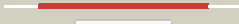



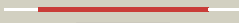
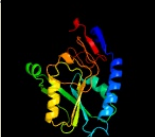


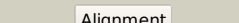



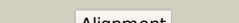














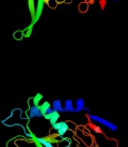


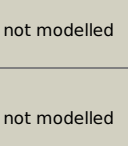


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3624c_(hpt)_4063433_4064083
Date	Fri Aug 9 18:20:31 BST 2019
Unique Job ID	a33ef0880857c149

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1fsqa_	 Alignment		100.0	27	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
2	d1cjba_	 Alignment		100.0	30	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
3	c3kb8A_	 Alignment		100.0	50	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
4	c6ar9A_	 Alignment		100.0	29	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
5	c4rhyC_	 Alignment		100.0	100	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
6	c4rqbB_	 Alignment		100.0	48	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)
7	c4pqfF_	 Alignment		100.0	55	PDB header: transferase Chain: F: PDB Molecule: hypoxanthine phosphoribosyltransferase; PDBTitle: crystal structure of hypoxanthine phosphoribosyltransferase from2 brachy bacterium faecium dsm 4810, nysgrc target 029763.
8	d1p17b_	 Alignment		100.0	40	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
9	c5ipfA_	 Alignment		100.0	29	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
10	c2jbhA_	 Alignment		100.0	34	PDB header: transferase Chain: A: PDB Molecule: phosphoribosyltransferase domain-containing protein 1; PDBTitle: human phosphoribosyl transferase domain containing 1
11	d1yfza1	 Alignment		100.0	57	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)

12	c1yfaA	Alignment		100.0	57	PDB header: transferase Chain: A: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: novel imp binding in feedback inhibition of hypoxanthine-guanine2 phosphoribosyltransferase from thermoanaerobacter tengcongensis
13	c5eswB	Alignment		100.0	20	PDB header: transferase Chain: B: PDB Molecule: purine/pyrimidine phosphoribosyltransferase; PDBTitle: crystal structure of apo hypoxanthine-guanine2 phosphoribosyltransferase from legionella pneumophila
14	dlz7ga1	Alignment		100.0	29	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
15	dlg9sa	Alignment		100.0	48	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
16	c6apsA	Alignment		100.0	32	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
17	dltc1a	Alignment		100.0	45	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
18	c5kapA	Alignment		100.0	34	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: trypanosoma brucei hypoxanthine-guanine phosphoribosyltransferase in2 complex with a 9-(4-(phosphonobutyl)hypoxanthine
19	dlpzma	Alignment		100.0	37	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
20	dl1dqa	Alignment		100.0	24	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
21	dlhgxa	Alignment	not modelled	100.0	42	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
22	c4lyyA	Alignment	not modelled	100.0	46	PDB header: transferase Chain: A: PDB Molecule: hypoxanthine phosphoribosyltransferase; PDBTitle: crystal structure of hypoxanthine phosphoribosyltransferase from2 shewanella pealeana atcc 700345, nysgrc target 029677.
23	c2ywtA	Alignment	not modelled	100.0	46	PDB header: transferase Chain: A: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: crystal structure of hypoxanthine-guanine2 phosphoribosyltransferase with gmp from thermus3 thermophilus hb8
24	c1pzmB	Alignment	not modelled	100.0	37	PDB header: transferase Chain: B: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: crystal structure of hgprt-ase from leishmania tarentolae in complex2 with gmp
25	c3o7mD	Alignment	not modelled	100.0	43	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'
26	dlj7ja	Alignment	not modelled	100.0	49	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
27	dlw30a	Alignment	not modelled	100.0	19	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)

28	d2igba1	Alignment	not modelled	100.0	15	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
29	d1ufra	Alignment	not modelled	100.0	20	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
30	c4z1oB	Alignment	not modelled	100.0	21	PDB header: transferase Chain: B: PDB Molecule: phosphoribosyltransferase; PDBTitle: hypoxanthine-guanine-xanthine phosphoribosyltransferase (hgxpvt) from2 sulfolobus solfataricus in complex with alpha-3 phosphoribosylpyrophosphoric acid (prpp) and magnesium
31	d1a3ca	Alignment	not modelled	100.0	20	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
32	c5vogA	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: putative phosphoribosyltransferase; PDBTitle: crystal structure of a hypothetical protein from neisseria gonorrhoeae2 with bound ppgpp
33	c4trbA	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: purine phosphoribosyltransferase (gpt-1); PDBTitle: sulfolobus solfataricus adenine phosphoribosyltransferase
34	c2jkzB	Alignment	not modelled	100.0	18	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)
35	d1vdma1	Alignment	not modelled	100.0	23	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
36	d1nula	Alignment	not modelled	99.9	18	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
37	d1wd5a	Alignment	not modelled	99.9	18	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
38	d1gph11	Alignment	not modelled	99.9	17	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
39	d1ecfa1	Alignment	not modelled	99.9	21	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
40	c1ecjB	Alignment	not modelled	99.8	18	PDB header: transferase Chain: B: PDB Molecule: glutamine phosphoribosylpyrophosphate PDBTitle: escherichia coli glutamine phosphoribosylpyrophosphate2 (prpp) amidotransferase complexed with 2 amp per tetramer
41	d1g2qa	Alignment	not modelled	99.8	14	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
42	c1gph1	Alignment	not modelled	99.8	16	PDB header: transferase Chain: 1: PDB Molecule: glutamine phosphoribosyl-pyrophosphate amidotransferase; PDBTitle: structure of the allosteric regulatory enzyme of purine biosynthesis
43	d1zn7a1	Alignment	not modelled	99.8	20	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
44	c5yw2D	Alignment	not modelled	99.8	13	PDB header: transferase Chain: D: PDB Molecule: adenine phosphoribosyltransferase; PDBTitle: crystal structure of adenine phosphoribosyltransferase from2 francisella tularensis.
45	c5zgoB	Alignment	not modelled	99.7	19	PDB header: transferase Chain: B: PDB Molecule: adenine phosphoribosyltransferase; PDBTitle: crystal structure of apt2 from thermus thermophilus hb8
46	c4pawA	Alignment	not modelled	99.7	21	PDB header: transferase Chain: A: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: structure of hypothetical protein hp1257.
47	d1vcha1	Alignment	not modelled	99.7	15	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
48	c4m0kD	Alignment	not modelled	99.7	15	PDB header: transferase Chain: D: PDB Molecule: adenine phosphoribosyltransferase; PDBTitle: crystal structure of adenine phosphoribosyltransferase from2 rhodothermus marinus dsm 4252, nysgrc target 029775.
49	c4lzaB	Alignment	not modelled	99.7	20	PDB header: transferase Chain: B: PDB Molecule: adenine phosphoribosyltransferase; PDBTitle: crystal structure of adenine phosphoribosyltransferase from2 thermoanaerobacter pseudethanolicus atcc 33223, nysgrc target 029700.
50	c5t3oB	Alignment	not modelled	99.7	13	PDB header: transferase Chain: B: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: crystal structure of the phosphorybosylpyrophosphate synthetase ii2 from thermus thermophilus
51	c2dy0A	Alignment	not modelled	99.7	17	PDB header: transferase Chain: A: PDB Molecule: adenine phosphoribosyltransferase; PDBTitle: crystal structure of project jw0458 from escherichia coli
52	d1y0ba1	Alignment	not modelled	99.7	12	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
53	c5hkiD	Alignment	not modelled	99.7	16	PDB header: transferase Chain: D: PDB Molecule: orotate phosphoribosyltransferase;

53	c9hkd_	Alignment	not modelled	99.7	10	PDBTitle: crystal structure of mycobacterium tuberculosis h37rv orotate2 phosphoribosyltransferase in complex with fe(iii) dicitrate PDB header: dna binding protein
54	c1o57A_	Alignment	not modelled	99.7	19	Chain: A: PDB Molecule: pur operon repressor; PDBTitle: crystal structure of the purine operon repressor of2 bacillus subtilis
55	c5e38D_	Alignment	not modelled	99.7	19	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
56	c2wnsB_	Alignment	not modelled	99.7	19	PDB header: transferase Chain: B: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: human orotate phosphoribosyltransferase (oprtae) domain of2 uridine 5'-monophosphate synthase (umps) in complex with3 its substrate orotidine 5'-monophosphate (omp)
57	c2ehjA_	Alignment	not modelled	99.6	17	PDB header: transferase Chain: A: PDB Molecule: uracil phosphoribosyltransferase; PDBTitle: structure of uracil phosphoribosyl transferase
58	d1i5ea_	Alignment	not modelled	99.6	20	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
59	d1o5oa_	Alignment	not modelled	99.6	11	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
60	d1o57a2	Alignment	not modelled	99.6	17	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
61	d1mzva_	Alignment	not modelled	99.6	13	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
62	c2yzkC_	Alignment	not modelled	99.6	19	PDB header: transferase Chain: C: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: crystal structure of orotate phosphoribosyltransferase from2 aeropyrum pernix
63	d1qb7a_	Alignment	not modelled	99.6	13	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
64	d1l1qa_	Alignment	not modelled	99.6	14	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
65	c2p1zA_	Alignment	not modelled	99.6	18	PDB header: transferase Chain: A: PDB Molecule: phosphoribosyltransferase; PDBTitle: crystal structure of phosphoribosyltransferase from corynebacterium2 diphtheriae
66	d1lh0a_	Alignment	not modelled	99.6	17	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
67	d1xtta1	Alignment	not modelled	99.6	15	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
68	c3mjdA_	Alignment	not modelled	99.5	14	PDB header: transferase Chain: A: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: 1.9 angstrom crystal structure of orotate phosphoribosyltransferase2 (pyre) francisella tularensis.
69	d2aeaa1	Alignment	not modelled	99.5	16	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
70	c2e55D_	Alignment	not modelled	99.5	14	PDB header: transferase Chain: D: PDB Molecule: uracil phosphoribosyltransferase; PDBTitle: structure of aq2163 protein from aquifex aeolicus
71	c2przB_	Alignment	not modelled	99.5	11	PDB header: transferase Chain: B: PDB Molecule: orotate phosphoribosyltransferase 1; PDBTitle: s. cerevisiae orotate phosphoribosyltransferase complexed with omp
72	c3dezA_	Alignment	not modelled	99.5	12	PDB header: transferase Chain: A: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: crystal structure of orotate phosphoribosyltransferase from2 streptococcus mutans
73	c3n2lA_	Alignment	not modelled	99.5	13	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
74	c5vn4A_	Alignment	not modelled	99.5	10	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
75	c3lpnB_	Alignment	not modelled	99.5	21	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).
76	c5mp7C_	Alignment	not modelled	99.5	18	PDB header: transferase Chain: C: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: crystal structure of phosphoribosylpyrophosphate synthetase from2 mycobacterium smegmatis
77	c4s2uA_	Alignment	not modelled	99.5	21	PDB header: transferase Chain: A: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: crystal structure of the phosphorybosylpyrophosphate synthetase from2 e. coli
						PDB header: ligase Chain: B: PDB Molecule: ribose-phosphate pyrophosphokinase;

78	c6nfeB	Alignment	not modelled	99.5	17	PDBTitle: crystal structure of ribose-phosphate pyrophosphokinase from2 legionella pneumophila with bound amp, adp, and ribose-5-phosphate
79	d1bd3a	Alignment	not modelled	99.5	15	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
80	c3efhB	Alignment	not modelled	99.5	17	PDB header: transferase Chain: B: PDB Molecule: ribose-phosphate pyrophosphokinase 1; PDBTitle: crystal structure of human phosphoribosyl pyrophosphate2 synthetase 1
81	c2c4kD	Alignment	not modelled	99.5	16	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)
82	d1v9sa1	Alignment	not modelled	99.4	16	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
83	c1dkrB	Alignment	not modelled	99.4	16	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.
84	c4twbB	Alignment	not modelled	99.4	23	PDB header: transferase Chain: B: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: sulfolobus solfataricus ribose-phosphate pyrophosphokinase
85	d1dkua2	Alignment	not modelled	99.4	18	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
86	c3dmpD	Alignment	not modelled	99.4	20	PDB header: transferase Chain: D: PDB Molecule: uracil phosphoribosyltransferase; PDBTitle: 2.6 a crystal structure of uracil phosphoribosyltransferase from2 burkholderia pseudomallei
87	d2c4ka2	Alignment	not modelled	99.4	18	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
88	c3m3hA	Alignment	not modelled	99.4	19	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	d1u9ya2	Alignment	not modelled	99.4	21	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
90	c1u9yD	Alignment	not modelled	99.3	18	PDB header: transferase Chain: D: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: crystal structure of phosphoribosyl diphosphate synthase2 from methanocaldococcus jannaschii
91	c3dahB	Alignment	not modelled	99.3	23	PDB header: transferase Chain: B: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: 2.3 a crystal structure of ribose-phosphate pyrophosphokinase from2 burkholderia pseudomallei
92	c3qw4B	Alignment	not modelled	99.2	14	PDB header: transferase, lyase Chain: B: PDB Molecule: cump synthase; PDBTitle: structure of leishmania donovani ump synthase
93	c4fymA	Alignment	not modelled	99.1	12	PDB header: transferase Chain: A: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: crystal structure of plasmodium falciparum orotate2 phosphoribosyltransferase
94	d1u9ya1	Alignment	not modelled	96.1	7	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
95	d2c4ka1	Alignment	not modelled	93.9	11	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
96	d1dkua1	Alignment	not modelled	93.5	16	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
97	c3o8qB	Alignment	not modelled	75.6	21	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
98	c3mnmA	Alignment	not modelled	74.7	23	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+
99	d1vi2a1	Alignment	not modelled	74.2	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
100	c3pgjB	Alignment	not modelled	73.0	21	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
101	c3tumA	Alignment	not modelled	64.5	17	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+
102	d1npya1	Alignment	not modelled	59.4	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
103	c5d7eA	Alignment	not modelled	58.9	18	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase (nadp(+));

