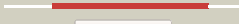



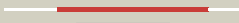


















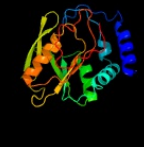


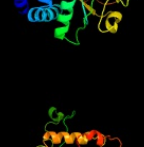



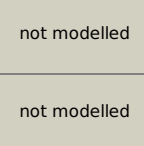


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2584c_(apt)_2910239_2910910
Date	Wed Aug 7 12:50:22 BST 2019
Unique Job ID	ec13af857272b652

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1l1qa_</a>	 Alignment		100.0	32	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
2	<a href="#">c4lzaB_</a>	 Alignment		100.0	43	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> adenine phosphoribosyltransferase; <b>PDBTitle:</b> crystal structure of adenine phosphoribosyltransferase from2 thermoanaerobacter pseudethanolicus atcc 33223, nysgrc target 029700.
3	<a href="#">c5vn4A_</a>	 Alignment		100.0	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> adenine phosphoribosyltransferase, putative; <b>PDBTitle:</b> crystal structure of adenine phosphoribosyl transferase from2 trypanosoma brucei in complex with amp, pyrophosphate, and ribose-5-3 phosphate
4	<a href="#">c5yw2D_</a>	 Alignment		100.0	43	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> adenine phosphoribosyltransferase; <b>PDBTitle:</b> crystal structure of adenine phosphoribosyltransferase from2 francisella tularensis.
5	<a href="#">c2dy0A_</a>	 Alignment		100.0	39	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> adenine phosphoribosyltransferase; <b>PDBTitle:</b> crystal structure of project jw0458 from escherichia coli
6	<a href="#">d1mzva_</a>	 Alignment		100.0	28	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
7	<a href="#">d1zn7a1</a>	 Alignment		100.0	43	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
8	<a href="#">d1g2qa_</a>	 Alignment		100.0	35	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
9	<a href="#">c4m0kD_</a>	 Alignment		100.0	43	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> adenine phosphoribosyltransferase; <b>PDBTitle:</b> crystal structure of adenine phosphoribosyltransferase from2 rhodothermus marinus dsm 4252, nysgrc target 029775.
10	<a href="#">d1qb7a_</a>	 Alignment		100.0	29	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
11	<a href="#">d1y0ba1</a>	 Alignment		100.0	21	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)

12	<a href="#">d1o57a2</a>	Alignment		100.0	27	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
13	<a href="#">c1o57A</a>	Alignment		99.9	30	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> pur operon repressor; <b>PDBTitle:</b> crystal structure of the purine operon repressor of2 bacillus subtilis
14	<a href="#">c3dezA</a>	Alignment		99.9	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> orotate phosphoribosyltransferase; <b>PDBTitle:</b> crystal structure of orotate phosphoribosyltransferase from2 streptococcus mutans
