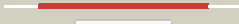



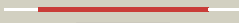


















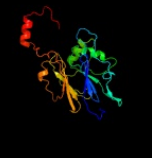



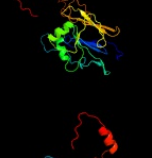
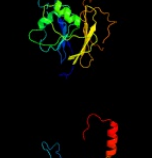

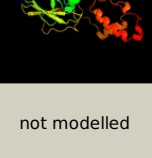


Phyre2

| | |
|---------------|------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD3577_(-)_4019441_4020307 |
| Date | Fri Aug 9 18:20:26 BST 2019 |
| Unique Job ID | a05b83f9634e7055 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | c4qn9A_ | Alignment  |  | 100.0 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: n-acyl-phosphatidylethanolamine-hydrolyzing phospholipase PDBTitle: structure of human nape-pld |
| 2 | c2wylF_ | Alignment  |  | 100.0 | 16 | PDB header: hydrolase Chain: F: PDB Molecule: l-ascorbate-6-phosphate lactonase ulag; PDBTitle: apo structure of a metallo-b-lactamase |
| 3 | c3bv6D_ | Alignment  |  | 100.0 | 15 | 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 |
| 4 | c3rpcD_ | Alignment  |  | 100.0 | 15 | 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 |
| 5 | c4jo0A_ | Alignment  |  | 100.0 | 15 | PDB header: oxidoreductase Chain: A: PDB Molecule: cmla; PDBTitle: crystal structure of cmla, a diiron beta-hydroxylase from streptomyces2 venezuelae |
| 6 | c3kl7A_ | Alignment  |  | 100.0 | 16 | 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 |
| 7 | c6brmC_ | Alignment  |  | 100.0 | 15 | 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 |
| 8 | d1vjna_ | Alignment  |  | 100.0 | 19 | Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Hypothetical protein TM0207 |
| 9 | c3x30A_ | Alignment  |  | 100.0 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: upf0173 metal-dependent hydrolase tm_1162; PDBTitle: crystal structure of metallo-beta-lactamase from thermotoga maritima |
| 10 | c6b9vA_ | Alignment  |  | 99.9 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase-like protein; PDBTitle: crystal structure of a new diphosphatase from the phnp family |
| 11 | c1zkpD_ | Alignment  |  | 99.9 | 21 | 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 |

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|----|-------------------------|-----------|---|------|----|--|
| 12 | c3g1pA | Alignment |  | 99.9 | 17 | PDB header: lyase Chain: A; PDB Molecule: protein phnp; PDBTitle: crystals structure of phnp from e.coli k-12 |
| 13 | c2xr1A | Alignment |  | 99.9 | 16 | 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 |
| 14 | d1zkpa1 | Alignment |  | 99.9 | 17 | Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Yhfl-like |
| 15 | c5a0tA | Alignment |  | 99.9 | 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 |
| 16 | c6j4nD | Alignment |  | 99.9 | 18 | PDB header: hydrolase Chain: D; PDB Molecule: metallo-beta-lactamases pngm-1; PDBTitle: structure of papua new guinea mbl-1(pngm-1) native |
| 17 | c2xr1B | Alignment |  | 99.9 | 17 | 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 |
| 18 | c2ycbA | Alignment |  | 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 |
| 19 | c4xwwA | Alignment |  | 99.9 | 16 | PDB header: rna binding protein/rna Chain: A; PDB Molecule: dr2417; PDBTitle: crystal structure of rnase j complexed with rna |
| 20 | c6i1dA | Alignment |  | 99.9 | 15 | PDB header: gene regulation Chain: A; PDB Molecule: endoribonuclease ysh1; PDBTitle: structure of the ysh1-mpe1 nuclease complex from s.cerevisiae |
| 21 | c3md7A | Alignment | not modelled | 99.9 | 22 | 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 |
| 22 | d2i7ta1 | Alignment | not modelled | 99.9 | 13 | Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: beta-CASP RNA-metabolising hydrolases |
| 23 | c3zwfA | Alignment | not modelled | 99.9 | 17 | PDB header: hydrolase Chain: A; PDB Molecule: zinc phosphodiesterase elac protein 1; PDBTitle: crystal structure of human tnase z, short form (elac1). |
| 24 | c3af5A | Alignment | not modelled | 99.9 | 17 | PDB header: hydrolase Chain: A; PDB Molecule: putative uncharacterized protein ph1404; PDBTitle: the crystal structure of an archaeal cpsf subunit, ph1404 from2 pyrococcus horikoshii |
| 25 | c3zq4C | Alignment | not modelled | 99.9 | 14 | 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 |
| 26 | d1y44a1 | Alignment | not modelled | 99.9 | 16 | Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: RNase Z-like |
| 27 | c4z7rA | Alignment | not modelled | 99.9 | 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 |
| 28 | c3bk2A | Alignment | not modelled | 99.9 | 14 | PDB header: hydrolase Chain: A; PDB Molecule: metal dependent hydrolase; PDBTitle: crystal structure analysis of the rnase j/ump complex |
| | | | | | | Fold: Metallo-hydrolase/oxidoreductase |

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|----|-------------------------|-----------|--------------|------|----|--|
| 29 | d2dkfa1 | Alignment | not modelled | 99.9 | 22 | Superfamily: Metallo-hydrolase/oxidoreductase Family: beta-CASP RNA-metabolising hydrolases |
| 30 | c5habB | Alignment | not modelled | 99.9 | 11 | 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 |
| 31 | 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 |
| 32 | d2cbna1 | Alignment | not modelled | 99.8 | 17 | Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: RNase Z-like |
| 33 | 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 |
| 34 | c2bibA | Alignment | not modelled | 99.8 | 13 | 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 |
| 35 | d1k07a | Alignment | not modelled | 99.8 | 17 | Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase |
| 36 | d1xtoa | Alignment | not modelled | 99.8 | 18 | Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Coenzyme PQQ synthesis protein B, PqqB |
| 37 | c6dn4A | Alignment | not modelled | 99.8 | 18 | PDB header: metal binding protein Chain: A: PDB Molecule: beta-lactamase; PDBTitle: cronobacter sakazakii (enterobacter sakazakii) metallo-beta-lactamase2 harldq motif |
| 38 | c2i7xA | Alignment | not modelled | 99.8 | 16 | PDB header: rna binding protein, protein binding Chain: A: PDB Molecule: protein cft2; PDBTitle: structure of yeast cpsf-100 (ydh1p) |
| 39 | d2i7xa1 | Alignment | not modelled | 99.8 | 16 | Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: beta-CASP RNA-metabolising hydrolases |
| 40 | c6qnmB | Alignment | not modelled | 99.8 | 12 | PDB header: signaling protein Chain: B: PDB Molecule: oxygen-binding di-iron protein; PDBTitle: apo state of chemotaxis sensor odp from t. denticola |
| 41 | c5aebA | Alignment | not modelled | 99.8 | 20 | 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. |
| 42 | c4awyB | Alignment | not modelled | 99.8 | 21 | 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 |
| 43 | c6n36A | Alignment | not modelled | 99.8 | 19 | PDB header: ligase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: beta-lactamase from chitinophaga pinensis |
| 44 | c6e0sA | Alignment | not modelled | 99.8 | 18 | 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 |
| 45 | d2aioa1 | Alignment | not modelled | 99.8 | 25 | Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase |
| 46 | c4efzB | Alignment | not modelled | 99.8 | 21 | PDB header: hydrolase Chain: B: PDB Molecule: metallo-beta-lactamase family protein; PDBTitle: crystal structure of a hypothetical metallo-beta-lactamase from2 burkholderia pseudomallei |
| 47 | c6aufB | Alignment | not modelled | 99.8 | 22 | PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase-like protein; PDBTitle: crystal structure of metallo beta lactamases mim-1 from novosphingobium2 pentaromativorans |
| 48 | c3lvzA | Alignment | not modelled | 99.7 | 24 | 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 |
| 49 | c6qqrB | Alignment | not modelled | 99.7 | 11 | PDB header: signaling protein Chain: B: PDB Molecule: oxygen-binding diiron protein; PDBTitle: apo conformation of chemotaxis sensor odp |
| 50 | c5iqkB | Alignment | not modelled | 99.7 | 19 | PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase rm3; PDBTitle: rm3 metallo-beta-lactamase |
| 51 | 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 sulfobolus tokodaii |
| 52 | c4b87A | Alignment | not modelled | 99.7 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: dna cross-link repair 1a protein; PDBTitle: crystal structure of human dna cross-link repair 1a |
| 53 | d2gmna1 | Alignment | not modelled | 99.7 | 22 | Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase |
| 54 | c4ojvA | Alignment | not modelled | 99.7 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: 3',5'-cyclic-nucleotide phosphodiesterase 1; PDBTitle: crystal structure of unliganded yeast pde1 |

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|----|-------------------------|-----------|--------------|------|----|---|
| 55 | c4yskA | Alignment | not modelled | 99.7 | 22 | PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase domain protein; PDBTitle: crystal structure of apo-form sdoa from pseudomonas putida |
| 56 | c3vqzA | Alignment | not modelled | 99.7 | 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 |
| 57 | c2ohiB | Alignment | not modelled | 99.7 | 27 | PDB header: oxidoreductase Chain: B: PDB Molecule: type a flavoprotein fpra; PDBTitle: crystal structure of coenzyme f420h2 oxidase (fpra), a diiron2 flavoprotein, reduced state |
| 58 | c1vmeB | Alignment | not modelled | 99.7 | 18 | PDB header: electron transport Chain: B: PDB Molecule: flavoprotein; PDBTitle: crystal structure of flavoprotein (tm0755) from thermotoga maritima at2 1.80 a resolution |
| 59 | c2q9uB | Alignment | not modelled | 99.7 | 23 | PDB header: oxidoreductase Chain: B: PDB Molecule: a-type flavoprotein; PDBTitle: crystal structure of the flavodiiron protein from giardia2 intestinalis |
| 60 | c2p4zA | Alignment | not modelled | 99.7 | 15 | 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 |
| 61 | c4d02A | Alignment | not modelled | 99.7 | 22 | PDB header: electron transport Chain: A: PDB Molecule: anaerobic nitric oxide reductase flavorubredoxin; PDBTitle: the crystallographic structure of flavorubredoxin from escherichia2 coli |
| 62 | c5mtzA | Alignment | not modelled | 99.6 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease z; PDBTitle: crystal structure of a long form rnase z from yeast |
| 63 | d1wraa1 | Alignment | not modelled | 99.6 | 13 | Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Pce catalytic domain-like |
| 64 | c2zo4A | Alignment | not modelled | 99.6 | 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 |
| 65 | d1m2xa | Alignment | not modelled | 99.6 | 14 | Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase |
| 66 | d1znba | Alignment | not modelled | 99.6 | 14 | Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase |
| 67 | c6h0cA | Alignment | not modelled | 99.6 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: putative diflavin flavoprotein a 3; PDBTitle: flv1 flavodiiron core from synechocystis sp. pcc6803 |
| 68 | c1e5dA | Alignment | not modelled | 99.6 | 21 | PDB header: oxidoreductase Chain: A: PDB Molecule: rubredoxin\oxygen oxidoreductase; PDBTitle: rubredoxin oxygen:oxidoreductase (roo) from anaerobe desulfovibrio2 gigas |
| 69 | c3l6nA | Alignment | not modelled | 99.6 | 12 | PDB header: hydrolase Chain: A: PDB Molecule: metallo-beta-lactamase; PDBTitle: crystal structure of metallo-beta-lactamase ind-7 |
| 70 | c1ychD | Alignment | not modelled | 99.6 | 21 | 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 |
| 71 | c3zdkA | Alignment | not modelled | 99.6 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: 5' exonuclease apollo; PDBTitle: crystal structure of human 5' exonuclease apollo |
| 72 | d2e7ya1 | Alignment | not modelled | 99.6 | 18 | Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: RNase Z-like |
| 73 | d1xm8a | Alignment | not modelled | 99.6 | 20 | Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Glyoxalase II (hydroxyacylglutathione hydrolase) |
| 74 | c3tp9B | Alignment | not modelled | 99.6 | 25 | 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 |
| 75 | c2r2dC | Alignment | not modelled | 99.6 | 18 | PDB header: hydrolase Chain: C: PDB Molecule: zn-dependent hydrolases; PDBTitle: structure of a quorum-quenching lactonase (aiib) from agrobacterium2 tumefaciens |
| 76 | d1ko3a | Alignment | not modelled | 99.6 | 16 | Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase |
| 77 | d1qh5a | Alignment | not modelled | 99.6 | 22 | Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Glyoxalase II (hydroxyacylglutathione hydrolase) |
| 78 | c3eshB | Alignment | not modelled | 99.6 | 12 | 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 |
| 79 | c3r2uC | Alignment | not modelled | 99.6 | 22 | 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 |

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|-----|-------------------------|-----------|--------------|------|----|--|
| 80 | c6ch0L | Alignment | not modelled | 99.6 | 17 | PDB header: hydrolase Chain: I: PDB Molecule: beta-lactamase; PDBTitle: structure of the quorum quenching lactonase from alicyclobacillus2 acidoterrestris bound to a glycerol molecule |
| 81 | c4zo3A | Alignment | not modelled | 99.6 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: acylhomoserine lactonase; PDBTitle: aidc, a dizinc quorum-quenching lactonase, in complex with a product2 n-hexnoyl-l-homoserine |
| 82 | d1vmea2 | Alignment | not modelled | 99.6 | 16 | Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: ROO N-terminal domain-like |
| 83 | c4ad9E | Alignment | not modelled | 99.6 | 10 | PDB header: hydrolase Chain: E: PDB Molecule: beta-lactamase-like protein 2; PDBTitle: crystal structure of human lactb2. |
| 84 | d1ycga2 | Alignment | not modelled | 99.5 | 23 | Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: ROO N-terminal domain-like |
| 85 | c4xukB | Alignment | not modelled | 99.5 | 18 | PDB header: hydrolase Chain: B: PDB Molecule: putative hydrolase; PDBTitle: crystal structure of hydrolase aboph in beta lactamase superfamily |
| 86 | c2br6A | Alignment | not modelled | 99.5 | 15 | PDB header: hydrolase Chain: A: PDB Molecule: aiia-like protein; PDBTitle: crystal structure of quorum-quenching n-acyl homoserine2 lactone lactonase |
| 87 | c2ynuB | Alignment | not modelled | 99.5 | 19 | 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 |
| 88 | c5ve5C | Alignment | not modelled | 99.5 | 19 | 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 |
| 89 | d2az4a1 | Alignment | not modelled | 99.5 | 13 | Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: beta-CASP RNA-metabolising hydrolases |
| 90 | c5i0pB | Alignment | not modelled | 99.5 | 18 | PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase domain protein; PDBTitle: crystal structure of a beta-lactamase domain protein from burkholderia2 ambifaria |
| 91 | c1p9eA | Alignment | not modelled | 99.5 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: methyl parathion hydrolase; PDBTitle: crystal structure analysis of methyl parathion hydrolase from2 pseudomonas sp wbc-3 |
| 92 | d1p9ea | Alignment | not modelled | 99.5 | 18 | Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Methyl parathion hydrolase |
| 93 | c4wd6B | Alignment | not modelled | 99.5 | 17 | PDB header: hydrolase Chain: B: PDB Molecule: metallo-beta-lactamase; PDBTitle: crystal structure of dim-1 metallo-beta-lactamase |
| 94 | c3aj3A | Alignment | not modelled | 99.5 | 14 | PDB header: hydrolase Chain: A: PDB Molecule: 4-pyridoxolactonase; PDBTitle: crystal structure of selenomethionine substituted 4-pyridoxolactonase2 from mesorhizobium loti |
| 95 | c3hnnD | Alignment | not modelled | 99.5 | 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 |
| 96 | c3spuB | Alignment | not modelled | 99.5 | 13 | PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase ndm-1; PDBTitle: apo ndm-1 crystal structure |
| 97 | d1e5da2 | Alignment | not modelled | 99.5 | 14 | Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: ROO N-terminal domain-like |
| 98 | c2fxhB | Alignment | not modelled | 99.5 | 13 | PDB header: hydrolase, metal binding protein Chain: B: PDB Molecule: spm-1; PDBTitle: pseudomonas aeruginosa spm-1 metallo-beta-lactamase |
| 99 | c4chlA | Alignment | not modelled | 99.5 | 25 | PDB header: oxidoreductase Chain: A: PDB Molecule: persulfide dioxygenase ethe1, mitochondrial; PDBTitle: human ethylmalonic encephalopathy protein 1 (hethe1) |
| 100 | c2gcuD | Alignment | not modelled | 99.5 | 18 | PDB header: hydrolase Chain: D: PDB Molecule: putative hydroxyacylglutathione hydrolase 3; PDBTitle: x-ray structure of gene product from arabidopsis thaliana at1g53580 |
| 101 | c6cqsA | Alignment | not modelled | 99.5 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: sediminispirochaeta smaragdinae sps-1 metallo-beta-lactamase |
| 102 | c4nurB | Alignment | not modelled | 99.5 | 16 | PDB header: hydrolase Chain: B: PDB Molecule: psdsa; PDBTitle: crystal structure of thermostable alkylsulfatase sdsap from2 pseudomonas sp. s9 |
| 103 | d2q0ia1 | Alignment | not modelled | 99.4 | 20 | Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: PqsE-like |
| 104 | c4ysbB | Alignment | not modelled | 99.4 | 23 | PDB header: hydrolase Chain: B: PDB Molecule: metallo-beta-lactamase family protein; PDBTitle: crystal structure of ethe1 from myxococcus xanthus |
| 105 | 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 |

