Phyre2

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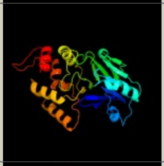
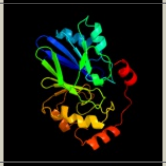
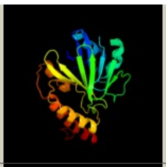
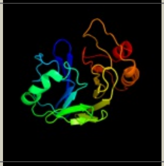
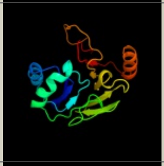
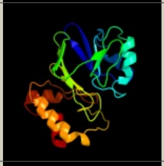
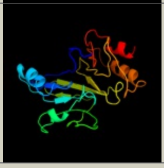
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2qeda1	Alignment		100.0	78	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Glyoxalase II (hydroxyacylglutathione hydrolase)
2	d1qh5a_	Alignment		100.0	38	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Glyoxalase II (hydroxyacylglutathione hydrolase)
3	d1xm8a_	Alignment		100.0	41	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Glyoxalase II (hydroxyacylglutathione hydrolase)
4	c2p18A_	Alignment		100.0	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glyoxalase ii; **PDBTitle:** crystal structure of the leishmania infantum glyoxalase ii
5	c3tp9B_	Alignment		100.0	28	**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
6	c3r2uC_	Alignment		100.0	23	**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
7	c2gcuD_	Alignment		100.0	25	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative hydroxyacylglutathione hydrolase 3; **PDBTitle:** x-ray structure of gene product from arabidopsis thaliana2 at1g53580
8	c2xf4A_	Alignment		100.0	37	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydroxyacylglutathione hydrolase; **PDBTitle:** crystal structure of salmonella enterica serovar2 typhimurium ycbl
9	c2zwrA_	Alignment		100.0	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metallo-beta-lactamase superfamily protein; **PDBTitle:** crystal structure of ttha1623 from thermus thermophilus hb8
10	d2q0ia1	Alignment		100.0	23	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**PqsE-like
11	d2gmna1	Alignment		100.0	20	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase

12	c3lvzA_	Alignment		100.0	19	**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	c3adrA_	Alignment		100.0	25	**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
14	d1jjta_	Alignment		100.0	19	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
15	c2zo4A_	Alignment		100.0	23	**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
16	d2aioa1	Alignment		100.0	21	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
17	c1vmeB_	Alignment		100.0	19	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**flavoprotein; **PDBTitle:** crystal structure of flavoprotein (tm0755) from thermotoga maritima at2 1.80 a resolution
18	c2ohiB_	Alignment		100.0	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**type a flavoprotein fpra; **PDBTitle:** crystal structure of coenzyme f420h2 oxidase (fpra), a diiron2 flavoprotein, reduced state
19	d1k07a_	Alignment		100.0	17	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
20	c3l6nA_	Alignment		100.0	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metallo-beta-lactamase; **PDBTitle:** crystal structure of metallo-beta-lactamase ind-7
21	c2q9uB_	Alignment	not modelled	99.9	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**a-type flavoprotein; **PDBTitle:** crystal structure of the flavodiiron protein from giardia2 intestinalis
22	d1ko3a_	Alignment	not modelled	99.9	19	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
23	d1m2xa_	Alignment	not modelled	99.9	17	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
24	c1ychD_	Alignment	not modelled	99.9	16	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**nitric oxide reductase; **PDBTitle:** x-ray crystal structures of moorella thermoacetica fpra.2 novel diiron site structure and mechanistic insights into3 a scavenging nitric oxide reductase
25	c3rkjA_	Alignment	not modelled	99.9	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-lactamase ndm-1; **PDBTitle:** crystal structure of new delhi metallo-beta-lactamase-1 from2 klebsiella pnueumoniae
26	d1znba_	Alignment	not modelled	99.9	19	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
27	c3hnnD_	Alignment	not modelled	99.9	21	**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
28	c1e5dA_	Alignment	not modelled	99.9	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**rubredoxin\:oxygen oxidoreductase; **PDBTitle:** rubredoxin oxygen:oxidoreductase (roo) from anaerobe2

