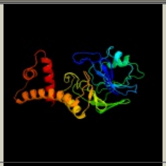
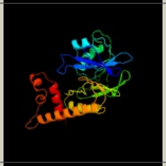
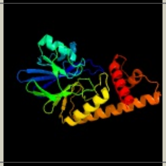
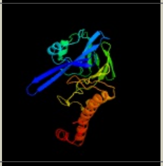
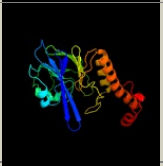
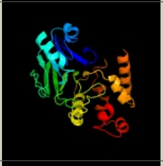
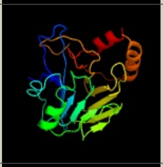
Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3677c_(-)_4117436_4118230
Date	Fri Aug 9 18:20:36 BST 2019
Unique Job ID	677daadd3646814f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4ad9E_	Alignment		100.0	32	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**beta-lactamase-like protein 2; **PDBTitle:** crystal structure of human lactb2.
2	c5i0pB_	Alignment		100.0	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-lactamase domain protein; **PDBTitle:** crystal structure of a beta-lactamase domain protein from burkholderia2 ambifaria
3	c2zo4A_	Alignment		100.0	32	**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
4	c4nurB_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**psdsa; **PDBTitle:** crystal structure of thermostable alkylsulfatase sdsap from2 pseudomonas sp. s9
5	c2yheD_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**sec-alkyl sulfatase; **PDBTitle:** structure determination of the stereoselective inverting sec-2 alkylsulfatase pisa1 from pseudomonas sp.
6	d2cfua2	Alignment		100.0	23	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Alkylsulfatase-like
7	c2cfuA_	Alignment		100.0	21	**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.
8	c4efzB_	Alignment		100.0	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**metallo-beta-lactamase family protein; **PDBTitle:** crystal structure of a hypothetical metallo-beta-lactamase from2 burkholderia pseudomallei
9	c3r2uC_	Alignment		100.0	20	**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
10	d1xm8a_	Alignment		100.0	21	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Glyoxalase II (hydroxyacylglutathione hydrolase)
11	d2q0ia1	Alignment		100.0	24	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**PqsE-like

12	c4ysbB_	Alignment		100.0	28	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**metallo-beta-lactamase family protein; **PDBTitle:** crystal structure of ethe1 from myxococcus xanthus
13	c4chlA_	Alignment		100.0	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**persulfide dioxygenase ethe1, mitochondrial; **PDBTitle:** human ethylmalonic encephalopathy protein 1 (hethe1)
14	c3tp9B_	Alignment		100.0	27	**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
15	c5ve5C_	Alignment		100.0	26	**PDB header:**oxidoreductase, transferase **Chain:** C: **PDB Molecule:**bpprf; **PDBTitle:** crystal structure of persulfide dioxygenase rhodanese fusion protein2 with rhodanese domain inactivating mutation (c314s) from burkholderia3 phytofirmans in complex with glutathione
16	c4yskA_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-lactamase domain protein; **PDBTitle:** crystal structure of apo-form sdoa from pseudomonas putida
17	d2qeda1	Alignment		100.0	22	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Glyoxalase II (hydroxyacylglutathione hydrolase)
18	c6h0cA_	Alignment		100.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative diflavin flavoprotein a 3; **PDBTitle:** flv1 flavodiiron core from synechocystis sp. pcc6803
19	c2ohiB_	Alignment		100.0	26	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**type a flavoprotein fpra; **PDBTitle:** crystal structure of coenzyme f420h2 oxidase (fpra), a diiron2 flavoprotein, reduced state
20	c1vmeB_	Alignment		100.0	22	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**flavoprotein; **PDBTitle:** crystal structure of flavoprotein (tm0755) from thermotoga maritima at2 1.80 a resolution
21	d2gmna1	Alignment	not modelled	100.0	23	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
22	c2gcuD_	Alignment	not modelled	100.0	22	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative hydroxyacylglutathione hydrolase 3; **PDBTitle:** x-ray structure of gene product from arabidopsis thaliana at1g53580
23	c2q9uB_	Alignment	not modelled	100.0	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**a-type flavoprotein; **PDBTitle:** crystal structure of the flavodiiron protein from giardia2 intestinalis
24	c1ychD_	Alignment	not modelled	100.0	19	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**nitric oxide reductase; **PDBTitle:** x-ray crystal structures of moorella thermoacetica fpra. novel diiron2 site structure and mechanistic insights into a scavenging nitric3 oxide reductase
25	c4pdxB_	Alignment	not modelled	100.0	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative alkyl/aryl-sulfatase yjcs; **PDBTitle:** crystal structure of escherchia coli uncharacterized protein yjcs
26	c5k0wA_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**class b carbapenemase gob-18; **PDBTitle:** crystal structure of the metallo-beta-lactamase gob-18 from2 elizabethkingia meningoseptica
27	c6dn4A_	Alignment	not modelled	100.0	23	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**beta-lactamase; **PDBTitle:** cronobacter sakazakii (enterobacter sakazakii) metallo-beta-lactamse2 harldq motif
28	d1m2xa_	Alignment	not modelled	100.0	18	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase

						Family: Zn metallo-beta-lactamase
29	c3adrA_	Alignment	not modelled	100.0	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
30	c1e5dA_	Alignment	not modelled	100.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**rubredoxin\:oxygen oxidoreductase; **PDBTitle:** rubredoxin oxygen:oxidoreductase (roo) from anaerobe desulfovibrio2 gigas
31	d1jjta_	Alignment	not modelled	100.0	17	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
32	c5aebA_	Alignment	not modelled	100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lra-12; **PDBTitle:** crystal structure of the class b3 di-zinc metallo-beta-lactamase lra-2 12 from an alaskan soil metagenome.
33	d1ko3a_	Alignment	not modelled	100.0	20	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
34	c3lvzA_	Alignment	not modelled	100.0	23	**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
35	c2p18A_	Alignment	not modelled	100.0	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glyoxalase ii; **PDBTitle:** crystal structure of the leishmania infantum glyoxalase ii
36	c6n36A_	Alignment	not modelled	100.0	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**beta-lactamase; **PDBTitle:** beta-lactamase from chitinophaga pinensis
37	c3rkjA_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-lactamase ndm-1; **PDBTitle:** crystal structure of new delhi metallo-beta-lactamase-1 from2 klebsiella pnueumoniae
38	c5iqkB_	Alignment	not modelled	100.0	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-lactamase rm3; **PDBTitle:** rm3 metallo-beta-lactamase
39	c4awyB_	Alignment	not modelled	100.0	26	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**metallo-beta-lactamase aim-1; **PDBTitle:** crystal structure of the mobile metallo-beta-lactamase aim-1 from2 pseudomonas aeruginosa: insights into antibiotic binding and the role3 of gln157
40	d1qh5a_	Alignment	not modelled	100.0	24	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Glyoxalase II (hydroxyacylglutathione hydrolase)
41	d1k07a_	Alignment	not modelled	100.0	21	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
42	c6aufB_	Alignment	not modelled	100.0	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-lactamase-like protein; **PDBTitle:** crystal structure of metalo beta lactamases mim-1 from novosphingobium2 pentaromativorans
43	c4d02A_	Alignment	not modelled	100.0	19	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**anaerobic nitric oxide reductase flavorubredoxin; **PDBTitle:** the crystallographic structure of flavorubredoxin from escherichia2 coli
44	c2ynuB_	Alignment	not modelled	100.0	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**gim-1 protein; **PDBTitle:** apo gim-1 with 2mol. crystal structures of pseudomonas aeruginosa2 gim-1: active site plasticity in metallo-beta-lactamases
45	d1e5da2	Alignment	not modelled	100.0	16	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**ROO N-terminal domain-like
46	c3hnnD_	Alignment	not modelled	100.0	20	**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
47	d2aioa1	Alignment	not modelled	100.0	25	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
48	d1znba_	Alignment	not modelled	100.0	17	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
49	c4wd6B_	Alignment	not modelled	100.0	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**metallo-beta-lactamase; **PDBTitle:** crystal structure of dim-1 metallo-beta-lactamase
50	c3spuB_	Alignment	not modelled	100.0	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-lactamase ndm-1; **PDBTitle:** apo ndm-1 crystal structure
51	c2yz3B_	Alignment	not modelled	100.0	19	**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
52	c3vqzA_	Alignment	not modelled	100.0	22	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**metallo-beta-lactamase; **PDBTitle:** crystal structure of metallo-beta-lactamase, smb-1, in a complex with2 mercaptoacetic acid
53	c6e0sA_	Alignment	not modelled	100.0	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mem-a1; **PDBTitle:** crystal structure of mem-a1, a subclass b3 metallo-beta-lactamase2 isolated from a soil metagenome library
						Fold: Metallo-hydrolase/oxidoreductase

54	d1ycga2	Alignment	not modelled	100.0	20	**Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**ROO N-terminal domain-like
55	c5mmdF_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**metallo-beta-lactamase 1; **PDBTitle:** tmb-1. structural insights into tmb-1 and the role of residue 119 and2 228 in substrate and inhibitor binding
56	c3l6nA_	Alignment	not modelled	100.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metallo-beta-lactamase; **PDBTitle:** crystal structure of metallo-beta-lactamase ind-7
57	d1mqoa_	Alignment	not modelled	100.0	21	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
58	c2xf4A_	Alignment	not modelled	100.0	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydroxyacylglutathione hydrolase; **PDBTitle:** crystal structure of salmonella enterica serovar2 typhimurium ycbl
59	c6qrqB_	Alignment	not modelled	100.0	17	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**oxygen-binding diiron protein; **PDBTitle:** apo conformation of chemotaxis sensor odp
60	c2fhxB_	Alignment	not modelled	99.9	19	**PDB header:**hydrolase, metal binding protein **Chain:** B: **PDB Molecule:**spm-1; **PDBTitle:** pseudomonas aeruginosa spm-1 metallo-beta-lactamase
61	d2p97a1	Alignment	not modelled	99.9	15	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Ava3068-like
62	d1vmea2	Alignment	not modelled	99.9	22	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**ROO N-terminal domain-like
63	c6cqsA_	Alignment	not modelled	99.9	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-lactamase; **PDBTitle:** sediminispirochaeta smaragdinae sps-1 metallo-beta-lactamase
64	c6qnmB_	Alignment	not modelled	99.9	16	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**oxygen-binding di-iron protein; **PDBTitle:** apo state of chemotaxis sensor odp from t. denticola
65	d1x8ha_	Alignment	not modelled	99.9	22	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
66	c2zwrA_	Alignment	not modelled	99.9	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metallo-beta-lactamase superfamily protein; **PDBTitle:** crystal structure of ttha1623 from thermus thermophilus hb8
67	c3sd9B_	Alignment	not modelled	99.9	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
68	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 mesorhizobium loti
69	c6ch0I_	Alignment	not modelled	99.8	20	**PDB header:**hydrolase **Chain:** I: **PDB Molecule:**beta-lactamase; **PDBTitle:** structure of the quorum quenching lactonase from alicyclobacillus2 acidoterrestris bound to a glycerol molecule
70	c4v0hC_	Alignment	not modelled	99.8	22	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**metallo-beta-lactamase domain-containing protein 1 1; **PDBTitle:** human metallo beta lactamase domain containing protein 1 (hmblac1)
71	c2r2dC_	Alignment	not modelled	99.8	22	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**zn-dependent hydrolases; **PDBTitle:** structure of a quorum-quenching lactonase (aiib) from agrobacterium2 tumefaciens
72	c3eshB_	Alignment	not modelled	99.8	20	**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
73	c4xukB_	Alignment	not modelled	99.8	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative hydrolase; **PDBTitle:** crystal structure of hydrolase aboph in beta lactamase superfamily
74	c4zo3A_	Alignment	not modelled	99.8	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acylhomoserine lactonase; **PDBTitle:** aidc, a dizinc quorum-quenching lactonase, in complex with a product2 n-hexnoyl-l-homoserine
75	c1p9eA_	Alignment	not modelled	99.8	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**methyl parathion hydrolase; **PDBTitle:** crystal structure analysis of methyl parathion hydrolase from2 pseudomonas sp wbc-3
76	d1p9ea_	Alignment	not modelled	99.8	20	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Methyl parathion hydrolase
77	c4le6B_	Alignment	not modelled	99.8	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**organophosphorus hydrolase; **PDBTitle:** crystal structure of the phosphotriesterase ophc2 from pseudomonas2 pseudoalcaligenes
78	c2br6A_	Alignment	not modelled	99.8	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aiia-like protein; **PDBTitle:** crystal structure of quorum-quenching n-acyl homoserine2 lactone lactonase
						PDB header:hydrolase **Chain:** A: **PDB Molecule:**metal-dependent hydrolases of the beta-

79	c2p4zA_	Alignment	not modelled	99.8	20	lactamase **PDBTitle:** a ferredoxin-like metallo-beta-lactamase superfamily protein from2 thermoanaerobacter tengcongensis
80	c5a0tA_	Alignment	not modelled	99.8	27	**PDB header:**hydrolase/rna **Chain:** A: **PDB Molecule:**ribonuclease j; **PDBTitle:** catalysis and 5' end sensing by ribonuclease rnase j of the2 metallo-beta-lactamase family
81	c3zq4C_	Alignment	not modelled	99.7	23	**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
82	d1ztca1	Alignment	not modelled	99.7	21	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**TM0894-like
83	c4xwwA_	Alignment	not modelled	99.7	25	**PDB header:**rna binding protein/rna **Chain:** A: **PDB Molecule:**dr2417; **PDBTitle:** crystal structure of rnase j complexed with rna
84	c1zkpD_	Alignment	not modelled	99.7	18	**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
85	c5habB_	Alignment	not modelled	99.7	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ribonuclease j; **PDBTitle:** crystal structure of mpy-rnase j (mutant h84a), an archaeal rnase j2 from methanolobus psychrophilus r15, complex with rna
86	c3x30A_	Alignment	not modelled	99.7	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**upf0173 metal-dependent hydrolase tm_1162; **PDBTitle:** crystal structure of metallo-beta-lactamase from thermotoga maritima
87	c3bk2A_	Alignment	not modelled	99.6	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metal dependent hydrolase; **PDBTitle:** crystal structure analysis of the rnase j/ump complex
88	c6b9vA_	Alignment	not modelled	99.6	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-lactamase-like protein; **PDBTitle:** crystal structure of a new diphosphatase from the phnp family
89	d1zkpa1	Alignment	not modelled	99.5	17	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**YhfI-like
90	c3h3eA_	Alignment	not modelled	99.5	22	**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
91	c6i1dA_	Alignment	not modelled	99.5	26	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**endoribonuclease ysh1; **PDBTitle:** structure of the ysh1-mpe1 nuclease complex from s.cerevisiae
92	d2i7ta1	Alignment	not modelled	99.5	25	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**beta-CASP RNA-metabolising hydrolases
93	c2az4A_	Alignment	not modelled	99.5	24	**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
94	c3af5A_	Alignment	not modelled	99.5	32	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein ph1404; **PDBTitle:** the crystal structure of an archaeal cpsf subunit, ph1404 from2 pyrococcus horikoshii
95	c2xr1A_	Alignment	not modelled	99.5	30	**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
96	d2dkfa1	Alignment	not modelled	99.5	27	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**beta-CASP RNA-metabolising hydrolases
97	c2ycbA_	Alignment	not modelled	99.4	30	**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
98	c2xr1B_	Alignment	not modelled	99.4	28	**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
99	c3g1pA_	Alignment	not modelled	99.4	23	**PDB header:**lyase **Chain:** A: **PDB Molecule:**protein phnp; **PDBTitle:** crystals structure of phnp from e.coli k-12
100	c6j4nD_	Alignment	not modelled	99.4	19	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**metallo-beta-lactamases pngm-1; **PDBTitle:** structure of papua new guinea mbl-1(pngm-1) native
101	c3md7A_	Alignment	not modelled	99.4	15	**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
102	d1y44a1	Alignment	not modelled	99.3	13	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**RNase Z-like
						PDB header:hydrolase

103	c3zwfA_	Alignment	not modelled	99.3	21	**Chain:** A: **PDB Molecule:**zinc phosphodiesterase elac protein 1; **PDBTitle:** crystal structure of human trnase z, short form (elac1).
104	c3kl7A_	Alignment	not modelled	99.2	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
105	c4z7rA_	Alignment	not modelled	99.2	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**coenzyme pqq synthesis protein b; **PDBTitle:** the 1.98-angstrom crystal structure of zn(2+)-bound pqqb from2 methylobacterium extorquens
106	d2i7xa1	Alignment	not modelled	99.2	17	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**beta-CASP RNA-metabolising hydrolases
107	c2i7xA_	Alignment	not modelled	99.2	17	**PDB header:**rna binding protein, protein binding **Chain:** A: **PDB Molecule:**protein cft2; **PDBTitle:** structure of yeast cpsf-100 (ydh1p)
108	d2az4a1	Alignment	not modelled	99.1	20	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**beta-CASP RNA-metabolising hydrolases
109	d1xtoa_	Alignment	not modelled	99.1	14	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Coenzyme PQQ synthesis protein B, PqqB
110	d2cbna1	Alignment	not modelled	99.0	18	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**RNase Z-like
111	c2bibA_	Alignment	not modelled	99.0	23	**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 streptococcus pneumoniae
112	c6brmC_	Alignment	not modelled	99.0	22	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**putative metal-dependent isothiocyanate hydrolase saxa; **PDBTitle:** the crystal structure of isothiocyanate hydrolase from delia radicum2 gut bacteria
113	d1wraa1	Alignment	not modelled	99.0	21	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Pce catalytic domain-like
114	c4b87A_	Alignment	not modelled	98.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dna cross-link repair 1a protein; **PDBTitle:** crystal structure of human dna cross-link repair 1a
115	c4ojvA_	Alignment	not modelled	98.8	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**3',5'-cyclic-nucleotide phosphodiesterase 1; **PDBTitle:** crystal structure of unliganded yeast pde1
116	c3bv6D_	Alignment	not modelled	98.8	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
117	d1vjna_	Alignment	not modelled	98.8	21	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Hypothetical protein TM0207
118	c2wyIF_	Alignment	not modelled	98.7	18	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**l-ascorbate-6-phosphate lactonase ulag; **PDBTitle:** apo structure of a metallo-b-lactamase
119	c4jo0A_	Alignment	not modelled	98.7	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cmla; **PDBTitle:** crystal structure of cmla, a diiron beta-hydroxylase from streptomyces2 venezuelae
120	c4qn9A_	Alignment	not modelled	98.7	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**n-acyl-phosphatidylethanolamine-hydrolyzing phospholipase **PDBTitle:** structure of human nape-pld