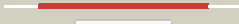
































Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0808_purF_902114_903697
Date	Fri Jul 26 01:50:39 BST 2019
Unique Job ID	310ec5ef0159936b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1gph1_	 Alignment		100.0	47	PDB header: transferase Chain: 1: PDB Molecule: glutamine phosphoribosyl-pyrophosphate amidotransferase; PDBTitle: structure of the allosteric regulatory enzyme of purine biosynthesis
2	c1ecjB_	 Alignment		100.0	39	PDB header: transferase Chain: B: PDB Molecule: glutamine phosphoribosylpyrophosphate PDBTitle: escherichia coli glutamine phosphoribosylpyrophosphate2 (prpp) amidotransferase complexed with 2 amp per tetramer
3	d1gph11	 Alignment		100.0	52	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
4	d1ecfa1	 Alignment		100.0	41	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
5	d1gph12	 Alignment		100.0	41	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases
6	c1jxaA_	 Alignment		100.0	30	PDB header: transferase Chain: A: PDB Molecule: glucosamine 6-phosphate synthase; PDBTitle: glucosamine 6-phosphate synthase with glucose 6-phosphate
7	d1ecfa2	 Alignment		100.0	38	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases
8	d1xffa_	 Alignment		100.0	27	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases
9	d1ofda3	 Alignment		100.0	26	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases
10	d1ea0a3	 Alignment		100.0	32	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases
11	c1ct9D_	 Alignment		100.0	22	PDB header: ligase Chain: D: PDB Molecule: asparagine synthetase b; PDBTitle: crystal structure of asparagine synthetase b from2 escherichia coli

12	d1ct9a2	Alignment		100.0	28	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases
13	d1te5a_	Alignment		100.0	25	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases
14	c4zfb_	Alignment		100.0	20	PDB header: hydrolase Chain: B: PDB Molecule: amidohydrolase egtc; PDBTitle: ergothioneine-biosynthetic ntn hydrolase egtc, apo form
15	c3mdnD_	Alignment		100.0	23	PDB header: transferase Chain: D: PDB Molecule: glutamine aminotransferase class-ii domain protein; PDBTitle: structure of glutamine aminotransferase class-ii domain protein2 (spo2029) from silicibacter pomeroyi
16	c1m1zB_	Alignment		99.9	21	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactam synthetase; PDBTitle: beta-lactam synthetase apo enzyme
17	c1lm1A_	Alignment		99.9	29	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin-dependent glutamate synthase; PDBTitle: structural studies on the synchronization of catalytic centers in2 glutamate synthase: native enzyme
18	c2vdcF_	Alignment		99.9	33	PDB header: oxidoreductase Chain: F: PDB Molecule: glutamate synthase [nadh] large chain; PDBTitle: the 9.5 a resolution structure of glutamate synthase from cryo-2 electron microscopy and its oligomerization behavior in solution:3 functional implications.
