





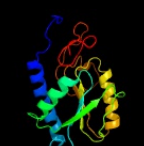




Phyre2

Email: mdejesus@rockefeller.edu
 Description: RVBD1379_(pyrR)_1552660_1553241
 Date: Wed Jul 31 22:05:48 BST 2019
 Unique Job ID: 14c3dc1c9d45b5b0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1w30a_	Alignment		100.0	98	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
2	d2igba1	Alignment		100.0	56	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
3	d1a3ca_	Alignment		100.0	52	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
4	d1ufra_	Alignment		100.0	53	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
5	d1fsga_	Alignment		100.0	19	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
6	d1cjba_	Alignment		100.0	17	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
7	c6ar9A_	Alignment		100.0	17	PDB header: transferase Chain: A: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase, putative; PDBTitle: 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
8	c3kb8A_	Alignment		100.0	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
9	d1p17b_	Alignment		100.0	16	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
10	c5eswB_	Alignment		100.0	24	PDB header: transferase Chain: B: PDB Molecule: purine/pyrimidine phosphoribosyltransferase; PDBTitle: crystal structure of apo hypoxanthine-guanine2 phosphoribosyltransferase from legionella pneumophila
11	c2jbaA_	Alignment		100.0	19	PDB header: transferase Chain: A: PDB Molecule: phosphoribosyltransferase domain-containing protein 1; PDBTitle: human phosphoribosyl transferase domain containing 1

12	c5ipfA_	Alignment		100.0	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
13	c4rqbB_	Alignment		100.0	18	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)
14	c4pfgF_	Alignment		100.0	25	PDB header: transferase Chain: F: PDB Molecule: hypoxanthine phosphoribosyltransferase; PDBTitle: crystal structure of hypoxanthine phosphoribosyltransferase from2 brachybacterium faecium dsm 4810, nysgrc target 029763.
15	c4rhyC_	Alignment		100.0	18	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
16	d1tc1a_	Alignment		100.0	18	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
17	d1z7ga1	Alignment		100.0	17	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
18	d1pzma_	Alignment		100.0	17	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
19	d1g9sa_	Alignment		100.0	19	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
20	c5kapA_	Alignment		100.0	21	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
21	d1yfa1	Alignment	not modelled	100.0	17	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
22	c1yfaA_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: novel imp binding in feedback inhibition of hypoxanthine-guanine2 phosphoribosyltransferase from thermoanaerobacter tengcongensis
23	c4lyyA_	Alignment	not modelled	100.0	21	PDB header: transferase Chain: A: PDB Molecule: hypoxanthine phosphoribosyltransferase; PDBTitle: crystal structure of hypoxanthine phosphoribosyltransferase from2 shewanella pealeana atcc 700345, nysgrc target 029677.
24	c6apsA_	Alignment	not modelled	100.0	19	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
25	c1pzmB_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: B: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: crystal structure of hgprt-ase from leishmania tarentolae in complex2 with gmp
26	d1dqna_	Alignment	not modelled	100.0	12	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
						PDB header: transferase Chain: D: PDB Molecule: hypoxanthine phosphoribosyltransferase;

27	c3o7mD_	Alignment	not modelled	100.0	21	PDBTitle: 1.98 angstrom resolution crystal structure of a hypoxanthine-guanine2 phosphoribosyltransferase (hpt-2) from bacillus anthracis str. 'ames3 ancestor'
28	d1hgxa_	Alignment	not modelled	100.0	18	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
29	c2ywtA_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: crystal structure of hypoxanthine-guanine2 phosphoribosyltransferase with gmp from thermus3 thermophilus hb8
30	d1j7ja_	Alignment	not modelled	100.0	19	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
31	c4trbA_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: purine phosphoribosyltransferase (gpt-1); PDBTitle: sulfobolus solfataricus adenine phosphoribosyltransferase
32	c4z1oB_	Alignment	not modelled	100.0	20	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
33	c5vogA_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: putative phosphoribosyltransferase; PDBTitle: crystal structure of a hypothetical protein from neisseria gonorrhoeae2 with bound pppp
34	d1vdma1	Alignment	not modelled	99.9	24	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
35	c2jkbB_	Alignment	not modelled	99.9	23	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)
36	d1nula_	Alignment	not modelled	99.9	16	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
37	d1wd5a_	Alignment	not modelled	99.8	29	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
38	d1g2qa_	Alignment	not modelled	99.7	13	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
39	d1ecfa1	Alignment	not modelled	99.7	19	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
40	d1gph11	Alignment	not modelled	99.7	21	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
41	d1zn7a1	Alignment	not modelled	99.7	18	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
42	c5yw2D_	Alignment	not modelled	99.7	15	PDB header: transferase Chain: D: PDB Molecule: adenine phosphoribosyltransferase; PDBTitle: crystal structure of adenine phosphoribosyltransferase from2 francisella tularensis.
43	c1ecjB_	Alignment	not modelled	99.6	20	PDB header: transferase Chain: B: PDB Molecule: glutamine phosphoribosylpyrophosphate PDBTitle: escherichia coli glutamine phosphoribosylpyrophosphate2 (prpp) amidotransferase complexed with 2 amp per tetramer
44	c5zgoB_	Alignment	not modelled	99.6	16	PDB header: transferase Chain: B: PDB Molecule: adenine phosphoribosyltransferase; PDBTitle: crystal structure of apt2 from thermus thermophilus hb8
45	c4pawA_	Alignment	not modelled	99.6	15	PDB header: transferase Chain: A: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: structure of hypothetical protein hp1257.
46	c4lzaB_	Alignment	not modelled	99.6	12	PDB header: transferase Chain: B: PDB Molecule: adenine phosphoribosyltransferase; PDBTitle: crystal structure of adenine phosphoribosyltransferase from2 thermoanaerobacter pseudethanolicus atcc 33223, nysgrc target 029700.
47	c4m0kD_	Alignment	not modelled	99.6	15	PDB header: transferase Chain: D: PDB Molecule: adenine phosphoribosyltransferase; PDBTitle: crystal structure of adenine phosphoribosyltransferase from2 rhodothermus marinus dsm 4252, nysgrc target 029775.
48	c2dy0A_	Alignment	not modelled	99.6	13	PDB header: transferase Chain: A: PDB Molecule: adenine phosphoribosyltransferase; PDBTitle: crystal structure of project jw0458 from escherichia coli
49	d1lh0a_	Alignment	not modelled	99.6	19	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
50	c5hkiD_	Alignment	not modelled	99.6	24	PDB header: transferase Chain: D: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: crystal structure of mycobacterium tuberculosis h37rv orotate2 phosphoribosyltransferase in complex with fe(iii) dicitrate
51	d1y0ba1	Alignment	not modelled	99.6	14	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
						Fold: PRTase-like

52	d1vcha1	Alignment	not modelled	99.6	18	Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
53	c1o57A	Alignment	not modelled	99.6	15	PDB header: dna binding protein Chain: A: PDB Molecule: pur operon repressor; PDBTitle: crystal structure of the purine operon repressor of2 bacillus subtilis
54	c5t3oB	Alignment	not modelled	99.5	18	PDB header: transferase Chain: B: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: crystal structure of the phosphoribosylpyrophosphate synthetase ii2 from thermus thermophilus
55	d1o57a2	Alignment	not modelled	99.5	15	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
56	c3n2IA	Alignment	not modelled	99.5	19	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
57	c2przB	Alignment	not modelled	99.5	19	PDB header: transferase Chain: B: PDB Molecule: orotate phosphoribosyltransferase 1; PDBTitle: s. cerevisiae orotate phosphoribosyltransferase complexed with omp
58	c1gph1	Alignment	not modelled	99.5	22	PDB header: transferase Chain: 1: PDB Molecule: glutamine phosphoribosyl-pyrophosphate amidotransferase; PDBTitle: structure of the allosteric regulatory enzyme of purine biosynthesis
59	c3mjdA	Alignment	not modelled	99.5	17	PDB header: transferase Chain: A: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: 1.9 angstrom crystal structure of orotate phosphoribosyltransferase2 (pyre) francisella tularensis.
60	c2wnsB	Alignment	not modelled	99.5	18	PDB header: transferase Chain: B: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: human orotate phosphoribosyltransferase (optase) domain of2 uridine 5'-monophosphate synthase (umps) in complex with3 its substrate orotidine 5'-monophosphate (omp)
61	c2p1zA	Alignment	not modelled	99.5	22	PDB header: transferase Chain: A: PDB Molecule: phosphoribosyltransferase; PDBTitle: crystal structure of phosphoribosyltransferase from corynebacterium2 diphtheriae
62	d1l1qa	Alignment	not modelled	99.5	16	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
63	c2yzkC	Alignment	not modelled	99.5	25	PDB header: transferase Chain: C: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: crystal structure of orotate phosphoribosyltransferase from2 aeropyrum pernix
64	c2ehjA	Alignment	not modelled	99.4	20	PDB header: transferase Chain: A: PDB Molecule: uracil phosphoribosyltransferase; PDBTitle: structure of uracil phosphoribosyl transferase
65	c5e38D	Alignment	not modelled	99.4	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
66	d1o5oa	Alignment	not modelled	99.4	19	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
67	d1i5ea	Alignment	not modelled	99.4	18	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
68	c4fymA	Alignment	not modelled	99.4	18	PDB header: transferase Chain: A: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: crystal structure of plasmodium falciparum orotate2 phosphoribosyltransferase
69	d2aeaa1	Alignment	not modelled	99.4	15	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
70	d1mzva	Alignment	not modelled	99.4	20	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
71	c3dezA	Alignment	not modelled	99.4	15	PDB header: transferase Chain: A: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: crystal structure of orotate phosphoribosyltransferase from2 streptococcus mutans
72	c2e55D	Alignment	not modelled	99.3	15	PDB header: transferase Chain: D: PDB Molecule: uracil phosphoribosyltransferase; PDBTitle: structure of aq2163 protein from aquifex aeolicus
73	d1bd3a	Alignment	not modelled	99.3	19	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
74	d1qb7a	Alignment	not modelled	99.3	16	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
75	c5vn4A	Alignment	not modelled	99.3	15	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
76	c3lpnB	Alignment	not modelled	99.3	15	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). PDB header: transferase

