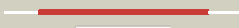








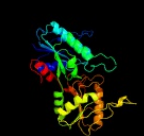




















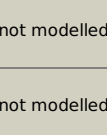


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1017c_(prsA)_1135505_1136485
Date	Wed Jul 31 22:05:08 BST 2019
Unique Job ID	1d9d3a4279257811

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5t3oB_</a>	 Alignment		100.0	44	<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
2	<a href="#">c1dkrB_</a>	 Alignment		100.0	47	<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.
3	<a href="#">c5mp7C_</a>	 Alignment		100.0	88	<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
4	<a href="#">c3efhB_</a>	 Alignment		100.0	44	<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
5	<a href="#">c4s2uA_</a>	 Alignment		100.0	45	<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
6	<a href="#">c6nfeB_</a>	 Alignment		100.0	42	<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
7	<a href="#">c3dahB_</a>	 Alignment		100.0	47	<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
8	<a href="#">c2c4kD_</a>	 Alignment		100.0	36	<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)
9	<a href="#">c4twbB_</a>	 Alignment		100.0	28	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> ribose-phosphate pyrophosphokinase; <b>PDBTitle:</b> sulfolobus solfataricus ribose-phosphate pyrophosphokinase
10	<a href="#">c1u9yD_</a>	 Alignment		100.0	30	<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
11	<a href="#">c3lpnB_</a>	 Alignment		100.0	27	<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).

12	<a href="#">d1dkua1</a>	Alignment		100.0	48	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosylpyrophosphate synthetase-like
13	<a href="#">d1u9ya1</a>	Alignment		100.0	30	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosylpyrophosphate synthetase-like
14	<a href="#">d2c4ka1</a>	Alignment		100.0	39	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosylpyrophosphate synthetase-like
15	<a href="#">d2c4ka2</a>	Alignment		100.0	33	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosylpyrophosphate synthetase-like
16	<a href="#">d1dkua2</a>	Alignment		100.0	46	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosylpyrophosphate synthetase-like
17	<a href="#">d1u9ya2</a>	Alignment		100.0	33	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosylpyrophosphate synthetase-like
18	<a href="#">c5yw2D_</a>	Alignment		99.7	17	<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.
19	<a href="#">d1wd5a_</a>	Alignment		99.6	31	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
20	<a href="#">c1yfaA_</a>	Alignment		99.6	16	<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
21	<a href="#">d1yfa1</a>	Alignment	not modelled	99.6	16	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
22	<a href="#">d1zn7a1</a>	Alignment	not modelled	99.6	19	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
23	<a href="#">d1ecfa1</a>	Alignment	not modelled	99.6	22	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
24	<a href="#">c3o7mD_</a>	Alignment	not modelled	99.6	12	<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'
25	<a href="#">d1hgxa_</a>	Alignment	not modelled	99.6	18	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
26	<a href="#">c5eswB_</a>	Alignment	not modelled	99.5	25	<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
27	<a href="#">c3kb8A_</a>	Alignment	not modelled	99.5	17	<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 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypoxanthine phosphoribosyltransferase;

