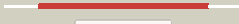



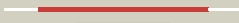



















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2581c (-) _2906099_2906773
Date	Wed Aug 7 12:50:22 BST 2019
Unique Job ID	5b6a42a287a3d375

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2xf4A_</a>	 Alignment		100.0	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hydroxyacylglutathione hydrolase; <b>PDBTitle:</b> crystal structure of salmonella enterica serovar2 typhimurium ycb1
2	<a href="#">c3r2uC_</a>	 Alignment		100.0	28	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> metallo-beta-lactamase family protein; <b>PDBTitle:</b> 2.1 angstrom resolution crystal structure of metallo-beta-lactamase2 from staphylococcus aureus subsp. aureus col
3	<a href="#">c4efzB_</a>	 Alignment		100.0	28	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> metallo-beta-lactamase family protein; <b>PDBTitle:</b> crystal structure of a hypothetical metallo-beta-lactamase from2 burkholderia pseudomallei
4	<a href="#">c5ve5C_</a>	 Alignment		100.0	29	<b>PDB header:</b> oxidoreductase, transferase <b>Chain:</b> C: <b>PDB Molecule:</b> bpprf; <b>PDBTitle:</b> crystal structure of persulfide dioxygenase rhodanese fusion protein2 with rhodanese domain inactivating mutation (c314s) from burkholderia3 phytotfirmans in complex with glutathione
5	<a href="#">c3tp9B_</a>	 Alignment		100.0	30	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-lactamase and rhodanese domain protein; <b>PDBTitle:</b> crystal structure of alicyclobacillus acidocaldarius protein with2 beta-lactamase and rhodanese domains
6	<a href="#">c4yskA_</a>	 Alignment		100.0	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase domain protein; <b>PDBTitle:</b> crystal structure of apo-form sdoa from pseudomonas putida
7	<a href="#">c4ysbB_</a>	 Alignment		100.0	30	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> metallo-beta-lactamase family protein; <b>PDBTitle:</b> crystal structure of ethe1 from myxococcus xanthus
8	<a href="#">d1qh5a_</a>	 Alignment		100.0	29	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> Glyoxalase II (hydroxyacylglutathione hydrolase)
9	<a href="#">c4chlA_</a>	 Alignment		100.0	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> persulfide dioxygenase ethe1, mitochondrial; <b>PDBTitle:</b> human ethylmalonic encephalopathy protein 1 (hethe1)
10	<a href="#">c2zwrA_</a>	 Alignment		100.0	32	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> metallo-beta-lactamase superfamily protein; <b>PDBTitle:</b> crystal structure of ttha1623 from thermus thermophilus hb8
11	<a href="#">c2gcuD_</a>	 Alignment		100.0	28	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> putative hydroxyacylglutathione hydrolase 3; <b>PDBTitle:</b> x-ray structure of gene product from arabidopsis thaliana at1g53580

12	<a href="#">d1xm8a_</a>	Alignment		100.0	32	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> Glyoxalase II (hydroxyacylglutathione hydrolase)
13	<a href="#">c2p18A_</a>	Alignment		100.0	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxalase ii; <b>PDBTitle:</b> crystal structure of the leishmania infantum glyoxalase ii
14	<a href="#">d2qeda1</a>	Alignment		100.0	32	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> Glyoxalase II (hydroxyacylglutathione hydrolase)
15	<a href="#">c5i0pB_</a>	Alignment		100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-lactamase domain protein; <b>PDBTitle:</b> crystal structure of a beta-lactamase domain protein from burkholderia2 ambifaria
16	<a href="#">c4wd6B_</a>	Alignment		100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> metallo-beta-lactamase; <b>PDBTitle:</b> crystal structure of dim-1 metallo-beta-lactamase
17	<a href="#">d1ko3a_</a>	Alignment		100.0	17	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> Zn metallo-beta-lactamase
18	<a href="#">d2q0ia1</a>	Alignment		100.0	18	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> PqsE-like
19	<a href="#">c2ynuB_</a>	Alignment		100.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> gim-1 protein; <b>PDBTitle:</b> apo gim-1 with 2mol. crystal structures of pseudomonas aeruginosa2 gim-1: active site plasticity in metallo-beta-lactamases
20	<a href="#">c3l6nA_</a>	Alignment		100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> metallo-beta-lactamase; <b>PDBTitle:</b> crystal structure of metallo-beta-lactamase ind-7
21	<a href="#">c3rkjA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase ndm-1; <b>PDBTitle:</b> crystal structure of new delhi metallo-beta-lactamase-1 from2 klebsiella pnueumoniae
22	<a href="#">c3spuB_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-lactamase ndm-1; <b>PDBTitle:</b> apo ndm-1 crystal structure
23	<a href="#">c5k0wA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> class b carbapenemase gob-18; <b>PDBTitle:</b> crystal structure of the metallo-beta-lactamase gob-18 from2 elizabethkingia meningoseptica
24	<a href="#">c5iqkB_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-lactamase rm3; <b>PDBTitle:</b> rm3 metallo-beta-lactamase
25	<a href="#">c5aebA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lra-12; <b>PDBTitle:</b> crystal structure of the class b3 di-zinc metallo-beta-lactamase lra-2 12 from an alaskan soil metagenome.
26	<a href="#">d1jita_</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> Zn metallo-beta-lactamase
27	<a href="#">d1m2xa_</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> Zn metallo-beta-lactamase
28	<a href="#">d1mqoa_</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> Zn metallo-beta-lactamase
29	<a href="#">c2zo4A_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> metallo-beta-lactamase family protein;

29	<a href="#">c2z9A_</a>	Alignment	not modelled	100.0	20	<b>PDBTitle:</b> crystal structure of metallo-beta-lactamase family protein ttha14292 from thermus thermophilus hb8 <b>PDB header:</b> metal binding protein
30	<a href="#">c6dn4A_</a>	Alignment	not modelled	100.0	18	<b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> cronobacter sakazakii (enterobacter sakazakii) metallo-beta-lactamse2 harldq motif
31	<a href="#">c6n36A_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> beta-lactamase from chitinophaga pinensis
32	<a href="#">c4ad9E_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> beta-lactamase-like protein 2; <b>PDBTitle:</b> crystal structure of human lactb2.
33	<a href="#">c5mmdF_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> metallo-beta-lactamase 1; <b>PDBTitle:</b> tmb-1. structural insights into tmb-1 and the role of residue 119 and2 228 in substrate and inhibitor binding
34	<a href="#">c3lvzA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> blr6230 protein; <b>PDBTitle:</b> new refinement of the crystal structure of bjp-1, a subclass b32 metallo-beta-lactamase of bradyrhizobium japonicum
35	<a href="#">c2yz3B_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> metallo-beta-lactamase; <b>PDBTitle:</b> crystallographic investigation of inhibition mode of the2 vim-2 metallo-beta-lactamase from pseudomonas aeruginosa3 with mercaptocarboxylate inhibitor
36	<a href="#">d1znba_</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> Zn metallo-beta-lactamase
37	<a href="#">d1k07a_</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> Zn metallo-beta-lactamase
38	<a href="#">c4awyB_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> metallo-beta-lactamase aim-1; <b>PDBTitle:</b> crystal structure of the mobile metallo-beta-lactamase aim-1 from2 pseudomonas aeruginosa: insights into antibiotic binding and the role3 of gln157
39	<a href="#">c6aufB_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-lactamase-like protein; <b>PDBTitle:</b> crystal structure of metallo beta lactamases mim-1 from novosphingobium2 pentaromativorans
40	<a href="#">d2gmna1</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> Zn metallo-beta-lactamase
41	<a href="#">d2aioa1</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> Zn metallo-beta-lactamase
42	<a href="#">c6grqB_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> oxygen-binding diiron protein; <b>PDBTitle:</b> apo conformation of chemotaxis sensor odp
43	<a href="#">c3adrA_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein st1585; <b>PDBTitle:</b> the first crystal structure of an archaeal metallo-beta-lactamase2 superfamily protein; st1585 from sulfolobus tokodaii
44	<a href="#">c4nurB_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> psdsa; <b>PDBTitle:</b> crystal structure of thermostable alkylsulfatase sdsap from2 pseudomonas sp. s9
45	<a href="#">c2ohiB_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> type a flavoprotein fpra; <b>PDBTitle:</b> crystal structure of coenzyme f420h2 oxidase (fpra), a diiron2 flavoprotein, reduced state
46	<a href="#">c6qnmB_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> oxygen-binding di-iron protein; <b>PDBTitle:</b> apo state of chemotaxis sensor odp from t. denticola
47	<a href="#">c2q9uB_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> a-type flavoprotein; <b>PDBTitle:</b> crystal structure of the flavodiiron protein from giardia2 intestinalis
48	<a href="#">c6h0cA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative diflavin flavoprotein a 3; <b>PDBTitle:</b> flv1 flavodiiron core from synechocystis sp. pcc6803
49	<a href="#">c6e0sA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mem-a-1; <b>PDBTitle:</b> crystal structure of mem-a-1, a subclass b3 metallo-beta-lactamase2 isolated from a soil metagenome library
50	<a href="#">c3vqzA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> metallo-beta-lactamase; <b>PDBTitle:</b> crystal structure of metallo-beta-lactamase, smb-1, in a complex with2 mercaptoacetic acid
51	<a href="#">d1x8ha_</a>	Alignment	not modelled	99.9	12	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> Zn metallo-beta-lactamase
52	<a href="#">c6cqsA_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> sediminispirochaeta smaragdinae sps-1 metallo-beta-lactamase
53	<a href="#">c2cfuA_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sdsa1; <b>PDBTitle:</b> crystal structure of sdsa1, an alkylsulfatase from2 pseudomonas aeruginosa, in complex with 1-decane-sulfonic-3 acid.
54	<a href="#">c1ychD_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> nitric oxide reductase; <b>PDBTitle:</b> x-ray crystal structures of moorella thermoacetica fpra. novel diiron2 site structure and mechanistic insights into a scavenging nitric3 oxide reductase
						<b>PDB header:</b> hydrolase, metal binding protein

55	<a href="#">c2fhxB_</a>	Alignment	not modelled	99.9	17	<b>Chain:</b> B; <b>PDB Molecule:</b> spm-1; <b>PDBTitle:</b> pseudomonas aeruginosa spm-1 metallo-beta-lactamase
56	<a href="#">d2cfua2</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> Alkylsulfatase-like
57	<a href="#">c2yheD</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> D; <b>PDB Molecule:</b> sec-alkyl sulfatase; <b>PDBTitle:</b> structure determination of the stereoselective inverting sec-2 alkylsulfatase pisa1 from pseudomonas sp.
58	<a href="#">c1e5dA</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> rubredoxin\;oxygen oxidoreductase; <b>PDBTitle:</b> rubredoxin oxygen:oxidoreductase (roo) from anaerobe desulfovibrio2 gigas
59	<a href="#">c3hnnD</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D; <b>PDB Molecule:</b> putative diflavin flavoprotein a 5; <b>PDBTitle:</b> crystal structure of putative diflavin flavoprotein a 5 (fragment 1-2 254) from nostoc sp. pcc 7120, northeast structural genomics3 consortium target nsr435a
60	<a href="#">c1vmeB</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> electron transport <b>Chain:</b> B; <b>PDB Molecule:</b> flavoprotein; <b>PDBTitle:</b> crystal structure of flavoprotein (tm0755) from thermotoga maritima at2 1.80 a resolution
61	<a href="#">c4d02A</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> electron transport <b>Chain:</b> A; <b>PDB Molecule:</b> anaerobic nitric oxide reductase flavorubredoxin; <b>PDBTitle:</b> the crystallographic structure of flavorubredoxin from escherichia2 coli
62	<a href="#">c3aj3A</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> 4-pyridoxolactonase; <b>PDBTitle:</b> crystal structure of selenomethionine substituted 4-pyridoxolactonase2 from mesorhizobium loti
63	<a href="#">c6ch0L</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> I; <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> structure of the quorum quenching lactonase from alicyclobacillus2 acidoterrestris bound to a glycerol molecule
64	<a href="#">c3sd9B</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> crystal structure of serratia fonticola sfh-i: source of the2 nucleophile in the catalytic mechanism of mono-zinc metallo-beta-3 lactamases
65	<a href="#">c3eshB</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> protein similar to metal-dependent hydrolase; <b>PDBTitle:</b> crystal structure of a probable metal-dependent hydrolase2 from staphylococcus aureus. northeast structural genomics3 target zr314
66	<a href="#">d1ycga2</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> ROO N-terminal domain-like
67	<a href="#">d1vmea2</a>	Alignment	not modelled	99.9	21	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> ROO N-terminal domain-like
68	<a href="#">d1e5da2</a>	Alignment	not modelled	99.9	16	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> ROO N-terminal domain-like
69	<a href="#">c2r2dC</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> zn-dependent hydrolases; <b>PDBTitle:</b> structure of a quorum-quenching lactonase (aiib) from agrobacterium2 tumefaciens
70	<a href="#">c4xukB</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> putative hydrolase; <b>PDBTitle:</b> crystal structure of hydrolase aboph in beta lactamase superfamily
71	<a href="#">d2p97a1</a>	Alignment	not modelled	99.9	21	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> Ava3068-like
72	<a href="#">c4zo3A</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> acylhomoserine lactonase; <b>PDBTitle:</b> aidc, a dizinc quorum-quenching lactonase, in complex with a product2 n-hexnoyl-l-homoserine
73	<a href="#">c4pdxB</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> putative alkyl/aryl-sulfatase yjcs; <b>PDBTitle:</b> crystal structure of escherchia coli uncharacterized protein yjcs
74	<a href="#">c1p9eA</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> methyl parathion hydrolase; <b>PDBTitle:</b> crystal structure analysis of methyl parathion hydrolase from2 pseudomonas sp wbc-3
75	<a href="#">d1p9ea</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> Methyl parathion hydrolase
76	<a href="#">c4v0hC</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> metallo-beta-lactamase domain-containing protein 1 1; <b>PDBTitle:</b> human metallo beta lactamase domain containing protein 1 (hmblac1)
77	<a href="#">c4le6B</a>	Alignment	not modelled	99.9	25	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> organophosphorus hydrolase; <b>PDBTitle:</b> crystal structure of the phosphotriesterase ophc2 from pseudomonas2 pseudoalcaligenes
78	<a href="#">c3zq4C</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> ribonuclease j 1; <b>PDBTitle:</b> unusual, dual endo- and exo-nuclease activity in the degradosome2 explained by crystal structure analysis of rnase j1
79	<a href="#">c5habB</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> ribonuclease j; <b>PDBTitle:</b> crystal structure of mpy-rnase j (mutant h84a), an archaeal rnase j2 from methanobolus psychrophilus r15, complex

						with rna
80	<a href="#">c2br6A_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> aiia-like protein; <b>PDBTitle:</b> crystal structure of quorum-quenching n-acyl homoserine2 lactone lactonase
81	<a href="#">c4xwwA_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> A: <b>PDB Molecule:</b> dr2417; <b>PDBTitle:</b> crystal structure of rnaase j complexed with rna
82	<a href="#">d1ztca1</a>	Alignment	not modelled	99.8	21	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> TM0894-like
83	<a href="#">c5a0tA_</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> ribonuclease j; <b>PDBTitle:</b> catalysis and 5' end sensing by ribonuclease rnaase j of the2 metallo-beta-lactamase family
84	<a href="#">c3bk2A_</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> metal dependent hydrolase; <b>PDBTitle:</b> crystal structure analysis of the rnaase j/ump complex
85	<a href="#">c2p4zA_</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> metal-dependent hydrolases of the beta-lactamase <b>PDBTitle:</b> a ferredoxin-like metallo-beta-lactamase superfamily protein from2 thermoanaerobacter tengcongensis
86	<a href="#">c6i1dA_</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> endoribonuclease ysh1; <b>PDBTitle:</b> structure of the ysh1-mpe1 nuclease complex from s.cerevisiae
87	<a href="#">c3af5A_</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein ph1404; <b>PDBTitle:</b> the crystal structure of an archaeal cpsf subunit, ph1404 from2 pyrococcus horikoshii
88	<a href="#">d2dkfa1</a>	Alignment	not modelled	99.8	22	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> beta-CASP RNA-metabolising hydrolases
89	<a href="#">c2ycbA_</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cleavage and polyadenylation specificity factor; <b>PDBTitle:</b> structure of the archaeal beta-casp protein with n-terminal2 kh domains from methanothermobacter thermautotrophicus
90	<a href="#">d2i7ta1</a>	Alignment	not modelled	99.8	21	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> beta-CASP RNA-metabolising hydrolases
91	<a href="#">c2bibA_</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> teichoic acid phosphorylcholine esterase/ choline binding <b>PDBTitle:</b> crystal structure of the complete modular teichoic acid2 phosphorylcholine esterase pce (cbpe) from streptococcus pneumoniae
92	<a href="#">c2xr1A_</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cleavage and polyadenylation specificity factor 100 kd <b>PDBTitle:</b> dimeric archaeal cleavage and polyadenylation specificity2 factor with n-terminal kh domains (kh-cpsf) from methanosarcina3 mazei
93	<a href="#">c2az4A_</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ef2904; <b>PDBTitle:</b> crystal structure of a protein of unknown function from enterococcus2 faecalis v583
94	<a href="#">d1wraa1</a>	Alignment	not modelled	99.7	14	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> Pce catalytic domain-like
95	<a href="#">c2xr1B_</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cleavage and polyadenylation specificity factor 100 kd <b>PDBTitle:</b> dimeric archaeal cleavage and polyadenylation specificity2 factor with n-terminal kh domains (kh-cpsf) from methanosarcina3 mazei
96	<a href="#">c2i7xA_</a>	Alignment	not modelled	99.7	12	<b>PDB header:</b> rna binding protein, protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> protein cft2; <b>PDBTitle:</b> structure of yeast cpsf-100 (ydh1p)
97	<a href="#">d2i7xa1</a>	Alignment	not modelled	99.7	12	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> beta-CASP RNA-metabolising hydrolases
98	<a href="#">c3x30A_</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> upf0173 metal-dependent hydrolase tm_1162; <b>PDBTitle:</b> crystal structure of metallo-beta-lactamase from thermotoga maritima
99	<a href="#">c3zwfA_</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> zinc phosphodiesterase elac protein 1; <b>PDBTitle:</b> crystal structure of human trnaase z, short form (elac1).
100	<a href="#">c3h3eA_</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> structural genomics, metal binding prote <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein tm1679; <b>PDBTitle:</b> crystal structure of tm1679, a metal-dependent hydrolase of2 the beta-lactamase superfamily
101	<a href="#">c1zkdD_</a>	Alignment	not modelled	99.6	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> hypothetical protein ba1088; <b>PDBTitle:</b> 1.5a resolution crystal structure of a metallo beta lactamase family2 protein, the elac homologue of bacillus anthracis, a putative3 ribonuclease
102	<a href="#">c6b9vA_</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase-like protein; <b>PDBTitle:</b> crystal structure of a new diphosphatase from the phnp family
						<b>PDB header:</b> hydrolase

103	<a href="#">c6j4nD_</a>	Alignment	not modelled	99.5	21	<b>Chain:</b> D: <b>PDB Molecule:</b> metallo-beta-lactamases pngm-1; <b>PDBTitle:</b> structure of papua new guinea mbl-1(pngm-1) native
104	<a href="#">c4z7rA_</a>	Alignment	not modelled	99.5	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> coenzyme pqq synthesis protein b; <b>PDBTitle:</b> the 1.98-angstrom crystal structure of zn(2+)-bound pqqb from2 methylobacterium extorquens
105	<a href="#">d1xtoa_</a>	Alignment	not modelled	99.5	8	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> Coenzyme PQQ synthesis protein B, PqqB
106	<a href="#">c3g1pA_</a>	Alignment	not modelled	99.5	17	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> protein phnp; <b>PDBTitle:</b> crystals structure of phnp from e.coli k-12
107	<a href="#">d1y44a1</a>	Alignment	not modelled	99.4	14	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> RNase Z-like
108	<a href="#">c3md7A_</a>	Alignment	not modelled	99.4	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase-like; <b>PDBTitle:</b> crystal structure of a beta-lactamase-like protein bound to gmp from2 brucella melitensis
109	<a href="#">c3ki7A_</a>	Alignment	not modelled	99.4	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative metal-dependent hydrolase; <b>PDBTitle:</b> crystal structure of putative metal-dependent hydrolase2 (yp_001302908.1) from parabacteroides distasonis atcc 8503 at 2.30 a3 resolution
110	<a href="#">c4ojvA_</a>	Alignment	not modelled	99.4	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 3',5'-cyclic-nucleotide phosphodiesterase 1; <b>PDBTitle:</b> crystal structure of unliganded yeast pde1
111	<a href="#">d2az4a1</a>	Alignment	not modelled	99.4	22	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> beta-CASP RNA-metabolising hydrolases
112	<a href="#">d1zkpa1</a>	Alignment	not modelled	99.4	16	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> Yhfl-like
113	<a href="#">c3zdkA_</a>	Alignment	not modelled	99.3	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 5' exonuclease apollo; <b>PDBTitle:</b> crystal structure of human 5' exonuclease apollo
114	<a href="#">d2cbna1</a>	Alignment	not modelled	99.2	18	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> RNase Z-like
115	<a href="#">c4b87A_</a>	Alignment	not modelled	99.2	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dna cross-link repair 1a protein; <b>PDBTitle:</b> crystal structure of human dna cross-link repair 1a
116	<a href="#">d2e7ya1</a>	Alignment	not modelled	99.1	22	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> RNase Z-like
117	<a href="#">c5mtzA_</a>	Alignment	not modelled	99.1	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ribonuclease z; <b>PDBTitle:</b> crystal structure of a long form rnase z from yeast
118	<a href="#">c6brmC_</a>	Alignment	not modelled	99.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> putative metal-dependent isothiocyanate hydrolase saxa; <b>PDBTitle:</b> the crystal structure of isothiocyanate hydrolase from delia radicum2 gut bacteria
119	<a href="#">c2wylF_</a>	Alignment	not modelled	98.9	25	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> l-ascorbate-6-phosphate lactonase ulag; <b>PDBTitle:</b> apo structure of a metallo-b-lactamase
120	<a href="#">d1vjna_</a>	Alignment	not modelled	98.8	22	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> Hypothetical protein TM0207