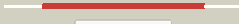



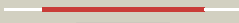



















Phyre2

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|------------------|----------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD1096 (-)_1224390_1225265 |
| Date | Wed Jul 31 22:05:17 BST 2019 |
| Unique Job ID | 8507a9ce4cb14cee |

Detailed template
information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|---|
| 1 | c2c1iA_ |  Alignment |  | 100.0 | 36 | PDB header: hydrolase Chain: A: PDB Molecule: peptidoglycan glcnac deacetylase; PDBTitle: structure of streptococcus pneumoniae peptidoglycan deacetylase2 (sppgda) d 275 n mutant. |
| 2 | c5jp6A_ |  Alignment |  | 100.0 | 29 | PDB header: hydrolase Chain: A: PDB Molecule: putative polysaccharide deacetylase; PDBTitle: bdellovibrio bacteriovorus peptidoglycan deacetylase bd3279 |
| 3 | c4nz3A_ |  Alignment |  | 100.0 | 23 | PDB header: hydrolase Chain: A: PDB Molecule: deacetylase da1; PDBTitle: structure of vibrio cholerae chitin de-n-acetylase in complex with2 di(n-acetyl-d-glucosamine) (cbs) in p 21 21 21 |
| 4 | c5lqcA_ |  Alignment |  | 100.0 | 38 | PDB header: hydrolase Chain: A: PDB Molecule: arce4a; PDBTitle: t48 deacetylase with substrate |
| 5 | c1w17A_ |  Alignment |  | 100.0 | 27 | PDB header: hydrolase Chain: A: PDB Molecule: probable polysaccharide deacetylase pdaa; PDBTitle: structure of bacillus subtilis pdaa, a family 4 carbohydrate esterase. |
| 6 | d1ny1a_ |  Alignment |  | 100.0 | 28 | Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase |
| 7 | d2cc0a1 |  Alignment |  | 100.0 | 36 | Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase |
| 8 | d2c1ia1 |  Alignment |  | 100.0 | 37 | Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase |
| 9 | c5ncdA_ |  Alignment |  | 100.0 | 31 | PDB header: hydrolase Chain: A: PDB Molecule: peptidoglycan n-acetylglucosamine deacetylase; PDBTitle: crystal structure of the polysaccharide deacetylase bc1974 from2 bacillus cereus in complex with (2s)-2-amino-5-3 (diaminomethylideneamino)-n-hydroxypentanamide |
| 10 | c4m1bA_ |  Alignment |  | 100.0 | 26 | PDB header: hydrolase Chain: A: PDB Molecule: polysaccharide deacetylase; PDBTitle: structural determination of ba0150, a polysaccharide deacetylase from2 bacillus anthracis |
| 11 | d2j13a1 |  Alignment |  | 100.0 | 27 | Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase |

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|----|-------------------------|-----------|--------------|-------|----|--|
| 12 | c2vvoA_ | Alignment | | 100.0 | 20 | PDB header: hydrolase Chain: A: PDB Molecule: polysaccharide deacetylase domain-containing protein PDBTitle: chitin deacetylase family member from encephalitozoon cuniculi |
| 13 | c2y8uA_ | Alignment | | 100.0 | 31 | PDB header: hydrolase Chain: A: PDB Molecule: chitin deacetylase; PDBTitle: a. nidulans chitin deacetylase |
| 14 | c4l1gB_ | Alignment | | 100.0 | 30 | PDB header: hydrolase Chain: B: PDB Molecule: peptidoglycan n-acetylglucosamine deacetylase; PDBTitle: crystal structure of the bc1960 peptidoglycan n-acetylglucosamine2 deacetylase from bacillus cereus |
| 15 | d2iw0a1 | Alignment | | 100.0 | 32 | Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase |
| 16 | d2c71a1 | Alignment | | 100.0 | 31 | Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase |
| 17 | c2iw0A_ | Alignment | | 100.0 | 32 | PDB header: hydrolase Chain: A: PDB Molecule: chitin deacetylase; PDBTitle: structure of the chitin deacetylase from the fungal2 pathogen colletotrichum lindemuthianum |