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|-----|-------------------------|-----------|--------------|------|----|---|
| | | | | | | vim-2 metallo-beta-lactamase from pseudomonas aeruginosa3 with mercaptocarboxylate inhibitor |
| 106 | d1mqoa_ | Alignment | not modelled | 99.4 | 14 | Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase |
| 107 | d1jita_ | Alignment | not modelled | 99.4 | 15 | Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase |
| 108 | c3rkjA_ | Alignment | not modelled | 99.4 | 13 | PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase ndm-1; PDBTitle: crystal structure of new delhi metallo-beta-lactamase-1 from2 klebsiella pnueumoniae |
| 109 | c2yheD_ | Alignment | not modelled | 99.4 | 19 | PDB header: hydrolase Chain: D: PDB Molecule: sec-alkyl sulfatase; PDBTitle: structure determination of the stereoselective inverting sec-2 alkylsulfatase pisa1 from pseudomonas sp. |
| 110 | c4le6B_ | Alignment | not modelled | 99.4 | 23 | PDB header: hydrolase Chain: B: PDB Molecule: organophosphorus hydrolase; PDBTitle: crystal structure of the phosphotriesterase ophc2 from pseudomonas2 pseudoalcaligenes |
| 111 | c2p18A_ | Alignment | not modelled | 99.4 | 22 | PDB header: hydrolase Chain: A: PDB Molecule: glyoxalase ii; PDBTitle: crystal structure of the leishmania infantum glyoxalase ii |
| 112 | d2qeda1 | Alignment | not modelled | 99.3 | 14 | Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Glyoxalase II (hydroxyacylglutathione hydrolase) |
| 113 | c2zwrA_ | Alignment | not modelled | 99.3 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: metallo-beta-lactamase superfamily protein; PDBTitle: crystal structure of ttha1623 from thermus thermophilus hb8 |
| 114 | c3sd9B_ | Alignment | not modelled | 99.3 | 15 | 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 |
| 115 | d2cfua2 | Alignment | not modelled | 99.3 | 14 | Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Alkylsulfatase-like |
| 116 | c2cfuA_ | Alignment | not modelled | 99.3 | 15 | 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. |
| 117 | c3h3eA_ | Alignment | not modelled | 99.3 | 16 | 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 |
| 118 | d1x8ha_ | Alignment | not modelled | 99.3 | 14 | Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase |
| 119 | c4pdxB_ | Alignment | not modelled | 99.3 | 17 | PDB header: hydrolase Chain: B: PDB Molecule: putative alkyl/aryl-sulfatase yjcs; PDBTitle: crystal structure of escherchia coli uncharacterized protein yjcs |
| 120 | c2xf4A_ | Alignment | not modelled | 99.3 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: hydroxyacylglutathione hydrolase; PDBTitle: crystal structure of salmonella enterica serovar2 typhimurium ycb1 |