled	99.1	15	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
29	c1yfzA_	Alignment	not modelled	99.1	13	PDB header: transferase Chain: A: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: novel imp binding in feedback inhibition of hypoxanthine-guanine2 phosphoribosyltransferase from thermoanaerobacter tengcongensis
30	d1yfza1	Alignment	not modelled	99.1	13	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
31	d1lh0a_	Alignment	not modelled	99.1	23	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
32	c2wnsB_	Alignment	not modelled	99.1	21	PDB header: transferase Chain: B: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: human orotate phosphoribosyltransferase (oprtae) domain of2 uridine 5'-monophosphate synthase (umps) in complex with3 its substrate orotidine 5'-monophosphate (omp)
33	d1ufra_	Alignment	not modelled	99.1	22	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
34	c1o57A_	Alignment	not modelled	99.1	16	PDB header: dna binding protein Chain: A: PDB Molecule: pur operon repressor; PDBTitle: crystal structure of the purine operon repressor of2 bacillus subtilis
35	c5vogA_	Alignment	not modelled	99.1	11	PDB header: transferase Chain: A: PDB Molecule: putative phosphoribosyltransferase; PDBTitle: crystal structure of a hypothetical protein from neisseria gonorrhoeae2 with bound ppgpp
36	c4pawA_	Alignment	not modelled	99.0	21	PDB header: transferase Chain: A: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: structure of hypothetical protein hp1257.
37	c4rqbB_	Alignment	not modelled	99.0	17	PDB header: transferase Chain: B: PDB Molecule: hypoxanthine phosphoribosyltransferase; PDBTitle: crystal structure of a hypoxanthine phosphoribosyltransferase (target2 id nysgrc-029686) from staphylococcus aureus (tetragonal space group)
38	c4lyyA_	Alignment	not modelled	99.0	12	PDB header: transferase Chain: A: PDB Molecule: hypoxanthine phosphoribosyltransferase; PDBTitle: crystal structure of hypoxanthine phosphoribosyltransferase from2 shewanella pealeana atcc 700345, nysgrc target 029677.
39	d1pzma_	Alignment	not modelled	99.0	16	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
40	d1hqxa_	Alignment	not modelled	99.0	17	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
41	c5hkiD_	Alignment	not modelled	99.0	21	PDB header: transferase Chain: D: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: crystal structure of mycobacterium tuberculosis h37rv orotate2 phosphoribosyltransferase in complex with fe(iii) dicitrate
42	c3dezA_	Alignment	not modelled	99.0	14	PDB header: transferase Chain: A: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: crystal structure of orotate phosphoribosyltransferase from2 streptococcus mutans
43	d1g9sa_	Alignment	not modelled	99.0	15	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
44	d2aeaa1	Alignment	not modelled	99.0	13	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
45	d1z7ga1	Alignment	not modelled	99.0	16	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
46	d1p17b_	Alignment	not modelled	99.0	12	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
47	c3o7mD_	Alignment	not modelled	99.0	12	PDB header: transferase Chain: D: PDB Molecule: hypoxanthine phosphoribosyltransferase; PDBTitle: 1.98 angstrom resolution crystal structure of a hypoxanthine-guanine2 phosphoribosyltransferase (hpt-2) from bacillus anthracis str. 'ames3 ancestor'
48	c3mjda_	Alignment	not modelled	99.0	14	PDB header: transferase Chain: A: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: 1.9 angstrom crystal structure of orotate phosphoribosyltransferase2 (pyre) francisella tularensis.