| 18 | c2w3zA_ | Alignment | | 100.0 | 26 | PDB header: hydrolase Chain: A: PDB Molecule: putative deacetylase; PDBTitle: structure of a streptococcus mutans ce4 esterase |
| 19 | d2nlya1 | Alignment | | 100.0 | 19 | Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: Divergent polysaccharide deacetylase |
| 20 | c3qbuD_ | Alignment | | 100.0 | 25 | PDB header: hydrolase Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of putative peptidoglycan deactelyase (hp0310) from2 helicobacter pylori |
| 21 | d1z7aa1 | Alignment | not modelled | 100.0 | 16 | Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: PA1517-like |
| 22 | c3rxzA_ | Alignment | not modelled | 100.0 | 27 | PDB header: hydrolase Chain: A: PDB Molecule: polysaccharide deacetylase; PDBTitle: crystal structure of putative polysaccharide deacetylase from2 mycobacterium smegmatis |
| 23 | c3s6oD_ | Alignment | not modelled | 100.0 | 18 | PDB header: hydrolase Chain: D: PDB Molecule: polysaccharide deacetylase family protein; PDBTitle: crystal structure of a polysaccharide deacetylase family protein from2 burkholderia pseudomallei |
| 24 | c5z34A_ | Alignment | not modelled | 100.0 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: chitin deacetylase; PDBTitle: the structure of a chitin deacetylase from bombyx mori provide the2 first insight into insect chitin deacetylation mechanism |
| 25 | c6dq3B_ | Alignment | not modelled | 100.0 | 25 | PDB header: hydrolase Chain: B: PDB Molecule: polysaccharide deacetylase; PDBTitle: streptococcus pyogenes deacetylase pdi in complex with acetate |
| 26 | c5znsA_ | Alignment | not modelled | 99.9 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: chitin deacetylase; PDBTitle: insect chitin deacetylase |
| 27 | c4wcjA_ | Alignment | not modelled | 99.9 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: polysaccharide deacetylase; PDBTitle: structure of icab from ammonifex degensii |
| 28 | c4f9dA_ | Alignment | not modelled | 99.9 | 20 | PDB header: hydrolase Chain: A: PDB Molecule: poly-beta-1,6-n-acetyl-d-glucosamine n-deacetylase; PDBTitle: structure of escherichia coli pgab 42-655 in complex with nickel |
| | | | | | | PDB header: hydrolase Chain: B: PDB Molecule: bpsb (dqab), poly-beta-1,6-n-acetyl-d- |

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|----|-------------------------|-----------|--------------|------|----|---|
| 29 | c5bu6B_ | Alignment | not modelled | 99.9 | 23 | glucosamine n- PDBTitle: structure of bpsb deacetylase domain from bordetella bronchiseptica PDB header: hydrolase Chain: B: PDB Molecule: poly-beta-1,6-n-acetyl-d-glucosamine n-deacetylase; PDBTitle: probing the structure and mechanism of de-n-acetylase from2 aggregatibacter actinomycetemcomitans |
| 30 | c4u10B_ | Alignment | not modelled | 99.9 | 28 | PDB header: hydrolase Chain: A: PDB Molecule: polysaccharide deacetylase-like protein; PDBTitle: crystal structure of a bacillus anthracis peptidoglycan deacetylase |
| 31 | c6go1A_ | Alignment | not modelled | 99.8 | 28 | PDB header: hydrolase Chain: A: PDB Molecule: polysaccharide deacetylase; PDBTitle: crystal structure of bc0361, a polysaccharide deacetylase from2 bacillus cereus |
| 32 | c4hd5A_ | Alignment | not modelled | 99.8 | 24 | Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: 4-alpha-glucanotransferase, N-terminal domain |
| 33 | d1k1xa3 | Alignment | not modelled | 98.8 | 19 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atu2773; PDBTitle: crystal structure of uncharacterized protein atu2773 from2 agrobacterium tumefaciens c58 |