28	<a href="#">c4lyyA_</a>	Alignment	not modelled	99.5	17	<b>PDBTitle:</b> crystal structure of hypoxanthine phosphoribosyltransferase from2 shewanella pealeana atcc 700345, nysgrc target 029677.
29	<a href="#">d1cjba_</a>	Alignment	not modelled	99.5	16	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
30	<a href="#">c5zgoB_</a>	Alignment	not modelled	99.5	24	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> adenine phosphoribosyltransferase; <b>PDBTitle:</b> crystal structure of aprt2 from thermus thermophilus hb8
31	<a href="#">c3dezA_</a>	Alignment	not modelled	99.5	23	<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
32	<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
33	<a href="#">d1gph11</a>	Alignment	not modelled	99.5	23	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
34	<a href="#">c2dy0A_</a>	Alignment	not modelled	99.5	20	<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
35	<a href="#">d1z7ga1</a>	Alignment	not modelled	99.5	16	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
36	<a href="#">c2ywtA_</a>	Alignment	not modelled	99.5	19	<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
37	<a href="#">d1g9sa_</a>	Alignment	not modelled	99.5	20	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
38	<a href="#">c4pfgF_</a>	Alignment	not modelled	99.5	20	<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="#">c4rqbB_</a>	Alignment	not modelled	99.5	13	<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)
40	<a href="#">c2yzkC_</a>	Alignment	not modelled	99.5	24	<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
41	<a href="#">c4lzaB_</a>	Alignment	not modelled	99.5	16	<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.
42	<a href="#">d1vdma1</a>	Alignment	not modelled	99.5	26	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
43	<a href="#">d1j7ja_</a>	Alignment	not modelled	99.5	20	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
44	<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 (hgxpirt) from2 sulfobolus solfataricus in complex with alpha-3 phosphoribosylpyrophosphoric acid (prpp) and magnesium
45	<a href="#">d1l1qa_</a>	Alignment	not modelled	99.4	20	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
46	<a href="#">d2aeaa1</a>	Alignment	not modelled	99.4	23	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
47	<a href="#">c5vogA_</a>	Alignment	not modelled	99.4	16	<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 pppp
48	<a href="#">d1vcha1</a>	Alignment	not modelled	99.4	17	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
49	<a href="#">d1g2qa_</a>	Alignment	not modelled	99.4	21	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
50	<a href="#">c4pawA_</a>	Alignment	not modelled	99.4	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> orotate phosphoribosyltransferase; <b>PDBTitle:</b> structure of hypothetical protein hp1257.
51	<a href="#">d1a3ca_</a>	Alignment	not modelled	99.4	19	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
52	<a href="#">d1ufra_</a>	Alignment	not modelled	99.4	19	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)

53	<a href="#">c1ecjB_</a>	Alignment	not modelled	99.4	22	<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
54	<a href="#">d1p17b_</a>	Alignment	not modelled	99.4	14	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
55	<a href="#">c4m0kD_</a>	Alignment	not modelled	99.4	18	<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.
56	<a href="#">c4trbA_</a>	Alignment	not modelled	99.4	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> purine phosphoribosyltransferase (gpt-1); <b>PDBTitle:</b> sulfolobus solfataricus adenine phosphoribosyltransferase
57	<a href="#">c2wnsB_</a>	Alignment	not modelled	99.4	16	<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)
58	<a href="#">d2igba1</a>	Alignment	not modelled	99.4	21	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
59	<a href="#">d1w30a_</a>	Alignment	not modelled	99.4	15	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
60	<a href="#">d1y0ba1</a>	Alignment	not modelled	99.4	20	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
61	<a href="#">d1fsga_</a>	Alignment	not modelled	99.4	17	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
62	<a href="#">c5hkiD_</a>	Alignment	not modelled	99.3	19	<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
63	<a href="#">c1gph1_</a>	Alignment	not modelled	99.3	23	<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
64	<a href="#">d1tc1a_</a>	Alignment	not modelled	99.3	13	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
65	<a href="#">c3m3hA_</a>	Alignment	not modelled	99.3	17	<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'
66	<a href="#">c5ipfA_</a>	Alignment	not modelled	99.3	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
67	<a href="#">c2p1zA_</a>	Alignment	not modelled	99.3	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosyltransferase; <b>PDBTitle:</b> crystal structure of phosphoribosyltransferase from corynebacterium2 diphtheriae
68	<a href="#">d1mzva_</a>	Alignment	not modelled	99.3	20	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
69	<a href="#">c1pzmB_</a>	Alignment	not modelled	99.3	14	<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
70	<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-9h-yl)methyl)propane-1,3 diyl)bis(oxy)3 ]bis(methylene)diphosphonic acid
71	<a href="#">d1pzma_</a>	Alignment	not modelled	99.2	13	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
72	<a href="#">c5vn4A_</a>	Alignment	not modelled	99.2	24	<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
73	<a href="#">c5kapA_</a>	Alignment	not modelled	99.2	18	<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
74	<a href="#">d1qb7a_</a>	Alignment	not modelled	99.2	21	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
75	<a href="#">d1o57a2</a>	Alignment	not modelled	99.2	20	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
						<b>PDB header:</b> transferase

76	<a href="#">c2jbhA_</a>	Alignment	not modelled	99.2	14	<b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosyltransferase domain-containing protein 1; <b>PDBTitle:</b> human phosphoribosyl transferase domain containing 1
77	<a href="#">d1lh0a_</a>	Alignment	not modelled	99.1	21	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
78	<a href="#">c1o57A_</a>	Alignment	not modelled	99.1	23	<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
79	<a href="#">c6ar9A_</a>	Alignment	not modelled	99.1	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
80	<a href="#">c3mjdA_</a>	Alignment	not modelled	99.0	14	<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.
81	<a href="#">c2jkzB_</a>	Alignment	not modelled	99.0	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="#">c2e55D_</a>	Alignment	not modelled	99.0	17	<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
83	<a href="#">d1o5oa_</a>	Alignment	not modelled	98.9	18	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
84	<a href="#">c2ehjA_</a>	Alignment	not modelled	98.9	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> uracil phosphoribosyltransferase; <b>PDBTitle:</b> structure of uracil phosphoribosyl transferase
85	<a href="#">d1dqna_</a>	Alignment	not modelled	98.9	18	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
86	<a href="#">d1i5ea_</a>	Alignment	not modelled	98.9	15	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
87	<a href="#">c3qw4B_</a>	Alignment	not modelled	98.9	18	<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
88	<a href="#">c5e38D_</a>	Alignment	not modelled	98.8	17	<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
89	<a href="#">c2przB_</a>	Alignment	not modelled	98.8	17	<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
90	<a href="#">c3dmpD_</a>	Alignment	not modelled	98.8	17	<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
91	<a href="#">d1nula_</a>	Alignment	not modelled	98.8	16	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
92	<a href="#">c3n2IA_</a>	Alignment	not modelled	98.7	19	<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
93	<a href="#">d1xtta1</a>	Alignment	not modelled	98.7	15	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
94	<a href="#">d1bd3a_</a>	Alignment	not modelled	98.7	17	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
95	<a href="#">d1v9sa1</a>	Alignment	not modelled	98.5	23	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
96	<a href="#">c4fymA_</a>	Alignment	not modelled	98.4	14	<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
97	<a href="#">c1sy7B_</a>	Alignment	not modelled	90.2	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> catalase 1; <b>PDBTitle:</b> crystal structure of the catalase-1 from neurospora crassa, native2 structure at 1.75a resolution.
98	<a href="#">c1zuwA_</a>	Alignment	not modelled	85.8	17	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate racemase 1; <b>PDBTitle:</b> crystal structure of b.subtilis glutamate racemase (race) with d-glu
99	<a href="#">c2zskA_</a>	Alignment	not modelled	85.8	13	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> 226aa long hypothetical aspartate racemase; <b>PDBTitle:</b> crystal structure of ph1733, an aspartate racemase2 homologue, from pyrococcus horikoshii ot3
100	<a href="#">c2jfzB_</a>	Alignment	not modelled	85.8	11	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> glutamate racemase; <b>PDBTitle:</b> crystal structure of helicobacter pylori glutamate