103	c0uz3A_	Alignment	not modelled	58.9	18	PDBTitle: 1.5 angstrom crystal structure of shikimate dehydrogenase 1 from2 peptoclostridium difficile. PDB header: oxidoreductase
104	c2hk8B_	Alignment	not modelled	56.1	20	Chain: B: PDB Molecule: shikimate dehydrogenase; PDBTitle: crystal structure of shikimate dehydrogenase from aquifex2 aeolicus at 2.35 angstrom resolution
105	c3fbtB_	Alignment	not modelled	54.0	21	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
106	c3tozA_	Alignment	not modelled	53.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase; PDBTitle: 2.2 angstrom crystal structure of shikimate 5-dehydrogenase from2 listeria monocytogenes in complex with nad.
107	d1dcfa_	Alignment	not modelled	53.1	21	Fold: Flavodoxin-like Superfamily: CheY-like Family: Receiver domain of the ethylene receptor
108	d1vmea1	Alignment	not modelled	52.7	13	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
109	c3pwzA_	Alignment	not modelled	52.5	19	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase 3; PDBTitle: crystal structure of an ael1 enzyme from pseudomonas putida
110	c6bwqB_	Alignment	not modelled	51.9	17	PDB header: metal binding protein Chain: B: PDB Molecule: pyridinium-3,5-bisthiocarboxylic acid mononucleotide nickel PDBTitle: larc2, the c-terminal domain of a cyclometallase involved in the2 synthesis of the npn cofactor of lactate racemase, in complex with3 mnctp
111	d1p77a1	Alignment	not modelled	51.2	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
112	c3donA_	Alignment	not modelled	50.3	19	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase; PDBTitle: crystal structure of shikimate dehydrogenase from staphylococcus2 epidermidis
113	c2wu8A_	Alignment	not modelled	47.6	14	PDB header: isomerase Chain: A: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: structural studies of phosphoglucose isomerase from2 mycobacterium tuberculosis h37rv
114	c2nloA_	Alignment	not modelled	46.3	20	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase; PDBTitle: crystal structure of the quinate dehydrogenase from corynebacterium2 glutamicum
115	d1u0sy_	Alignment	not modelled	46.3	28	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
116	c4lzlA_	Alignment	not modelled	46.1	23	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)
117	c1nytC_	Alignment	not modelled	43.4	19	PDB header: oxidoreductase Chain: C: PDB Molecule: shikimate 5-dehydrogenase; PDBTitle: shikimate dehydrogenase aroe complexed with nadp+
118	d1pjqa1	Alignment	not modelled	43.0	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Siroheme synthase N-terminal domain-like
119	c6oecD_	Alignment	not modelled	42.4	24	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
120	c5x5jA_	Alignment	not modelled	41.8	22	PDB header: dna binding protein Chain: A: PDB Molecule: ader; PDBTitle: crystal structure of response regulator ader receiver domain