| 34 | c2qv5A_ | Alignment | not modelled | 98.6 | 16 | Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: AmyC N-terminal domain-like |
| 35 | d2b5dx2 | Alignment | not modelled | 98.6 | 18 | PDB header: hydrolase Chain: X: PDB Molecule: alpha-amylase; PDBTitle: crystal structure of the novel alpha-amylase amyc from thermotoga2 maritima |
| 36 | c2b5dX_ | Alignment | not modelled | 98.5 | 18 | PDB header: transferase Chain: A: PDB Molecule: 4-alpha-glucanotransferase; PDBTitle: crystal structure of thermococcus litoralis 4-alpha-glucanotransferase2 complexed with acarbose |
| 37 | c1k1yA_ | Alignment | not modelled | 98.4 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of gh57-type branching enzyme from hyperthermophilic2 archaeon pyrococcus horikoshii |
| 38 | c5wu7A_ | Alignment | not modelled | 98.2 | 19 | Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: AmyC N-terminal domain-like |
| 39 | d1ufaa2 | Alignment | not modelled | 98.0 | 22 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: tt1467 protein; PDBTitle: crystal structure of tt1467 from thermus thermophilus hb8 |
| 40 | c1ufaA_ | Alignment | not modelled | 98.0 | 19 | PDB header: transferase Chain: A: PDB Molecule: alpha-amylase, gh57 family; PDBTitle: crystal structure of tk1436, a gh57 branching enzyme from2 hyperthermophilic archaeon thermococcus kodakaraensis, in complex3 with glucose |
| 41 | c3n92A_ | Alignment | not modelled | 97.8 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: wbms, polysaccharide deacetylase involved in o-antigen PDBTitle: crystal structure of a putative polysaccharide deacetylase involved in2 o-antigen biosynthesis (wbms, bb0128) from bordetella bronchiseptica3 at 1.90 a resolution |
| 42 | c3hftA_ | Alignment | not modelled | 97.4 | 15 | Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: LamB/YcsF-like |
| 43 | d1v6ta_ | Alignment | not modelled | 97.3 | 19 | Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: YdjC-like |
| 44 | d2i5ia1 | Alignment | not modelled | 95.0 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: alpha-mannosidase; PDBTitle: structure of the streptococcus pyogenes family gh38 alpha-2 mannosidase |
| 45 | c2wyhA_ | Alignment | not modelled | 94.4 | 15 | PDB header: hydrolase Chain: A: PDB Molecule: alpha-mannosidase 2; PDBTitle: golgi alpha-mannosidase ii complex with (1r,6s,7r,8s)-1-2 thioniabicyclo[4.3.0]nonan-7,8-diol chloride |
| 46 | c2ow7A_ | Alignment | not modelled | 94.0 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: alpha-mannosidase ii; PDBTitle: golgi alpha-mannosidase ii |
| 47 | c1htyA_ | Alignment | not modelled | 93.6 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: lysosomal alpha-mannosidase; PDBTitle: the structure of the bovine lysosomal a-mannosidase suggests a novel2 mechanism for low ph activation |
| 48 | c1o7dA_ | Alignment | not modelled | 91.6 | 15 | Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: alpha-mannosidase |
| 49 | d3bvua3 | Alignment | not modelled | 91.6 | 17 | Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: LamB/YcsF-like |
| 50 | d2dfaa1 | Alignment | not modelled | 90.6 | 20 | PDB header: hydrolase Chain: A: PDB Molecule: glycosyl hydrolase, family 38; PDBTitle: the crystal structure of a protein in the glycosyl hydrolase family 382 from enterococcus faecalis to 2.55a |