						racemase2 in complex with d-glutamate and an inhibitor <b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (udp-n-acetylmuramoyl-l-alanine:d- <b>PDBTitle:</b> udp-n-acetylmuramoyl-l-alanine:d-glutamate ligase
101	<a href="#">c3uagA_</a>	Alignment	not modelled	83.6	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of hypothetical protein opag_01669 from rhodococcus2 opacus pd630, target 016205
102	<a href="#">c4ix1B_</a>	Alignment	not modelled	83.1	12	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> trka domain protein; <b>PDBTitle:</b> gsuk channel
103	<a href="#">c4gx5D_</a>	Alignment	not modelled	81.0	22	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> uroporphyrinogen-iii synthase; <b>PDBTitle:</b> crystal structure of an uroporphyrinogen-iii synthase (sama_3255) from2 shewanella amazonensis sb2b at 1.65 a resolution
104	<a href="#">c3mw8A_</a>	Alignment	not modelled	74.6	16	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> 223aa long hypothetical arylmalonate decarboxylase; <b>PDBTitle:</b> crystal structure of st0656, a function unknown protein from2 sulfolobus tokodaii
105	<a href="#">c2dgdD_</a>	Alignment	not modelled	72.7	9	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> metallo-beta-lactamase family protein; <b>PDBTitle:</b> crystal structure of ethe1 from myxococcus xanthus
106	<a href="#">c4ysbB_</a>	Alignment	not modelled	72.6	29	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> putative maleate isomerase; <b>PDBTitle:</b> nocardia farcinica maleate cis-trans isomerase bound to2 tris
107	<a href="#">c2xecD_</a>	Alignment	not modelled	71.5	16	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> aspartate racemase; <b>PDBTitle:</b> crystal structure of pyrococcus horikoshii ot3 aspartate racemase2 complex with citric acid
108	<a href="#">c2dx7B_</a>	Alignment	not modelled	70.8	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> mcyf; <b>PDBTitle:</b> crystal structure of microcystis aeruginosa pcc 7806 aspartate2 racemase in complex with d-aspartate
109	<a href="#">c5wxzA_</a>	Alignment	not modelled	70.4	14	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> C-terminal domain of adrenodoxin reductase-like
110	<a href="#">d1gtea3</a>	Alignment	not modelled	69.8	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate racemase; <b>PDBTitle:</b> crystal structure of glutamate racemase from listeria monocytogenes
111	<a href="#">c3hfrA_</a>	Alignment	not modelled	69.0	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
112	<a href="#">d1vi2a1</a>	Alignment	not modelled	68.7	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hydroxyacylglutathione hydrolase; <b>PDBTitle:</b> crystal structure of salmonella enterica serovar2 typhimurium ycb1
113	<a href="#">c2xf4A_</a>	Alignment	not modelled	68.7	28	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Cytochrome p450 reductase N-terminal domain-like
114	<a href="#">d1b1ca_</a>	Alignment	not modelled	68.0	14	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> orotidine 5'-phosphate decarboxylase; <b>PDBTitle:</b> crystal structure of orotidine 5'-phosphate decarboxylase from2 lactobacillus acidophilus
115	<a href="#">c3tfxB_</a>	Alignment	not modelled	65.6	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> shikimate 5-dehydrogenase i alpha; <b>PDBTitle:</b> 1.45 angstrom resolution crystal structure of shikimate 5-2 dehydrogenase (aroe) from vibrio cholerae
116	<a href="#">c3o8qB_</a>	Alignment	not modelled	65.5	26	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
117	<a href="#">d1p77a1</a>	Alignment	not modelled	65.3	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> metallo-beta-lactamase family protein; <b>PDBTitle:</b> crystal structure of a hypothetical metallo-beta-lactamase from2 burkholderia pseudomallei
118	<a href="#">c4efzB_</a>	Alignment	not modelled	64.8	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> light-independent protochlorophyllide reductase subunit n; <b>PDBTitle:</b> dark operative protochlorophyllide oxidoreductase (chl-chlb)2 complex
119	<a href="#">c2xdqA_</a>	Alignment	not modelled	64.7	10	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
120	<a href="#">d1qsga_</a>	Alignment	not modelled	64.6	22	