15	<a href="#">d2aeea1</a>	Alignment		99.9	19	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
16	<a href="#">c2p1zA</a>	Alignment		99.9	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosyltransferase; <b>PDBTitle:</b> crystal structure of phosphoribosyltransferase from corynebacterium2 diphtheriae
17	<a href="#">c2wnsB</a>	Alignment		99.9	30	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> orotate phosphoribosyltransferase; <b>PDBTitle:</b> human orotate phosphoribosyltransferase (oprtae) domain of2 uridine 5'-monophosphate synthase (umps) in complex with3 its substrate orotidine 5'-monophosphate (omp)
18	<a href="#">c5hkiD</a>	Alignment		99.9	27	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> orotate phosphoribosyltransferase; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis h37rv orotate2 phosphoribosyltransferase in complex with fe(iii) dicitrate
19	<a href="#">c3qw4B</a>	Alignment		99.9	26	<b>PDB header:</b> transferase, lyase <b>Chain:</b> B: <b>PDB Molecule:</b> ump synthase; <b>PDBTitle:</b> structure of leishmania donovani ump synthase
20	<a href="#">d1vcha1</a>	Alignment		99.9	20	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
21	<a href="#">c2yzkC</a>	Alignment	not modelled	99.9	29	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> orotate phosphoribosyltransferase; <b>PDBTitle:</b> crystal structure of orotate phosphoribosyltransferase from2 aeropyrum pernix
22	<a href="#">c5zgoB</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> adenine phosphoribosyltransferase; <b>PDBTitle:</b> crystal structure of apt2 from thermus thermophilus hb8
23	<a href="#">c3m3hA</a>	Alignment	not modelled	99.9	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> orotate phosphoribosyltransferase; <b>PDBTitle:</b> 1.75 angstrom resolution crystal structure of an orotate2 phosphoribosyltransferase from bacillus anthracis str. 'ames3 ancestor'
24	<a href="#">c4pawA</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> orotate phosphoribosyltransferase; <b>PDBTitle:</b> structure of hypothetical protein hp1257.
25	<a href="#">d1lh0a</a>	Alignment	not modelled	99.9	29	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
26	<a href="#">c3mjdA</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> orotate phosphoribosyltransferase; <b>PDBTitle:</b> 1.9 angstrom crystal structure of orotate phosphoribosyltransferase2 (pyre) francisella tularensis.
27	<a href="#">c2przB</a>	Alignment	not modelled	99.8	24	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> orotate phosphoribosyltransferase 1; <b>PDBTitle:</b> s. cerevisiae orotate phosphoribosyltransferase complexed with omp
28	<a href="#">c3n2IA</a>	Alignment	not modelled	99.7	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> orotate phosphoribosyltransferase; <b>PDBTitle:</b> 2.1 angstrom resolution crystal structure of an orotate2 phosphoribosyltransferase (pyre) from vibrio cholerae o1 biovar