| 51 | c3lvtA_ | Alignment | not modelled | 87.8 | 12 | PDB header: hydrolase Chain: A: PDB Molecule: alpha-mannosidase from canavalia ensiformis (jack bean); PDBTitle: structure of gh 38 jack bean alpha-mannosidase in complex with a 36-2 valent iminosugar cluster inhibitor |
| 52 | c6b9pA_ | Alignment | not modelled | 86.8 | 14 | PDB header: isomerase Chain: A: PDB Molecule: xylose isomerase domain protein tim barrel; PDBTitle: crystal structure of xylose isomerase domain protein from planctomyces2 limnophilus dsm 3776 |
| 53 | c4ovxA_ | Alignment | not modelled | 85.4 | 11 | |

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|----|-------------------------|-----------|--------------|------|----|---|
| 54 | c5exkG | Alignment | not modelled | 84.4 | 13 | PDB header: transferase Chain: G: PDB Molecule: lipoyl synthase; PDBTitle: crystal structure of m. tuberculosis lipoyl synthase with 6-2 thiooctanoyl peptide intermediate |
| 55 | c2x5eA | Alignment | not modelled | 76.2 | 13 | PDB header: unknown function Chain: A: PDB Molecule: upf0271 protein pa4511; PDBTitle: crystal structure of the hypothetical protein pa4511 from2 pseudomonas aeruginosa |
| 56 | c5hk8A | Alignment | not modelled | 75.0 | 24 | PDB header: hydrolase Chain: A: PDB Molecule: probable pheophorbidase; PDBTitle: crystal structure of a methylsterase protein mes16 from arabidopsis |
| 57 | d2i7xa1 | Alignment | not modelled | 72.7 | 10 | Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: beta-CASP RNA-metabolising hydrolases |
| 58 | c2i7xA | Alignment | not modelled | 72.7 | 10 | PDB header: rna binding protein, protein binding Chain: A: PDB Molecule: protein cft2; PDBTitle: structure of yeast cpsf-100 (ydh1p) |
| 59 | c3stxB | Alignment | not modelled | 72.7 | 19 | PDB header: hydrolase Chain: B: PDB Molecule: methylketone synthase 1; PDBTitle: crystal structure of tomato methylketone synthase i h243a variant2 complexed with beta-ketoheptanoate |
| 60 | c5dqpA | Alignment | not modelled | 71.3 | 21 | PDB header: oxidoreductase Chain: A: PDB Molecule: edta monooxygenase; PDBTitle: edta monooxygenase (emoa) from chelatorvans sp. bnc1 |
| 61 | c3zoqA | Alignment | not modelled | 71.1 | 27 | PDB header: hydrolase/viral protein Chain: A: PDB Molecule: uracil-dna glycosylase; PDBTitle: structure of bsudg-p56 complex |
| 62 | d3c70a1 | Alignment | not modelled | 68.4 | 25 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hydroxynitrile lyase-like |
| 63 | c3wwoA | Alignment | not modelled | 68.1 | 25 | PDB header: lyase Chain: A: PDB Molecule: (s)-hydroxynitrile lyase; PDBTitle: s-selective hydroxynitrile lyase from baliospermum montanum (apo1) |
| 64 | c3dqzB | Alignment | not modelled | 68.0 | 25 | PDB header: lyase Chain: B: PDB Molecule: alpha-hydroxynitrile lyase-like protein; PDBTitle: structure of the hydroxynitrile lyase from arabidopsis thaliana |
| 65 | d1tqha | Alignment | not modelled | 67.2 | 20 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/lipase |
| 66 | c5jm0A | Alignment | not modelled | 64.8 | 11 | PDB header: hydrolase Chain: A: PDB Molecule: alpha-mannosidase,alpha-mannosidase,alpha-mannosidase; PDBTitle: structure of the s. cerevisiae alpha-mannosidase 1 |
| 67 | d1e89a | Alignment | not modelled | 63.6 | 22 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hydroxynitrile lyase-like |
| 68 | c2mhcA | Alignment | not modelled | 63.5 | 10 | PDB header: recombination Chain: A: PDB Molecule: tnpx; PDBTitle: nmr structure of the catalytic domain of the large serine resolvase2 tnpX |