19	c1q15A_	Alignment		99.9	17	PDB header: biosynthetic protein Chain: A: PDB Molecule: carc; PDBTitle: carbapenam synthetase
20	c1o57A_	Alignment		99.9	19	PDB header: dna binding protein Chain: A: PDB Molecule: pur operon repressor; PDBTitle: crystal structure of the purine operon repressor of2 bacillus subtilis
21	d1jgta2	Alignment	not modelled	99.9	22	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases
22	d1q15a2	Alignment	not modelled	99.9	19	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases
23	c3kb8A_	Alignment	not modelled	99.8	19	PDB header: transferase Chain: A: PDB Molecule: hypoxanthine phosphoribosyltransferase; PDBTitle: 2.09 angstrom resolution structure of a hypoxanthine-guanine2 phosphoribosyltransferase (hpt-1) from bacillus anthracis str. 'ames3 ancestor' in complex with gmp
24	d1wd5a_	Alignment	not modelled	99.8	25	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
25	d1z7ga1	Alignment	not modelled	99.8	16	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
26	c3o7mD_	Alignment	not modelled	99.7	16	PDB header: transferase Chain: D: PDB Molecule: hypoxanthine phosphoribosyltransferase; PDBTitle: 1.98 angstrom resolution crystal structure of a hypoxanthine-guanine2 phosphoribosyltransferase (hpt-2) from bacillus anthracis str. 'ames3 ancestor'
27	d1o57a2	Alignment	not modelled	99.7	22	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
28	d1g9sa_	Alignment	not modelled	99.6	19	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)

29	c2jhbA_	Alignment	not modelled	99.6	14	PDB header: transferase Chain: A: PDB Molecule: phosphoribosyltransferase domain-containing protein 1; PDBTitle: human phosphoribosyl transferase domain containing 1
30	c4z1oB_	Alignment	not modelled	99.6	18	PDB header: transferase Chain: B: PDB Molecule: phosphoribosyltransferase; PDBTitle: hypoxanthine-guanine-xanthine phosphoribosyltransferase (hgxpvt) from2 sulfobolus solfataricus in complex with alpha-3 phosphoribosylpyrophosphoric acid (prpp) and magnesium
31	c5vogA_	Alignment	not modelled	99.6	21	PDB header: transferase Chain: A: PDB Molecule: putative phosphoribosyltransferase; PDBTitle: crystal structure of a hypothetical protein from neisseria gonorrhoeae2 with bound pppp
32	d2igba1	Alignment	not modelled	99.6	22	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
33	c1yfaA_	Alignment	not modelled	99.6	20	PDB header: transferase Chain: A: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: novel imp binding in feedback inhibition of hypoxanthine-guanine2 phosphoribosyltransferase from thermoanaerobacter tengcongensis
34	d1yfa1	Alignment	not modelled	99.6	20	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
35	c4pfqF_	Alignment	not modelled	99.6	20	PDB header: transferase Chain: F: PDB Molecule: hypoxanthine phosphoribosyltransferase; PDBTitle: crystal structure of hypoxanthine phosphoribosyltransferase from2 brachy bacterium faecium dsm 4810, nysgrc target 029763.
36	c4rqbB_	Alignment	not modelled	99.6	14	PDB header: transferase Chain: B: PDB Molecule: hypoxanthine phosphoribosyltransferase; PDBTitle: crystal structure of a hypoxanthine phosphoribosyltransferase (target2 id nysgrc-029686) from staphylococcus aureus (tetragonal space group)
37	d1hgxa_	Alignment	not modelled	99.6	18	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
38	d1y0ba1	Alignment	not modelled	99.6	16	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
39	c5zgoB_	Alignment	not modelled	99.6	19	PDB header: transferase Chain: B: PDB Molecule: adenine phosphoribosyltransferase; PDBTitle: crystal structure of apt2 from thermus thermophilus hb8
40	d1cjba_	Alignment	not modelled	99.6	13	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
41	c4rhyC_	Alignment	not modelled	99.6	25	PDB header: transferase/transferase inhibitor Chain: C: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: crystal structures of mycobacterium tuberculosis 6-oxopurine2 phosphoribosyltransferase which is a potential target for drug3 development against this disease
42	d1vdma1	Alignment	not modelled	99.6	22	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
43	c5eswB_	Alignment	not modelled	99.5	18	PDB header: transferase Chain: B: PDB Molecule: purine/pyrimidine phosphoribosyltransferase; PDBTitle: crystal structure of apo hypoxanthine-guanine2 phosphoribosyltransferase from legionella pneumophila
44	c2ywtA_	Alignment	not modelled	99.5	20	PDB header: transferase Chain: A: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: crystal structure of hypoxanthine-guanine2 phosphoribosyltransferase with gmp from thermus3 thermophilus hb8
45	d1j7ja_	Alignment	not modelled	99.5	20	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
46	d1a3ca_	Alignment	not modelled	99.5	20	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
47	d1w30a_	Alignment	not modelled	99.5	21	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
48	c5ipfA_	Alignment	not modelled	99.5	16	PDB header: transferase Chain: A: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase (hgprt); PDBTitle: crystal structure of hypoxanthine-guanine phosphoribosyltransferase2 from schistosoma mansoni in complex with imp
49	c4trbA_	Alignment	not modelled	99.5	14	PDB header: transferase Chain: A: PDB Molecule: purine phosphoribosyltransferase (gpt-1); PDBTitle: sulfobolus solfataricus adenine phosphoribosyltransferase
50	c4lyvA_	Alignment	not modelled	99.5	15	PDB header: transferase Chain: A: PDB Molecule: hypoxanthine phosphoribosyltransferase; PDBTitle: crystal structure of hypoxanthine phosphoribosyltransferase from2 shewanella pealeana atcc 700345, nysgrc target 029677.