						desulfovibrio gigas
29	c3spuB_	Alignment	not modelled	99.9	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-lactamase ndm-1; **PDBTitle:** apo ndm-1 crystal structure
30	c2cfuA_	Alignment	not modelled	99.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sdsa1; **PDBTitle:** crystal structure of sdsa1, an alkylsulfatase from2 pseudomonas aeruginosa, in complex with 1-decane-sulfonic-3 acid.
31	c2yz3B_	Alignment	not modelled	99.9	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
32	d2cfua2	Alignment	not modelled	99.9	17	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Alkylsulfatase-like
33	d1mqoa_	Alignment	not modelled	99.9	16	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
34	d2p97a1	Alignment	not modelled	99.9	18	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Ava3068-like
35	d1e5da2	Alignment	not modelled	99.9	21	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**ROO N-terminal domain-like
36	d1vmea2	Alignment	not modelled	99.9	21	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**ROO N-terminal domain-like
37	c3aj3A_	Alignment	not modelled	99.9	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**4-pyridoxolactonase; **PDBTitle:** crystal structure of selenomethionine substituted 4-pyridoxolactonase2 from mesorhizobium loti
38	d1ycga2	Alignment	not modelled	99.9	16	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**ROO N-terminal domain-like
39	c2fhxB_	Alignment	not modelled	99.9	17	**PDB header:**hydrolase, metal binding protein **Chain:** B: **PDB Molecule:**spm-1; **PDBTitle:** pseudomonas aeruginosa spm-1 metallo-beta-lactamase
40	d1x8ha_	Alignment	not modelled	99.9	21	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
41	c2r2dC_	Alignment	not modelled	99.9	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**zn-dependent hydrolases; **PDBTitle:** structure of a quorum-quenching lactonase (aiib) from agrobacterium2 tumefaciens
42	c3eshB_	Alignment	not modelled	99.9	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein similar to metal-dependent hydrolase; **PDBTitle:** crystal structure of a probable metal-dependent hydrolase2 from staphylococcus aureus. northeast structural genomics3 target zr314
43	c1p9eA_	Alignment	not modelled	99.8	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**methyl parathion hydrolase; **PDBTitle:** crystal structure analysis of methyl parathion hydrolase from2 pseudomonas sp wbc-3
44	d1p9ea_	Alignment	not modelled	99.8	27	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Methyl parathion hydrolase
45	c3sd9B_	Alignment	not modelled	99.8	16	**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
46	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 from2 thermoanaerobacter tengcongensis
47	c2br6A_	Alignment	not modelled	99.8	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aiia-like protein; **PDBTitle:** crystal structure of quorum-quenching n-acyl homoserine2 lactone lactonase
48	d1ztca1	Alignment	not modelled	99.7	21	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**TM0894-like
49	c3zq4C_	Alignment	not modelled	99.7	20	**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
50	c2bibA_	Alignment	not modelled	99.6	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**teichoic acid phosphorylcholine esterase/ choline binding **PDBTitle:** crystal structure of the complete modular teichioic acid2 phosphorylcholine esterase pce (cbpe) from streptococcus3 pneumoniae
51	c3bk2A_	Alignment	not modelled	99.6	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metal dependent hydrolase; **PDBTitle:** crystal structure analysis of the rnase j/ump complex
52	d2i7ta1	Alignment	not modelled	99.6	22	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**beta-CASP RNA-metabolising hydrolases
53	c3h3eA	Alignment	not modelled	99.6	20	**PDB header:**structural genomics, metal binding prote **Chain:** A: **PDB Molecule:**uncharacterized protein tm1679;

		Alignment	not modelled	99.6	20	**PDBTitle:** crystal structure of tm1679, a metal-dependent hydrolase of2 the beta-lactamase superfamily
54	d1wraa1	Alignment	not modelled	99.5	22	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Pce catalytic domain-like
55	d2dkfa1	Alignment	not modelled	99.5	22	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**beta-CASP RNA-metabolising hydrolases
56	c2az4A_	Alignment	not modelled	99.4	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
57	c3af5A_	Alignment	not modelled	99.4	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein ph1404; **PDBTitle:** the crystal structure of an archaeal cpsf subunit, ph1404 from2 pyrococcus horikoshii
58	c2ycbA_	Alignment	not modelled	99.4	25	**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
59	c2xr1A_	Alignment	not modelled	99.4	24	**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
60	c3kl7A_	Alignment	not modelled	99.4	15	**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
61	c1zkpD_	Alignment	not modelled	99.3	17	**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 homolgue of bacillus anthracis, a putative3 ribonuclease
62	c2xr1B_	Alignment	not modelled	99.3	25	**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
63	c3zwfA_	Alignment	not modelled	99.3	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zinc phosphodiesterase elac protein 1; **PDBTitle:** crystal structure of human trnase z, short form (elac1).
64	c3g1pA_	Alignment	not modelled	99.3	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**protein phnp; **PDBTitle:** crystals structure of phnp from e.coli k-12
65	c3md7A_	Alignment	not modelled	99.3	13	**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
66	d2az4a1	Alignment	not modelled	99.1	20	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**beta-CASP RNA-metabolising hydrolases
67	d2i7xa1	Alignment	not modelled	99.1	18	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**beta-CASP RNA-metabolising hydrolases
68	c2i7xA_	Alignment	not modelled	99.1	18	**PDB header:**rna binding protein, protein binding **Chain:** A: **PDB Molecule:**protein cft2; **PDBTitle:** structure of yeast cpsf-100 (ydh1p)
69	d1y44a1	Alignment	not modelled	99.0	28	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**RNase Z-like
70	d1zkpa1	Alignment	not modelled	99.0	21	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**YhfI-like
71	d2cbna1	Alignment	not modelled	98.9	22	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**RNase Z-like
72	d1vjna_	Alignment	not modelled	98.7	22	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Hypothetical protein TM0207
73	d1xtoa_	Alignment	not modelled	98.6	14	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Coenzyme PQQ synthesis protein B, PqqB
74	c3bv6D_	Alignment	not modelled	98.6	19	**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	98.6	24	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**l-ascorbate-6-phosphate lactonase ulag; **PDBTitle:** apo structure of a metallo-b-lactamase
76	d2e7ya1	Alignment	not modelled	98.5	24	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**RNase Z-like
77	c3rpcD_	Alignment	not modelled	98.5	21	**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
						PDB header:lyase/lyase inhibitor

78	c3ucoB_	Alignment	not modelled	57.2	16	**Chain:** B: **PDB Molecule:**carbonic anhydrase; **PDBTitle:** coccomyxa beta-carbonic anhydrase in complex with iodide
79	c3dmpD_	Alignment	not modelled	52.0	14	**PDB header:**transferase **Chain:** D: **PDB Molecule:**uracil phosphoribosyltransferase; **PDBTitle:** 2.6 a crystal structure of uracil phosphoribosyltransferase2 from burkholderia pseudomallei
80	d1bd3a_	Alignment	not modelled	35.3	11	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
81	d1ulza2	Alignment	not modelled	34.2	14	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
82	d1i5ea_	Alignment	not modelled	33.8	22	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
83	c2ehjA_	Alignment	not modelled	33.1	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uracil phosphoribosyltransferase; **PDBTitle:** structure of uracil phosphoribosyl transferase
84	c3lpnB_	Alignment	not modelled	32.9	23	**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).
85	d2j9ga2	Alignment	not modelled	32.1	14	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
86	d1xtta1	Alignment	not modelled	31.5	19	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
87	d1v9sa1	Alignment	not modelled	30.0	19	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
88	c3efhB_	Alignment	not modelled	28.6	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribose-phosphate pyrophosphokinase 1; **PDBTitle:** crystal structure of human phosphoribosyl pyrophosphate2 synthetase 1
89	d2f06a1	Alignment	not modelled	27.3	6	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**BT0572-like
90	c1okgA_	Alignment	not modelled	26.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**possible 3-mercaptopyruvate sulfurtransferase; **PDBTitle:** 3-mercaptopyruvate sulfurtransferase from leishmania major
91	d1dkua2	Alignment	not modelled	25.0	29	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
92	c3eyxB_	Alignment	not modelled	23.7	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**carbonic anhydrase; **PDBTitle:** crystal structure of carbonic anhydrase nce103 from2 saccharomyces cerevisiae
93	c2c4kD_	Alignment	not modelled	23.2	20	**PDB header:**regulatory protein **Chain:** D: **PDB Molecule:**phosphoribosyl pyrophosphate synthetase- **PDBTitle:** crystal structure of human phosphoribosylpyrophosphate2 synthetase-associated protein 39 (pap39)
94	c3dahB_	Alignment	not modelled	22.7	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribose-phosphate pyrophosphokinase; **PDBTitle:** 2.3 a crystal structure of ribose-phosphate pyrophosphokinase from2 burkholderia pseudomallei
95	d2c4ka2	Alignment	not modelled	22.6	20	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
96	d1ii7a_	Alignment	not modelled	21.2	20	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**DNA double-strand break repair nuclease
97	d1ddza1	Alignment	not modelled	19.8	12	**Fold:**Resolvase-like **Superfamily:**beta-carbonic anhydrase, cab **Family:**beta-carbonic anhydrase, cab
98	c1dkrB_	Alignment	not modelled	18.7	29	**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.
99	c3bbnB_	Alignment	not modelled	17.1	17	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**ribosomal protein s2; **PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.