| 69 | d1xkla | Alignment | not modelled | 60.5 | 22 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hydroxynitrile lyase-like |
| 70 | c5nn7A | Alignment | not modelled | 59.9 | 14 | PDB header: hydrolase Chain: A: PDB Molecule: uracil-dna glycosylase; PDBTitle: kshv uracil-dna glycosylase, apo form |
| 71 | c5esrA | Alignment | not modelled | 58.9 | 28 | PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of haloalkane dehalogenase (dcca) from caulobacter2 crescentus |
| 72 | c2owrD | Alignment | not modelled | 58.0 | 19 | PDB header: hydrolase Chain: D: PDB Molecule: uracil-dna glycosylase; PDBTitle: crystal structure of vaccinia virus uracil-dna glycosylase |
| 73 | c3gzjB | Alignment | not modelled | 56.8 | 25 | PDB header: hydrolase Chain: B: PDB Molecule: polynucleotide-aldehyde esterase; PDBTitle: crystal structure of polynucleotide aldehyde esterase complexed with2 16-epi-vellosimine |
| 74 | c3cxmA | Alignment | not modelled | 56.4 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: uracil-dna glycosylase; PDBTitle: leishmania naiffi uracil-dna glycosylase in complex with 5-bromouracil |
| 75 | c2gm4B | Alignment | not modelled | 56.1 | 19 | PDB header: recombination, dna Chain: B: PDB Molecule: transposon gamma-delta resolvase; PDBTitle: an activated, tetrameric gamma-delta resolvase: hin chimaera bound to2 cleaved dna |
| 76 | c3dyvA | Alignment | not modelled | 55.5 | 22 | PDB header: hydrolase Chain: A: PDB Molecule: esterase d; PDBTitle: snapshots of esterase d from lactobacillus rhamnosus:2 insights into a rotation driven catalytic mechanism |
| 77 | c6d6zA | Alignment | not modelled | 54.6 | 12 | PDB header: isomerase Chain: A: PDB Molecule: nickel-dependent lactate racemase; PDBTitle: structure of the 2nd lactate racemase homolog apoprotein from2 thermoanaerobacterium thermosaccharolyticum |
| 78 | d1jdqa | Alignment | not modelled | 54.2 | 15 | Fold: IF3-like Superfamily: SirA-like Family: SirA-like |
| 79 | c4y7dA | Alignment | not modelled | 53.2 | 25 | PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase fold protein; PDBTitle: alpha/beta hydrolase fold protein from nakamurella multipartita |
| 80 | c4fhmA | Alignment | not modelled | 53.1 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: lips lipolytic enzyme; |

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|-----|-------------------------|-----------|--------------|------|----|---|
| 80 | c4rmlA | Alignment | not modelled | 53.1 | 10 | PDBTitle: lips and lip1, two metagenome-derived lipolytic enzymes increase the2 diversity of known lipase and esterase families |
| 81 | d1xw8a | Alignment | not modelled | 52.9 | 24 | Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: LamB/YcsF-like |
| 82 | d1fi4a2 | Alignment | not modelled | 52.4 | 35 | Fold: Ferredoxin-like Superfamily: GHMP Kinase, C-terminal domain Family: Mevalonate 5-diphosphate decarboxylase |
| 83 | c3tr7A | Alignment | not modelled | 52.3 | 24 | PDB header: hydrolase Chain: A: PDB Molecule: uracil-dna glycosylase; PDBTitle: structure of a uracil-dna glycosylase (ung) from coxiella burnetii |
| 84 | c5xksB | Alignment | not modelled | 51.4 | 9 | PDB header: hydrolase Chain: B: PDB Molecule: thermostable monoacylglycerol lipase; PDBTitle: crystal structure of monoacylglycerol lipase from thermophilic2 geobacillus sp. 12amor |
| 85 | d1m0sa1 | Alignment | not modelled | 50.9 | 16 | Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: D-ribose-5-phosphate isomerase (RpiA), catalytic domain |
