







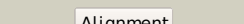

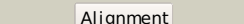

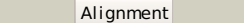

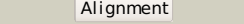

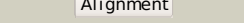

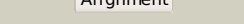

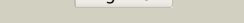



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2xf4A_	 Alignment		100.0	91	PDB header: hydrolase Chain: A: PDB Molecule: hydroxyacylglutathione hydrolase; PDBTitle: crystal structure of salmonella enterica serovar2 typhimurium ycb1
2	c3r2uC_	 Alignment		100.0	33	PDB header: hydrolase Chain: C: PDB Molecule: metallo-beta-lactamase family protein; PDBTitle: 2.1 angstrom resolution crystal structure of metallo-beta-lactamase2 from staphylococcus aureus subsp. aureus col
3	c3tp9B_	 Alignment		100.0	37	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase and rhodanese domain protein; PDBTitle: crystal structure of alicyclobacillus acidocaldarius protein with2 beta-lactamase and rhodanese domains
4	d1qh5a_	 Alignment		100.0	31	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Glyoxalase II (hydroxyacylglutathione hydrolase)
5	d1xm8a_	 Alignment		100.0	32	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Glyoxalase II (hydroxyacylglutathione hydrolase)
6	c2zwrA_	 Alignment		100.0	36	PDB header: hydrolase Chain: A: PDB Molecule: metallo-beta-lactamase superfamily protein; PDBTitle: crystal structure of ttha1623 from thermus thermophilus hb8
7	d2qeda1	 Alignment		100.0	35	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Glyoxalase II (hydroxyacylglutathione hydrolase)
8	c2p18A_	 Alignment		100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: glyoxalase ii; PDBTitle: crystal structure of the leishmania infantum glyoxalase ii
9	c2gcuD_	 Alignment		100.0	30	PDB header: hydrolase Chain: D: PDB Molecule: putative hydroxyacylglutathione hydrolase 3; PDBTitle: x-ray structure of gene product from arabidopsis thaliana2 at1g53580
10	d2q0ia1	 Alignment		100.0	24	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: PqsE-like
11	d2gmna1	 Alignment		100.0	22	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase

12	c3lvzA_	Alignment		100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: blr6230 protein; PDBTitle: new refinement of the crystal structure of bjp-1, a subclass b32 metallo-beta-lactamase of bradyrhizobium japonicum
13	d1jjta_	Alignment		100.0	19	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase
14	c3l6nA_	Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: metallo-beta-lactamase; PDBTitle: crystal structure of metallo-beta-lactamase ind-7
15	d1ko3a_	Alignment		100.0	20	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase
16	c3rkjA_	Alignment		100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase ndm-1; PDBTitle: crystal structure of new delhi metallo-beta-lactamase-1 from2 klebsiella pneumoniae
17	c3spuB_	Alignment		100.0	15	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase ndm-1; PDBTitle: apo ndm-1 crystal structure
18	d2aioa1	Alignment		100.0	22	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase
19	c2z04A_	Alignment		100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: metallo-beta-lactamase family protein; PDBTitle: crystal structure of metallo-beta-lactamase family protein ttha14292 from thermus thermophilus hb8
20	d1m2xa_	Alignment		100.0	16	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase
21	d1k07a_	Alignment	not modelled	100.0	20	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase
22	c2q9uB_	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: B: PDB Molecule: a-type flavoprotein; PDBTitle: crystal structure of the flavodiiron protein from giardia2 intestinalis
23	d1znba_	Alignment	not modelled	100.0	18	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase
24	d1mqoa_	Alignment	not modelled	100.0	19	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase
25	c2ohiB_	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: B: PDB Molecule: type a flavoprotein fpfa; PDBTitle: crystal structure of coenzyme f420h2 oxidase (fpfa), a diiron2 flavoprotein, reduced state
26	c2yz3B_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: metallo-beta-lactamase; PDBTitle: crystallographic investigation of inhibition mode of the2 vim-2 metallo-beta-lactamase from pseudomonas aeruginosa3 with mercaptocarboxylate inhibitor
27	c3adrA_	Alignment	not modelled	99.9	21	PDB header: signaling protein Chain: A: PDB Molecule: putative uncharacterized protein st1585; PDBTitle: the first crystal structure of an archaeal metallo-beta-lactamase2 superfamily protein; st1585 from sulfolobus tokodaii
28	c1ychD_	Alignment	not modelled	99.9	19	PDB header: oxidoreductase Chain: D: PDB Molecule: nitric oxide reductase; PDBTitle: x-ray crystal structures of moorella thermoacetica fpfa.2 novel diiron site structure and mechanistic insights into3 a

