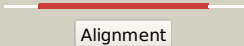

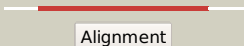

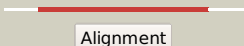







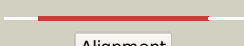

















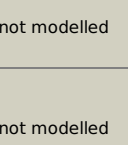


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2407_(-)_2704707_2705528
Date	Wed Aug 7 12:50:02 BST 2019
Unique Job ID	42ed8d24a9ba7518

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6j4nD_	 Alignment		100.0	24	PDB header: hydrolase Chain: D: PDB Molecule: metallo-beta-lactamases pngm-1; PDBTitle: structure of papua new guinea mbl-1(pngm-1) native
2	d2cbna1	 Alignment		100.0	30	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: RNase Z-like
3	d1y44a1	 Alignment		100.0	26	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: RNase Z-like
4	c3zwfA_	 Alignment		100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: zinc phosphodiesterase elac protein 1; PDBTitle: crystal structure of human trnase z, short form (elac1).
5	c5mtzA_	 Alignment		100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease z; PDBTitle: crystal structure of a long form rnase z from yeast
6	c1zkpD_	 Alignment		100.0	24	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
7	d1zka1	 Alignment		100.0	24	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Yhfl-like
8	c4z7rA_	 Alignment		100.0	17	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
9	c3md7A_	 Alignment		100.0	25	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
10	c6b9vA_	 Alignment		100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase-like protein; PDBTitle: crystal structure of a new diphosphatase from the phnp family
11	d1xtoa_	 Alignment		100.0	12	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Coenzyme PQQ synthesis protein B, PqqB

12	c3g1pA	Alignment		100.0	23	PDB header: lyase Chain: A: PDB Molecule: protein phnp; PDBTitle: crystals structure of phnp from e.coli k-12
13	c4ojvA	Alignment		100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: 3',5'-cyclic-nucleotide phosphodiesterase 1; PDBTitle: crystal structure of unliganded yeast pde1
14	d2e7ya1	Alignment		100.0	20	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: RNase Z-like
15	d2i7ta1	Alignment		99.9	15	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: beta-CASP RNA-metabolising hydrolases
16	c2p4zA	Alignment		99.9	14	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
17	c6i1dA	Alignment		99.9	12	PDB header: gene regulation Chain: A: PDB Molecule: endoribonuclease ysh1; PDBTitle: structure of the ysh1-mpe1 nuclease complex from s.cerevisiae
18	c6brmC	Alignment		99.9	17	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
19	c3x30A	Alignment		99.9	20	PDB header: hydrolase Chain: A: PDB Molecule: upf0173 metal-dependent hydrolase tm_1162; PDBTitle: crystal structure of metallo-beta-lactamase from thermotoga maritima
20	d2dkfa1	Alignment		99.9	19	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: beta-CASP RNA-metabolising hydrolases
21	c3rpcD	Alignment	not modelled	99.9	17	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
22	c2ycbA	Alignment	not modelled	99.9	16	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
23	c5a0tA	Alignment	not modelled	99.9	22	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
24	c2xr1A	Alignment	not modelled	99.9	15	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
25	c2az4A	Alignment	not modelled	99.9	13	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
26	c2xr1B	Alignment	not modelled	99.9	15	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
27	c1gn9A	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: n-acyl-phosphatidylethanolamine-

27	c4q19A	Alignment	not modelled	99.9	10	hydrolyzing phospholipase PDBTitle: structure of human nape-pld
28	c3af5A	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A; PDB Molecule: putative uncharacterized protein ph1404; PDBTitle: the crystal structure of an archaeal cpsf subunit, ph1404 from2 pyrococcus horikoshii
29	c4xwwA	Alignment	not modelled	99.9	21	PDB header: rna binding protein/rna Chain: A; PDB Molecule: dr2417; PDBTitle: crystal structure of rnase j complexed with rna
30	c3bk2A	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: A; PDB Molecule: metal dependent hydrolase; PDBTitle: crystal structure analysis of the rnase j/ump complex
31	c3zq4C	Alignment	not modelled	99.9	17	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
32	c2wy1F	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: F; PDB Molecule: l-ascorbate-6-phosphate lactonase ulag; PDBTitle: apo structure of a metallo-b-lactamase
33	c3h3eA	Alignment	not modelled	99.9	17	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
34	c5habB	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: B; PDB Molecule: ribonuclease j; PDBTitle: crystal structure of mpy-rnase j (mutant h84a), an archaeal rnase j2 from methanobolus psychrophilus r15, complex with rna
35	c3ki7A	Alignment	not modelled	99.9	21	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
36	c3bv6D	Alignment	not modelled	99.9	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
37	d2i7xa1	Alignment	not modelled	99.9	13	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: beta-CASP RNA-metabolising hydrolases
38	c2i7xA	Alignment	not modelled	99.9	13	PDB header: rna binding protein, protein binding Chain: A; PDB Molecule: protein cft2; PDBTitle: structure of yeast cpsf-100 (ydh1p)
39	c4jo0A	Alignment	not modelled	99.8	14	PDB header: oxidoreductase Chain: A; PDB Molecule: cm1a; PDBTitle: crystal structure of cm1a, a diiron beta-hydroxylase from streptomyces2 venezuelae
40	d1vjna	Alignment	not modelled	99.8	23	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Hypothetical protein TM0207
41	d1k07a	Alignment	not modelled	99.8	16	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase
42	c5iqkB	Alignment	not modelled	99.8	14	PDB header: hydrolase Chain: B; PDB Molecule: beta-lactamase rm3; PDBTitle: rm3 metallo-beta-lactamase
43	c6qrqB	Alignment	not modelled	99.8	12	PDB header: signaling protein Chain: B; PDB Molecule: oxygen-binding diiron protein; PDBTitle: apo conformation of chemotaxis sensor odp
44	c5aebA	Alignment	not modelled	99.8	14	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.
45	c5k0wA	Alignment	not modelled	99.8	13	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
46	c6e0sA	Alignment	not modelled	99.8	14	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
47	c6ch0I	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: I; PDB Molecule: beta-lactamase; PDBTitle: structure of the quorum quenching lactonase from alicyclobacillus2 acidoterrestris bound to a glycerol molecule
48	c6dn4A	Alignment	not modelled	99.8	16	PDB header: metal binding protein Chain: A; PDB Molecule: beta-lactamase; PDBTitle: cronobacter sakazakii (enterobacter sakazakii) metallo-beta-lactamase2 harldq motif
49	c6aufB	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: B; PDB Molecule: beta-lactamase-like protein; PDBTitle: crystal structure of metalo beta lactamases mim-1 from novosphingobium2 pentaromativorans
50	c2r2dC	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: C; PDB Molecule: zn-dependent hydrolases; PDBTitle: structure of a quorum-quenching lactonase (aiib) from agrobacterium2 tumefaciens
51	c4awyB	Alignment	not modelled	99.7	14	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
52	c2zo4A	Alignment	not modelled	99.7	16	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 PDB header: hydrolase/hydrolase inhibitor

53	c3vqzA	Alignment	not modelled	99.7	15	Chain: A: PDB Molecule: metallo-beta-lactamase; PDBTitle: crystal structure of metallo-beta-lactamase, smb-1, in a complex with2 mercaptoacetic acid
54	c4zo3A	Alignment	not modelled	99.7	14	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
55	c1vmeB	Alignment	not modelled	99.7	15	PDB header: electron transport Chain: B: PDB Molecule: flavoprotein; PDBTitle: crystal structure of flavoprotein (tm0755) from thermotoga maritima at2 1.80 a resolution
56	d2aioa1	Alignment	not modelled	99.7	20	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase
57	c6n36A	Alignment	not modelled	99.7	12	PDB header: ligase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: beta-lactamase from chitinophaga pinensis
58	c3lvzA	Alignment	not modelled	99.7	16	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
59	d2gmna1	Alignment	not modelled	99.7	16	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase
60	d2q0ia1	Alignment	not modelled	99.7	14	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: PqsE-like
61	c3eshB	Alignment	not modelled	99.7	17	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
62	c6qnmB	Alignment	not modelled	99.7	10	PDB header: signaling protein Chain: B: PDB Molecule: oxygen-binding di-iron protein; PDBTitle: apo state of chemotaxis sensor odp from t. denticola
63	c6h0cA	Alignment	not modelled	99.7	13	PDB header: oxidoreductase Chain: A: PDB Molecule: putative diflavin flavoprotein a 3; PDBTitle: flv1 flavodiiron core from synechocystis sp. pcc6803
64	c2q9uB	Alignment	not modelled	99.7	11	PDB header: oxidoreductase Chain: B: PDB Molecule: ia-type flavoprotein; PDBTitle: crystal structure of the flavodiiron protein from giardia2 intestinalis
65	d1ztca1	Alignment	not modelled	99.7	17	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: TM0894-like
66	c2bibA	Alignment	not modelled	99.7	14	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 streptococcus pneumoniae
67	c3adrA	Alignment	not modelled	99.7	15	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
68	c4xukB	Alignment	not modelled	99.7	19	PDB header: hydrolase Chain: B: PDB Molecule: putative hydrolase; PDBTitle: crystal structure of hydrolase aboph in beta lactamase superfamily
69	c1e5dA	Alignment	not modelled	99.7	15	PDB header: oxidoreductase Chain: A: PDB Molecule: rubredoxin\;oxygen oxidoreductase; PDBTitle: rubredoxin oxygen:oxidoreductase (roo) from anaerobe desulfovibrio2 gigas
70	d1p9ea	Alignment	not modelled	99.7	20	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Methyl parathion hydrolase
71	c1p9eA	Alignment	not modelled	99.7	20	PDB header: hydrolase Chain: A: PDB Molecule: methyl parathion hydrolase; PDBTitle: crystal structure analysis of methyl parathion hydrolase from2 pseudomonas sp wbc-3
72	c2ohiB	Alignment	not modelled	99.6	14	PDB header: oxidoreductase Chain: B: PDB Molecule: type a flavoprotein fpfa; PDBTitle: crystal structure of coenzyme f420h2 oxidase (fpfa), a diiron2 flavoprotein, reduced state
73	c3aj3A	Alignment	not modelled	99.6	13	PDB header: hydrolase Chain: A: PDB Molecule: 4-pyridoxolactonase; PDBTitle: crystal structure of selenomethionine substituted 4-pyridoxolactonase2 from mesorhizobium loti
74	c4efzB	Alignment	not modelled	99.6	20	PDB header: hydrolase Chain: B: PDB Molecule: metallo-beta-lactamase family protein; PDBTitle: crystal structure of a hypothetical metallo-beta-lactamase from2 burkholderia pseudomallei
75	c3hnnD	Alignment	not modelled	99.6	13	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
76	c4d02A	Alignment	not modelled	99.6	15	PDB header: electron transport Chain: A: PDB Molecule: anaerobic nitric oxide reductase flavorubredoxin; PDBTitle: the crystallographic structure of flavorubredoxin from escherichia2 coli
77	c5i0pB	Alignment	not modelled	99.6	21	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase domain protein; PDBTitle: crystal structure of a beta-lactamase domain protein from burkholderia2 ambifaria

78	c4yskA	Alignment	not modelled	99.6	20	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase domain protein; PDBTitle: crystal structure of apo-form sdoa from pseudomonas putida
79	c1ychD	Alignment	not modelled	99.6	9	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
80	d1vmea2	Alignment	not modelled	99.6	14	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: ROO N-terminal domain-like
81	c2br6A	Alignment	not modelled	99.6	15	PDB header: hydrolase Chain: A: PDB Molecule: aiia-like protein; PDBTitle: crystal structure of quorum-quenching n-acyl homoserine2 lactone lactonase
82	c4b87A	Alignment	not modelled	99.6	20	PDB header: hydrolase Chain: A: PDB Molecule: dna cross-link repair 1a protein; PDBTitle: crystal structure of human dna cross-link repair 1a
83	c4nurB	Alignment	not modelled	99.6	16	PDB header: hydrolase Chain: B: PDB Molecule: psdsa; PDBTitle: crystal structure of thermostable alkylsulfatase sdsap from2 pseudomonas sp. s9
84	d1ycga2	Alignment	not modelled	99.6	11	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: ROO N-terminal domain-like
85	d1e5da2	Alignment	not modelled	99.6	17	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: ROO N-terminal domain-like
86	c3l6nA	Alignment	not modelled	99.6	14	PDB header: hydrolase Chain: A: PDB Molecule: metallo-beta-lactamase; PDBTitle: crystal structure of metallo-beta-lactamase ind-7
87	c4ad9E	Alignment	not modelled	99.6	14	PDB header: hydrolase Chain: E: PDB Molecule: beta-lactamase-like protein 2; PDBTitle: crystal structure of human lactb2.
88	c3sd9B	Alignment	not modelled	99.5	9	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
89	c4pdxB	Alignment	not modelled	99.5	16	PDB header: hydrolase Chain: B: PDB Molecule: putative alkyl/aryl-sulfatase yjcs; PDBTitle: crystal structure of escherchia coli uncharacterized protein yjcs
90	d1znba	Alignment	not modelled	99.5	14	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase
91	c6cqsA	Alignment	not modelled	99.5	14	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: sediminispirochaeta smaragdinae sps-1 metallo-beta-lactamase
92	c3zdkA	Alignment	not modelled	99.5	16	PDB header: hydrolase Chain: A: PDB Molecule: 5' exonuclease apollo; PDBTitle: crystal structure of human 5' exonuclease apollo
93	d1m2xa	Alignment	not modelled	99.5	10	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase
94	d2az4a1	Alignment	not modelled	99.5	13	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: beta-CASP RNA-metabolising hydrolases
95	c2yheD	Alignment	not modelled	99.5	11	PDB header: hydrolase Chain: D: PDB Molecule: sec-alkyl sulfatase; PDBTitle: structure determination of the stereoselective inverting sec-2 alkylsulfatase pisa1 from pseudomonas sp.
96	d1x8ha	Alignment	not modelled	99.5	12	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase
97	c4le6B	Alignment	not modelled	99.5	28	PDB header: hydrolase Chain: B: PDB Molecule: organophosphorus hydrolase; PDBTitle: crystal structure of the phosphotriesterase ophc2 from pseudomonas2 pseudoalcaligenes
98	c2fxbB	Alignment	not modelled	99.5	10	PDB header: hydrolase, metal binding protein Chain: B: PDB Molecule: spm-1; PDBTitle: pseudomonas aeruginosa spm-1 metallo-beta-lactamase
99	c4wd6B	Alignment	not modelled	99.5	16	PDB header: hydrolase Chain: B: PDB Molecule: metallo-beta-lactamase; PDBTitle: crystal structure of dim-1 metallo-beta-lactamase
100	d1ko3a	Alignment	not modelled	99.5	18	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase
101	c2cfuA	Alignment	not modelled	99.5	13	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.
102	d1jita	Alignment	not modelled	99.5	11	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase
103	c2zwrA	Alignment	not modelled	99.5	15	PDB header: hydrolase Chain: A: PDB Molecule: metallo-beta-lactamase superfamily protein; PDBTitle: crystal structure of ttha1623 from thermus thermophilus hb8
						PDB header: hydrolase

104	c2ynuB_	Alignment	not modelled	99.5	16	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
105	d2cfua2	Alignment	not modelled	99.4	12	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Alkylsulfatase-like
106	c3tp9B_	Alignment	not modelled	99.4	19	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
107	d1mqoa_	Alignment	not modelled	99.4	12	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase
108	c3rkjA_	Alignment	not modelled	99.4	17	PDB header: hydrolase Chain: A; PDB Molecule: beta-lactamase ndm-1; PDBTitle: crystal structure of new delhi metallo-beta-lactamase-1 from2 klebsiella pneumoniae
109	c2yz3B_	Alignment	not modelled	99.4	15	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
110	c5mmdF_	Alignment	not modelled	99.4	14	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
111	c3spuB_	Alignment	not modelled	99.4	18	PDB header: hydrolase Chain: B; PDB Molecule: beta-lactamase ndm-1; PDBTitle: apo ndm-1 crystal structure
112	d1xm8a_	Alignment	not modelled	99.4	20	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Glyoxalase II (hydroxyacylglutathione hydrolase)
113	c4v0hC_	Alignment	not modelled	99.4	27	PDB header: hydrolase Chain: C; PDB Molecule: metallo-beta-lactamase domain-containing protein 1 1; PDBTitle: human metallo beta lactamase domain containing protein 1 (hmb1ac1)
114	d1wraa1	Alignment	not modelled	99.4	13	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Pce catalytic domain-like
115	c5ve5C_	Alignment	not modelled	99.3	24	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
116	d1qh5a_	Alignment	not modelled	99.3	23	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Glyoxalase II (hydroxyacylglutathione hydrolase)
117	c3r2uC_	Alignment	not modelled	99.3	13	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
118	d2qeda1	Alignment	not modelled	99.3	19	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Glyoxalase II (hydroxyacylglutathione hydrolase)
119	c2xf4A_	Alignment	not modelled	99.2	19	PDB header: hydrolase Chain: A; PDB Molecule: hydroxyacylglutathione hydrolase; PDBTitle: crystal structure of salmonella enterica serovar2 typhimurium ycb1
120	c2p18A_	Alignment	not modelled	99.2	16	PDB header: hydrolase Chain: A; PDB Molecule: glyoxalase ii; PDBTitle: crystal structure of the leishmania infantum glyoxalase ii