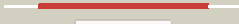



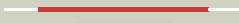




























# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3309c_(upp)_3696641_3697264
Date	Thu Aug 8 16:20:51 BST 2019
Unique Job ID	5e00db846b0b89b5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1i5ea_</a>	 Alignment		100.0	45	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
2	<a href="#">d1bd3a_</a>	 Alignment		100.0	36	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
3	<a href="#">d1o5oa_</a>	 Alignment		100.0	47	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
4	<a href="#">c2e55D_</a>	 Alignment		100.0	34	<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
5	<a href="#">c2ehjA_</a>	 Alignment		100.0	45	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> uracil phosphoribosyltransferase; <b>PDBTitle:</b> structure of uracil phosphoribosyl transferase
6	<a href="#">c5e38D_</a>	 Alignment		100.0	100	<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
7	<a href="#">c3dmpD_</a>	 Alignment		100.0	48	<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
8	<a href="#">d1v9sa1</a>	 Alignment		100.0	43	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
9	<a href="#">d1xtta1</a>	 Alignment		100.0	35	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
10	<a href="#">d1qb7a_</a>	 Alignment		99.9	15	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
11	<a href="#">d1wd5a_</a>	 Alignment		99.4	25	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)

12	<a href="#">c1yfzA</a>	Alignment		99.4	18	<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="#">d1yfza1</a>	Alignment		99.4	18	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
14	<a href="#">c4rhyC</a>	Alignment		99.4	21	<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
15	<a href="#">c4rqbB</a>	Alignment		99.4	16	<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)
16	<a href="#">c3kb8A</a>	Alignment		99.2	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
17	<a href="#">d1p17b</a>	Alignment		99.2	14	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
18	<a href="#">d1tc1a</a>	Alignment		99.2	15	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
19	<a href="#">c4z1oB</a>	Alignment		99.2	15	<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
20	<a href="#">d2igba1</a>	Alignment		99.2	19	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
21	<a href="#">c5eswB</a>	Alignment	not modelled	99.2	20	<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
22	<a href="#">c4pfqF</a>	Alignment	not modelled	99.2	25	<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="#">d1vdma1</a>	Alignment	not modelled	99.1	21	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
24	<a href="#">c1pzmB</a>	Alignment	not modelled	99.1	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
25	<a href="#">c4lyyA</a>	Alignment	not modelled	99.1	14	<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.
26	<a href="#">d1a3ca</a>	Alignment	not modelled	99.1	20	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
27	<a href="#">d1cjba</a>	Alignment	not modelled	99.1	13	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
						<b>Fold:</b> PRTase-like

28	<a href="#">d1pzma_</a>	Alignment	not modelled	99.1	13	<b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
29	<a href="#">c3o7mD_</a>	Alignment	not modelled	99.1	16	<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'
30	<a href="#">d1z7ga1</a>	Alignment	not modelled	99.1	14	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
31	<a href="#">d1ufra_</a>	Alignment	not modelled	99.1	22	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
32	<a href="#">d1hgxa_</a>	Alignment	not modelled	99.1	21	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
33	<a href="#">d1j7ja_</a>	Alignment	not modelled	99.0	18	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
34	<a href="#">d1fsga_</a>	Alignment	not modelled	99.0	13	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
35	<a href="#">c2jbhA_</a>	Alignment	not modelled	99.0	16	<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
36	<a href="#">c4trbA_</a>	Alignment	not modelled	99.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> purine phosphoribosyltransferase (gpt-1); <b>PDBTitle:</b> sulfolobus solfataricus adenine phosphoribosyltransferase
37	<a href="#">c2ywtA_</a>	Alignment	not modelled	99.0	22	<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
38	<a href="#">d1w30a_</a>	Alignment	not modelled	99.0	16	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
39	<a href="#">d1g9sa_</a>	Alignment	not modelled	99.0	16	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
40	<a href="#">c5ipfA_</a>	Alignment	not modelled	99.0	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
41	<a href="#">c6apsA_</a>	Alignment	not modelled	99.0	19	<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
42	<a href="#">c5t3oB_</a>	Alignment	not modelled	98.9	15	<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
43	<a href="#">d1ecfa1</a>	Alignment	not modelled	98.9	12	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
44	<a href="#">c5vogA_</a>	Alignment	not modelled	98.9	17	<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
45	<a href="#">c4s2uA_</a>	Alignment	not modelled	98.8	16	<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
46	<a href="#">c6nfeB_</a>	Alignment	not modelled	98.8	14	<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
47	<a href="#">c5mp7C_</a>	Alignment	not modelled	98.8	17	<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
48	<a href="#">c5kapA_</a>	Alignment	not modelled	98.8	17	<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
49	<a href="#">c3lpnB_</a>	Alignment	not modelled	98.8	19	<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).
50	<a href="#">d1u9ya2</a>	Alignment	not modelled	98.7	26	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosylpyrophosphate synthetase-like
51	<a href="#">c1ecjB_</a>	Alignment	not modelled	98.7	14	<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