						eltor3 str. n16961
29	<a href="#">c3kb8A</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypoxanthine phosphoribosyltransferase; <b>PDBTitle:</b> 2.09 angstrom resolution structure of a hypoxanthine-guanine2 phosphoribosyltransferase (hpt-1) from bacillus anthracis str. 'ames3 ancestor' in complex with gmp
30	<a href="#">c2ywtA</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypoxanthine-guanine phosphoribosyltransferase; <b>PDBTitle:</b> crystal structure of hypoxanthine-guanine2 phosphoribosyltransferase with gmp from thermus3 thermophilus hb8
31	<a href="#">c4fymA</a>	Alignment	not modelled	99.6	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> orotate phosphoribosyltransferase; <b>PDBTitle:</b> crystal structure of plasmodium falciparum orotate2 phosphoribosyltransferase
32	<a href="#">d1vdma1</a>	Alignment	not modelled	99.6	22	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
33	<a href="#">d1z7ga1</a>	Alignment	not modelled	99.6	17	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
34	<a href="#">c4lyyA</a>	Alignment	not modelled	99.6	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypoxanthine phosphoribosyltransferase; <b>PDBTitle:</b> crystal structure of hypoxanthine phosphoribosyltransferase from2 shewanella pealeana atcc 700345, nysgrc target 029677.
35	<a href="#">d1yfa1</a>	Alignment	not modelled	99.5	12	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
36	<a href="#">c1yfaA</a>	Alignment	not modelled	99.5	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypoxanthine-guanine phosphoribosyltransferase; <b>PDBTitle:</b> novel imp binding in feedback inhibition of hypoxanthine-guanine2 phosphoribosyltransferase from thermoanaerobacter tengcongensis
37	<a href="#">c4rqbB</a>	Alignment	not modelled	99.5	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> hypoxanthine phosphoribosyltransferase; <b>PDBTitle:</b> crystal structure of a hypoxanthine phosphoribosyltransferase (target2 id nysgrc-029686) from staphylococcus aureus (tetragonal space group)
38	<a href="#">c4pqfF</a>	Alignment	not modelled	99.5	18	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> hypoxanthine phosphoribosyltransferase; <b>PDBTitle:</b> crystal structure of hypoxanthine phosphoribosyltransferase from2 brachybacterium faecium dsm 4810, nysgrc target 029763.
39	<a href="#">d1hgxa</a>	Alignment	not modelled	99.5	13	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
40	<a href="#">c4z1oB</a>	Alignment	not modelled	99.5	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosyltransferase; <b>PDBTitle:</b> hypoxanthine-guanine-xanthine phosphoribosyltransferase (hgxpvt) from2 sulfobolus solfataricus in complex with alpha-3 phosphoribosylpyrophosphoric acid (prpp) and magnesium
41	<a href="#">c3o7mD</a>	Alignment	not modelled	99.5	14	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> hypoxanthine phosphoribosyltransferase; <b>PDBTitle:</b> 1.98 angstrom resolution crystal structure of a hypoxanthine-guanine2 phosphoribosyltransferase (hpt-2) from bacillus anthracis str. 'ames3 ancestor'
42	<a href="#">c4rhyC</a>	Alignment	not modelled	99.5	17	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> C: <b>PDB Molecule:</b> hypoxanthine-guanine phosphoribosyltransferase; <b>PDBTitle:</b> crystal structures of mycobacterium tuberculosis 6-oxopurine2 phosphoribosyltransferase which is a potential target for drug3 development against this disease
43	<a href="#">c5vogA</a>	Alignment	not modelled	99.5	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative phosphoribosyltransferase; <b>PDBTitle:</b> crystal structure of a hypothetical protein from neisseria gonorrhoeae2 with bound ppgrp
44	<a href="#">c5eswB</a>	Alignment	not modelled	99.5	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> purine/pyrimidine phosphoribosyltransferase; <b>PDBTitle:</b> crystal structure of apo hypoxanthine-guanine2 phosphoribosyltransferase from legionella pneumophila
45	<a href="#">c3lpnB</a>	Alignment	not modelled	99.5	24	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ribose-phosphate pyrophosphokinase; <b>PDBTitle:</b> crystal structure of the phosphoribosylpyrophosphate (prpp) synthetase2 from thermoplasma volcanium in complex with an atp analog (ampcpp).
46	<a href="#">d1a3ca</a>	Alignment	not modelled	99.5	22	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
47	<a href="#">c5t3oB</a>	Alignment	not modelled	99.5	23	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ribose-phosphate pyrophosphokinase; <b>PDBTitle:</b> crystal structure of the phosphorybosylpyrophosphate synthetase ii2 from thermus thermophilus
48	<a href="#">d1j7ja</a>	Alignment	not modelled	99.5	14	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
49	<a href="#">d1g9sa</a>	Alignment	not modelled	99.5	15	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
50	<a href="#">d1fsga</a>	Alignment	not modelled	99.4	19	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
						<b>Fold:</b> PRTase-like

51	<a href="#">d1ufra_</a>	Alignment	not modelled	99.4	22	<b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
52	<a href="#">d2igba1</a>	Alignment	not modelled	99.4	26	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
53	<a href="#">c5ipfA_</a>	Alignment	not modelled	99.4	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypoxanthine-guanine phosphoribosyltransferase (hgprt); <b>PDBTitle:</b> crystal structure of hypoxanthine-guanine phosphoribosyltransferase2 from schistosoma mansoni in complex with imp
54	<a href="#">d1gph11</a>	Alignment	not modelled	99.4	22	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
55	<a href="#">c3efhB_</a>	Alignment	not modelled	99.4	23	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ribose-phosphate pyrophosphokinase 1; <b>PDBTitle:</b> crystal structure of human phosphoribosyl pyrophosphate2 synthetase 1
56	<a href="#">d1dkua2</a>	Alignment	not modelled	99.3	23	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosylpyrophosphate synthetase-like
57	<a href="#">d1cjba_</a>	Alignment	not modelled	99.3	19	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
58	<a href="#">c4trbA_</a>	Alignment	not modelled	99.3	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> purine phosphoribosyltransferase (gpt-1); <b>PDBTitle:</b> sulfolobus solfataricus adenine phosphoribosyltransferase
59	<a href="#">c6apsA_</a>	Alignment	not modelled	99.3	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypoxanthine-guanine phosphoribosyltransferase; <b>PDBTitle:</b> trypanosoma brucei hypoxanthine guanine phosphoribosyltransferase in2 complex with [(2-((guanine-9-h-yl)methyl)propane-1,3 diyl)bis(oxy)3 ]bis(methylene)diphosphonic acid
60	<a href="#">d2c4ka2</a>	Alignment	not modelled	99.3	18	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosylpyrophosphate synthetase-like
61	<a href="#">d1ecfa1</a>	Alignment	not modelled	99.3	15	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
62	<a href="#">d1tc1a_</a>	Alignment	not modelled	99.3	14	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
63	<a href="#">d1p17b_</a>	Alignment	not modelled	99.3	15	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
64	<a href="#">d1pzma_</a>	Alignment	not modelled	99.3	18	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
65	<a href="#">c1pzmB_</a>	Alignment	not modelled	99.3	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> hypoxanthine-guanine phosphoribosyltransferase; <b>PDBTitle:</b> crystal structure of hgprt-ase from leishmania tarentolae in complex2 with gmp
66	<a href="#">c2c4kD_</a>	Alignment	not modelled	99.3	15	<b>PDB header:</b> regulatory protein <b>Chain:</b> D: <b>PDB Molecule:</b> phosphoribosyl pyrophosphate synthetase-associated protein <b>PDBTitle:</b> crystal structure of human phosphoribosylpyrophosphate synthetase-2 associated protein 39 (pap39)
67	<a href="#">d1w30a_</a>	Alignment	not modelled	99.3	19	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
68	<a href="#">c4twbB_</a>	Alignment	not modelled	99.2	25	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ribose-phosphate pyrophosphokinase; <b>PDBTitle:</b> sulfolobus solfataricus ribose-phosphate pyrophosphokinase
69	<a href="#">c1dkrB_</a>	Alignment	not modelled	99.2	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosyl pyrophosphate synthetase; <b>PDBTitle:</b> crystal structures of bacillus subtilis phosphoribosylpyrophosphate2 synthetase: molecular basis of allosteric inhibition and activation.
70	<a href="#">d1wd5a_</a>	Alignment	not modelled	99.2	32	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
71	<a href="#">c4s2uA_</a>	Alignment	not modelled	99.2	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ribose-phosphate pyrophosphokinase; <b>PDBTitle:</b> crystal structure of the phosphorybosylpyrophosphate synthetase from2 e. coli
72	<a href="#">c6nfeB_</a>	Alignment	not modelled	99.2	20	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> ribose-phosphate pyrophosphokinase; <b>PDBTitle:</b> crystal structure of ribose-phosphate pyrophosphokinase from2 legionella pneumophila with bound amp, adp, and ribose-5-phosphate
73	<a href="#">c2jbhA_</a>	Alignment	not modelled	99.2	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosyltransferase domain-containing protein 1; <b>PDBTitle:</b> human phosphoribosyl transferase domain containing 1
74	<a href="#">d1u9ya2</a>	Alignment	not modelled	99.2	24	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosylpyrophosphate synthetase-like
75	<a href="#">c5mp7C_</a>	Alignment	not modelled	99.1	23	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> ribose-phosphate pyrophosphokinase; <b>PDBTitle:</b> crystal structure of phosphoribosylpyrophosphate synthetase from2 mycobacterium smegmatis

76	<a href="#">c1ecjB_</a>	Alignment	not modelled	99.1	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glutamine phosphoribosylpyrophosphate <b>PDBTitle:</b> escherichia coli glutamine phosphoribosylpyrophosphate2 (prpp) amidotransferase complexed with 2 amp per tetramer
77	<a href="#">c5kapA_</a>	Alignment	not modelled	99.1	23	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> hypoxanthine-guanine phosphoribosyltransferase; <b>PDBTitle:</b> trypanosome brucei hypoxanthine-guanine phosphoribosyltransferase in2 complex with a 9-(4-(phosphonobutyl)hypoxanthine
78	<a href="#">c1gph1_</a>	Alignment	not modelled	99.1	21	<b>PDB header:</b> transferase <b>Chain:</b> 1: <b>PDB Molecule:</b> glutamine phosphoribosyl-pyrophosphate amidotransferase; <b>PDBTitle:</b> structure of the allosteric regulatory enzyme of purine biosynthesis
79	<a href="#">c1u9yD_</a>	Alignment	not modelled	99.1	23	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> ribose-phosphate pyrophosphokinase; <b>PDBTitle:</b> crystal structure of phosphoribosyl diphosphate synthase2 from methanocaldococcus jannaschii
80	<a href="#">d1nula_</a>	Alignment	not modelled	99.0	22	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
81	<a href="#">c2jkzB_</a>	Alignment	not modelled	98.8	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> hypoxanthine-guanine phosphoribosyltransferase; <b>PDBTitle:</b> saccharomyces cerevisiae hypoxanthine-guanine2 phosphoribosyltransferase in complex with gmp (guanosine 5'-3 monophosphate) (orthorhombic crystal form)
82	<a href="#">c3dahB_</a>	Alignment	not modelled	98.8	30	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ribose-phosphate pyrophosphokinase; <b>PDBTitle:</b> 2.3 a crystal structure of ribose-phosphate pyrophosphokinase from2 burkholderia pseudomallei
83	<a href="#">c6ar9A_</a>	Alignment	not modelled	98.6	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypoxanthine-guanine phosphoribosyltransferase, putative; <b>PDBTitle:</b> crystal structure of hypoxanthine-guanine-xanthine2 phosphorybosyltransferase 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
84	<a href="#">d1o5oa_</a>	Alignment	not modelled	97.8	21	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
85	<a href="#">c2ehjA_</a>	Alignment	not modelled	97.8	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> uracil phosphoribosyltransferase; <b>PDBTitle:</b> structure of uracil phosphoribosyl transferase
86	<a href="#">d1i5ea_</a>	Alignment	not modelled	97.8	20	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
87	<a href="#">c2e55D_</a>	Alignment	not modelled	97.8	21	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> uracil phosphoribosyltransferase; <b>PDBTitle:</b> structure of aq2163 protein from aquifex aeolicus
88	<a href="#">d1bd3a_</a>	Alignment	not modelled	97.5	16	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
89	<a href="#">d1dqna_</a>	Alignment	not modelled	97.5	13	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
90	<a href="#">d1xtta1</a>	Alignment	not modelled	97.2	14	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
91	<a href="#">c5e38D_</a>	Alignment	not modelled	97.2	33	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> uracil phosphoribosyltransferase; <b>PDBTitle:</b> structural basis of mapping the spontaneous mutations with 5-2 flourouracil in uracil phosphoribosyltransferase from mycobacterium3 tuberculosis
92	<a href="#">c3dmpD_</a>	Alignment	not modelled	96.9	21	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> uracil phosphoribosyltransferase; <b>PDBTitle:</b> 2.6 a crystal structure of uracil phosphoribosyltransferase from2 burkholderia pseudomallei
93	<a href="#">d1v9sa1</a>	Alignment	not modelled	96.4	33	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
94	<a href="#">c6fahB_</a>	Alignment	not modelled	79.0	23	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> caffeyl-coa reductase-etf complex subunit card; <b>PDBTitle:</b> molecular basis of the flavin-based electron-bifurcating caffeyl-coa2 reductase reaction
95	<a href="#">c4kpuB_</a>	Alignment	not modelled	72.4	13	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> electron transfer flavoprotein alpha/beta-subunit; <b>PDBTitle:</b> electron transferring flavoprotein of acidaminococcus fermentans:2 towards a mechanism of flavin-based electron bifurcation
96	<a href="#">d1wi4a1</a>	Alignment	not modelled	68.2	14	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain
97	<a href="#">d1efpb_</a>	Alignment	not modelled	67.9	15	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> ETFP subunits
98	<a href="#">c2hk8B_</a>	Alignment	not modelled	66.8	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> shikimate dehydrogenase; <b>PDBTitle:</b> crystal structure of shikimate dehydrogenase from aquifex2 aeolicus at 2.35 angstrom resolution <b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> electron transfer flavoprotein, beta



99	<a href="#">c5ow0B_</a>	Alignment	not modelled	63.1	19	subunit; <b>PDBTitle:</b> crystal structure of an electron transfer flavoprotein from <i>Geobacillus metallireducens</i>
100	<a href="#">c5ol2E_</a>	Alignment	not modelled	60.8	14	<b>PDB header:</b> flavoprotein <b>Chain:</b> E; <b>PDB Molecule:</b> electron transfer flavoprotein small subunit; <b>PDBTitle:</b> the electron transferring flavoprotein/butyryl-coa dehydrogenase2 complex from <i>Clostridium difficile</i>
101	<a href="#">c4lzlA_</a>	Alignment	not modelled	58.0	13	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> structure of the inactive form of the regulatory domain from the $\lambda$ repressor of iron transport regulator (ritr)
102	<a href="#">d1efvb_</a>	Alignment	not modelled	53.0	22	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> ETFP subunits
103	<a href="#">c5f67A_</a>	Alignment	not modelled	49.0	15	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> inactivation-no-after-potential d protein; <b>PDBTitle:</b> an exquisitely specific pdz/target recognition revealed by the structure of inad pdz3 in complex with trp channel tail
104	<a href="#">d1u9ya1</a>	Alignment	not modelled	48.9	20	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosylpyrophosphate synthetase-like
105	<a href="#">d1p1da2</a>	Alignment	not modelled	48.4	16	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain
106	<a href="#">c3eggC_</a>	Alignment	not modelled	46.9	16	<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
107	<a href="#">c2krqA_</a>	Alignment	not modelled	46.1	22	<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)
108	<a href="#">d1dcfa_</a>	Alignment	not modelled	45.7	28	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> Receiver domain of the ethylene receptor
109	<a href="#">c2jikB_</a>	Alignment	not modelled	44.5	14	<b>PDB header:</b> membrane protein <b>Chain:</b> B; <b>PDB Molecule:</b> synaptojanin-2 binding protein; <b>PDBTitle:</b> crystal structure of pdz domain of synaptojanin-2 binding2 protein
110	<a href="#">c2o2tB_</a>	Alignment	not modelled	42.0	14	<b>PDB header:</b> structural protein <b>Chain:</b> B; <b>PDB Molecule:</b> multiple pdz domain protein; <b>PDBTitle:</b> the crystal structure of the 1st pdz domain of mppdz
111	<a href="#">c4xh7A_</a>	Alignment	not modelled	41.9	12	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> multiple pdz domain protein; <b>PDBTitle:</b> crystal structure of mupp1 pdz4
112	<a href="#">c3qglD_</a>	Alignment	not modelled	38.0	15	<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 esekv peptide corresponding to the c-terminal tail of girk3
113	<a href="#">c2yubA_</a>	Alignment	not modelled	37.8	9	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> lim domain kinase 2; <b>PDBTitle:</b> solution structure of the pdz domain from mouse lim domain2 kinase
114	<a href="#">d2fe5a1</a>	Alignment	not modelled	37.6	13	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain
115	<a href="#">c1z87A_</a>	Alignment	not modelled	37.2	13	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> alpha-1-syntrophin; <b>PDBTitle:</b> solution structure of the split ph-pdz supramodule of alpha-2 syntrophin
116	<a href="#">d1ihja_</a>	Alignment	not modelled	37.2	15	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain
117	<a href="#">c2ehrA_</a>	Alignment	not modelled	36.5	10	<b>PDB header:</b> structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> inad-like protein; <b>PDBTitle:</b> solution structure of the sixth pdz domain of human inad-2 like protein
118	<a href="#">d1vaea_</a>	Alignment	not modelled	36.3	25	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain
119	<a href="#">c3fetA_</a>	Alignment	not modelled	35.8	15	<b>PDB header:</b> electron transport <b>Chain:</b> A; <b>PDB Molecule:</b> electron transfer flavoprotein subunit alpha related <b>PDBTitle:</b> crystal structure of the electron transfer flavoprotein subunit alpha2 related protein ta0212 from <i>Thermoplasma acidophilum</i>
120	<a href="#">d1qlca_</a>	Alignment	not modelled	35.2	13	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain