


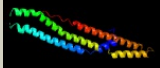

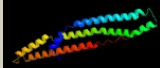

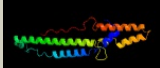











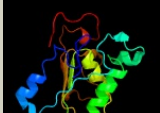




Phyre2

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|---------------|----------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD2608_(PPE42)_2935056_2936798 |
| Date | Wed Aug 7 12:50:25 BST 2019 |
| Unique Job ID | 5c24209d52c6614d |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | c5xfsB_ |  Alignment |  | 100.0 | 55 | PDB header: protein transport Chain: B: PDB Molecule: ppe family protein ppe15; PDBTitle: crystal structure of pe8-ppe15 in complex with esp95 from m.2 tuberculosis |
| 2 | c2g38B_ |  Alignment |  | 100.0 | 35 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: ppe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis |
| 3 | d2g38b1 |  Alignment |  | 100.0 | 35 | Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE |
| 4 | c4xy3A_ |  Alignment |  | 100.0 | 17 | PDB header: protein transport Chain: A: PDB Molecule: esx-1 secretion-associated protein espb; PDBTitle: structure of esx-1 secreted protein espb |
| 5 | c3ajaA_ |  Alignment |  | 99.8 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of msmeg_6394 |
| 6 | d1qoza_ |  Alignment |  | 99.4 | 17 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like |
| 7 | d1g66a_ |  Alignment |  | 99.3 | 16 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like |
| 8 | c3hc7A_ |  Alignment |  | 99.2 | 20 | PDB header: cell adhesion Chain: A: PDB Molecule: gene 12 protein; PDBTitle: crystal structure of lysin b from mycobacteriophage d29 |
| 9 | c2czaB_ |  Alignment |  | 99.0 | 19 | PDB header: hydrolase Chain: B: PDB Molecule: cutinase-like protein; PDBTitle: a novel cutinase-like protein from cryptococcus sp. |
| 10 | c3dd5F_ |  Alignment |  | 98.8 | 13 | PDB header: hydrolase Chain: F: PDB Molecule: cutinase; PDBTitle: glomerella cingulata e600-cutinase complex |
| 11 | d1cexa_ |  Alignment |  | 98.8 | 10 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like |

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|----|-------------------------|-----------|--------------|------|----|--|
| 12 | c5x88A_ | Alignment | | 98.7 | 15 | PDB header: hydrolase Chain: A: PDB Molecule: cutinase; PDBTitle: a crystal structure of cutinases from malbranchea cinnamomea |
| 13 | c3gbsA_ | Alignment | | 98.6 | 8 | PDB header: hydrolase Chain: A: PDB Molecule: cutinase 1; PDBTitle: crystal structure of aspergillus oryzae cutinase |
| 14 | c4oylC_ | Alignment | | 98.4 | 13 | PDB header: hydrolase Chain: C: PDB Molecule: cutinase; PDBTitle: humicola insolens cutinase in complex with monoethylphosphate |
| 15 | c4psdA_ | Alignment | | 98.4 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: carbohydrate esterase family 5; PDBTitle: structure of trichoderma reesei cutinase native form. |
| 16 | c4wj2A_ | Alignment | | 98.2 | 18 | PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein |
| 17 | c2vs0B_ | Alignment | | 97.6 | 11 | PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa |
| 18 | c4iogD_ | Alignment | | 97.4 | 13 | PDB header: unknown function Chain: D: PDB Molecule: secreted protein esxb; PDBTitle: the crystal structure of a secreted protein esxb (wild-type, in p212 space group) from bacillus anthracis str. sterne |
| 19 | c3gvmA_ | Alignment | | 97.3 | 10 | PDB header: viral protein Chain: A: PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae |
| 20 | c3zbcC_ | Alignment | | 97.2 | 15 | PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i |
| 21 | d1wa8a1 | Alignment | not modelled | 96.8 | 16 | Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like |
| 22 | c4lwsA_ | Alignment | not modelled | 95.2 | 16 | PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata |
| 23 | c4lwsB_ | Alignment | not modelled | 95.0 | 16 | PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata |
| 24 | c5xavB_ | Alignment | not modelled | 94.8 | 15 | PDB header: biosynthetic protein Chain: B: PDB Molecule: intracellular polyhydroxyalkanoate synthase; PDBTitle: structure of phac from chromobacterium sp. usm2 |
| 25 | d1wa8b1 | Alignment | not modelled | 94.5 | 24 | Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like |
| 26 | c5t6oA_ | Alignment | not modelled | 94.2 | 18 | 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 |
| 27 | d1ei9a_ | Alignment | not modelled | 93.4 | 15 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterases |
| 28 | d1tcaa_ | Alignment | not modelled | 93.3 | 17 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases |
| | | | | | | Fold: alpha/beta-Hydrolases |