					scavenging nitric oxide reductase
29	d1x8ha	Alignment	not modelled	99.9	14 Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase
30	c1e5dA	Alignment	not modelled	99.9	20 PDB header: oxidoreductase Chain: A: PDB Molecule: rubredoxin; oxygen oxidoreductase; PDBTitle: rubredoxin oxygen: oxidoreductase (roo) from anaerobe2 desulfovibrio gigas
31	c1vmeB	Alignment	not modelled	99.9	21 PDB header: electron transport Chain: B: PDB Molecule: flavoprotein; PDBTitle: crystal structure of flavoprotein (tm0755) from thermotoga maritima at 2.1.80 Å resolution
32	c2cfuA	Alignment	not modelled	99.9	21 PDB header: hydrolase Chain: A: PDB Molecule: sdsA1; PDBTitle: crystal structure of sdsA1, an alkylsulfatase from <i>Pseudomonas aeruginosa</i> , in complex with 1-decane-sulfonic-3 acid.
33	c3hnnD	Alignment	not modelled	99.9	16 PDB header: oxidoreductase Chain: D: PDB Molecule: putative diflavin flavoprotein a 5; PDBTitle: crystal structure of putative diflavin flavoprotein a 5 (fragment 1-2254) from <i>Nostoc</i> sp. pcc 7120, northeast structural genomics3 consortium target nsr435a
34	d2cfua2	Alignment	not modelled	99.9	18 Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Alkylsulfatase-like
35	c2fhxB	Alignment	not modelled	99.9	18 PDB header: hydrolase, metal binding protein Chain: B: PDB Molecule: spm-1; PDBTitle: <i>Pseudomonas aeruginosa</i> spm-1 metallo-beta-lactamase
36	c3eshB	Alignment	not modelled	99.9	17 PDB header: hydrolase Chain: B: PDB Molecule: protein similar to metal-dependent hydrolase; PDBTitle: crystal structure of a probable metal-dependent hydrolase2 from <i>Staphylococcus aureus</i> . northeast structural genomics3 target zr314
37	d1ycga2	Alignment	not modelled	99.9	18 Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: ROO N-terminal domain-like
38	c3aj3A	Alignment	not modelled	99.9	19 PDB header: hydrolase Chain: A: PDB Molecule: 4-pyridoxolactonase; PDBTitle: crystal structure of selenomethionine substituted 4-pyridoxolactonase2 from <i>Mesorhizobium loti</i>
39	d2p97a1	Alignment	not modelled	99.9	19 Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Ava3068-like
40	d1e5da2	Alignment	not modelled	99.9	19 Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: ROO N-terminal domain-like
41	d1vmea2	Alignment	not modelled	99.9	19 Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: ROO N-terminal domain-like
42	c2r2dC	Alignment	not modelled	99.9	16 PDB header: hydrolase Chain: C: PDB Molecule: zn-dependent hydrolases; PDBTitle: structure of a quorum-quenching lactonase (aiib) from <i>Agrobacterium tumefaciens</i>
43	c3sd9B	Alignment	not modelled	99.9	13 PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of serratia fonticola sfh-i: source of the2 nucleophile in the catalytic mechanism of mono-zinc metallo-beta-3 lactamases
44	c1p9eA	Alignment	not modelled	99.9	22 PDB header: hydrolase Chain: A: PDB Molecule: methyl parathion hydrolase; PDBTitle: crystal structure analysis of methyl parathion hydrolase from <i>Pseudomonas</i> sp wbc-3
45	d1p9ea	Alignment	not modelled	99.9	22 Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Methyl parathion hydrolase
46	c2bibA	Alignment	not modelled	99.8	18 PDB header: hydrolase Chain: A: PDB Molecule: teichoic acid phosphorylcholine esterase/ choline binding PDBTitle: crystal structure of the complete modular teichoic acid2 phosphorylcholine esterase pce (cbpe) from <i>Streptococcus pneumoniae</i>
47	c2br6A	Alignment	not modelled	99.8	21 PDB header: hydrolase Chain: A: PDB Molecule: aiia-like protein; PDBTitle: crystal structure of quorum-quenching n-acyl homoserine2 lactone lactonase
48	c3zq4C	Alignment	not modelled	99.8	16 PDB header: hydrolase Chain: C: PDB Molecule: ribonuclease j 1; PDBTitle: unusual, dual endo- and exo-nuclease activity in the degradosome2 explained by crystal structure analysis of rnase j1
49	d1ztca1	Alignment	not modelled	99.8	17 Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: TM0894-like
50	c2p4zA	Alignment	not modelled	99.8	18 PDB header: hydrolase Chain: A: PDB Molecule: metal-dependent hydrolases of the beta-lactamase PDBTitle: a ferredoxin-like metallo-beta-lactamase superfamily protein from <i>Thermoanaerobacter tengcongensis</i>
51	d1wraa1	Alignment	not modelled	99.8	23 Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Pce catalytic domain-like
52	c3bk2A	Alignment	not modelled	99.7	18 PDB header: hydrolase Chain: A: PDB Molecule: metal dependent hydrolase; PDBTitle: crystal structure analysis of the rnase j/ump complex
					Fold: Metallo-hydrolase/oxidoreductase