51	d1fsga_	Alignment	not modelled	99.5	14	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)

52	d1ufra_	Alignment	not modelled	99.5	23	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
53	d1tc1a_	Alignment	not modelled	99.5	15	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
54	d1vcha1	Alignment	not modelled	99.5	20	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
55	c2dy0A_	Alignment	not modelled	99.4	17	PDB header: transferase Chain: A: PDB Molecule: adenine phosphoribosyltransferase; PDBTitle: crystal structure of project jw0458 from escherichia coli
56	d1p17b_	Alignment	not modelled	99.4	14	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
57	d2c4ka2	Alignment	not modelled	99.4	18	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
58	c4m0kD_	Alignment	not modelled	99.4	19	PDB header: transferase Chain: D: PDB Molecule: adenine phosphoribosyltransferase; PDBTitle: crystal structure of adenine phosphoribosyltransferase from2 rhodothermus marinus dsm 4252, nysgrc target 029775.
59	c5hkiD_	Alignment	not modelled	99.4	22	PDB header: transferase Chain: D: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: crystal structure of mycobacterium tuberculosis h37rv orotate2 phosphoribosyltransferase in complex with fe(iii) dicitrate
60	c4lzaB_	Alignment	not modelled	99.4	19	PDB header: transferase Chain: B: PDB Molecule: adenine phosphoribosyltransferase; PDBTitle: crystal structure of adenine phosphoribosyltransferase from2 thermoanaerobacter pseudethanolicus atcc 33223, nysgrc target 029700.
61	c5t3oB_	Alignment	not modelled	99.4	21	PDB header: transferase Chain: B: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: crystal structure of the phosphorybosylpyrophosphate synthetase ii2 from thermus thermophilus
62	d1zn7a1	Alignment	not modelled	99.4	19	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
63	c1pzmB_	Alignment	not modelled	99.3	17	PDB header: transferase Chain: B: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: crystal structure of hgprt-ase from leishmania tarentolae in complex2 with gmp
64	c5yw2D_	Alignment	not modelled	99.3	16	PDB header: transferase Chain: D: PDB Molecule: adenine phosphoribosyltransferase; PDBTitle: crystal structure of adenine phosphoribosyltransferase from2 francisella tularensis.
65	d1pzma_	Alignment	not modelled	99.3	12	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
66	c2wnsB_	Alignment	not modelled	99.3	17	PDB header: transferase Chain: B: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: human orotate phosphoribosyltransferase (oprtase) domain of2 uridine 5'-monophosphate synthase (umps) in complex with3 its substrate orotidine 5'-monophosphate (omp)
67	d1g2qa_	Alignment	not modelled	99.3	21	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
68	d1l1qa_	Alignment	not modelled	99.2	15	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
69	c3dezA_	Alignment	not modelled	99.2	21	PDB header: transferase Chain: A: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: crystal structure of orotate phosphoribosyltransferase from2 streptococcus mutans
70	c4pawA_	Alignment	not modelled	99.2	19	PDB header: transferase Chain: A: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: structure of hypothetical protein hp1257.
71	c3efhB_	Alignment	not modelled	99.2	15	PDB header: transferase Chain: B: PDB Molecule: ribose-phosphate pyrophosphokinase 1; PDBTitle: crystal structure of human phosphoribosyl pyrophosphate2 synthetase 1
72	d1nula_	Alignment	not modelled	99.2	23	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
73	c2p1zA_	Alignment	not modelled	99.2	25	PDB header: transferase Chain: A: PDB Molecule: phosphoribosyltransferase; PDBTitle: crystal structure of phosphoribosyltransferase from corynebacterium2 diphtheriae
74	d2aeaa1	Alignment	not modelled	99.2	19	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
75	c5mp7C_	Alignment	not modelled	99.2	22	PDB header: transferase Chain: C: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: crystal structure of phosphoribosylpyrophosphate synthetase from2 mycobacterium smegmatis
76	c6apsA_	Alignment	not modelled	99.2	17	PDB header: transferase Chain: A: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: trypanosoma brucei hypoxanthine guanine phosphoribosyltransferase in2 complex with [(2-((guanine-9h-yl)methyl)propane-1,3 diyl)bis(oxy)3]bis(methylene)diphosphonic acid
						PDB header: transferase

77	c1dkrB_	Alignment	not modelled	99.1	20	Chain: B: PDB Molecule: phosphoribosyl pyrophosphate synthetase; PDBTitle: crystal structures of bacillus subtilis phosphoribosylpyrophosphate2 synthetase: molecular basis of allosteric inhibition and activation.
78	c2przB_	Alignment	not modelled	99.1	16	PDB header: transferase Chain: B: PDB Molecule: orotate phosphoribosyltransferase 1; PDBTitle: s. cerevisiae orotate phosphoribosyltransferase complexed with omp
79	c2c4kD_	Alignment	not modelled	99.1	17	PDB header: regulatory protein Chain: D: PDB Molecule: phosphoribosyl pyrophosphate synthetase-associated protein PDBTitle: crystal structure of human phosphoribosylpyrophosphate synthetase-2 associated protein 39 (pap39)
80	c5kapA_	Alignment	not modelled	99.1	19	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: trypanosome brucei hypoxanthine-guanine phosphoribosyltransferase in2 complex with a 9-(4-(phosphonobutyl)hypoxanthine
81	c3mjdA_	Alignment	not modelled	99.1	15	PDB header: transferase Chain: A: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: 1.9 angstrom crystal structure of orotate phosphoribosyltransferase2 (pyre) francisella tularensis.
82	c3lpnB_	Alignment	not modelled	99.1	25	PDB header: transferase Chain: B: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: crystal structure of the phosphoribosylpyrophosphate (prpp) synthetase2 from thermoplasma volcanium in complex with an atp analog (ampcpp).
83	d1u9ya2	Alignment	not modelled	99.1	21	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
84	d1lh0a_	Alignment	not modelled	99.1	22	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
85	d1dkua2	Alignment	not modelled	99.1	30	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
86	c6nfeB_	Alignment	not modelled	99.0	17	PDB header: ligase Chain: B: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: crystal structure of ribose-phosphate pyrophosphokinase from2 legionella pneumophila with bound amp, adp, and ribose-5-phosphate
87	c4s2uA_	Alignment	not modelled	99.0	16	PDB header: transferase Chain: A: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: crystal structure of the phosphorybosylpyrophosphate synthetase from2 e. coli
88	c3m3hA_	Alignment	not modelled	99.0	26	PDB header: transferase Chain: A: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: 1.75 angstrom resolution crystal structure of an orotate2 phosphoribosyltransferase from bacillus anthracis str. 'ames3 ancestor'
89	c2yzkC_	Alignment	not modelled	99.0	20	PDB header: transferase Chain: C: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: crystal structure of orotate phosphoribosyltransferase from2 aeropyrum pernix
90	c3n2lA_	Alignment	not modelled	99.0	24	PDB header: transferase Chain: A: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: 2.1 angstrom resolution crystal structure of an orotate2 phosphoribosyltransferase (pyre) from vibrio cholerae o1 biovar eltor3 str. n16961
91	d1qb7a_	Alignment	not modelled	99.0	15	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
92	d1mzva_	Alignment	not modelled	99.0	14	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
93	c5vn4A_	Alignment	not modelled	98.9	18	PDB header: transferase Chain: A: PDB Molecule: adenine phosphoribosyltransferase, putative; PDBTitle: crystal structure of adenine phosphoribosyl transferase from2 trypanosoma brucei in complex with amp, pyrophosphate, and ribose-5-3 phosphate
94	c3dahB_	Alignment	not modelled	98.9	20	PDB header: transferase Chain: B: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: 2.3 a crystal structure of ribose-phosphate pyrophosphokinase from2 burkholderia pseudomallei
95	c4twbB_	Alignment	not modelled	98.9	19	PDB header: transferase Chain: B: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: sulfolobus solfataricus ribose-phosphate pyrophosphokinase
96	c1u9yD_	Alignment	not modelled	98.8	23	PDB header: transferase Chain: D: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: crystal structure of phosphoribosyl diphosphate synthase2 from methanocaldococcus jannaschii
97	c3qw4B_	Alignment	not modelled	98.8	22	PDB header: transferase, lyase Chain: B: PDB Molecule: ump synthase; PDBTitle: structure of leishmania donovani ump synthase
98	c6ar9A_	Alignment	not modelled	98.7	20	PDB header: transferase Chain: A: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase, putative; PDBTitle: 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
99	c2jkzB_	Alignment	not modelled	98.7	14	PDB header: transferase Chain: B: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: saccharomyces cerevisiae hypoxanthine-guanine2 phosphoribosyltransferase in complex with gmp (guanosine 5'-3

						monophosphate) (orthorhombic crystal form)
100	c4fymA	Alignment	not modelled	98.6	14	PDB header: transferase Chain: A: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: crystal structure of plasmodium falciparum orotate2 phosphoribosyltransferase
101	c2ehjA	Alignment	not modelled	98.1	18	PDB header: transferase Chain: A: PDB Molecule: uracil phosphoribosyltransferase; PDBTitle: structure of uracil phosphoribosyl transferase
102	d1o5oa	Alignment	not modelled	98.0	20	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
103	c5e38D	Alignment	not modelled	98.0	20	PDB header: transferase Chain: D: PDB Molecule: uracil phosphoribosyltransferase; PDBTitle: structural basis of mapping the spontaneous mutations with 5-2 flourouracil in uracil phosphoribosyltransferase from mycobacterium3 tuberculosis
104	d1xtta1	Alignment	not modelled	97.9	10	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
105	d1i5ea	Alignment	not modelled	97.9	17	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
106	d1dqna	Alignment	not modelled	97.7	15	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
107	c2e55D	Alignment	not modelled	97.5	18	PDB header: transferase Chain: D: PDB Molecule: uracil phosphoribosyltransferase; PDBTitle: structure of aq2163 protein from aquifex aeolicus
108	d1v9sa1	Alignment	not modelled	97.4	19	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
109	d1bd3a	Alignment	not modelled	97.1	18	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
110	c3dmpD	Alignment	not modelled	96.8	19	PDB header: transferase Chain: D: PDB Molecule: uracil phosphoribosyltransferase; PDBTitle: 2.6 a crystal structure of uracil phosphoribosyltransferase from2 burkholderia pseudomallei
111	d1dkua1	Alignment	not modelled	96.8	23	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
112	d1u9ya1	Alignment	not modelled	95.2	12	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
113	d2c4ka1	Alignment	not modelled	94.9	21	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
114	c1a1sA	Alignment	not modelled	90.2	24	PDB header: transcarbamylyase Chain: A: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: ornithine carbamoyltransferase from pyrococcus furiosus
115	c3sdsA	Alignment	not modelled	89.9	22	PDB header: transferase Chain: A: PDB Molecule: ornithine carbamoyltransferase, mitochondrial; PDBTitle: crystal structure of a mitochondrial ornithine carbamoyltransferase2 from coccidioides immitis
116	c2d92A	Alignment	not modelled	88.6	24	PDB header: protein binding Chain: A: PDB Molecule: inad-like protein; PDBTitle: solution structure of the fifth pdz domain of inad-like2 protein
117	c3mnmA	Alignment	not modelled	88.1	33	PDB header: transferase Chain: A: PDB Molecule: histidine kinase homolog; PDBTitle: crystal structure of the receiver domain of the histidine kinase cki12 from arabidopsis thaliana complexed with mg2+
118	d1qh8a	Alignment	not modelled	87.5	12	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
119	c3txxD	Alignment	not modelled	87.1	20	PDB header: transferase Chain: D: PDB Molecule: putrescine carbamoyltransferase; PDBTitle: crystal structure of putrescine transcarbamylyase from enterococcus2 faecalis
120	c3gd5D	Alignment	not modelled	84.9	20	PDB header: transferase Chain: D: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: crystal structure of ornithine carbamoyltransferase from gloebacter2 violaceus