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|----|-------------------------|-----------|--------------|------|----|--|
| 29 | d1jmkc_ | Alignment | not modelled | 93.1 | 11 | Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases |
| 30 | c4i0xA_ | Alignment | not modelled | 92.6 | 19 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: esat-6-like protein mab_3112; PDBTitle: crystal structure of the mycobacterium abscessus esxf (mab_3112-2 mab_3113) complex |
| 31 | c3ds8A_ | Alignment | not modelled | 89.5 | 14 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin2722 protein; PDBTitle: the crystal structure of the gene lin2722 products from listeria2 innocua |
| 32 | c2kg7B_ | Alignment | not modelled | 87.9 | 16 | PDB header: unknown function Chain: B: PDB Molecule: esat-6-like protein esxh; PDBTitle: structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288 |
| 33 | c3icvA_ | Alignment | not modelled | 85.5 | 15 | PDB header: hydrolase Chain: A: PDB Molecule: lipase b; PDBTitle: structural consequences of a circular permutation on lipase b from2 candida antarctica |
| 34 | c4nfuB_ | Alignment | not modelled | 85.2 | 19 | 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 |
| 35 | c1mo2A_ | Alignment | not modelled | 84.5 | 19 | 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 |
| 36 | d1mo2a_ | Alignment | not modelled | 84.5 | 19 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases |
| 37 | d3b5ea1 | Alignment | not modelled | 83.7 | 11 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1 |
| 38 | c4qnnC_ | Alignment | not modelled | 83.4 | 18 | 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 |
| 39 | c3og9A_ | Alignment | not modelled | 81.8 | 11 | PDB header: hydrolase Chain: A: PDB Molecule: protein yahd a copper inducible hydrolase; PDBTitle: structure of yahd with malic acid |
| 40 | d1ispa_ | Alignment | not modelled | 81.4 | 13 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase |
| 41 | c2zyiB_ | Alignment | not modelled | 81.0 | 12 | PDB header: hydrolase Chain: B: PDB Molecule: lipase, putative; PDBTitle: a. fulgidus lipase with fatty acid fragment and calcium |
| 42 | d2h7xa1 | Alignment | not modelled | 81.0 | 17 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases |
| 43 | c4h0cA_ | Alignment | not modelled | 80.8 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: phospholipase/carboxylesterase; PDBTitle: crystal structure of phospholipase/carboxylesterase from dyadobacter2 fermentans dsm 18053 |
| 44 | c2vsqA_ | Alignment | not modelled | 79.3 | 16 | 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 |
| 45 | c3lp5A_ | Alignment | not modelled | 79.2 | 17 | 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 |
| 46 | c2cbgA_ | Alignment | not modelled | 79.0 | 20 | PDB header: hydrolase Chain: A: PDB Molecule: fengycin synthetase; PDBTitle: crystal structure of the pmsf-inhibited thioesterase domain of the2 fengycin biosynthesis cluster |
| 47 | d2h1ia1 | Alignment | not modelled | 78.2 | 20 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1 |
| 48 | c2oryA_ | Alignment | not modelled | 78.2 | 10 | PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: crystal structure of m37 lipase |
| 49 | c3lcrA_ | Alignment | not modelled | 76.4 | 20 | PDB header: hydrolase Chain: A: PDB Molecule: tautomycetin biosynthetic pks; PDBTitle: thioesterase from tautomycetin biosynthetic pathway |
| 50 | c6e6uA_ | Alignment | not modelled | 74.6 | 19 | PDB header: biosynthetic protein Chain: A: PDB Molecule: dieckmann cyclase, ncmc; PDBTitle: variant c89s of dieckmann cyclase, ncmc |
| 51 | c5d8mA_ | Alignment | not modelled | 73.2 | 10 | PDB header: hydrolase Chain: A: PDB Molecule: metagenomic carboxyl esterase mgs0156; PDBTitle: crystal structure of the metagenomic carboxyl esterase mgs0156 |
| 52 | c4f21G_ | Alignment | not modelled | 70.5 | 28 | PDB header: hydrolase/hydrolase inhibitor Chain: G: PDB Molecule: carboxylesterase/phospholipase family protein; PDBTitle: crystal structure of carboxylesterase/phospholipase family protein2 from francisella tularensis |
| 53 | c5f2hA_ | Alignment | not modelled | 69.7 | 16 | 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 |
| 54 | c2vtvA_ | Alignment | not modelled | 69.1 | 15 | PDB header: hydrolase Chain: A: PDB Molecule: phb depolymerase phaz7; PDBTitle: phaz7 depolymerase from paucimonas lemoignei |

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|----|-------------------------|-----------|--------------|------|----|--|
| 55 | d2r8ba1 | Alignment | not modelled | 69.1 | 12 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1 |
| 56 | c6cl4A | Alignment | not modelled | 67.1 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: lipase c12; PDBTitle: lipc12 - lipase from metagenomics |
| 57 | c4x96B | Alignment | not modelled | 65.2 | 16 | PDB header: transferase Chain: B: PDB Molecule: phosphatidylcholine-sterol acyltransferase; PDBTitle: low resolution crystal structure of lecithin:cholesterol2 acyltransferase (lcat; residues 21-397) |
| 58 | c2h7xA | Alignment | not modelled | 63.1 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: type i polyketide synthase pikaiv; PDBTitle: pikromycin thioesterase adduct with reduced triketide2 affinity label |
| 59 | c4x91C | Alignment | not modelled | 62.4 | 16 | PDB header: transferase Chain: C: PDB Molecule: group xv phospholipase a2; PDBTitle: crystal structure of lysosomal phospholipase a2 in complex with2 isopropyl dodec-11-enylfluorophosphonate (idfp) |
| 60 | c4eziA | Alignment | not modelled | 61.7 | 11 | 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 |
| 61 | c2q0xA | Alignment | not modelled | 61.7 | 18 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: alpha/beta hydrolase fold protein of unknown function |
| 62 | c3p3dA | Alignment | not modelled | 58.5 | 26 | PDB header: nuclear protein Chain: A: PDB Molecule: nucleoporin 53; PDBTitle: crystal structure of the nup53 rrm domain from pichia guilliermondii |
| 63 | d1pbb2 | Alignment | not modelled | 57.7 | 21 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain |
| 64 | c3h2iA | Alignment | not modelled | 57.5 | 20 | 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 |
| 65 | c4xjvA | Alignment | not modelled | 56.1 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: s-acyl fatty acid synthase thioesterase, medium chain; PDBTitle: crystal structure of human thioesterase 2 |
| 66 | c2veoA | Alignment | not modelled | 55.7 | 22 | PDB header: hydrolase Chain: A: PDB Molecule: lipase a; PDBTitle: x-ray structure of candida antarctica lipase a in its closed state. |
| 67 | d1bu8a2 | Alignment | not modelled | 55.7 | 20 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain |
| 68 | d1hpla2 | Alignment | not modelled | 54.8 | 16 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain |
| 69 | c2rauA | Alignment | not modelled | 54.5 | 8 | PDB header: hydrolase Chain: A: PDB Molecule: putative esterase; PDBTitle: crystal structure of a putative lipase (np_343859.1) from sulfolobus2 solfataricus at 1.85 a resolution |
| 70 | c2r8bA | Alignment | not modelled | 53.4 | 12 | 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 |
| 71 | c2vijA | Alignment | not modelled | 53.2 | 12 | PDB header: hydrolase Chain: A: PDB Molecule: phospholipase a1-igamma; PDBTitle: crystal structure of phospholipase a1 |
| 72 | d1etha2 | Alignment | not modelled | 52.7 | 19 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain |
| 73 | d1gpla2 | Alignment | not modelled | 52.6 | 26 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain |
| 74 | c3bdvB | Alignment | not modelled | 52.6 | 15 | 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 |
| 75 | c5uazB | Alignment | not modelled | 52.4 | 17 | PDB header: protein transport Chain: B: PDB Molecule: nucleoporin nup53; PDBTitle: crystal structure of the yeast nucleoporin |
| 76 | c4fleA | Alignment | not modelled | 51.0 | 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 |
| 77 | c2qjwA | Alignment | not modelled | 49.9 | 23 | 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 |
| 78 | c3fleB | Alignment | not modelled | 49.8 | 12 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: se_1780 protein; PDBTitle: se_1780 protein of unknown function from staphylococcus epidermidis. |
| 79 | d1xkta | Alignment | not modelled | 49.3 | 16 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases |
| 80 | c4r1dA | Alianment | not modelled | 46.8 | 20 | PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: uncharacterized protein; |

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|-----|-------------------------|-----------|--------------|------|----|--|
| | | | | | | PDBTitle: the crystal structure of tle4-tli4 complex |
| 81 | c2h1iA_ | Alignment | not modelled | 46.6 | 20 | PDB header: hydrolase Chain: A; PDB Molecule: carboxylesterase; PDBTitle: crystal structure of the bacillus cereus carboxylesterase |
| 82 | d3tqla_ | Alignment | not modelled | 45.9 | 17 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases |
| 83 | c5d6oB_ | Alignment | not modelled | 43.4 | 12 | PDB header: transferase Chain: B; PDB Molecule: homoserine o-acetyltransferase; PDBTitle: orthorhombic crystal structure of an acetylester hydrolase from2 corynebacterium glutamicum |
| 84 | c4nfaA_ | Alignment | not modelled | 42.3 | 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 |
| 85 | c1pjaA_ | Alignment | not modelled | 41.7 | 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) |
| 86 | d1pjaa_ | Alignment | not modelled | 41.7 | 14 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterases |
| 87 | c6qppA_ | Alignment | not modelled | 40.6 | 18 | PDB header: hydrolase Chain: A; PDB Molecule: lipase; PDBTitle: rhizomucor miehei lipase propeptide complex, native |
| 88 | c4zxiA_ | Alignment | not modelled | 40.3 | 13 | 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 |
| 89 | c2qs9A_ | Alignment | not modelled | 40.3 | 14 | PDB header: structural protein Chain: A; PDB Molecule: retinoblastoma-binding protein 9; PDBTitle: crystal structure of the human retinoblastoma-binding2 protein 9 (rbbp-9). nesg target hr2978 |
| 90 | c2m4mA_ | Alignment | not modelled | 39.9 | 30 | PDB header: unknown function Chain: A; PDB Molecule: hypothetical protein; PDBTitle: solution structure of the rrm domain of the hypothetical protein2 cagl0m09691g from candida glabrata |
| 91 | c6n8eA_ | Alignment | not modelled | 39.9 | 20 | PDB header: hydrolase Chain: A; PDB Molecule: holo-obif1; PDBTitle: crystal structure of holo-obif1, a five domain nonribosomal peptide2 synthetase from burkholderia diffusa |
| 92 | d1rpl2_ | Alignment | not modelled | 39.8 | 19 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain |
| 93 | c2pvsB_ | Alignment | not modelled | 39.3 | 21 | PDB header: hydrolase Chain: B; PDB Molecule: pancreatic lipase-related protein 2; PDBTitle: structure of human pancreatic lipase related protein 22 mutant n336q |
| 94 | d1ex9a_ | Alignment | not modelled | 38.1 | 21 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase |
| 95 | c5h3bA_ | Alignment | not modelled | 37.5 | 9 | PDB header: hydrolase Chain: A; PDB Molecule: uncharacterized protein hi_1552; PDBTitle: crystal structure of semet-biog from haemophilus influenzae at 1.492 angstroms resolution |
| 96 | c5h6bA_ | Alignment | not modelled | 37.2 | 14 | PDB header: hydrolase Chain: A; PDB Molecule: putative secreted lipase; PDBTitle: crystal structure of a thermostable lipase from marine streptomyces |
| 97 | c3g7nA_ | Alignment | not modelled | 35.4 | 11 | PDB header: hydrolase Chain: A; PDB Molecule: lipase; PDBTitle: crystal structure of a triacylglycerol lipase from penicillium2 expansum at 1.3 |
| 98 | c3flaB_ | Alignment | not modelled | 34.7 | 15 | PDB header: hydrolase Chain: B; PDB Molecule: rifr; PDBTitle: rifr - type ii thioesterase from rifamycin nrps/pks biosynthetic2 pathway - form 1 |
| 99 | c4i0xl_ | Alignment | not modelled | 34.2 | 21 | PDB header: structural genomics, unknown function Chain: J; PDB Molecule: esat-6-like protein mab_3113; PDBTitle: crystal structure of the mycobacterium abscessus esxf (mab_3112-2 mab_3113) complex |
| 100 | d1uwca_ | Alignment | not modelled | 34.2 | 18 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases |
| 101 | d1uxoa_ | Alignment | not modelled | 33.7 | 10 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: YdeN-like |
| 102 | c4gw3A_ | Alignment | not modelled | 33.6 | 19 | PDB header: hydrolase Chain: A; PDB Molecule: putative lipase; PDBTitle: crystal structure of the lipase from proteus mirabilis |
| 103 | c3qmwD_ | Alignment | not modelled | 32.9 | 14 | PDB header: hydrolase Chain: D; PDB Molecule: thioesterase; PDBTitle: redj with peg molecule bound in the active site |
| 104 | d1tiaa_ | Alignment | not modelled | 32.7 | 18 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases |
| 105 | c1qgeD_ | Alignment | not modelled | 31.6 | 22 | PDB header: hydrolase Chain: D; PDB Molecule: protein (triacylglycerol hydrolase); PDBTitle: new crystal form of pseudomonas glumae (formerly chromobacterium2 viscosum atcc 6918) lipase |
| 106 | c5xk2A_ | Alignment | not modelled | 30.4 | 14 | PDB header: hydrolase Chain: A; PDB Molecule: diacylglycerol lipase; PDBTitle: crystal structure of mono- and diacylglycerol lipase from aspergillus2 oryzae |

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|-----|-------------------------|-----------|--------------|------|----|---|
| 107 | c5gw8A_ | Alignment | not modelled | 30.4 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: hypothetical secretory lipase (family 3); PDBTitle: crystal structure of a putative dag-like lipase (mgmdl2) from <i>malassezia globosa</i> |
| 108 | c3fqnB_ | Alignment | not modelled | 29.4 | 30 | PDB header: dna binding protein Chain: B: PDB Molecule: geobacillus stearothermophilus uvrb interaction domain; PDBTitle: crystal structure of uvra-uvrb interaction domains |
| 109 | d1lgya_ | Alignment | not modelled | 29.1 | 21 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases |
| 110 | c4b6gA_ | Alignment | not modelled | 29.0 | 14 | PDB header: hydrolase Chain: A: PDB Molecule: putative esterase; PDBTitle: the crystal structure of the neisserial esterase d. |
| 111 | c2ronA_ | Alignment | not modelled | 29.0 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: surfactin synthetase thioesterase subunit; PDBTitle: the external thioesterase of the surfactin-synthetase |
| 112 | c1hplB_ | Alignment | not modelled | 28.6 | 18 | PDB header: hydrolase(carboxylic esterase) Chain: B: PDB Molecule: lipase; PDBTitle: horse pancreatic lipase. the crystal structure at 2.3 angstroms2 resolution |
| 113 | c3uuuA_ | Alignment | not modelled | 28.4 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: lip1, secretory lipase (family 3); PDBTitle: crystal structure of mono- and diacylglycerol lipase from <i>malassezia2 globosa</i> |
| 114 | d1tiba_ | Alignment | not modelled | 27.9 | 17 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases |
| 115 | c2w6cX_ | Alignment | not modelled | 27.9 | 19 | PDB header: hydrolase Chain: X: PDB Molecule: acetylcholinesterase; PDBTitle: ache in complex with a bis-(-)-nor-meptazinol derivative |
| 116 | c2hihB_ | Alignment | not modelled | 26.3 | 17 | PDB header: hydrolase Chain: B: PDB Molecule: lipase 46 kda form; PDBTitle: crystal structure of staphylococcus hyicus lipase |
| 117 | c2pplA_ | Alignment | not modelled | 25.4 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: pancreatic lipase-related protein 1; PDBTitle: human pancreatic lipase-related protein 1 |
| 118 | d1k8qa_ | Alignment | not modelled | 25.1 | 15 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Gastric lipase |
| 119 | c6e7kB_ | Alignment | not modelled | 24.9 | 18 | PDB header: hydrolase Chain: B: PDB Molecule: lipoprotein lipase; PDBTitle: structure of the lipoprotein lipase gp1hbp1 complex that mediates2 plasma triglyceride hydrolysis |
| 120 | d1fyea_ | Alignment | not modelled | 24.7 | 22 | Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Aspartyl dipeptidase PepE |