| 86 | c2vjgB | Alignment | not modelled | 50.3 | 13 | PDB header: isomerase Chain: B: PDB Molecule: lactate racemase apoprotein; PDBTitle: structure of the lactate racemase apoprotein from2 thermoanaerobacterium thermosaccharolyticum |
| 87 | c2p6yA | Alignment | not modelled | 50.2 | 14 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein vca0587; PDBTitle: x-ray structure of the protein q9km02_vibch from vibrio cholerae at2 the resolution 1.63 a. northeast structural genomics consortium3 target vcr80. |
| 88 | c3l2iB | Alignment | not modelled | 49.8 | 14 | PDB header: lyase Chain: B: PDB Molecule: 3-dehydroquinone dehydratase; PDBTitle: 1.85 angstrom crystal structure of the 3-dehydroquinone dehydratase2 (arod) from salmonella typhimurium lt2. |
| 89 | d7reqa2 | Alignment | not modelled | 49.1 | 15 | Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain |
| 90 | d1hx7a | Alignment | not modelled | 49.0 | 13 | Fold: Resolvase-like Superfamily: Resolvase-like Family: gamma,delta resolvase, catalytic domain |
| 91 | c4gf5S | Alignment | not modelled | 48.8 | 19 | PDB header: transferase Chain: S: PDB Molecule: rcals11; PDBTitle: crystal structure of calicheamicin methyltransferase, cals11 |
| 92 | c5w4zA | Alignment | not modelled | 48.4 | 21 | PDB header: flavoprotein Chain: A: PDB Molecule: riboflavin lyase; PDBTitle: crystal structure of riboflavin lyase (rcae) with modified fmn and2 substrate riboflavin |
| 93 | c3b9nB | Alignment | not modelled | 48.4 | 18 | PDB header: oxidoreductase Chain: B: PDB Molecule: alkane monooxygenase; PDBTitle: crystal structure of long-chain alkane monooxygenase (lada) |
| 94 | c5uroA | Alignment | not modelled | 48.2 | 28 | PDB header: hydrolase Chain: A: PDB Molecule: predicted protein; PDBTitle: structure of a soluble epoxide hydrolase identified in trichoderma2 reesei |
| 95 | c4ycsC | Alignment | not modelled | 48.0 | 8 | PDB header: hydrolase Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of putative lipoprotein from peptoclostridium2 difficile 630 (fragment) |
| 96 | c5h3hB | Alignment | not modelled | 47.8 | 25 | PDB header: hydrolase Chain: B: PDB Molecule: abhydrolase domain-containing protein; PDBTitle: esterase (eaest) from exiguobacterium antarcticum |
| 97 | c4rrfD | Alignment | not modelled | 47.5 | 12 | PDB header: ligase Chain: D: PDB Molecule: threonine--trna ligase; PDBTitle: editing domain of threonyl-trna synthetase from methanococcus2 jannaschii with l-ser3aa |
| 98 | d1a8qa | Alignment | not modelled | 46.6 | 22 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase |
| 99 | c2hkeB | Alignment | not modelled | 46.6 | 21 | PDB header: lyase Chain: B: PDB Molecule: diphosphomevalonate decarboxylase, putative; PDBTitle: mevalonate diphosphate decarboxylase from trypanosoma brucei |
| 100 | c3rm3A | Alignment | not modelled | 46.5 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: thermostable monoacylglycerol lipase; PDBTitle: crystal structure of monoacylglycerol lipase from bacillus sp. h257 |
| 101 | c4z8zA | Alignment | not modelled | 45.9 | 11 | PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the hypothetical protein from ruminiclostridium2 thermocellum atcc 27405 |
| 102 | c6g80C | Alignment | not modelled | 45.0 | 11 | PDB header: transferase Chain: C: PDB Molecule: methyltransferase domain protein; PDBTitle: structure of mycobacterium hassiacum met1 from orthorhombic crystals. |
| 103 | d1va4a | Alignment | not modelled | 44.8 | 22 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase |
| 104 | c5y51F | Alignment | not modelled | 44.7 | 25 | PDB header: hydrolase Chain: F: PDB Molecule: pyrethroid hydrolase; PDBTitle: crystal structure of pyth_h230a |
| 105 | c4k3zA | Alignment | not modelled | 44.4 | 15 | PDB header: oxidoreductase Chain: A: PDB Molecule: d-erythrulose 4-phosphate dehydrogenase; PDBTitle: crystal structure of d-erythrulose 4-phosphate dehydrogenase from2 brucella melitensis, solved by iodide sad PDB header: hydrolase |

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|-----|-------------------------|-----------|--------------|------|----|--|
| 106 | c4f0jA_ | Alignment | not modelled | 44.4 | 28 | Chain: A: PDB Molecule: probable hydrolytic enzyme; PDBTitle: crystal structure of a probable hydrolytic enzyme (pa3053) from2 pseudomonas aeruginosa pao1 at 1.50 a resolution |
| 107 | c3h5oB_ | Alignment | not modelled | 44.0 | 9 | PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator gntr; PDBTitle: the crystal structure of transcription regulator gntr from2 chromobacterium violaceum |
| 108 | c4df3B_ | Alignment | not modelled | 43.9 | 18 | PDB header: transferase Chain: B: PDB Molecule: fibrillar-like rrna/trna 2'-o-methyltransferase; PDBTitle: crystal structure of aeropyrum pernix fibrillar in complex with2 natively bound s-adenosyl-l-methionine at 1.7a |
| 109 | c4zwnD_ | Alignment | not modelled | 43.8 | 26 | PDB header: hydrolase Chain: D: PDB Molecule: monoglyceride lipase; PDBTitle: crystal structure of a soluble variant of the monoglyceride lipase2 from saccharomyces cerevisiae |
| 110 | c4rpcA_ | Alignment | not modelled | 43.1 | 22 | PDB header: hydrolase Chain: A: PDB Molecule: putative alpha/beta hydrolase; PDBTitle: crystal structure of the putative alpha/beta hydrolase family protein2 from desulfitobacterium hafniense |
| 111 | d1brta_ | Alignment | not modelled | 43.1 | 28 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase |
| 112 | c2cjpA_ | Alignment | not modelled | 42.7 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: structure of potato (solanum tuberosum) epoxide hydrolase i (steh1) |
| 113 | c5xmdA_ | Alignment | not modelled | 41.8 | 25 | PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase a; PDBTitle: crystal structure of epoxide hydrolase vreh1 from vigna radiata |
| 114 | c3hazA_ | Alignment | not modelled | 41.7 | 9 | PDB header: oxidoreductase Chain: A: PDB Molecule: proline dehydrogenase; PDBTitle: crystal structure of bifunctional proline utilization a2 (puta) protein |
| 115 | c2r0qF_ | Alignment | not modelled | 41.6 | 15 | PDB header: recombination/dna Chain: F: PDB Molecule: putative transposon tn552 dna-invertase bin3; PDBTitle: crystal structure of a serine recombinase- dna regulatory2 complex |
| 116 | d1jr2a_ | Alignment | not modelled | 41.2 | 10 | Fold: HemD-like Superfamily: HemD-like Family: HemD-like |
| 117 | c1jr2A_ | Alignment | not modelled | 41.2 | 10 | PDB header: lyase Chain: A: PDB Molecule: uroporphyrinogen-iii synthase; PDBTitle: structure of uroporphyrinogen iii synthase |
| 118 | d1b6ga_ | Alignment | not modelled | 41.1 | 19 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloalkane dehalogenase |
| 119 | c5oluA_ | Alignment | not modelled | 40.8 | 13 | PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase family protein; PDBTitle: the crystal structure of a highly thermostable carboxyl esterase from2 bacillus coagulans in complex with glycerol |
| 120 | d1a8sa_ | Alignment | not modelled | 40.6 | 25 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase |