

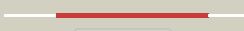























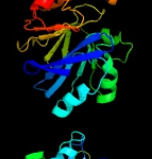
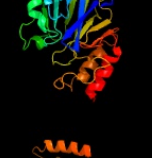
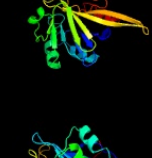




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1637C_(-)_1842905_1843699
Date	Fri Aug 2 13:30:23 BST 2019
Unique Job ID	877864e8f912a2e2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	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
2	c3r2uC_	 Alignment		100.0	25	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	c4efzB_	 Alignment		100.0	26	PDB header: hydrolase Chain: B: PDB Molecule: metallo-beta-lactamase family protein; PDBTitle: crystal structure of a hypothetical metallo-beta-lactamase from2 burkholderia pseudomallei
4	c5ve5C_	 Alignment		100.0	27	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 phytotfirmans in complex with glutathione
5	c4yskA_	 Alignment		100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase domain protein; PDBTitle: crystal structure of apo-form sdoa from pseudomonas putida
6	d1qh5a_	 Alignment		100.0	24	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Glyoxalase II (hydroxyacylglutathione hydrolase)
7	c4ysbB_	 Alignment		100.0	30	PDB header: hydrolase Chain: B: PDB Molecule: metallo-beta-lactamase family protein; PDBTitle: crystal structure of ethe1 from myxococcus xanthus
8	c4chlA_	 Alignment		100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: persulfide dioxygenase ethe1, mitochondrial; PDBTitle: human ethylmalonic encephalopathy protein 1 (hethe1)
9	c2p18A_	 Alignment		100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: glyoxalase ii; PDBTitle: crystal structure of the leishmania infantum glyoxalase ii
10	c2gcuD_	 Alignment		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
11	d2qed1	 Alignment		100.0	21	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Glyoxalase II (hydroxyacylglutathione hydrolase)

12	d1xm8a_	Alignment		100.0	29	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Glyoxalase II (hydroxyacylglutathione hydrolase)
13	c2xf4A_	Alignment		100.0	32	PDB header: hydrolase Chain: A: PDB Molecule: hydroxyacylglutathione hydrolase; PDBTitle: crystal structure of salmonella enterica serovar2 typhimurium ycbI
14	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
15	c5i0pB_	Alignment		100.0	21	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase domain protein; PDBTitle: crystal structure of a beta-lactamase domain protein from burkholderia2 ambifaria
16	c2ynuB_	Alignment		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
17	d1m2xa_	Alignment		100.0	14	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase
18	d2gmn1	Alignment		100.0	22	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase
19	c5k0wA_	Alignment		100.0	20	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
20	c4ad9E_	Alignment		100.0	23	PDB header: hydrolase Chain: E: PDB Molecule: beta-lactamase-like protein 2; PDBTitle: crystal structure of human lactb2.
21	d1jita_	Alignment	not modelled	100.0	18	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase
22	d2q0ia1	Alignment	not modelled	100.0	19	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: PqsE-like
23	c3l6nA_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: metallo-beta-lactamase; PDBTitle: crystal structure of metallo-beta-lactamase ind-7
24	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
25	c3rkjA_	Alignment	not modelled	100.0	20	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	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
27	d1znba_	Alignment	not modelled	100.0	19	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase
28	d1ko3a_	Alignment	not modelled	100.0	19	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase
29	c6dn4A_	Alignment	not modelled	100.0	20	PDB header: metal binding protein Chain: A: PDB Molecule: beta-lactamase;

29	c00n4A	Alignment	not modelled	100.0	20	PDBTitle: cronobacter sakazakii (enterobacter sakazakii) metallo-beta-lactamase2 harldq motif
30	c5iqkB	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase rm3; PDBTitle: rm3 metallo-beta-lactamase
31	c6aufB	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase-like protein; PDBTitle: crystal structure of metallo beta lactamases mim-1 from novosphingobium2 pentaromativorans
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	c6n36A	Alignment	not modelled	100.0	22	PDB header: ligase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: beta-lactamase from chitinophaga pinensis
34	c4awyB	Alignment	not modelled	100.0	24	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
35	c5mmdF	Alignment	not modelled	100.0	18	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
36	c3adrA	Alignment	not modelled	100.0	23	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
37	c2zo4A	Alignment	not modelled	100.0	24	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
38	c3spuB	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase ndm-1; PDBTitle: apo ndm-1 crystal structure
39	c6e0sA	Alignment	not modelled	100.0	22	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
40	d2aioa1	Alignment	not modelled	100.0	24	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase
41	d1mqoa	Alignment	not modelled	100.0	16	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase
42	d1k07a	Alignment	not modelled	100.0	18	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase
43	c2q9uB	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: a-type flavoprotein; PDBTitle: crystal structure of the flavodiiron protein from giardia2 intestinalis
44	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
45	d2p97a1	Alignment	not modelled	99.9	20	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Ava3068-like
46	c2ohiB	Alignment	not modelled	99.9	21	PDB header: oxidoreductase Chain: B: PDB Molecule: type a flavoprotein fpra; PDBTitle: crystal structure of coenzyme f420h2 oxidase (fpra), a diiron2 flavoprotein, reduced state
47	c3vqzA	Alignment	not modelled	99.9	19	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
48	c6h0cA	Alignment	not modelled	99.9	16	PDB header: oxidoreductase Chain: A: PDB Molecule: putative diflavin flavoprotein a 3; PDBTitle: flv1 flavodiiron core from synechocystis sp. pcc6803
49	c1e5dA	Alignment	not modelled	99.9	19	PDB header: oxidoreductase Chain: A: PDB Molecule: rubredoxin\oxygen oxidoreductase; PDBTitle: rubredoxin oxygen:oxidoreductase (roo) from anaerobe desulfovibrio2 gigas
50	c6qnmB	Alignment	not modelled	99.9	18	PDB header: signaling protein Chain: B: PDB Molecule: oxygen-binding di-iron protein; PDBTitle: apo state of chemotaxis sensor odp from t. denticola
51	c1ychD	Alignment	not modelled	99.9	23	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
52	c4d02A	Alignment	not modelled	99.9	23	PDB header: electron transport Chain: A: PDB Molecule: anaerobic nitric oxide reductase flavorubredoxin; PDBTitle: the crystallographic structure of flavorubredoxin from escherichia2 coli
53	c6qrgB	Alignment	not modelled	99.9	18	PDB header: signaling protein Chain: B: PDB Molecule: oxygen-binding diiron protein; PDBTitle: apo conformation of chemotaxis sensor odp
54	c4nurB	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: B: PDB Molecule: psdsa; PDBTitle: crystal structure of thermostable alkylsulfatase sdsap from2 pseudomonas sp. s9

55	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 at2 1.80 a resolution
56	c3hnnD_	Alignment	not modelled	99.9	14	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
57	d1e5da2	Alignment	not modelled	99.9	19	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: ROO N-terminal domain-like
58	c6cqsA_	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: sediminispirochaeta smaragdinae sps-1 metallo-beta-lactamase
59	d1x8ha_	Alignment	not modelled	99.9	15	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase
60	d1ycga2	Alignment	not modelled	99.9	24	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: ROO N-terminal domain-like
61	d2cfua2	Alignment	not modelled	99.9	17	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Alkylsulfatase-like
62	c2yheD_	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: D: PDB Molecule: sec-alkyl sulfatase; PDBTitle: structure determination of the stereoselective inverting sec-2 alkylsulfatase pisa1 from pseudomonas sp.
63	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
64	c4v0hC_	Alignment	not modelled	99.9	25	PDB header: hydrolase Chain: C: PDB Molecule: metallo-beta-lactamase domain-containing protein 1 1; PDBTitle: human metallo beta lactamase domain containing protein 1 (hmbiac1)
65	c2cfuA_	Alignment	not modelled	99.9	16	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.
66	d1vmea2	Alignment	not modelled	99.9	22	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: ROO N-terminal domain-like
67	c4xukB_	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: B: PDB Molecule: putative hydrolase; PDBTitle: crystal structure of hydrolase aboph in beta lactamase superfamily
68	c3eshB_	Alignment	not modelled	99.9	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
69	c3aj3A_	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: A: PDB Molecule: 4-pyridoxolactonase; PDBTitle: crystal structure of selenomethionine substituted 4-pyridoxolactonase2 from mesorhizobium loti
70	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 from2 pseudomonas sp wbc-3
71	d1p9ea_	Alignment	not modelled	99.9	22	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Methyl parathion hydrolase
72	c4le6B_	Alignment	not modelled	99.9	25	PDB header: hydrolase Chain: B: PDB Molecule: organophosphorus hydrolase; PDBTitle: crystal structure of the phosphotriesterase ophc2 from pseudomonas2 pseudoalcaligenes
73	c3sd9B_	Alignment	not modelled	99.9	14	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
74	c6ch0l_	Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: I: PDB Molecule: beta-lactamase; PDBTitle: structure of the quorum quenching lactonase from alicyclobacillus2 acidoterrestris bound to a glycerol molecule
75	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
76	c4zo3A_	Alignment	not modelled	99.8	20	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
77	c4pdxB_	Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: B: PDB Molecule: putative alkyl/aryl-sulfatase yjcs; PDBTitle: crystal structure of escherchia coli uncharacterized protein yjcs
78	c4xwwA_	Alignment	not modelled	99.8	23	PDB header: rna binding protein/rna Chain: A: PDB Molecule: dr2417; PDBTitle: crystal structure of rnase j complexed with rna
79	c3zq4C_	Alignment	not modelled	99.8	22	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

80	c2bibA	Alignment	not modelled	99.8	17	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
81	c5habB	Alignment	not modelled	99.8	21	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
82	c5a0tA	Alignment	not modelled	99.7	17	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
83	c2br6A	Alignment	not modelled	99.7	21	PDB header: hydrolase Chain: A: PDB Molecule: aiia-like protein; PDBTitle: crystal structure of quorum-quenching n-acyl homoserine2 lactone lactonase
84	d1ztca1	Alignment	not modelled	99.7	15	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: TM0894-like
85	c2p4zA	Alignment	not modelled	99.7	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
86	c3bk2A	Alignment	not modelled	99.7	19	PDB header: hydrolase Chain: A: PDB Molecule: metal dependent hydrolase; PDBTitle: crystal structure analysis of the rnase j/ump complex
87	d2i7ta1	Alignment	not modelled	99.6	17	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: beta-CASP RNA-metabolising hydrolases
88	d1wraa1	Alignment	not modelled	99.6	14	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Pce catalytic domain-like
89	c6i1dA	Alignment	not modelled	99.6	21	PDB header: gene regulation Chain: A: PDB Molecule: endoribonuclease ysh1; PDBTitle: structure of the ysh1-mpe1 nuclease complex from s.cerevisiae
90	c3x30A	Alignment	not modelled	99.6	16	PDB header: hydrolase Chain: A: PDB Molecule: upf0173 metal-dependent hydrolase tm_1162; PDBTitle: crystal structure of metallo-beta-lactamase from thermotoga maritima
91	d2dkfa1	Alignment	not modelled	99.5	24	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: beta-CASP RNA-metabolising hydrolases
92	c2az4A	Alignment	not modelled	99.5	21	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
93	d2i7xa1	Alignment	not modelled	99.5	16	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: beta-CASP RNA-metabolising hydrolases
94	c2i7xA	Alignment	not modelled	99.5	16	PDB header: rna binding protein, protein binding Chain: A: PDB Molecule: protein cft2; PDBTitle: structure of yeast cpsf-100 (ydh1p)
95	c3af5A	Alignment	not modelled	99.5	25	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein ph1404; PDBTitle: the crystal structure of an archaeal cpsf subunit, ph1404 from2 pyrococcus horikoshii
96	c3h3eA	Alignment	not modelled	99.4	18	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
97	c2xr1A	Alignment	not modelled	99.4	20	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
98	c2ycbA	Alignment	not modelled	99.4	21	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
99	c3zwfA	Alignment	not modelled	99.4	19	PDB header: hydrolase Chain: A: PDB Molecule: zinc phosphodiesterase elac protein 1; PDBTitle: crystal structure of human trnase z, short form (elac1).
100	c6b9vA	Alignment	not modelled	99.4	26	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase-like protein; PDBTitle: crystal structure of a new diphosphatase from the phnp family
101	c2xr1B	Alignment	not modelled	99.4	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
102	c1zkpD	Alignment	not modelled	99.3	20	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 PDB header: hydrolase

103	c3kl7A_	Alignment	not modelled	99.3	16	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
104	c6j4nD_	Alignment	not modelled	99.2	20	PDB header: hydrolase Chain: D; PDB Molecule: metallo-beta-lactamases pngm-1; PDBTitle: structure of papua new guinea mbl-1(pngm-1) native
105	c3g1pA_	Alignment	not modelled	99.2	18	PDB header: lyase Chain: A; PDB Molecule: protein phnp; PDBTitle: crystals structure of phnp from e.coli k-12
106	d2az4a1	Alignment	not modelled	99.2	22	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: beta-CASP RNA-metabolising hydrolases
107	d1y44a1	Alignment	not modelled	99.2	12	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: RNase Z-like
108	d1zkpa1	Alignment	not modelled	99.2	23	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: YhfI-like
109	c4b87A_	Alignment	not modelled	99.2	19	PDB header: hydrolase Chain: A; PDB Molecule: dna cross-link repair 1a protein; PDBTitle: crystal structure of human dna cross-link repair 1a
110	c3md7A_	Alignment	not modelled	99.1	20	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
111	c4z7rA_	Alignment	not modelled	99.1	15	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
112	c4ojvA_	Alignment	not modelled	99.1	20	PDB header: hydrolase Chain: A; PDB Molecule: 3',5'-cyclic-nucleotide phosphodiesterase 1; PDBTitle: crystal structure of unliganded yeast pde1
113	d1xtoa_	Alignment	not modelled	99.0	18	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Coenzyme PQQ synthesis protein B, PqqB
114	c3zdkA_	Alignment	not modelled	99.0	25	PDB header: hydrolase Chain: A; PDB Molecule: 5' exonuclease apollo; PDBTitle: crystal structure of human 5' exonuclease apollo
115	d2cbna1	Alignment	not modelled	98.9	14	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: RNase Z-like
116	d1vjna_	Alignment	not modelled	98.7	16	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Hypothetical protein TM0207
117	c4jo0A_	Alignment	not modelled	98.7	16	PDB header: oxidoreductase Chain: A; PDB Molecule: cmla; PDBTitle: crystal structure of cmla, a diiron beta-hydroxylase from streptomyces2 venezuelae
118	c3bv6D_	Alignment	not modelled	98.6	17	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
119	c2wylF_	Alignment	not modelled	98.6	14	PDB header: hydrolase Chain: F; PDB Molecule: l-ascorbate-6-phosphate lactonase ulag; PDBTitle: apo structure of a metallo-b-lactamase
120	c6brmC_	Alignment	not modelled	98.6	18	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