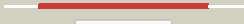



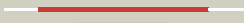



















Phyre2

| | |
|---------------|-----------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD3724B_(cut5b)_4169784_4170347 |
| Date | Fri Aug 9 18:20:42 BST 2019 |
| Unique Job ID | 09de406988130e47 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|---|
| 1 | d1qoza_ |  Alignment |  | 100.0 | 26 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like |
| 2 | d1g66a_ |  Alignment |  | 100.0 | 26 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like |
| 3 | c4psdA_ |  Alignment |  | 100.0 | 33 | PDB header: hydrolase Chain: A; PDB Molecule: carbohydrate esterase family 5; PDBTitle: structure of trichoderma reesei cutinase native form. |
| 4 | c5x88A_ |  Alignment |  | 100.0 | 25 | PDB header: hydrolase Chain: A; PDB Molecule: cutinase; PDBTitle: a crystal structure of cutinases from malbranchea cinnamomea |
| 5 | d1cexa_ |  Alignment |  | 100.0 | 23 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like |
| 6 | c3dd5F_ |  Alignment |  | 100.0 | 26 | PDB header: hydrolase Chain: F; PDB Molecule: cutinase; PDBTitle: glomerella cingulata e600-cutinase complex |
| 7 | c2czqB_ |  Alignment |  | 100.0 | 26 | PDB header: hydrolase Chain: B; PDB Molecule: cutinase-like protein; PDBTitle: a novel cutinase-like protein from cryptococcus sp. |
| 8 | c3gbsA_ |  Alignment |  | 100.0 | 25 | PDB header: hydrolase Chain: A; PDB Molecule: cutinase 1; PDBTitle: crystal structure of aspergillus oryzae cutinase |
| 9 | c4oylC_ |  Alignment |  | 100.0 | 25 | PDB header: hydrolase Chain: C; PDB Molecule: cutinase; PDBTitle: humicola insolens cutinase in complex with monoethylphosphate |
| 10 | c3ajaA_ |  Alignment |  | 100.0 | 29 | PDB header: hydrolase Chain: A; PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of msmeg_6394 |
| 11 | c3hc7A_ |  Alignment |  | 99.9 | 22 | PDB header: cell adhesion Chain: A; PDB Molecule: gene 12 protein; PDBTitle: crystal structure of lysin b from mycobacteriophage d29 |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|--|
| 12 | c3g7nA_ | Alignment | | 97.6 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: crystal structure of a triacylglycerol lipase from penicillium2 expansum at 1.3 |
| 13 | c3ngmB_ | Alignment | | 97.2 | 21 | PDB header: hydrolase Chain: B: PDB Molecule: extracellular lipase; PDBTitle: crystal structure of lipase from gibberella zeae |
| 14 | d1uwca_ | Alignment | | 97.0 | 26 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases |
| 15 | d1tcaa_ | Alignment | | 96.9 | 11 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases |
| 16 | c5gw8A_ | Alignment | | 96.8 | 21 | PDB header: hydrolase Chain: A: PDB Molecule: hypothetical secretory lipase (family 3); PDBTitle: crystal structure of a putative dag-like lipase (mgmdl2) from2 malassezia globosa |
| 17 | c3uuuA_ | Alignment | | 96.8 | 20 | PDB header: hydrolase Chain: A: PDB Molecule: lip1, secretory lipase (family 3); PDBTitle: crystal structure of mono- and diacylglycerol lipase from malassezia2 globosa |
| 18 | c5f2hA_ | Alignment | | 96.4 | 15 | PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: 2.75 angstrom resolution crystal structure of uncharacterized protein2 from bacillus cereus atcc 10987 |
| 19 | d3tgla_ | Alignment | | 96.2 | 13 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases |
| 20 | c5h6bA_ | Alignment | | 96.2 | 12 | PDB header: hydrolase Chain: A: PDB Molecule: putative secreted lipase; PDBTitle: crystal structure of a thermostable lipase from marine streptomyces |
| 21 | d1tiba_ | Alignment | not modelled | 96.2 | 20 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases |
| 22 | c3icvA_ | Alignment | not modelled | 96.2 | 13 | PDB header: hydrolase Chain: A: PDB Molecule: lipase b; PDBTitle: structural consequences of a circular permutation on lipase b from2 candida antarctica |
| 23 | d1tiaa_ | Alignment | not modelled | 96.2 | 20 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases |
| 24 | c6cl4A_ | Alignment | not modelled | 96.2 | 29 | PDB header: hydrolase Chain: A: PDB Molecule: lipase c12; PDBTitle: lipc12 - lipase from metagenomics |
| 25 | d1lgva_ | Alignment | not modelled | 96.0 | 19 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases |
| 26 | c3og9A_ | Alignment | not modelled | 95.9 | 15 | PDB header: hydrolase Chain: A: PDB Molecule: protein yahd a copper inducible hydrolase; PDBTitle: structure of yahd with malic acid |
| 27 | d4lipd_ | Alignment | not modelled | 95.8 | 28 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase |
| 28 | c5xk2A_ | Alignment | not modelled | 95.8 | 25 | PDB header: hydrolase Chain: A: PDB Molecule: diacylglycerol lipase; PDBTitle: crystal structure of mono- and diacylglycerol lipase from aspergillus2 oryzae |
| 29 | c3n0dE_ | Alignment | not modelled | 95.7 | 22 | PDB header: hydrolase Chain: F: PDB Molecule: triacylglycerol lipase; |

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|----|-------------------------|-----------|--------------|------|----|---|
| 29 | c3000r_ | Alignment | not modelled | 95.7 | 42 | PDBTitle: crystal structure of lip2 lipase from yarrowia lipolytica at 1.7 a2 resolution |
| 30 | c6qppA_ | Alignment | not modelled | 95.6 | 14 | PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: rhizomucor miehei lipase propeptide complex, native |
| 31 | c2veoA_ | Alignment | not modelled | 95.5 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: lipase a; PDBTitle: x-ray structure of candida antarctica lipase a in its closed state. |
| 32 | c2h7xA_ | Alignment | not modelled | 95.5 | 15 | PDB header: hydrolase Chain: A: PDB Molecule: type i polyketide synthase pikaiv; PDBTitle: pikromycin thioesterase adduct with reduced triketide2 affinity label |
| 33 | c2zyiB_ | Alignment | not modelled | 95.5 | 18 | PDB header: hydrolase Chain: B: PDB Molecule: lipase, putative; PDBTitle: a. fulgidus lipase with fatty acid fragment and calcium |
| 34 | c2r8bA_ | Alignment | not modelled | 95.5 | 23 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atu2452; PDBTitle: the crystal structure of the protein atu2452 of unknown function from2 agrobacterium tumefaciens str. c58 |
| 35 | d2r8ba1 | Alignment | not modelled | 95.5 | 22 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1 |
| 36 | d2h7xa1 | Alignment | not modelled | 95.4 | 15 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases |
| 37 | c1mo2A_ | Alignment | not modelled | 95.3 | 16 | PDB header: transferase Chain: A: PDB Molecule: erythronolide synthase, modules 5 and 6; PDBTitle: thioesterase domain from 6-deoxyerythronolide synthase (debs te), ph2 8.5 |
| 38 | d1mo2a_ | Alignment | not modelled | 95.3 | 16 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases |
| 39 | d2h1ia1 | Alignment | not modelled | 95.3 | 19 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1 |
| 40 | c5xavB_ | Alignment | not modelled | 95.3 | 15 | PDB header: biosynthetic protein Chain: B: PDB Molecule: intracellular polyhydroxyalkanoate synthase; PDBTitle: structure of phac from chromobacterium sp. usm2 |
| 41 | d1etha2 | Alignment | not modelled | 95.3 | 9 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain |
| 42 | d1ex9a_ | Alignment | not modelled | 95.3 | 27 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase |
| 43 | d1cvla_ | Alignment | not modelled | 95.2 | 30 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase |
| 44 | c5t6oA_ | Alignment | not modelled | 95.1 | 26 | PDB header: biosynthetic protein Chain: A: PDB Molecule: poly-beta-hydroxybuterate polymerase; PDBTitle: structure of the catalytic domain of the class i polyhydroxybutyrate2 synthase from cupriavidus necator |
| 45 | c4gw3A_ | Alignment | not modelled | 94.9 | 25 | PDB header: hydrolase Chain: A: PDB Molecule: putative lipase; PDBTitle: crystal structure of the lipase from proteus mirabilis |
| 46 | c5d8mA_ | Alignment | not modelled | 94.9 | 30 | PDB header: hydrolase Chain: A: PDB Molecule: metagenomic carboxyl esterase mgs0156; PDBTitle: crystal structure of the metagenomic carboxyl esterase mgs0156 |
| 47 | d3b5ea1 | Alignment | not modelled | 94.9 | 22 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1 |
| 48 | d1lpbb2 | Alignment | not modelled | 94.8 | 9 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain |
| 49 | c6e6uA_ | Alignment | not modelled | 94.8 | 16 | PDB header: biosynthetic protein Chain: A: PDB Molecule: dieckmann cyclase, ncmc; PDBTitle: variant c89s of dieckmann cyclase, ncmc |
| 50 | d1ei9a_ | Alignment | not modelled | 94.7 | 21 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterases |
| 51 | c2q0xA_ | Alignment | not modelled | 94.5 | 15 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: alpha/beta hydrolase fold protein of unknown function |
| 52 | c4eziA_ | Alignment | not modelled | 94.4 | 13 | PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative hydrolase (lpg1103) from legionella2 pneumophila subsp. pneumophila str. philadelphia 1 at 1.15 a3 resolution |
| 53 | c3lp5A_ | Alignment | not modelled | 94.3 | 10 | PDB header: hydrolase Chain: A: PDB Molecule: putative cell surface hydrolase; PDBTitle: the crystal structure of the putative cell surface hydrolase from2 lactobacillus plantarum wcf51 |
| 54 | c4qnnC_ | Alignment | not modelled | 94.3 | 23 | PDB header: hydrolase Chain: C: PDB Molecule: phospholipase a 1 from hornet(vespa basalis) venom; PDBTitle: crystal structure of phospholipase a 1 from hornet(vespa basalis)2 venom |
| 55 | c2rauA_ | Alignment | not modelled | 94.3 | 23 | PDB header: hydrolase Chain: A: PDB Molecule: putative esterase; PDBTitle: crystal structure of a putative lipase (np_343859.1) from |

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|----|-------------------------|-----------|--------------|------|----|--|
| | | | | | | sulfolobus2 solfataricus at 1.85 a resolution |
| 56 | c6e7kB_ | Alignment | not modelled | 94.1 | 19 | PDB header: hydrolase Chain: B: PDB Molecule: lipoprotein lipase; PDBTitle: structure of the lipoprotein lipase gp1hbp1 complex that mediates2 plasma triglyceride hydrolysis |
| 57 | c3ds8A_ | Alignment | not modelled | 94.0 | 14 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin2722 protein; PDBTitle: the crysatl structure of the gene lin2722 products from listeria2 innocua |
| 58 | d1rp1a2 | Alignment | not modelled | 94.0 | 16 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain |
| 59 | d1bu8a2 | Alignment | not modelled | 94.0 | 11 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain |
| 60 | d1gpl2 | Alignment | not modelled | 94.0 | 12 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain |
| 61 | d1ispa_ | Alignment | not modelled | 93.9 | 18 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase |
| 62 | c1gplA_ | Alignment | not modelled | 93.5 | 13 | PDB header: serine esterase Chain: A: PDB Molecule: rp2 lipase; PDBTitle: rp2 lipase |
| 63 | d1hpl2 | Alignment | not modelled | 93.5 | 12 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain |
| 64 | c1qgeD_ | Alignment | not modelled | 93.4 | 32 | PDB header: hydrolase Chain: D: PDB Molecule: protein (triacylglycerol hydrolase); PDBTitle: new crystal form of pseudomonas glumae (formerly chromobacterium2 viscosum atcc 6918) lipase |
| 65 | c4f21G_ | Alignment | not modelled | 93.2 | 18 | PDB header: hydrolase/hydrolase inhibitor Chain: G: PDB Molecule: carboxylesterase/phospholipase family protein; PDBTitle: crystal structure of carboxylesterase/phospholipase family protein2 from francisella tularensis |
| 66 | c3h2iA_ | Alignment | not modelled | 93.2 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of n228w mutant of the rice cell wall2 degrading esterase lipa from xanthomonas oryzae |
| 67 | c1hplB_ | Alignment | not modelled | 92.9 | 13 | PDB header: hydrolase(carboxylic esterase) Chain: B: PDB Molecule: lipase; PDBTitle: horse pancreatic lipase. the crystal structure at 2.3 angstroms2 resolution |
| 68 | c2pvsB_ | Alignment | not modelled | 92.8 | 10 | PDB header: hydrolase Chain: B: PDB Molecule: pancreatic lipase-related protein 2; PDBTitle: structure of human pancreatic lipase related protein 22 mutant n336q |
| 69 | d1hlga_ | Alignment | not modelled | 92.5 | 16 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Gastric lipase |
| 70 | c2pplA_ | Alignment | not modelled | 92.3 | 20 | PDB header: hydrolase Chain: A: PDB Molecule: pancreatic lipase-related protein 1; PDBTitle: human pancreatic lipase-related protein 1 |
| 71 | d1jmkc_ | Alignment | not modelled | 92.0 | 23 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases |
| 72 | c2h1iA_ | Alignment | not modelled | 91.9 | 23 | PDB header: hydrolase Chain: A: PDB Molecule: carboxylesterase; PDBTitle: crystal structure of the bacillus cereus carboxylesterase |
| 73 | c2yijA_ | Alignment | not modelled | 91.6 | 14 | PDB header: hydrolase Chain: A: PDB Molecule: phospholipase a1-iigamma; PDBTitle: crystal structure of phospholipase a1 |
| 74 | c4nfuB_ | Alignment | not modelled | 91.6 | 16 | PDB header: signaling protein Chain: B: PDB Molecule: senescence-associated carboxylesterase 101; PDBTitle: structure of the central plant immunity signaling node eds1 in complex2 with its interaction partner sag101 |
| 75 | c4h0cA_ | Alignment | not modelled | 91.6 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: phospholipase/carboxylesterase; PDBTitle: crystal structure of phospholipase/carboxylesterase from dyadobacter2 fermentans dsm 18053 |
| 76 | c2cbgA_ | Alignment | not modelled | 91.4 | 26 | PDB header: hydrolase Chain: A: PDB Molecule: fengycin synthetase; PDBTitle: crystal structure of the pmsf-inhibited thioesterase domain of the2 fengycin biosynthesis cluster |
| 77 | c3l80A_ | Alignment | not modelled | 91.3 | 14 | PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein smu.1393c; PDBTitle: crystal structure of smu.1393c from streptococcus mutans ua159 |
| 78 | c2qjwA_ | Alignment | not modelled | 91.3 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein xcc1541; PDBTitle: crystal structure of a putative hydrolase of the alpha/beta2 superfamily (xcc1541) from xanthomonas campestris pv. campestris at3 1.35 a resolution |
| 79 | d1k8qa_ | Alignment | not modelled | 91.1 | 18 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Gastric lipase |
| 80 | c3h04A_ | Alignment | not modelled | 90.6 | 11 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of the protein with unknown function from2 staphylococcus aureus subsp. aureus mu50 |
| | | | | | | PDB header: structural genomics, unknown function |

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|-----|-------------------------|-----------|--------------|------|----|--|
| 81 | c3fleB_ | Alignment | not modelled | 90.4 | 7 | Chain: B: PDB Molecule: se_1780 protein; PDBTitle: se_1780 protein of unknown function from staphylococcus epidermidis. |
| 82 | c2vavL_ | Alignment | not modelled | 90.4 | 21 | PDB header: transferase Chain: L: PDB Molecule: acetyl-coa--deacetylcephalosporin c acetyltransferase; PDBTitle: crystal structure of deacetylcephalosporin c acetyltransferase (dac-2 soak) |
| 83 | c1rp1A_ | Alignment | not modelled | 89.9 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: pancreatic lipase related protein 1; PDBTitle: dog pancreatic lipase related protein 1 |
| 84 | c4zxiA_ | Alignment | not modelled | 88.9 | 24 | PDB header: biosynthetic protein Chain: A: PDB Molecule: tyrocidine synthetase 3; PDBTitle: crystal structure of holo-ab3403 a four domain nonribosomal peptide2 synthetase bound to amp and glycine |
| 85 | c3lcrA_ | Alignment | not modelled | 87.9 | 23 | PDB header: hydrolase Chain: A: PDB Molecule: tautomycetin biosynthetic pks; PDBTitle: thioesterase from tautomycetin biosynthetic pathway |
| 86 | c2oryA_ | Alignment | not modelled | 87.9 | 10 | PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: crystal structure of m37 lipase |
| 87 | c4nfuA_ | Alignment | not modelled | 87.7 | 17 | PDB header: signaling protein Chain: A: PDB Molecule: eds1; PDBTitle: structure of the central plant immunity signaling node eds1 in complex2 with its interaction partner sag101 |
| 88 | c2vsqA_ | Alignment | not modelled | 87.6 | 18 | PDB header: ligase Chain: A: PDB Molecule: surfactin synthetase subunit 3; PDBTitle: structure of surfactin a synthetase c (srfa-c), a nonribosomal peptide2 synthetase termination module |
| 89 | c4fleA_ | Alignment | not modelled | 85.8 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of the esterase yqia (ye3661) from yersinia2 enterocolitica, northeast structural genomics consortium target yer85 |
| 90 | c3bdvB_ | Alignment | not modelled | 85.2 | 19 | PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein duf1234; PDBTitle: crystal structure of a putative yden-like hydrolase (eca3091) from2 pectobacterium atrosepticum scri1043 at 1.66 a resolution |
| 91 | c3flaB_ | Alignment | not modelled | 85.0 | 21 | PDB header: hydrolase Chain: B: PDB Molecule: rifr; PDBTitle: rifr - type ii thioesterase from rifamycin nrps/pks biosynthetic2 pathway - form 1 |
| 92 | c5ugzA_ | Alignment | not modelled | 84.5 | 13 | PDB header: hydrolase Chain: A: PDB Molecule: putative thioesterase; PDBTitle: crystal structure of clbq from the colibactin nrps/pks pathway |
| 93 | c6gupB_ | Alignment | not modelled | 84.5 | 13 | PDB header: hydrolase Chain: B: PDB Molecule: siderophore biosynthesis lipase/esterase, putative; PDBTitle: siderophore hydrolase estb from aspergillus fumigatus |
| 94 | c4c87A_ | Alignment | not modelled | 84.0 | 25 | PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: esterase lpest1 from lactobacillus plantarum wcfs1 |
| 95 | c4xjvA_ | Alignment | not modelled | 82.2 | 22 | PDB header: hydrolase Chain: A: PDB Molecule: s-acyl fatty acid synthase thioesterase, medium chain; PDBTitle: crystal structure of human thioesterase 2 |
| 96 | c3visB_ | Alignment | not modelled | 82.1 | 10 | PDB header: hydrolase Chain: B: PDB Molecule: esterase; PDBTitle: crystal structure of cutinase est119 from thermobifida alba ahk119 |
| 97 | c3qmwD_ | Alignment | not modelled | 82.0 | 18 | PDB header: hydrolase Chain: D: PDB Molecule: thioesterase; PDBTitle: redj with peg molecule bound in the active site |
| 98 | c1pjaA_ | Alignment | not modelled | 81.3 | 14 | PDB header: hydrolase Chain: A: PDB Molecule: palmitoyl-protein thioesterase 2 precursor; PDBTitle: the crystal structure of palmitoyl protein thioesterase-2 reveals the2 basis for divergent substrate specificities of the two lysosomal3 thioesterases (ppt1 and ppt2) |
| 99 | d1pjaa_ | Alignment | not modelled | 81.3 | 14 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterases |
| 100 | c3mveB_ | Alignment | not modelled | 81.2 | 15 | PDB header: lyase Chain: B: PDB Molecule: upf0255 protein vv1_0328; PDBTitle: crystal structure of a novel pyruvate decarboxylase |
| 101 | c2zshA_ | Alignment | not modelled | 81.0 | 18 | PDB header: hormone receptor Chain: A: PDB Molecule: probable gibberellin receptor gid111; PDBTitle: structural basis of gibberellin(ga3)-induced della2 recognition by the gibberellin receptor |