52	<a href="#">d2c4ka2</a>	Alignment	not modelled	98.7	13	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosylpyrophosphate synthetase-like
53	<a href="#">d1dkua2</a>	Alignment	not modelled	98.7	14	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosylpyrophosphate synthetase-like
54	<a href="#">c6ar9A_</a>	Alignment	not modelled	98.6	15	<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
55	<a href="#">c3efhB_</a>	Alignment	not modelled	98.6	21	<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="#">c1dkrB_</a>	Alignment	not modelled	98.6	14	<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.
57	<a href="#">c2jkzB_</a>	Alignment	not modelled	98.6	18	<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)
58	<a href="#">c4twbB_</a>	Alignment	not modelled	98.6	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
59	<a href="#">d1mzva_</a>	Alignment	not modelled	98.6	17	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
60	<a href="#">c5yw2D_</a>	Alignment	not modelled	98.6	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 francisella tularensis.
61	<a href="#">c2c4kD_</a>	Alignment	not modelled	98.5	13	<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)
62	<a href="#">c5zgoB_</a>	Alignment	not modelled	98.5	21	<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
63	<a href="#">c1gph1_</a>	Alignment	not modelled	98.5	17	<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="#">d1zn7a1</a>	Alignment	not modelled	98.5	20	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
65	<a href="#">d1gph11</a>	Alignment	not modelled	98.5	14	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
66	<a href="#">d1g2qa_</a>	Alignment	not modelled	98.5	19	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
67	<a href="#">c2dy0A_</a>	Alignment	not modelled	98.4	18	<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
68	<a href="#">d1y0ba1</a>	Alignment	not modelled	98.4	16	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
69	<a href="#">c5hkiD_</a>	Alignment	not modelled	98.4	17	<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
70	<a href="#">d1vcha1</a>	Alignment	not modelled	98.4	21	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
71	<a href="#">c4pawA_</a>	Alignment	not modelled	98.4	17	<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="#">c1u9yD_</a>	Alignment	not modelled	98.3	24	<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
73	<a href="#">c5vn4A_</a>	Alignment	not modelled	98.3	18	<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
74	<a href="#">c4lzaB_</a>	Alignment	not modelled	98.3	17	<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.
75	<a href="#">d2aeaa1</a>	Alignment	not modelled	98.3	14	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)

76	<a href="#">d1l1qa_</a>	Alignment	not modelled	98.3	20	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
77	<a href="#">c2wnsB_</a>	Alignment	not modelled	98.3	13	<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)
78	<a href="#">c3dahB_</a>	Alignment	not modelled	98.3	18	<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
79	<a href="#">c4m0kD_</a>	Alignment	not modelled	98.3	20	<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.
80	<a href="#">c3dezA_</a>	Alignment	not modelled	98.2	16	<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
81	<a href="#">c2yzkC_</a>	Alignment	not modelled	98.2	26	<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
82	<a href="#">c2p1zA_</a>	Alignment	not modelled	98.2	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosyltransferase; <b>PDBTitle:</b> crystal structure of phosphoribosyltransferase from corynebacterium2 diphtheriae
83	<a href="#">d1o57a2</a>	Alignment	not modelled	98.2	13	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
84	<a href="#">c1o57A_</a>	Alignment	not modelled	98.1	12	<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
85	<a href="#">d1nula_</a>	Alignment	not modelled	97.9	21	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
86	<a href="#">d1lh0a_</a>	Alignment	not modelled	97.9	17	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
87	<a href="#">c2przB_</a>	Alignment	not modelled	97.8	12	<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
88	<a href="#">d1dqna_</a>	Alignment	not modelled	97.7	15	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
89	<a href="#">c3mjda_</a>	Alignment	not modelled	97.7	18	<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="#">c3m3ha_</a>	Alignment	not modelled	97.7	16	<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'
91	<a href="#">c3n21A_</a>	Alignment	not modelled	97.6	18	<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="#">c3qw4B_</a>	Alignment	not modelled	96.1	16	<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
93	<a href="#">c4fymA_</a>	Alignment	not modelled	95.7	13	<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
94	<a href="#">c4x84C_</a>	Alignment	not modelled	90.6	20	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> ribose-5-phosphate isomerase a; <b>PDBTitle:</b> crystal structure of ribose-5-phosphate isomerase a from pseudomonas2 aeruginosa
95	<a href="#">c2jfoB_</a>	Alignment	not modelled	90.0	19	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> glutamate racemase; <b>PDBTitle:</b> crystal structure of enterococcus faecalis glutamate2 racemase in complex with d- and l-glutamate
96	<a href="#">c3outC_</a>	Alignment	not modelled	89.9	20	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> glutamate racemase; <b>PDBTitle:</b> crystal structure of glutamate racemase from francisella tularensis2 subsp. tularensis schu s4 in complex with d-glutamate.
97	<a href="#">c5ijwA_</a>	Alignment	not modelled	89.4	21	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate racemase; <b>PDBTitle:</b> glutamate racemase (muri) from mycobacterium smegmatis with bound d-2 glutamate, 1.8 angstrom resolution, x-ray diffraction
98	<a href="#">c3hfrA_</a>	Alignment	not modelled	89.2	20	<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
99	<a href="#">d1b74a1</a>	Alignment	not modelled	88.7	24	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/glutamate racemase <b>Family:</b> Aspartate/glutamate racemase
100	<a href="#">c2ohoA_</a>	Alignment	not modelled	88.3	18	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate racemase; <b>PDBTitle:</b> structural basis for glutamate racemase inhibitor
						<b>PDB header:</b> isomerase

101	<a href="#">c5w16D_</a>	Alignment	not modelled	88.2	23	<b>Chain:</b> D; <b>PDB Molecule:</b> glutamate racemase; <b>PDBTitle:</b> crystal structure of glutamate racemase from thermus thermophilus in2 complex with d-glutamate
102	<a href="#">c2jfqA_</a>	Alignment	not modelled	87.6	18	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> glutamate racemase; <b>PDBTitle:</b> crystal structure of staphylococcus aureus glutamate racemase in2 complex with d- glutamate
103	<a href="#">c2gzmB_</a>	Alignment	not modelled	86.8	18	<b>PDB header:</b> isomerase <b>Chain:</b> B; <b>PDB Molecule:</b> glutamate racemase; <b>PDBTitle:</b> crystal structure of the glutamate racemase from bacillus anthracis
104	<a href="#">c3u7jA_</a>	Alignment	not modelled	85.2	18	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> ribose-5-phosphate isomerase a; <b>PDBTitle:</b> crystal structure of ribose-5-phosphate isomerase a from burkholderia2 thailandensis
105	<a href="#">c1b74A_</a>	Alignment	not modelled	85.1	24	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> glutamate racemase; <b>PDBTitle:</b> glutamate racemase from aquifex pyrophilus
106	<a href="#">d1u9ya1</a>	Alignment	not modelled	83.9	14	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosylpyrophosphate synthetase-like
107	<a href="#">c2dwuA_</a>	Alignment	not modelled	83.3	23	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> glutamate racemase; <b>PDBTitle:</b> crystal structure of glutamate racemase isoform race1 from bacillus2 anthracis
108	<a href="#">c3pwzA_</a>	Alignment	not modelled	82.8	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> shikimate dehydrogenase 3; <b>PDBTitle:</b> crystal structure of an ael1 enzyme from pseudomonas putida
109	<a href="#">d2c4ka1</a>	Alignment	not modelled	82.4	6	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosylpyrophosphate synthetase-like
110	<a href="#">c3uhfB_</a>	Alignment	not modelled	80.1	18	<b>PDB header:</b> isomerase <b>Chain:</b> B; <b>PDB Molecule:</b> glutamate racemase; <b>PDBTitle:</b> crystal structure of glutamate racemase from campylobacter jejuni2 subsp. jejuni
111	<a href="#">c4nmlA_</a>	Alignment	not modelled	80.0	19	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> ribulose 5-phosphate isomerase; <b>PDBTitle:</b> 2.60 angstrom resolution crystal structure of putative ribose 5-2 phosphate isomerase from toxoplasma gondii me49 in complex with dl-3 malic acid
112	<a href="#">c4omuA_</a>	Alignment	not modelled	79.7	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> shikimate dehydrogenase; <b>PDBTitle:</b> crystal structure of shikimate dehydrogenase (aroe) from pseudomonas2 putida
113	<a href="#">c2jfbB_</a>	Alignment	not modelled	78.1	16	<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
114	<a href="#">c2jfnA_</a>	Alignment	not modelled	78.1	20	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> glutamate racemase; <b>PDBTitle:</b> crystal structure of escherichia coli glutamate racemase2 in complex with l-glutamate and activator udp-murnac-ala
115	<a href="#">d1vi2a1</a>	Alignment	not modelled	77.8	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
116	<a href="#">c1zuwA_</a>	Alignment	not modelled	76.6	18	<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
117	<a href="#">c3o8qB_</a>	Alignment	not modelled	76.0	19	<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
118	<a href="#">d1dkua1</a>	Alignment	not modelled	73.3	6	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosylpyrophosphate synthetase-like
119	<a href="#">c3pgjB_</a>	Alignment	not modelled	73.1	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> shikimate dehydrogenase; <b>PDBTitle:</b> 2.49 angstrom resolution crystal structure of shikimate 5-2 dehydrogenase (aroe) from vibrio cholerae o1 biovar eltor str. n169613 in complex with shikimate
120	<a href="#">d1o8bb1</a>	Alignment	not modelled	71.9	17	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> D-ribose-5-phosphate isomerase (RpiA), catalytic domain