53	d2i7ta1	Alignment	not modelled	99.7	20	Superfamily: Metallo-hydrolase/oxidoreductase Family: beta-CASP RNA-metabolising hydrolases
54	c3af5A	Alignment	not modelled	99.6	21	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein ph1404; PDBTitle: the crystal structure of an archaeal cpsf subunit, ph1404 from2 pyrococcus horikoshii
55	c2ycbA	Alignment	not modelled	99.6	23	PDB header: hydrolase Chain: A: PDB Molecule: cleavage and polyadenylation specificity factor; PDBTitle: structure of the archaeal beta-casp protein with n-terminal2 kh domains from methanothermobacter thermautotrophicus
56	d2dkfa1	Alignment	not modelled	99.6	27	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: beta-CASP RNA-metabolising hydrolases
57	c2az4A	Alignment	not modelled	99.6	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ef2904; PDBTitle: crystal structure of a protein of unknown function from enterococcus2 faecalis v583
58	c2xr1A	Alignment	not modelled	99.6	19	PDB header: hydrolase Chain: A: PDB Molecule: cleavage and polyadenylation specificity factor 100 kd PDBTitle: dimeric archaeal cleavage and polyadenylation specificity2 factor with n-terminal kh domains (kh-cpsf) from methanosarcina3 mazei
59	c3h3eA	Alignment	not modelled	99.6	16	PDB header: structural genomics, metal binding prote Chain: A: PDB Molecule: uncharacterized protein tm1679; PDBTitle: crystal structure of tm1679, a metal-dependent hydrolase of2 the beta-lactamase superfamily
60	c2xr1B	Alignment	not modelled	99.5	19	PDB header: hydrolase Chain: B: PDB Molecule: cleavage and polyadenylation specificity factor 100 kd PDBTitle: dimeric archaeal cleavage and polyadenylation specificity2 factor with n-terminal kh domains (kh-cpsf) from methanosarcina3 mazei
61	d2i7xa1	Alignment	not modelled	99.5	17	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: beta-CASP RNA-metabolising hydrolases
62	c2i7xA	Alignment	not modelled	99.5	17	PDB header: rna binding protein, protein binding Chain: A: PDB Molecule: protein cft2; PDBTitle: structure of yeast cpsf-100 (ydh1p)
63	c3md7A	Alignment	not modelled	99.5	14	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase-like; PDBTitle: crystal structure of a beta-lactamase-like protein bound to gmp from2 brucella melitensis
64	c3zwfA	Alignment	not modelled	99.5	17	PDB header: hydrolase Chain: A: PDB Molecule: zinc phosphodiesterase elac protein 1; PDBTitle: crystal structure of human trnase z, short form (elac1).
65	c1zkpD	Alignment	not modelled	99.4	15	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein ba1088; PDBTitle: 1.5a resolution crystal structure of a metallo beta lactamase family2 protein, the elac homologue of bacillus anthracis, a putative3 ribonuclease
66	c3g1pA	Alignment	not modelled	99.4	15	PDB header: lyase Chain: A: PDB Molecule: protein phnp; PDBTitle: crystals structure of phnp from e.coli k-12
67	d1xtoa	Alignment	not modelled	99.3	13	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Coenzyme PQQ synthesis protein B, PqqB
68	d2az4a1	Alignment	not modelled	99.3	16	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: beta-CASP RNA-metabolising hydrolases
69	c3kl7A	Alignment	not modelled	99.3	19	PDB header: hydrolase Chain: A: PDB Molecule: putative metal-dependent hydrolase; PDBTitle: crystal structure of putative metal-dependent hydrolase2 (yp_001302908.1) from parabacteroides distasonis atcc 8503 at 2.30 a3 resolution
70	d1y44a1	Alignment	not modelled	99.2	21	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: RNase Z-like
71	d1zkpa1	Alignment	not modelled	99.2	16	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: YhfI-like
72	d2cbna1	Alignment	not modelled	99.2	16	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: RNase Z-like
73	d2e7ya1	Alignment	not modelled	98.8	20	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: RNase Z-like
74	c3bv6D	Alignment	not modelled	98.7	21	PDB header: hydrolase Chain: D: PDB Molecule: metal-dependent hydrolase; PDBTitle: crystal structure of uncharacterized metallo protein from vibrio2 cholerae with beta-lactamase like fold
75	c2wylF	Alignment	not modelled	98.7	21	PDB header: hydrolase Chain: F: PDB Molecule: l-ascorbate-6-phosphate lactonase ulag; PDBTitle: apo structure of a metallo-b-lactamase
76	c3rpcD	Alignment	not modelled	98.6	23	PDB header: hydrolase Chain: D: PDB Molecule: possible metal-dependent hydrolase; PDBTitle: the crystal structure of a possible metal-dependent hydrolase from2 veillonella parvula dsm 2008
77	d1vjna	Alignment	not modelled	98.4	22	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Hypothetical protein TM0207
						PDB header: transferase

