


























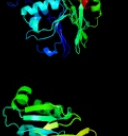


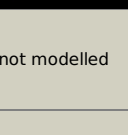


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3818 (- )_4282627_4284177
Date	Fri Aug 9 18:20:52 BST 2019
Unique Job ID	ea179a00074a6638

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4jo0A_</a>	 Alignment		100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cmla; <b>PDBTitle:</b> crystal structure of cmla, a diiron beta-hydroxylase from streptomyces2 venezuelae
2	<a href="#">c4qn9A_</a>	 Alignment		100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acyl-phosphatidylethanolamine-hydrolyzing phospholipase <b>PDBTitle:</b> structure of human nape-pld
3	<a href="#">c2wylF_</a>	 Alignment		100.0	18	<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
4	<a href="#">c3bv6D_</a>	 Alignment		100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> metal-dependent hydrolase; <b>PDBTitle:</b> crystal structure of uncharacterized metallo protein from vibrio2 cholerae with beta-lactamase like fold
5	<a href="#">c3rpcD_</a>	 Alignment		100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> possible metal-dependent hydrolase; <b>PDBTitle:</b> the crystal structure of a possible metal-dependent hydrolase from2 veillonella parvula dsm 2008
6	<a href="#">c6brmC_</a>	 Alignment		100.0	16	<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
7	<a href="#">c3kl7A_</a>	 Alignment		99.9	17	<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
8	<a href="#">d1vjna_</a>	 Alignment		99.9	27	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> Hypothetical protein TM0207
9	<a href="#">c3x30A_</a>	 Alignment		99.9	21	<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
10	<a href="#">c4xwwA_</a>	 Alignment		99.6	13	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> A: <b>PDB Molecule:</b> dr2417; <b>PDBTitle:</b> crystal structure of rnae j complexed with rna
11	<a href="#">c3g1pA_</a>	 Alignment		99.6	18	<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

12	<a href="#">d2i7ta1</a>	Alignment		99.6	13	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> beta-CASP RNA-metabolising hydrolases
13	<a href="#">c1zkpD</a>	Alignment		99.6	17	<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
14	<a href="#">c6i1dA</a>	Alignment		99.5	18	<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
15	<a href="#">c5a0tA</a>	Alignment		99.5	13	<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 rnase j of the2 metallo-beta-lactamase family
16	<a href="#">c3zwfA</a>	Alignment		99.5	15	<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 trnase z, short form (elac1).
17	<a href="#">c3zq4C</a>	Alignment		99.5	14	<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
18	<a href="#">c6b9vA</a>	Alignment		99.5	19	<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
19	<a href="#">c3bk2A</a>	Alignment		99.4	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> metal dependent hydrolase; <b>PDBTitle:</b> crystal structure analysis of the rnase j/ump complex
20	<a href="#">d1zkpa1</a>	Alignment		99.4	16	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> YhfI-like
21	<a href="#">c5habB</a>	Alignment	not modelled	99.4	11	<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 methanobus psychrophilus r15, complex with rna
22	<a href="#">c6j4nD</a>	Alignment	not modelled	99.4	14	<b>PDB header:</b> hydrolase <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
23	<a href="#">d2dkfa1</a>	Alignment	not modelled	99.4	16	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> beta-CASP RNA-metabolising hydrolases
24	<a href="#">c2bibA</a>	Alignment	not modelled	99.4	17	<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
25	<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
26	<a href="#">c2az4A</a>	Alignment	not modelled	99.3	16	<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
27	<a href="#">c4z7rA</a>	Alignment	not modelled	99.3	13	<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
						<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cleavage and polyadenylation specificity

28	<a href="#">c2xr1A_</a>	Alignment	not modelled	99.3	15	factor 100 kd <b>PDBTitle:</b> dimeric archaeal cleavage and polyadenylation specificity2 factor with n-terminal kh domains (kh-cpsf) from methanosarcina3 mazei
29	<a href="#">c3md7A_</a>	Alignment	not modelled	99.3	15	<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
30	<a href="#">c2ycbA_</a>	Alignment	not modelled	99.3	14	<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
31	<a href="#">c3af5A_</a>	Alignment	not modelled	99.3	16	<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
32	<a href="#">d2cbna1</a>	Alignment	not modelled	99.2	20	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> RNase Z-like
33	<a href="#">c2xr1B_</a>	Alignment	not modelled	99.2	15	<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
34	<a href="#">c2p4zA_</a>	Alignment	not modelled	99.2	14	<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
35	<a href="#">c6qrgB_</a>	Alignment	not modelled	99.2	13	<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
36	<a href="#">c6qnmB_</a>	Alignment	not modelled	99.1	11	<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
37	<a href="#">c5k0wA_</a>	Alignment	not modelled	99.0	16	<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
38	<a href="#">d2i7xa1</a>	Alignment	not modelled	99.0	16	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> beta-CASP RNA-metabolising hydrolases
39	<a href="#">c2i7xA_</a>	Alignment	not modelled	99.0	16	<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)
40	<a href="#">c5aebA_</a>	Alignment	not modelled	99.0	14	<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.
41	<a href="#">c2ohiB_</a>	Alignment	not modelled	98.9	18	<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
42	<a href="#">d1k07a_</a>	Alignment	not modelled	98.9	16	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> Zn metallo-beta-lactamase
43	<a href="#">c1vmeB_</a>	Alignment	not modelled	98.9	15	<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
44	<a href="#">c6dn4A_</a>	Alignment	not modelled	98.9	17	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> cronobacter sakazakii (enterobacter sakazakii) metallo-beta-lactamase2 harldq motif
45	<a href="#">c4xukB_</a>	Alignment	not modelled	98.8	13	<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
46	<a href="#">c3zdkA_</a>	Alignment	not modelled	98.8	16	<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
47	<a href="#">d1fqta_</a>	Alignment	not modelled	98.8	28	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> Rieske iron-sulfur protein (ISP)
48	<a href="#">c1p9eA_</a>	Alignment	not modelled	98.8	16	<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
49	<a href="#">d1p9ea_</a>	Alignment	not modelled	98.8	16	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> Methyl parathion hydrolase
50	<a href="#">c3lvzA_</a>	Alignment	not modelled	98.8	16	<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
51	<a href="#">c4efzB_</a>	Alignment	not modelled	98.8	15	<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
52	<a href="#">c3adrA_</a>	Alignment	not modelled	98.8	21	<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

53	<a href="#">c4b87A_</a>	Alignment	not modelled	98.8	17	<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
54	<a href="#">d2e7ya1</a>	Alignment	not modelled	98.7	14	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> RNase Z-like
55	<a href="#">c4yskA_</a>	Alignment	not modelled	98.7	11	<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
56	<a href="#">c4awyB_</a>	Alignment	not modelled	98.7	14	<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
57	<a href="#">c1e5dA_</a>	Alignment	not modelled	98.7	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
58	<a href="#">c6h0cA_</a>	Alignment	not modelled	98.7	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
59	<a href="#">c5mtzA_</a>	Alignment	not modelled	98.7	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
60	<a href="#">d1vmea2</a>	Alignment	not modelled	98.7	15	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> ROO N-terminal domain-like
61	<a href="#">c4zo3A_</a>	Alignment	not modelled	98.7	11	<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
62	<a href="#">c3eshB_</a>	Alignment	not modelled	98.7	17	<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
63	<a href="#">c3tp9B_</a>	Alignment	not modelled	98.7	19	<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
64	<a href="#">c4d02A_</a>	Alignment	not modelled	98.7	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
65	<a href="#">c2q9uB_</a>	Alignment	not modelled	98.7	13	<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
66	<a href="#">c6n36A_</a>	Alignment	not modelled	98.7	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-lactamase; <b>PDBTitle:</b> beta-lactamase from chitinophaga pinensis
67	<a href="#">c4qdfA_</a>	Alignment	not modelled	98.7	37	<b>PDB header:</b> oxidoreductase/oxidoreductase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> 3-ketosteroid 9alpha-hydroxylase oxygenase; <b>PDBTitle:</b> crystal structure of apo ksha5 and ksha1 in complex with 1,4-30q-coa2 from r. rhodochrous
68	<a href="#">c2de7E_</a>	Alignment	not modelled	98.7	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> ferredoxin component of carbazole; <b>PDBTitle:</b> the substrate-bound complex between oxygenase and2 ferredoxin in carbazole 1,9a-dioxygenase
69	<a href="#">c5iqkB_</a>	Alignment	not modelled	98.6	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-lactamase rm3; <b>PDBTitle:</b> rm3 metallo-beta-lactamase
70	<a href="#">c3d89A_</a>	Alignment	not modelled	98.6	21	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> rieske domain-containing protein; <b>PDBTitle:</b> crystal structure of a soluble rieske ferredoxin from mus musculus
71	<a href="#">c2de7B_</a>	Alignment	not modelled	98.6	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> terminal oxygenase component of carbazole; <b>PDBTitle:</b> the substrate-bound complex between oxygenase and2 ferredoxin in carbazole 1,9a-dioxygenase
72	<a href="#">c2i7fB_</a>	Alignment	not modelled	98.6	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ferredoxin component of dioxygenase; <b>PDBTitle:</b> sphingomonas yanoikuyae b1 ferredoxin
73	<a href="#">c2zylA_</a>	Alignment	not modelled	98.6	45	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> possible oxidoreductase; <b>PDBTitle:</b> crystal structure of 3-ketosteroid-9-alpha-hydroxylase2 (ksha) from m. tuberculosis
74	<a href="#">c4qdfB_</a>	Alignment	not modelled	98.6	38	<b>PDB header:</b> oxidoreductase/oxidoreductase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> 3-ketosteroid 9alpha-hydroxylase oxygenase; <b>PDBTitle:</b> crystal structure of apo ksha5 and ksha1 in complex with 1,4-30q-coa2 from r. rhodochrous
75	<a href="#">c4aivA_</a>	Alignment	not modelled	98.6	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable nitrite reductase [nad(p)h] small subunit nird; <b>PDBTitle:</b> crystal structure of putative nadh-dependent nitrite reductase small2 subunit from mycobacterium tuberculosis
76	<a href="#">c6e0sA_</a>	Alignment	not modelled	98.6	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mem-a1; <b>PDBTitle:</b> crystal structure of mem-a1, a subclass b3 metallo-beta-lactamase2 isolated from a soil metagenome library

77	<a href="#">d1z01a1</a>	Alignment	not modelled	98.6	27	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> Ring hydroxylating alpha subunit ISP domain
78	<a href="#">d2gmna1</a>	Alignment	not modelled	98.6	19	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> Zn metallo-beta-lactamase
79	<a href="#">d1wraa1</a>	Alignment	not modelled	98.6	17	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> Pce catalytic domain-like
80	<a href="#">d2aioa1</a>	Alignment	not modelled	98.6	13	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> Zn metallo-beta-lactamase
81	<a href="#">d3c0da1</a>	Alignment	not modelled	98.6	27	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> NirD-like
82	<a href="#">d2az4a1</a>	Alignment	not modelled	98.6	13	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> beta-CASP RNA-metabolising hydrolases
83	<a href="#">c3gkqB_</a>	Alignment	not modelled	98.6	34	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> terminal oxygenase component of carbazole 1,9a-dioxygenase; <b>PDBTitle:</b> terminal oxygenase of carbazole 1,9a-dioxygenase from novosphingobium2 sp. ka1
84	<a href="#">c3gceA_</a>	Alignment	not modelled	98.5	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin component of carbazole 1,9a- <b>PDBTitle:</b> ferredoxin of carbazole 1,9a-dioxygenase from nocardiooides2 aromaticivorans ic177
85	<a href="#">d1vm9a_</a>	Alignment	not modelled	98.5	30	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> Rieske iron-sulfur protein (ISP)
86	<a href="#">c4le6B_</a>	Alignment	not modelled	98.5	16	<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
87	<a href="#">d2jzaa1</a>	Alignment	not modelled	98.5	24	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> NirD-like
88	<a href="#">c6aufB_</a>	Alignment	not modelled	98.5	17	<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
89	<a href="#">c6ch0l_</a>	Alignment	not modelled	98.5	16	<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
90	<a href="#">c3hnnD_</a>	Alignment	not modelled	98.5	13	<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
91	<a href="#">c2qpzA_</a>	Alignment	not modelled	98.5	25	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> naphthalene 1,2-dioxygenase system ferredoxin <b>PDBTitle:</b> naphthalene 1,2-dioxygenase rieske ferredoxin
92	<a href="#">c1ychD_</a>	Alignment	not modelled	98.5	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
93	<a href="#">d2jo6a1</a>	Alignment	not modelled	98.5	20	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> NirD-like
94	<a href="#">c3gcfC_</a>	Alignment	not modelled	98.5	38	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> terminal oxygenase component of carbazole 1,9a- <b>PDBTitle:</b> terminal oxygenase of carbazole 1,9a-dioxygenase from2 nocardiooides aromaticivorans ic177
95	<a href="#">c2r2dC_</a>	Alignment	not modelled	98.4	16	<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
96	<a href="#">d2de6a1</a>	Alignment	not modelled	98.4	30	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> Ring hydroxylating alpha subunit ISP domain
97	<a href="#">d1ycga2</a>	Alignment	not modelled	98.4	20	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> ROO N-terminal domain-like
98	<a href="#">c1z01D_</a>	Alignment	not modelled	98.4	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> 2-oxo-1,2-dihydroquinoline 8-monoxygenase, oxygenase <b>PDBTitle:</b> 2-oxoquinoline 8-monoxygenase component: active site modulation by2 rieske-[2fe-2s] center oxidation/reduction
99	<a href="#">c3vqzA_</a>	Alignment	not modelled	98.4	19	<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
100	<a href="#">c4ojvA_</a>	Alignment	not modelled	98.4	13	<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
101	<a href="#">d1e5da2</a>	Alignment	not modelled	98.3	16	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> ROO N-terminal domain-like
102	<a href="#">c3r2uF_</a>	Alignment	not modelled	98.3	14	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> metallo-beta-lactamase family protein;

102	<a href="#">c3r2uA_</a>	Alignment	not modelled	98.3	14	<b>PDBTitle:</b> 2.1 angstrom resolution crystal structure of metallo-beta-lactamase2 from staphylococcus aureus subsp. aureus col <b>PDB header:</b> hydrolase
103	<a href="#">c3aj3A_</a>	Alignment	not modelled	98.3	20	<b>Chain:</b> A: <b>PDB Molecule:</b> 4-pyridoxolactonase; <b>PDBTitle:</b> crystal structure of selenomethionine substituted 4-pyridoxolactonase2 from mesorhizobium loti
104	<a href="#">d1xtoa_</a>	Alignment	not modelled	98.3	14	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> Coenzyme PQQ synthesis protein B, PqqB
105	<a href="#">d1m2xa_</a>	Alignment	not modelled	98.3	13	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> Zn metallo-beta-lactamase
106	<a href="#">c2zo4A_</a>	Alignment	not modelled	98.3	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> metallo-beta-lactamase family protein; <b>PDBTitle:</b> crystal structure of metallo-beta-lactamase family protein ttha14292 from thermus thermophilus hb8
107	<a href="#">c4ad9E_</a>	Alignment	not modelled	98.3	20	<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.
108	<a href="#">d2b1xa1</a>	Alignment	not modelled	98.2	16	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> Ring hydroxylating alpha subunit ISP domain
109	<a href="#">c3gteB_</a>	Alignment	not modelled	98.2	33	<b>PDB header:</b> electron transport, oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ddmc; <b>PDBTitle:</b> crystal structure of dicamba monooxygenase with non-heme iron
110	<a href="#">c3vcaA_</a>	Alignment	not modelled	98.2	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ring-hydroxylating dioxygenase; <b>PDBTitle:</b> quaternary ammonium oxidative demethylation: x-ray crystallographic,2 resonance raman and uv-visible spectroscopic analysis of a rieske-3 type demethylase
111	<a href="#">c3h3eA_</a>	Alignment	not modelled	98.2	15	<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
112	<a href="#">d1wqla1</a>	Alignment	not modelled	98.2	17	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> Ring hydroxylating alpha subunit ISP domain
113	<a href="#">c3n0qA_</a>	Alignment	not modelled	98.2	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative aromatic-ring hydroxylating dioxygenase; <b>PDBTitle:</b> crystal structure of a putative aromatic-ring hydroxylating2 dioxygenase (tm1040_3219) from silicibacter sp. tm1040 at 1.80 a3 resolution
114	<a href="#">c2zwrA_</a>	Alignment	not modelled	98.2	17	<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
115	<a href="#">d2bmoa1</a>	Alignment	not modelled	98.1	19	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> Ring hydroxylating alpha subunit ISP domain
116	<a href="#">c2br6A_</a>	Alignment	not modelled	98.1	14	<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
117	<a href="#">d1ulia1</a>	Alignment	not modelled	98.1	19	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> Ring hydroxylating alpha subunit ISP domain
118	<a href="#">c4wd6B_</a>	Alignment	not modelled	98.1	11	<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
119	<a href="#">c6cqsA_</a>	Alignment	not modelled	98.1	13	<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
120	<a href="#">d1znba_</a>	Alignment	not modelled	98.1	15	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> Zn metallo-beta-lactamase