49	c2ywtA_	Alignment	not modelled	99.0	17	PDB header: transferase Chain: A: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: crystal structure of hypoxanthine-guanine2 phosphoribosyltransferase with gmp from thermus3 thermophilus hb8
50	c1pzmB_	Alignment	not modelled	99.0	14	PDB header: transferase Chain: B: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: crystal structure of hgprt-ase from leishmania tarentolae in complex2 with gmp
51	d1l1qa_	Alignment	not modelled	99.0	17	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
52	c2vz6C_	Alignment	not modelled	99.0	25	PDB header: transferase Chain: C: PDB Molecule: orotate phosphoribosyltransferase;

52	c4yzkC_	Alignment	not modelled	98.9	23	PDBTitle: crystal structure of orotate phosphoribosyltransferase from2 aeropyrum pernix PDB header: transferase
53	c2p1zA_	Alignment	not modelled	98.9	22	Chain: A: PDB Molecule: phosphoribosyltransferase; PDBTitle: crystal structure of phosphoribosyltransferase from corynebacterium2 diphtheriae PDB header: transferase
54	c5vn4A_	Alignment	not modelled	98.9	18	Chain: A: PDB Molecule: adenine phosphoribosyltransferase, putative; PDBTitle: crystal structure of adenine phosphoribosyl transferase from2 trypanosoma brucei in complex with amp, pyrophosphate, and ribose-5-3 phosphate PDB header: transferase
55	c4pfqF_	Alignment	not modelled	98.9	19	Chain: F: PDB Molecule: hypoxanthine phosphoribosyltransferase; PDBTitle: crystal structure of hypoxanthine phosphoribosyltransferase from2 brachy bacterium faecium dsm 4810, nysgrc target 029763. PDB header: transferase
56	c3n2lA_	Alignment	not modelled	98.9	26	Chain: A: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: 2.1 angstrom resolution crystal structure of an orotate2 phosphoribosyltransferase (pyre) from vibrio cholerae o1 biovar eltor3 str. n16961 PDB header: transferase
57	c4twbB_	Alignment	not modelled	98.9	18	Chain: B: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: sulfolobus solfataricus ribose-phosphate pyrophosphokinase PDB header: transferase
58	c5t3oB_	Alignment	not modelled	98.9	25	Chain: B: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: crystal structure of the phosphorybosylpyrophosphate synthetase ii2 from thermus thermophilus PDB header: transferase
59	c3efhB_	Alignment	not modelled	98.9	23	Chain: B: PDB Molecule: ribose-phosphate pyrophosphokinase 1; PDBTitle: crystal structure of human phosphoribosyl pyrophosphate2 synthetase 1 PDB header: transferase
60	c2przB_	Alignment	not modelled	98.8	14	Chain: B: PDB Molecule: orotate phosphoribosyltransferase 1; PDBTitle: s. cerevisiae orotate phosphoribosyltransferase complexed with omp PDB header: transferase
61	c4trbA_	Alignment	not modelled	98.8	17	Chain: A: PDB Molecule: purine phosphoribosyltransferase (gpt-1); PDBTitle: sulfolobus solfataricus adenine phosphoribosyltransferase PDB header: transferase
62	c5mp7C_	Alignment	not modelled	98.8	24	Chain: C: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: crystal structure of phosphoribosylpyrophosphate synthetase from2 mycobacterium smegmatis PDB header: transferase
63	d1qb7a_	Alignment	not modelled	98.8	18	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
64	c2c4kD_	Alignment	not modelled	98.8	21	Chain: D: PDB Molecule: phosphoribosyl pyrophosphate synthetase-associated protein PDBTitle: crystal structure of human phosphoribosylpyrophosphate synthetase-2 associated protein 39 (pap39) PDB header: transferase/transferase inhibitor
65	c5kapA_	Alignment	not modelled	98.8	28	Chain: A: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: trypanosome brucei hypoxanthine-guanine phosphoribosyltransferase in2 complex with a 9-(4-(phosphonobutyl)hypoxanthine PDB header: transferase
66	c3m3hA_	Alignment	not modelled	98.7	18	Chain: A: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: 1.75 angstrom resolution crystal structure of an orotate2 phosphoribosyltransferase from bacillus anthracis str. 'ames3 ancestor' PDB header: transferase
67	d1cjba_	Alignment	not modelled	98.7	12	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
68	c3lpnB_	Alignment	not modelled	98.7	26	Chain: B: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: crystal structure of the phosphoribosylpyrophosphate (prpp) synthetase2 from thermoplasma volcanium in complex with an atp analog (ampcpp). PDB header: transferase
69	d1dkua2	Alignment	not modelled	98.7	26	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
70	c6nfeB_	Alignment	not modelled	98.7	21	Chain: B: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: crystal structure of ribose-phosphate pyrophosphokinase from2 legionella pneumophila with bound amp, adp, and ribose-5-phosphate PDB header: ligase
71	c4fymA_	Alignment	not modelled	98.7	13	Chain: A: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: crystal structure of plasmodium falciparum orotate2 phosphoribosyltransferase PDB header: transferase
72	c3qw4B_	Alignment	not modelled	98.7	18	Chain: B: PDB Molecule: ump synthase; PDBTitle: structure of leishmania donovani ump synthase PDB header: transferase
73	c2jkzB_	Alignment	not modelled	98.7	14	Chain: B: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: saccharomyces cerevisiae hypoxanthine-guanine2 phosphoribosyltransferase in complex with gmp (guanosine 5'-3 monophosphate) (orthorhombic crystal form) PDB header: transferase
74	c4s2uA_	Alignment	not modelled	98.7	25	Chain: A: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: crystal structure of the phosphorybosylpyrophosphate synthetase from2 e. coli PDB header: transferase
75	d1u9ya2	Alignment	not modelled	98.6	30	Fold: PRTase-like Superfamily: PRTase-like

						Family: Phosphoribosylpyrophosphate synthetase-like
76	c1dkrB_	Alignment	not modelled	98.6	24	PDB header: transferase Chain: B: PDB Molecule: phosphoribosyl pyrophosphate synthetase; PDBTitle: crystal structures of bacillus subtilis phosphoribosylpyrophosphate2 synthetase: molecular basis of allosteric inhibition and activation.
77	d2c4ka2	Alignment	not modelled	98.6	24	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
78	d1fsga_	Alignment	not modelled	98.5	15	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
79	c3dahB_	Alignment	not modelled	98.4	20	PDB header: transferase Chain: B: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: 2.3 a crystal structure of ribose-phosphate pyrophosphokinase from2 burkholderia pseudomallei
80	c1u9yD_	Alignment	not modelled	98.4	30	PDB header: transferase Chain: D: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: crystal structure of phosphoribosyl diphosphate synthase2 from methanocaldococcus jannaschii
81	c2jbhA_	Alignment	not modelled	98.3	17	PDB header: transferase Chain: A: PDB Molecule: phosphoribosyltransferase domain-containing protein 1; PDBTitle: human phosphoribosyl transferase domain containing 1
82	c6ar9A_	Alignment	not modelled	98.2	21	PDB header: transferase Chain: A: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase, putative; PDBTitle: crystal structure of hypoxanthine-guanine-xanthine2 phosphorybosyltranferase in complex with [(2-{{[2-(2-amino-6-oxo-1,6-3 dihydro-9h-purin-9-yl)ethyl]](e)-2-phosphonoethenyl]amino}ethoxy)4 methyl]phosphonic acid
83	d1nula_	Alignment	not modelled	98.2	23	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
84	d1i5ea_	Alignment	not modelled	98.0	21	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
85	c2ehjA_	Alignment	not modelled	98.0	26	PDB header: transferase Chain: A: PDB Molecule: uracil phosphoribosyltransferase; PDBTitle: structure of uracil phosphoribosyl transferase
86	c2e55D_	Alignment	not modelled	97.9	20	PDB header: transferase Chain: D: PDB Molecule: uracil phosphoribosyltransferase; PDBTitle: structure of aq2163 protein from aquifex aeolicus
87	c5e38D_	Alignment	not modelled	97.9	26	PDB header: transferase Chain: D: PDB Molecule: uracil phosphoribosyltransferase; PDBTitle: structural basis of mapping the spontaneous mutations with 5-2 flourouracil in uracil phosphoribosyltransferase from mycobacterium3 tuberculosis
88	d1dqna_	Alignment	not modelled	97.9	19	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
89	d1o5oa_	Alignment	not modelled	97.8	26	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
90	d1xtta1	Alignment	not modelled	97.6	15	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
91	c3dmpD_	Alignment	not modelled	97.3	30	PDB header: transferase Chain: D: PDB Molecule: uracil phosphoribosyltransferase; PDBTitle: 2.6 a crystal structure of uracil phosphoribosyltransferase from2 burkholderia pseudomallei
92	d1bd3a_	Alignment	not modelled	97.2	23	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
93	d1v9sa1	Alignment	not modelled	97.2	23	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
94	d1u9ya1	Alignment	not modelled	83.7	15	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
95	d1miob_	Alignment	not modelled	77.3	12	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
96	d2c4ka1	Alignment	not modelled	70.1	13	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
97	c4v195_	Alignment	not modelled	69.0	26	PDB header: ribosome Chain: 5: PDB Molecule: mitoribosomal protein bl32m, mrpl32; PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 12 of 2
98	d1wfga_	Alignment	not modelled	67.7	22	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
99	c1vw4W_	Alignment	not modelled	67.0	32	PDB header: ribosome Chain: W: PDB Molecule: 54s ribosomal protein l32, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
100	d1v6ba_	Alignment	not modelled	63.1	24	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
						Fold: PDZ domain-like

101	d1wifa_	Alignment	not modelled	62.9	20	Superfamily: PDZ domain-like Family: PDZ domain
102	c2hcuA_	Alignment	not modelled	62.8	10	PDB header: lyase Chain: A: PDB Molecule: 3-isopropylmalate dehydratase small subunit; PDBTitle: crystal structure of smu.1381 (or leud) from streptococcus mutans
103	c2komA_	Alignment	not modelled	62.5	18	PDB header: signaling protein Chain: A: PDB Molecule: partitioning defective 3 homolog; PDBTitle: solution structure of humar par-3b pdz2 (residues 451-549)
104	d1dgsa1	Alignment	not modelled	61.9	36	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: NAD+-dependent DNA ligase, domain 3
105	c3eggC_	Alignment	not modelled	61.9	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
106	c2jilA_	Alignment	not modelled	60.3	29	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)
107	d1vaea_	Alignment	not modelled	57.7	16	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
108	c1u38A_	Alignment	not modelled	57.6	5	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
109	d1ueqa_	Alignment	not modelled	56.9	15	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
110	d2cssa1	Alignment	not modelled	56.8	18	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
111	c2i04B_	Alignment	not modelled	55.4	20	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
112	c2opgB_	Alignment	not modelled	55.3	26	PDB header: structural protein Chain: B: PDB Molecule: multiple pdz domain protein; PDBTitle: the crystal structure of the 10th pdz domain of mpdz
113	c1u37A_	Alignment	not modelled	54.8	5	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
114	c4xh7A_	Alignment	not modelled	54.4	22	PDB header: signaling protein Chain: A: PDB Molecule: multiple pdz domain protein; PDBTitle: crystal structure of mupp1 pdz4
115	d1dkua1	Alignment	not modelled	54.0	8	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
116	c2d90A_	Alignment	not modelled	53.3	16	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
117	d1wjla_	Alignment	not modelled	52.3	21	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
118	c3q3wB_	Alignment	not modelled	51.1	12	PDB header: transferase Chain: B: PDB Molecule: 3-isopropylmalate dehydratase small subunit; PDBTitle: isopropylmalate isomerase small subunit from campylobacter jejuni.
119	c5f67A_	Alignment	not modelled	51.0	17	PDB header: protein binding Chain: A: PDB Molecule: inactivation-no-after-potential d protein; PDBTitle: an exquisitely specific pdz/target recognition revealed by the2 structure of inad pdz3 in complex with trp channel tail
120	c2ogpA_	Alignment	not modelled	49.8	17	PDB header: signaling protein Chain: A: PDB Molecule: partitioning-defective 3 homolog; PDBTitle: solution structure of the second pdz domain of par-3