78	c3lpnB_	Alignment	not modelled	83.8	25	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).
79	c3efhB_	Alignment	not modelled	81.9	39	PDB header: transferase Chain: B: PDB Molecule: ribose-phosphate pyrophosphokinase 1; PDBTitle: crystal structure of human phosphoribosyl pyrophosphate2 synthetase 1
80	d1u9ya2	Alignment	not modelled	81.6	22	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
81	c1dkrB_	Alignment	not modelled	80.4	25	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.
82	d1dkua2	Alignment	not modelled	80.1	25	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
83	c3dahB_	Alignment	not modelled	77.2	26	PDB header: transferase Chain: B: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: 2.3 a crystal structure of ribose-phosphate pyrophosphokinase from2 burkholderia pseudomallei
84	c1u9yD_	Alignment	not modelled	76.7	22	PDB header: transferase Chain: D: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: crystal structure of phosphoribosyl diphosphate synthase2 from methanocaldococcus jannaschii
85	d2c4ka2	Alignment	not modelled	76.6	28	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
86	c2c4kD_	Alignment	not modelled	75.2	24	PDB header: regulatory protein Chain: D: PDB Molecule: phosphoribosyl pyrophosphate synthetase- PDBTitle: crystal structure of human phosphoribosylpyrophosphate2 synthetase-associated protein 39 (pap39)
87	d1gph11	Alignment	not modelled	56.9	21	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
88	d1ecfa1	Alignment	not modelled	56.2	24	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
89	d1zn7a1	Alignment	not modelled	56.1	14	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
90	d1o57a2	Alignment	not modelled	48.3	18	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
91	c2dy0A_	Alignment	not modelled	46.5	20	PDB header: transferase Chain: A: PDB Molecule: adenine phosphoribosyltransferase; PDBTitle: crystal structure of project jw0458 from escherichia coli
92	c2wnsB_	Alignment	not modelled	46.2	12	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)
93	c3mjda_	Alignment	not modelled	46.2	15	PDB header: transferase Chain: A: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: 1.9 angstrom crystal structure of orotate2 phosphoribosyltransferase (pyre) francisella tularensis.
94	c3dmpD_	Alignment	not modelled	46.0	16	PDB header: transferase Chain: D: PDB Molecule: uracil phosphoribosyltransferase; PDBTitle: 2.6 a crystal structure of uracil phosphoribosyltransferase2 from burkholderia pseudomallei
95	d1l1qa_	Alignment	not modelled	45.4	16	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
96	d1ii7a_	Alignment	not modelled	44.6	22	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: DNA double-strand break repair nuclease
97	c2yzkC_	Alignment	not modelled	44.6	24	PDB header: transferase Chain: C: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: crystal structure of orotate phosphoribosyltransferase from2 aeropyrum pernix
98	c3dezA_	Alignment	not modelled	44.2	12	PDB header: transferase Chain: A: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: crystal structure of orotate phosphoribosyltransferase from2 streptococcus mutans
99	d1g2qa_	Alignment	not modelled	43.6	24	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
100	d1mzva_	Alignment	not modelled	43.6	29	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
101	d1lh0a_	Alignment	not modelled	43.4	24	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
102	d1vcha1	Alignment	not modelled	43.2	21	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
103	d2aeaa1	Alignment	not modelled	42.4	12	Fold: PRTase-like Superfamily: PRTase-like

					Family: Phosphoribosyltransferases (PRTases)
104	c3rl4A_	Alignment	not modelled	41.1	23 PDB header: hydrolase Chain: A: PDB Molecule: metallophosphoesterase mpped2; PDBTitle: rat metallophosphodiesterase mpped2 g252h mutant
105	c2p1zA_	Alignment	not modelled	38.1	12 PDB header: transferase Chain: A: PDB Molecule: phosphoribosyltransferase; PDBTitle: crystal structure of phosphoribosyltransferase from corynebacterium2 diphtheriae
106	c3m3hA_	Alignment	not modelled	36.7	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'
107	c1o57A_	Alignment	not modelled	36.1	18 PDB header: dna binding protein Chain: A: PDB Molecule: pur operon repressor; PDBTitle: crystal structure of the purine operon repressor of2 bacillus subtilis
108	c2przB_	Alignment	not modelled	35.8	9 PDB header: transferase Chain: B: PDB Molecule: orotate phosphoribosyltransferase 1; PDBTitle: s. cerevisiae orotate phosphoribosyltransferase complexed2 with omp
109	d1bd3a_	Alignment	not modelled	35.3	16 Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
110	d1y0ba1	Alignment	not modelled	35.0	21 Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
111	c3ib7A_	Alignment	not modelled	34.6	20 PDB header: hydrolase Chain: A: PDB Molecule: icc protein; PDBTitle: crystal structure of full length rv0805
112	c3n2lA_	Alignment	not modelled	31.9	22 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
113	d1dj3a_	Alignment	not modelled	30.8	10 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
114	d1dj2a_	Alignment	not modelled	30.6	12 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
115	d1uf3a_	Alignment	not modelled	28.5	13 Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: TT1561-like
116	c1ecjB_	Alignment	not modelled	27.7	24 PDB header: transferase Chain: B: PDB Molecule: glutamine phosphoribosylpyrophosphate PDBTitle: escherichia coli glutamine phosphoribosylpyrophosphate2 (prpp) amidotransferase complexed with 2 amp per tetramer
117	d1qb7a_	Alignment	not modelled	26.8	26 Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
118	d1vdma1	Alignment	not modelled	26.4	29 Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
119	c1gph1_	Alignment	not modelled	25.6	21 PDB header: transferase(glutamine amidotransferase) Chain: 1: PDB Molecule: glutamine phosphoribosyl-pyrophosphate amidotransferase; PDBTitle: structure of the allosteric regulatory enzyme of purine biosynthesis
120	d1yfza1	Alignment	not modelled	22.4	15 Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)