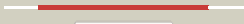
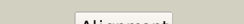
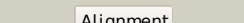
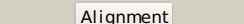
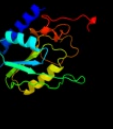
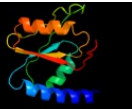
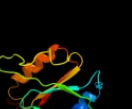
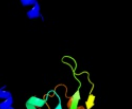


Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	dli5ea_	 Alignment		100.0	54	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
2	c2ehjA_	 Alignment		100.0	100	PDB header: transferase Chain: A: PDB Molecule: uracil phosphoribosyltransferase; PDBTitle: structure of uracil phosphoribosyl transferase
3	dlo5oa_	 Alignment		100.0	50	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
4	d1bd3a_	 Alignment		100.0	33	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
5	c2e55D_	 Alignment		100.0	40	PDB header: transferase Chain: D: PDB Molecule: uracil phosphoribosyltransferase; PDBTitle: structure of aq2163 protein from aquifex aeolicus
6	c3dmpD_	 Alignment		100.0	46	PDB header: transferase Chain: D: PDB Molecule: uracil phosphoribosyltransferase; PDBTitle: 2.6 a crystal structure of uracil phosphoribosyltransferase2 from burkholderia pseudomallei
7	d1v9sa1	 Alignment		100.0	49	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
8	d1xta1	 Alignment		100.0	30	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
9	d1qb7a_	 Alignment		99.9	14	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
10	c1yfaA_	 Alignment		99.4	16	PDB header: transferase Chain: A: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: novel imp binding in feedback inhibition of hypoxanthine-guanine2 phosphoribosyltransferase from thermoanaerobacter tengcongensis
11	d1yfa1	 Alignment		99.4	16	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)

12	c3kb8A_	Alignment		99.3	20	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
13	dlp17b_	Alignment		99.3	15	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
14	dlwd5a_	Alignment		99.3	23	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
15	dltc1a_	Alignment		99.3	15	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
16	d2igba1	Alignment		99.3	21	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
17	dlcjba_	Alignment		99.3	16	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
18	dla3ca_	Alignment		99.2	24	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
19	dlz7ga1	Alignment		99.2	17	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
20	c1pzmb_	Alignment		99.2	11	PDB header: transferase Chain: B: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: crystal structure of hgprt-ase from leishmania tarentolae in complex2 with gmp
21	c2jbhA_	Alignment	not modelled	99.2	21	PDB header: transferase Chain: A: PDB Molecule: phosphoribosyltransferase domain-containing protein 1; PDBTitle: human phosphoribosyl transferase domain containing 1
22	dlfsga_	Alignment	not modelled	99.2	18	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
23	dlufra_	Alignment	not modelled	99.2	19	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
24	dlpzma_	Alignment	not modelled	99.2	10	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
25	dlvdma1	Alignment	not modelled	99.2	21	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
26	c3o7mD_	Alignment	not modelled	99.2	17	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	dlw30a_	Alignment	not modelled	99.1	20	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
28	dlhgxa_	Alignment	not modelled	99.1	18	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
						PDB header: transferase Chain: A: PDB Molecule: hypoxanthine-guanine

29	c2ywtA	Alignment	not modelled	99.1	19	phosphoribosyltransferase; PDBTitle: crystal structure of hypoxanthine-guanine2 phosphoribosyltransferase with gmp from thermus3 thermophilus hb8
30	dlj7ja	Alignment	not modelled	99.1	18	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
31	dlg9sa	Alignment	not modelled	99.1	17	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
32	dlecfal	Alignment	not modelled	98.9	15	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
33	dlu9ya2	Alignment	not modelled	98.8	20	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
34	c3lpnB	Alignment	not modelled	98.8	17	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).
35	d2c4ka2	Alignment	not modelled	98.7	20	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
36	dldkua2	Alignment	not modelled	98.7	17	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
37	c3efhB	Alignment	not modelled	98.7	19	PDB header: transferase Chain: B: PDB Molecule: ribose-phosphate pyrophosphokinase 1; PDBTitle: crystal structure of human phosphoribosyl pyrophosphate2 synthetase 1
38	c2jkzB	Alignment	not modelled	98.7	16	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)
39	clecjB	Alignment	not modelled	98.7	12	PDB header: transferase Chain: B: PDB Molecule: glutamine phosphoribosylpyrophosphate PDBTitle: escherichia coli glutamine phosphoribosylpyrophosphate2 (prpp) amidotransferase complexed with 2 amp per tetramer
40	c2c4kD	Alignment	not modelled	98.6	19	PDB header: regulatory protein Chain: D: PDB Molecule: phosphoribosyl pyrophosphate synthetase- PDBTitle: crystal structure of human phosphoribosylpyrophosphate2 synthetase-associated protein 39 (pap39)
41	cldkrB	Alignment	not modelled	98.6	17	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.
42	clgph1	Alignment	not modelled	98.6	17	PDB header: transferase(glutamine amidotransferase) Chain: 1: PDB Molecule: glutamine phosphoribosyl-pyrophosphate amidotransferase; PDBTitle: structure of the allosteric regulatory enzyme of purine biosynthesis
43	dlzn7a1	Alignment	not modelled	98.6	17	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
44	dlg2qa	Alignment	not modelled	98.6	17	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
45	dlgph11	Alignment	not modelled	98.5	11	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
46	dlmzva	Alignment	not modelled	98.5	15	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
47	clu9yD	Alignment	not modelled	98.5	25	PDB header: transferase Chain: D: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: crystal structure of phosphoribosyl diphosphate synthase2 from methanocaldococcus jannaschii
48	dly0ba1	Alignment	not modelled	98.4	20	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
49	c3dahB	Alignment	not modelled	98.4	19	PDB header: transferase Chain: B: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: 2.3 a crystal structure of ribose-phosphate pyrophosphokinase from2 burkholderia pseudomallei
50	c2dy0A	Alignment	not modelled	98.4	23	PDB header: transferase Chain: A: PDB Molecule: adenine phosphoribosyltransferase; PDBTitle: crystal structure of project jw0458 from escherichia coli
51	dl1lga	Alignment	not modelled	98.3	23	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
52	dlvcha1	Alignment	not modelled	98.3	12	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
53	c2n1vA	Alignment	not modelled	98.3	15	PDB header: transferase Chain: A: PDB Molecule: phosphoribosyltransferase;

53	c2p1cA	Alignment	not modelled	98.3	13	PDBTitle: crystal structure of phosphoribosyltransferase from corynebacterium2 diphtheriae PDB header: transferase
54	c2wnsB	Alignment	not modelled	98.2	18	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)
55	c2yzkC	Alignment	not modelled	98.2	23	PDB header: transferase Chain: C: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: crystal structure of orotate phosphoribosyltransferase from2 aeropyrum pernix
56	d1dqna	Alignment	not modelled	98.2	17	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
57	c3dezA	Alignment	not modelled	98.1	18	PDB header: transferase Chain: A: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: crystal structure of orotate phosphoribosyltransferase from2 streptococcus mutans
58	d1o57a2	Alignment	not modelled	98.1	19	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
59	d2aeea1	Alignment	not modelled	98.1	16	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
60	c1o57A	Alignment	not modelled	98.0	17	PDB header: dna binding protein Chain: A: PDB Molecule: pur operon repressor; PDBTitle: crystal structure of the purine operon repressor of2 bacillus subtilis
61	d1nula	Alignment	not modelled	98.0	16	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
62	d1lh0a	Alignment	not modelled	97.8	10	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
63	c3n21A	Alignment	not modelled	97.8	15	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
64	c3m3hA	Alignment	not modelled	97.8	24	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'
65	c3mjda	Alignment	not modelled	97.7	10	PDB header: transferase Chain: A: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: 1.9 angstrom crystal structure of orotate2 phosphoribosyltransferase (pyre) francisella tularensis.
66	c2przB	Alignment	not modelled	97.7	10	PDB header: transferase Chain: B: PDB Molecule: orotate phosphoribosyltransferase 1; PDBTitle: s. cerevisiae orotate phosphoribosyltransferase complexed2 with omp
67	c3qw4B	Alignment	not modelled	95.9	25	PDB header: transferase, lyase Chain: B: PDB Molecule: ump synthase; PDBTitle: structure of leishmania donovani ump synthase
68	c3outC	Alignment	not modelled	89.2	17	PDB header: isomerase Chain: C: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of glutamate racemase from francisella tularensis2 subsp. tularensis schu s4 in complex with d-glutamate.
69	d1b74a1	Alignment	not modelled	89.1	21	Fold: ATC-like Superfamily: Aspartate/glutamate racemase Family: Aspartate/glutamate racemase
70	c2jfoB	Alignment	not modelled	89.0	18	PDB header: isomerase Chain: B: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of enterococcus faecalis glutamate2 racemase in complex with d- and l-glutamate
71	c3hfrA	Alignment	not modelled	89.0	16	PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of glutamate racemase from listeria monocytogenes
72	c2ohoA	Alignment	not modelled	89.0	18	PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: structural basis for glutamate racemase inhibitor
73	c2jfqA	Alignment	not modelled	88.0	14	PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of staphylococcus aureus glutamate2 racemase in complex with d-glutamate
74	d1u9ya1	Alignment	not modelled	87.6	17	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
75	c1b74A	Alignment	not modelled	87.3	21	PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: glutamate racemase from aquifex pyrophilus
76	c2gzmb	Alignment	not modelled	87.0	15	PDB header: isomerase Chain: B: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of the glutamate racemase from bacillus2 anthracis
77	d2c4ka1	Alignment	not modelled	85.5	10	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
78	c2dwuA	Alignment	not modelled	84.3	24	PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of glutamate racemase isoform race1 from bacillus2 anthracis
						PDB header: oxidoreductase

79	c3pwzA	Alignment	not modelled	82.2	19	Chain: A: PDB Molecule: shikimate dehydrogenase 3; PDBTitle: crystal structure of an ael1 enzyme from pseudomonas putida
80	d1dkua1	Alignment	not modelled	77.6	15	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
81	c3pgjB	Alignment	not modelled	77.4	16	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
82	d1vi2a1	Alignment	not modelled	77.1	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
83	c1zuwA	Alignment	not modelled	76.1	14	PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase 1; PDBTitle: crystal structure of b.subtilis glutamate racemase (race) with d-glu
84	c3u7jA	Alignment	not modelled	75.4	25	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase a from burkholderia2 thailandensis
85	c3o8qB	Alignment	not modelled	75.0	16	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
86	c2jfnA	Alignment	not modelled	74.7	20	PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of escherichia coli glutamate racemase2 in complex with l-glutamate and activator udp-murnac-ala
87	c2jfbB	Alignment	not modelled	74.5	18	PDB header: isomerase Chain: B: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of helicobacter pylori glutamate racemase2 in complex with d-glutamate and an inhibitor
88	d1o8bb1	Alignment	not modelled	73.3	22	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: D-ribose-5-phosphate isomerase (RpiA), catalytic domain
89	c3ca8B	Alignment	not modelled	72.9	19	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein ydcf; PDBTitle: crystal structure of escherichia coli ydcf, an s-adenosyl-l-methionine2 utilizing enzyme
90	d1npya1	Alignment	not modelled	66.5	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
91	c2pjmA	Alignment	not modelled	63.7	19	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: structure of ribose 5-phosphate isomerase a from2 methanocaldococcus jannaschii
92	c2eggA	Alignment	not modelled	60.4	15	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate 5-dehydrogenase; PDBTitle: crystal structure of shikimate 5-dehydrogenase (aroe) from2 geobacillus kaustophilus
93	c3fbtB	Alignment	not modelled	60.3	29	PDB header: oxidoreductase, lyase Chain: B: PDB Molecule: chorismate mutase and shikimate 5-dehydrogenase PDBTitle: crystal structure of a chorismate mutase/shikimate 5-2 dehydrogenase fusion protein from clostridium3 acetobutylicum
94	d3beda1	Alignment	not modelled	59.3	10	Fold: PTS system fructose IIA component-like Superfamily: PTS system fructose IIA component-like Family: EIIA-man component-like
95	c3tozA	Alignment	not modelled	56.1	17	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.
96	d1p77a1	Alignment	not modelled	55.5	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
97	c3k13A	Alignment	not modelled	52.8	21	PDB header: transferase Chain: A: PDB Molecule: 5-methyltetrahydrofolate-homocysteine methyltransferase; PDBTitle: structure of the pterin-binding domain metr of 5-2 methyltetrahydrofolate-homocysteine methyltransferase from3 bacteroides thetaiotaomicron
98	d2e7ya1	Alignment	not modelled	51.6	18	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: RNase Z-like
99	d2fwra2	Alignment	not modelled	49.6	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
100	c1npyA	Alignment	not modelled	49.2	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical shikimate 5-dehydrogenase-like PDBTitle: structure of shikimate 5-dehydrogenase-like protein hi0607
101	d1qh5a	Alignment	not modelled	47.6	25	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Glyoxalase II (hydroxyacylglutathione hydrolase)
102	c1lkzB	Alignment	not modelled	46.6	21	PDB header: isomerase Chain: B: PDB Molecule: ribose 5-phosphate isomerase a; PDBTitle: crystal structure of d-ribose-5-phosphate isomerase (rpiA)2 from escherichia coli.
103	c1xtzA	Alignment	not modelled	44.3	13	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase; PDBTitle: crystal structure of the s. cerevisiae d-ribose-5-phosphate isomerase:2 comparison with the archeal and bacterial

					enzymes
104	d1g60a_	Alignment	not modelled	43.5	22 Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Type II DNA methylase
105	c1vi2B_	Alignment	not modelled	43.4	23 PDB header: oxidoreductase Chain: B: PDB Molecule: shikimate 5-dehydrogenase 2; PDBTitle: crystal structure of shikimate-5-dehydrogenase with nad
106	c2ohiB_	Alignment	not modelled	42.7	11 PDB header: oxidoreductase Chain: B: PDB Molecule: type a flavoprotein fpra; PDBTitle: crystal structure of coenzyme f420h2 oxidase (fpra), a diiron2 flavoprotein, reduced state
107	c3kwmC_	Alignment	not modelled	40.7	22 PDB header: isomerase Chain: C: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-isomerase a
108	c3hnnD_	Alignment	not modelled	40.3	17 PDB header: oxidoreductase Chain: D: PDB Molecule: putative diflavin flavoprotein a 5; PDBTitle: crystal structure of putative diflavin flavoprotein a 5 (fragment 1-2 254) from nostoc sp. pcc 7120, northeast structural genomics3 consortium target nsr435a
109	c1vliA_	Alignment	not modelled	40.3	27 PDB header: biosynthetic protein Chain: A: PDB Molecule: spore coat polysaccharide biosynthesis protein spse; PDBTitle: crystal structure of spore coat polysaccharide biosynthesis protein2 spse (bsu37870) from bacillus subtilis at 2.38 a resolution
110	c2zifB_	Alignment	not modelled	39.7	20 PDB header: transferase Chain: B: PDB Molecule: putative modification methylase; PDBTitle: crystal structure of ttha0409, putative dna modification2 methylase from thermus thermophilus hb8- complexed with s-3 adenosyl-l-methionine
111	d2q0ia1	Alignment	not modelled	39.6	12 Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: PqsE-like
112	d1eg2a_	Alignment	not modelled	38.5	16 Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Type II DNA methylase
113	c3tbkA_	Alignment	not modelled	37.7	14 PDB header: hydrolase Chain: A: PDB Molecule: rig-i helicase domain; PDBTitle: mouse rig-i atpase domain
114	c1nw6A_	Alignment	not modelled	36.3	17 PDB header: transferase Chain: A: PDB Molecule: modification methylase rsri; PDBTitle: structure of the beta class n6-adenine dna methyltransferase rsri2 bound to sinefungin
115	c2hk8B_	Alignment	not modelled	35.8	27 PDB header: oxidoreductase Chain: B: PDB Molecule: shikimate dehydrogenase; PDBTitle: crystal structure of shikimate dehydrogenase from aquifex2 aeolicus at 2.35 angstrom resolution
116	d1f8fa1	Alignment	not modelled	34.8	16 Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain
117	c3hzhA_	Alignment	not modelled	34.5	15 PDB header: signaling protein Chain: A: PDB Molecule: chemotaxis response regulator (chey-3); PDBTitle: crystal structure of the cheX-chey-bef3-mg+2 complex from2 borrelia burgdorferi
118	c3donA_	Alignment	not modelled	34.5	25 PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase; PDBTitle: crystal structure of shikimate dehydrogenase from staphylococcus2 epidermidis
119	c2qkxA_	Alignment	not modelled	34.4	17 PDB header: transferase Chain: A: PDB Molecule: bifunctional protein glmu; PDBTitle: n-acetyl glucosamine 1-phosphate uridyltransferase from mycobacterium2 tuberculosis complex with n-acetyl glucosamine 1-phosphate
120	d1e5da2	Alignment	not modelled	32.2	14 Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: ROO N-terminal domain-like