| 102 | c5x6sB_ | Alignment | not modelled | 80.6 | 11 | PDB header: hydrolase Chain: B: PDB Molecule: acetylxylan esterase a; PDBTitle: acetyl xylan esterase from aspergillus awamori |
| 103 | c2y6vB_ | Alignment | not modelled | 80.1 | 19 | PDB header: hydrolase Chain: B: PDB Molecule: peroxisomal membrane protein lpx1; PDBTitle: peroxisomal alpha-beta-hydrolase lpx1 (yor084w) from saccharomyces2 cerevisiae (crystal form i) |
| 104 | c2jwbB_ | Alignment | not modelled | 80.0 | 10 | PDB header: hydrolase Chain: B: PDB Molecule: 2,6-dihydroxy-pseudo-oxynicotine hydrolase; PDBTitle: crystal structure of the 2,6-dihydroxy-pseudo-oxynicotine hydrolase. |
| 105 | c3qvmA_ | Alignment | not modelled | 77.3 | 13 | PDB header: hydrolase Chain: A: PDB Molecule: olei00960; PDBTitle: the structure of olei00960, a hydrolase from oleispira antarctica |
| | | | | | | PDB header: transferase |

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|-----|-------------------------|-----------|--------------|------|----|---|
| 106 | c4x91C_ | Alignment | not modelled | 77.1 | 19 | Chain: C; PDB Molecule: group xv phospholipase a2; PDBTitle: crystal structure of lysosomal phospholipase a2 in complex with2 isopropyl dodec-11-enylfluorophosphonate (idfp) |
| 107 | d1vkha_ | Alignment | not modelled | 76.1 | 22 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Putative serine hydrolase Ydr428c |
| 108 | d1uxoa_ | Alignment | not modelled | 74.8 | 12 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: YdeN-like |
| 109 | d2nn6i2 | Alignment | not modelled | 74.2 | 23 | Fold: Barrel-sandwich hybrid Superfamily: Ribosomal L27 protein-like Family: ECR1 N-terminal domain-like |
| 110 | c2o7vA_ | Alignment | not modelled | 73.9 | 10 | PDB header: hydrolase Chain: A; PDB Molecule: cxe carboxylesterase; PDBTitle: carboxylesterase aecxe1 from actinidia eriantha covalently inhibited2 by paraoxon |
| 111 | c3i28A_ | Alignment | not modelled | 72.8 | 25 | PDB header: hydrolase Chain: A; PDB Molecule: epoxide hydrolase 2; PDBTitle: crystal structure of soluble epoxide hydrolase |
| 112 | c4x96B_ | Alignment | not modelled | 72.7 | 16 | PDB header: transferase Chain: B; PDB Molecule: phosphatidylcholine-sterol acyltransferase; PDBTitle: low resolution crystal structure of lecithin:cholesterol2 acyltransferase (lcat; residues 21-397) |
| 113 | c5w8pA_ | Alignment | not modelled | 72.5 | 29 | PDB header: transferase Chain: A; PDB Molecule: homoserine o-acetyltransferase; PDBTitle: homoserine transacetylase meta from mycobacterium abscessus |
| 114 | d1xkta_ | Alignment | not modelled | 70.8 | 30 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases |
| 115 | c3fnbB_ | Alignment | not modelled | 70.6 | 20 | PDB header: hydrolase Chain: B; PDB Molecule: acylaminoacyl peptidase smu_737; PDBTitle: crystal structure of acylaminoacyl peptidase smu_737 from2 streptococcus mutans ua159 |
| 116 | c5ah0B_ | Alignment | not modelled | 70.6 | 11 | PDB header: hydrolase Chain: B; PDB Molecule: lipase; PDBTitle: structure of lipase 1 from pelosinus fermentans |
| 117 | c5hdfB_ | Alignment | not modelled | 70.3 | 15 | PDB header: hydrolase Chain: B; PDB Molecule: hydrolase; PDBTitle: hydrolase semet-stna |
| 118 | c3d0kA_ | Alignment | not modelled | 69.0 | 14 | PDB header: hydrolase Chain: A; PDB Molecule: putative poly(3-hydroxybutyrate) depolymerase lpqc; PDBTitle: crystal structure of the lpqc, poly(3-hydroxybutyrate) depolymerase2 from bordetella parapertussis |
| 119 | c3wydA_ | Alignment | not modelled | 67.9 | 18 | PDB header: hydrolase Chain: A; PDB Molecule: lc-est1c; PDBTitle: c-terminal esterase domain of lc-est1 |
| 120 | d2jbwa1 | Alignment | not modelled | 67.6 | 13 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: 2,6-dihdropseudooxynicotine hydrolase-like |