



























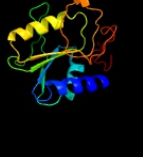




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2030c_(-)_2276449_2278494
Date	Mon Aug 5 13:25:14 BST 2019
Unique Job ID	9e7caa1db3d2ecdb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d3b55a1</a>	 Alignment		100.0	20	<b>Fold:</b> EreA/ChaN-like <b>Superfamily:</b> EreA/ChaN-like <b>Family:</b> EreA-like
2	<a href="#">c2radB_</a>	 Alignment		100.0	20	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> succinoglycan biosynthesis protein; <b>PDBTitle:</b> crystal structure of the succinoglycan biosynthesis2 protein. northeast structural genomics consortium target3 bcr135
3	<a href="#">d2qgma1</a>	 Alignment		100.0	24	<b>Fold:</b> EreA/ChaN-like <b>Superfamily:</b> EreA/ChaN-like <b>Family:</b> EreA-like
4	<a href="#">c2qgmA_</a>	 Alignment		100.0	24	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> succinoglycan biosynthesis protein; <b>PDBTitle:</b> crystal structure of succinoglycan biosynthesis protein at the2 resolution 1.7 a. northeast structural genomics consortium target3 bcr136.
5	<a href="#">d1wd5a_</a>	 Alignment		100.0	42	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
6	<a href="#">c1ecjB_</a>	 Alignment		99.7	23	<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
7	<a href="#">c1gph1_</a>	 Alignment		99.6	25	<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
8	<a href="#">d1hgxa_</a>	 Alignment		99.5	18	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
9	<a href="#">c5eswB_</a>	 Alignment		99.5	26	<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
10	<a href="#">d1ecfa1</a>	 Alignment		99.5	27	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
11	<a href="#">d1yfza1</a>	 Alignment		99.5	22	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)

12	<a href="#">c1yfaA</a>	Alignment		99.5	22	<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
13	<a href="#">d1gph1</a>	Alignment		99.5	24	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
14	<a href="#">c2ywtA</a>	Alignment		99.5	20	<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
15	<a href="#">c3kb8A</a>	Alignment		99.5	22	<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
16	<a href="#">d1j7ja</a>	Alignment		99.5	21	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
17	<a href="#">c4rhyC</a>	Alignment		99.4	20	<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
18	<a href="#">c4lyyA</a>	Alignment		99.4	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.
19	<a href="#">d1tc1a</a>	Alignment		99.4	18	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
20	<a href="#">c3o7mD</a>	Alignment		99.4	19	<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'
21	<a href="#">c5t3oB</a>	Alignment	not modelled	99.4	24	<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
22	<a href="#">c4pqfF</a>	Alignment	not modelled	99.4	23	<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.
23	<a href="#">c3lpnB</a>	Alignment	not modelled	99.4	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 (prpp) synthetase2 from thermoplasma volcanium in complex with an atp analog (ampcpp).
24	<a href="#">d1xtta1</a>	Alignment	not modelled	99.3	17	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
25	<a href="#">d1zn7a1</a>	Alignment	not modelled	99.3	31	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
26	<a href="#">c4rqbB</a>	Alignment	not modelled	99.3	17	<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)
27	<a href="#">d1z7ga1</a>	Alignment	not modelled	99.3	25	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
						<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosyltransferase;

28	<a href="#">c4z1oB_</a>	Alignment	not modelled	99.3	21	<b>PDBTitle:</b> hypoxanthine-guanine-xanthine phosphoribosyltransferase (hgxpirt) from2 sulfobolus solfataricus in complex with alpha-3 phosphoribosylpyrophosphoric acid (prpp) and magnesium
29	<a href="#">c5zgoB_</a>	Alignment	not modelled	99.3	19	<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
30	<a href="#">c3dezA_</a>	Alignment	not modelled	99.3	19	<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
31	<a href="#">c2dy0A_</a>	Alignment	not modelled	99.2	25	<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
32	<a href="#">c4lzaB_</a>	Alignment	not modelled	99.2	22	<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.
33	<a href="#">c1pzmB_</a>	Alignment	not modelled	99.2	25	<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
34	<a href="#">d1g9sa_</a>	Alignment	not modelled	99.2	18	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
35	<a href="#">d1vdma1</a>	Alignment	not modelled	99.2	33	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
36	<a href="#">d1pzma_</a>	Alignment	not modelled	99.2	21	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
37	<a href="#">c3efhB_</a>	Alignment	not modelled	99.2	16	<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
38	<a href="#">c5vogA_</a>	Alignment	not modelled	99.2	24	<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 ppgpp
39	<a href="#">d2aeaa1</a>	Alignment	not modelled	99.2	19	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
40	<a href="#">d1y0ba1</a>	Alignment	not modelled	99.1	16	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
41	<a href="#">c2c4kD_</a>	Alignment	not modelled	99.1	20	<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)
42	<a href="#">c5yw2D_</a>	Alignment	not modelled	99.1	26	<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.
43	<a href="#">c5mp7C_</a>	Alignment	not modelled	99.1	26	<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
44	<a href="#">c5ipfA_</a>	Alignment	not modelled	99.1	21	<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
45	<a href="#">d1g2qa_</a>	Alignment	not modelled	99.1	24	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
46	<a href="#">d1l1qa_</a>	Alignment	not modelled	99.1	19	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
47	<a href="#">c4trbA_</a>	Alignment	not modelled	99.1	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> purine phosphoribosyltransferase (gpt-1); <b>PDBTitle:</b> sulfobolus solfataricus adenine phosphoribosyltransferase
48	<a href="#">d1vcha1</a>	Alignment	not modelled	99.1	19	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
49	<a href="#">d2c4ka2</a>	Alignment	not modelled	99.1	22	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosylpyrophosphate synthetase-like
50	<a href="#">d1i5ea_</a>	Alignment	not modelled	99.1	21	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
51	<a href="#">c4s2uA_</a>	Alignment	not modelled	99.1	23	<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
52	<a href="#">d1u9ya2</a>	Alignment	not modelled	99.1	29	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosylpyrophosphate synthetase-like
53	<a href="#">d1w30a_</a>	Alignment	not modelled	99.0	27	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like

						<b>Family:</b> Phosphoribosyltransferases (PRTases)
54	<a href="#">d1p17b_</a>	Alignment	not modelled	99.0	20	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
55	<a href="#">c6nfeB_</a>	Alignment	not modelled	99.0	27	<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
56	<a href="#">c2ehjA_</a>	Alignment	not modelled	99.0	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> uracil phosphoribosyltransferase; <b>PDBTitle:</b> structure of uracil phosphoribosyl transferase
57	<a href="#">c2wnsB_</a>	Alignment	not modelled	99.0	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> orotate phosphoribosyltransferase; <b>PDBTitle:</b> human orotate phosphoribosyltransferase (oprtase) domain of2 uridine 5'-monophosphate synthase (umps) in complex with3 its substrate orotidine 5'-monophosphate (omp)
58	<a href="#">c1u9yD_</a>	Alignment	not modelled	99.0	34	<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
59	<a href="#">d1fsga_</a>	Alignment	not modelled	99.0	25	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
60	<a href="#">c5kapA_</a>	Alignment	not modelled	99.0	31	<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-(phosphonobutil)hypoxanthine
61	<a href="#">d1o5oa_</a>	Alignment	not modelled	99.0	27	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
62	<a href="#">c1dkrB_</a>	Alignment	not modelled	99.0	22	<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.
63	<a href="#">c5hkiD_</a>	Alignment	not modelled	98.9	34	<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
64	<a href="#">d1a3ca_</a>	Alignment	not modelled	98.9	31	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
65	<a href="#">d1cjbA_</a>	Alignment	not modelled	98.9	24	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
66	<a href="#">d1dkua2</a>	Alignment	not modelled	98.9	23	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosylpyrophosphate synthetase-like
67	<a href="#">c1o57A_</a>	Alignment	not modelled	98.9	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
68	<a href="#">c4m0kD_</a>	Alignment	not modelled	98.9	28	<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.
69	<a href="#">c4twbB_</a>	Alignment	not modelled	98.9	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ribose-phosphate pyrophosphokinase; <b>PDBTitle:</b> sulfobolus solfataricus ribose-phosphate pyrophosphokinase
70	<a href="#">c3dahB_</a>	Alignment	not modelled	98.9	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
71	<a href="#">c4pawA_</a>	Alignment	not modelled	98.9	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> orotate phosphoribosyltransferase; <b>PDBTitle:</b> structure of hypothetical protein hp1257.
72	<a href="#">d2igba1</a>	Alignment	not modelled	98.9	27	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
73	<a href="#">c2p1zA_</a>	Alignment	not modelled	98.9	37	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosyltransferase; <b>PDBTitle:</b> crystal structure of phosphoribosyltransferase from corynebacterium2 diphtheriae
74	<a href="#">c5e38D_</a>	Alignment	not modelled	98.8	23	<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
75	<a href="#">d1ufra_</a>	Alignment	not modelled	98.8	36	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
76	<a href="#">c5vn4A_</a>	Alignment	not modelled	98.8	21	<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
77	<a href="#">d1o57a2</a>	Alignment	not modelled	98.8	21	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
						<b>PDB header:</b> transferase

78	<a href="#">c2yzkC_</a>	Alignment	not modelled	98.7	33	<b>Chain:</b> C: <b>PDB Molecule:</b> orotate phosphoribosyltransferase; <b>PDBTitle:</b> crystal structure of orotate phosphoribosyltransferase from <i>2 aeropyrum pernix</i>
79	<a href="#">c6apsA_</a>	Alignment	not modelled	98.7	21	<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
80	<a href="#">c3m3hA_</a>	Alignment	not modelled	98.6	22	<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'
81	<a href="#">d1mzva_</a>	Alignment	not modelled	98.6	20	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
82	<a href="#">d2g5gx1</a>	Alignment	not modelled	98.6	21	<b>Fold:</b> EreA/ChaN-like <b>Superfamily:</b> EreA/ChaN-like <b>Family:</b> ChaN-like
83	<a href="#">c2e55D_</a>	Alignment	not modelled	98.6	20	<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
84	<a href="#">d1qb7a_</a>	Alignment	not modelled	98.6	17	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
85	<a href="#">c6ar9A_</a>	Alignment	not modelled	98.5	26	<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 phosphoribosyltransferase 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
86	<a href="#">d1lh0a_</a>	Alignment	not modelled	98.5	28	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
87	<a href="#">d1v9sa1</a>	Alignment	not modelled	98.5	22	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
88	<a href="#">c2jbhA_</a>	Alignment	not modelled	98.5	24	<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
89	<a href="#">c3mjdA_</a>	Alignment	not modelled	98.4	24	<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.
90	<a href="#">d1nula_</a>	Alignment	not modelled	98.4	24	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
91	<a href="#">c3n2IA_</a>	Alignment	not modelled	98.3	24	<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
92	<a href="#">c2przB_</a>	Alignment	not modelled	98.2	19	<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
93	<a href="#">c3qw4B_</a>	Alignment	not modelled	98.1	25	<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
94	<a href="#">c2jkbB_</a>	Alignment	not modelled	98.1	25	<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)
95	<a href="#">d1bd3a_</a>	Alignment	not modelled	98.0	15	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
96	<a href="#">c3dmpD_</a>	Alignment	not modelled	97.8	24	<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 from <i>2 burkholderia pseudomallei</i>
97	<a href="#">d1dqna_</a>	Alignment	not modelled	97.7	20	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
98	<a href="#">c4fymA_</a>	Alignment	not modelled	97.3	21	<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
99	<a href="#">d2c4ka1</a>	Alignment	not modelled	92.8	21	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosylpyrophosphate synthetase-like
100	<a href="#">d1dkua1</a>	Alignment	not modelled	92.6	22	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosylpyrophosphate synthetase-like
101	<a href="#">d1u9ya1</a>	Alignment	not modelled	90.9	15	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosylpyrophosphate synthetase-like
						<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> light-independent protochlorophyllide

102	<a href="#">c2ynmC_</a>	Alignment	not modelled	90.2	18	reductase subunit n; <b>PDBTitle:</b> structure of the adpxalf3-stabilized transition state of the2 nitrogenase-like dark-operative protochlorophyllide oxidoreductase3 complex from prochlorococcus marinus with its substrate4 protochlorophyllide a
103	<a href="#">d2ebfx2</a>	Alignment	not modelled	89.3	16	<b>Fold:</b> EreA/ChaN-like <b>Superfamily:</b> EreA/ChaN-like <b>Family:</b> PMT domain-like
104	<a href="#">c3pdiG_</a>	Alignment	not modelled	89.2	13	<b>PDB header:</b> protein binding <b>Chain:</b> G: <b>PDB Molecule:</b> nitrogenase mofe cofactor biosynthesis protein nife; <b>PDBTitle:</b> precursor bound nifen
105	<a href="#">d1vi2a1</a>	Alignment	not modelled	85.9	20	<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
106	<a href="#">c1e8cB_</a>	Alignment	not modelled	84.7	17	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-n-acetylmuramoyl-alanyl-d-glutamate-2,6-diaminopimelate <b>PDBTitle:</b> structure of mure the udp-n-acetylmuramyl tripeptide synthetase from2 e. coli
107	<a href="#">c1j6uA_</a>	Alignment	not modelled	81.0	15	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramate-alanine ligase murc; <b>PDBTitle:</b> crystal structure of udp-n-acetylmuramate-alanine ligase murc (tm0231)2 from thermotoga maritima at 2.3 a resolution
108	<a href="#">d1snna_</a>	Alignment	not modelled	81.0	17	<b>Fold:</b> YrdC/RibB <b>Superfamily:</b> YrdC/RibB <b>Family:</b> 3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
109	<a href="#">c2gn0A_</a>	Alignment	not modelled	80.9	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> threonine dehydratase catabolic; <b>PDBTitle:</b> crystal structure of dimeric biodegradative threonine deaminase (tdcb)2 from salmonella typhimurium at 1.7 a resolution (triclinic form with3 one complete subunit built in alternate conformation)
110	<a href="#">c2xjaD_</a>	Alignment	not modelled	80.8	15	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> udp-n-acetylmuramoyl-l-alanyl-d-glutamate--2,6- <b>PDBTitle:</b> structure of mure from m.tuberculosis with dipeptide and adp
111	<a href="#">c4ffjA_</a>	Alignment	not modelled	78.9	22	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> riboflavin biosynthesis protein ribba; <b>PDBTitle:</b> the crystal structure of spdhbps from s.pneumoniae
112	<a href="#">d1tdja1</a>	Alignment	not modelled	78.5	12	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
113	<a href="#">d1m1na_</a>	Alignment	not modelled	77.1	13	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> Nitrogenase iron-molybdenum protein
114	<a href="#">c4cvkA_</a>	Alignment	not modelled	76.6	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramoyl-tripeptide--d-alanyl-d-alanine <b>PDBTitle:</b> pamurf in complex with udp-murnac-tripeptide (mdap)
115	<a href="#">c6nbgD_</a>	Alignment	not modelled	75.6	22	<b>PDB header:</b> unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> glucosamine-6-phosphate deaminase; <b>PDBTitle:</b> 2.05 angstrom resolution crystal structure of hypothetical protein2 kp1_5497 from klebsiella pneumoniae.
116	<a href="#">d1g57a_</a>	Alignment	not modelled	75.0	18	<b>Fold:</b> YrdC/RibB <b>Superfamily:</b> YrdC/RibB <b>Family:</b> 3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
117	<a href="#">d1k4ia_</a>	Alignment	not modelled	74.5	21	<b>Fold:</b> YrdC/RibB <b>Superfamily:</b> YrdC/RibB <b>Family:</b> 3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
118	<a href="#">c6mgbA_</a>	Alignment	not modelled	74.2	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> capsular polysaccharide export system protein kpssc; <b>PDBTitle:</b> thermosulfurimonas dismutans kpssc, beta kdo 2,4 transferase
119	<a href="#">c5cvcB_</a>	Alignment	not modelled	73.5	18	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> serine racemase; <b>PDBTitle:</b> structure of maize serine racemase
120	<a href="#">c1tdja_</a>	Alignment	not modelled	72.2	14	<b>PDB header:</b> allostery <b>Chain:</b> A: <b>PDB Molecule:</b> biosynthetic threonine deaminase; <b>PDBTitle:</b> threonine deaminase (biosynthetic) from e. coli