77	c5mp7C_	Alignment	not modelled	99.3	26	Chain: C: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: crystal structure of phosphoribosylpyrophosphate synthetase from2 mycobacterium smegmatis
78	c4s2uA_	Alignment	not modelled	99.3	20	PDB header: transferase Chain: A: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: crystal structure of the phosphorybosylpyrophosphate synthetase from2 e. coli
79	d1xtta1	Alignment	not modelled	99.3	16	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
80	c3m3hA_	Alignment	not modelled	99.2	20	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'
81	c6nfeB_	Alignment	not modelled	99.2	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
82	d1v9sa1	Alignment	not modelled	99.2	21	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
83	d1dkua2	Alignment	not modelled	99.2	25	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
84	c3dmpD_	Alignment	not modelled	99.2	20	PDB header: transferase Chain: D: PDB Molecule: uracil phosphoribosyltransferase; PDBTitle: 2.6 a crystal structure of uracil phosphoribosyltransferase from2 burkholderia pseudomallei
85	c3efhB_	Alignment	not modelled	99.1	19	PDB header: transferase Chain: B: PDB Molecule: ribose-phosphate pyrophosphokinase 1; PDBTitle: crystal structure of human phosphoribosyl pyrophosphate2 synthetase 1
86	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)
87	d2c4ka2	Alignment	not modelled	99.1	18	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
88	d1u9ya2	Alignment	not modelled	99.1	21	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
89	c1dkrB_	Alignment	not modelled	99.1	24	PDB header: transferase Chain: B: PDB Molecule: phosphoribosyl pyrophosphate synthetase; PDBTitle: crystal structures of bacillus subtilis phosphoribosylpyrophosphate2 synthetase: molecular basis of allosteric inhibition and activation.
90	c4twbB_	Alignment	not modelled	99.1	24	PDB header: transferase Chain: B: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: sulfolobus solfataricus ribose-phosphate pyrophosphokinase
91	c1u9yD_	Alignment	not modelled	98.9	25	PDB header: transferase Chain: D: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: crystal structure of phosphoribosyl diphosphate synthase2 from methanocaldococcus jannaschii
92	c3qw4B_	Alignment	not modelled	98.9	22	PDB header: transferase, lyase Chain: B: PDB Molecule: ump synthase; PDBTitle: structure of leishmania donovani ump synthase
93	c3dahB_	Alignment	not modelled	98.8	18	PDB header: transferase Chain: B: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: 2.3 a crystal structure of ribose-phosphate pyrophosphokinase from2 burkholderia pseudomallei
94	d1u9ya1	Alignment	not modelled	92.4	17	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
95	d2c4ka1	Alignment	not modelled	89.8	11	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
96	d1dkua1	Alignment	not modelled	85.8	15	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
97	d1vi2a1	Alignment	not modelled	77.7	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
98	c3pgjB_	Alignment	not modelled	61.2	23	PDB header: oxidoreductase Chain: B: PDB Molecule: shikimate dehydrogenase; PDBTitle: 2.49 angstrom resolution crystal structure of shikimate 5-2 dehydrogenase (aroe) from vibrio cholerae o1 biovar eltor str. n169613 in complex with shikimate
99	d1dcfa_	Alignment	not modelled	57.8	18	Fold: Flavodoxin-like Superfamily: CheY-like Family: Receiver domain of the ethylene receptor
100	d1p77a1	Alignment	not modelled	55.2	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
101	d1npya1	Alignment	not modelled	55.0	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
102	c3pwzA_	Alignment	not modelled	54.3	31	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase 3; PDBTitle: crystal structure of an ael1 enzyme from pseudomonas

						putida
103	c4lz1A_	Alignment	not modelled	53.1	9	PDB header: transcription Chain: A: PDB Molecule: response regulator; PDBTitle: structure of the inactive form of the regulatory domain from the2 repressor of iron transport regulator (ritr)
104	c6oecD_	Alignment	not modelled	45.8	15	PDB header: structural protein Chain: D: PDB Molecule: response regulator/sensory box protein/ggdef domain PDBTitle: yeast spc42 trimeric coiled-coil amino acids 181-211 fused to pdb:2 3h5i
105	c2eggA_	Alignment	not modelled	45.5	19	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate 5-dehydrogenase; PDBTitle: crystal structure of shikimate 5-dehydrogenase (aroe) from geobacillus2 kaustophilus
106	c3o8qB_	Alignment	not modelled	45.0	22	PDB header: oxidoreductase Chain: B: PDB Molecule: shikimate 5-dehydrogenase i alpha; PDBTitle: 1.45 angstrom resolution crystal structure of shikimate 5-2 dehydrogenase (aroe) from vibrio cholerae
107	c3mmnA_	Alignment	not modelled	45.0	24	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+
108	c4omuA_	Alignment	not modelled	41.1	22	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase; PDBTitle: crystal structure of shikimate dehydrogenase (aroe) from pseudomonas2 putida
109	d1nyta1	Alignment	not modelled	36.4	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
110	d1u0sy_	Alignment	not modelled	35.2	22	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
111	c4jjaA_	Alignment	not modelled	34.6	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a duf1343 family protein (bf0379) from2 bacteroides fragilis nctc 9343 at 1.30 a resolution
112	c3tumA_	Alignment	not modelled	34.5	20	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase family protein; PDBTitle: 2.15 angstrom resolution crystal structure of a shikimate2 dehydrogenase family protein from pseudomonas putida kt2440 in3 complex with nad+
113	c5swvC_	Alignment	not modelled	34.4	25	PDB header: lyase Chain: C: PDB Molecule: pentafunctional arom polypeptide; PDBTitle: dehydroquinase dehydratase and shikimate dehydrogenase from s. pombe2 arom
114	d2jfga1	Alignment	not modelled	33.9	21	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
115	c5x5jA_	Alignment	not modelled	32.5	21	PDB header: dna binding protein Chain: A: PDB Molecule: ader; PDBTitle: crystal structure of response regulator ader receiver domain
116	d1h3da1	Alignment	not modelled	31.9	14	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
117	c2ekdD_	Alignment	not modelled	31.2	30	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein ph0250; PDBTitle: structural study of project id ph0250 from pyrococcus horikoshii ot3
118	c6otuA_	Alignment	not modelled	30.8	13	PDB header: isomerase Chain: A: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: crystal structure of a glucose-6-phosphate isomerase from chlamydia2 trachomatis d/uw-3/cx
119	c3eodA_	Alignment	not modelled	29.6	12	PDB header: signaling protein Chain: A: PDB Molecule: protein hnr; PDBTitle: crystal structure of n-terminal domain of e. coli rssb
120	c3fbtB_	Alignment	not modelled	29.0	29	PDB header: oxidoreductase, lyase Chain: B: PDB Molecule: chorismate mutase and shikimate 5-dehydrogenase fusion PDBTitle: crystal structure of a chorismate mutase/shikimate 5-dehydrogenase2 fusion protein from clostridium acetobutylicum