

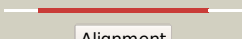

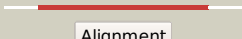

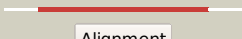

















Phyre2

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|---------------|---------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD3084_(lipR)_3449994_3450920 |
| Date | Thu Aug 8 16:20:26 BST 2019 |
| Unique Job ID | d75760277fc36796 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|--|---|------------|--------|---|
| 1 | c4xvcG_ |  Alignment |  | 100.0 | 31 | PDB header: hydrolase Chain: G; PDB Molecule: esterase e40; PDBTitle: crystal structure of an esterase from the bacterial hormone-sensitive2 lipase (hsl) family |
| 2 | c2zshA_ |  Alignment |  | 100.0 | 17 | 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 |
| 3 | c3dnmA_ |  Alignment |  | 100.0 | 28 | PDB header: hydrolase Chain: A; PDB Molecule: esterase/lipase; PDBTitle: crystal structure hormone-sensitive lipase from a2 metagenome library |
| 4 | c3d7rB_ |  Alignment |  | 100.0 | 22 | PDB header: hydrolase Chain: B; PDB Molecule: esterase; PDBTitle: crystal structure of a putative esterase from staphylococcus aureus |
| 5 | c3fakA_ |  Alignment |  | 100.0 | 29 | PDB header: hydrolase Chain: A; PDB Molecule: esterase/lipase; PDBTitle: structural and functional analysis of a hormone-sensitive2 lipase like este5 from a metagenome library |
| 6 | c4c87A_ |  Alignment |  | 100.0 | 23 | PDB header: hydrolase Chain: A; PDB Molecule: esterase; PDBTitle: esterase lpest1 from lactobacillus plantarum wcfs1 |
| 7 | c3ed1E_ |  Alignment |  | 100.0 | 17 | PDB header: hydrolase receptor Chain: E; PDB Molecule: gibberellin receptor gid1; PDBTitle: crystal structure of rice gid1 complexed with ga3 |
| 8 | c3ga7A_ |  Alignment |  | 100.0 | 19 | PDB header: hydrolase Chain: A; PDB Molecule: acetyl esterase; PDBTitle: 1.55 angstrom crystal structure of an acetyl esterase from salmonella2 typhimurium |
| 9 | c4krxB_ |  Alignment |  | 100.0 | 24 | PDB header: hydrolase Chain: B; PDB Molecule: acetyl esterase; PDBTitle: structure of aes from e. coli |
| 10 | c4q05A_ |  Alignment |  | 100.0 | 26 | PDB header: hydrolase Chain: A; PDB Molecule: esterase e25; PDBTitle: crystal structure of an esterase e25 |
| 11 | c5jd5A_ |  Alignment |  | 100.0 | 21 | PDB header: hydrolase Chain: A; PDB Molecule: mgs-mile3; PDBTitle: crystal structure of mgs-mile3, an alpha/beta hydrolase enzyme from2 the metagenome of pyrene-phenanthrene enrichment culture with3 sediment sample of milazzo harbor, italy |

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|----|-------------------------|-----------|--------------|-------|----|--|
| 12 | c5jd4D_ | Alignment | | 100.0 | 22 | PDB header: hydrolase Chain: D: PDB Molecule: lae6; PDBTitle: crystal structure of lae6 ser161ala mutant, an alpha/beta hydrolase2 enzyme from the metagenome of lake arreo, spain |
| 13 | d1lza_ | Alignment | | 100.0 | 22 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase |
| 14 | c4q3oB_ | Alignment | | 100.0 | 25 | PDB header: hydrolase Chain: B: PDB Molecule: mgs-mt1; PDBTitle: crystal structure of mgs-mt1, an alpha/beta hydrolase enzyme from a2 lake matapan deep-sea metagenome library |
| 15 | c4v2iB_ | Alignment | | 100.0 | 25 | PDB header: hydrolase Chain: B: PDB Molecule: esterase/lipase; PDBTitle: biochemical characterization and structural analysis of a2 new cold-active and salt tolerant esterase from the marine3 bacterium thalassospira sp |
| 16 | c4ob7A_ | Alignment | | 100.0 | 23 | PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase fold-3 domain protein; PDBTitle: crystal structure of esterase rppe mutant w187h |
| 17 | c5miiD_ | Alignment | | 100.0 | 22 | PDB header: hydrolase Chain: D: PDB Molecule: carboxyl esterase 2; PDBTitle: crystal structure of carboxyl esterase 2 (tmelest2) from mycorrhizal2 fungus tuber melanosporum |
| 18 | c3wj2A_ | Alignment | | 100.0 | 20 | PDB header: hydrolase Chain: A: PDB Molecule: carboxylesterase; PDBTitle: crystal structure of estfa (fe-lacking apo form) |
| 19 | c4ypvA_ | Alignment | | 100.0 | 24 | PDB header: hydrolase Chain: A: PDB Molecule: est8; PDBTitle: high-resolution structure of a metagenome-derived esterase est8 |
| 20 | c2wirB_ | Alignment | | 100.0 | 24 | PDB header: hydrolase Chain: B: PDB Molecule: alpha/beta hydrolase fold-3 domain protein; PDBTitle: hyperthermophilic esterase from the archeon pyrobaculum2 calidifontis |
| 21 | c5hc4A_ | Alignment | not modelled | 100.0 | 22 | PDB header: hydrolase Chain: A: PDB Molecule: lipolytic enzyme; PDBTitle: structure of esterase est22 |
| 22 | c6aaeA_ | Alignment | not modelled | 100.0 | 21 | PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of chloramphenicol-metabolizaing enzyme estdl136 |
| 23 | c4j7aB_ | Alignment | not modelled | 100.0 | 21 | PDB header: hydrolase Chain: B: PDB Molecule: esterase; PDBTitle: crystal structure of est25 - a bacterial homolog of hormone-sensitive2 lipase from a metagenomic library |
| 24 | d1jia_ | Alignment | not modelled | 100.0 | 24 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase |
| 25 | c2c7bA_ | Alignment | not modelled | 100.0 | 24 | PDB header: hydrolase Chain: A: PDB Molecule: carboxylesterase; PDBTitle: the crystal structure of este1, a new thermophilic and2 thermostable carboxylesterase cloned from a metagenomic3 library |
| 26 | c4wy8A_ | Alignment | not modelled | 100.0 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: structural analysis of two fungal esterases from rhizomucor miehei2 explaining their substrate specificity |
| 27 | d1u4na_ | Alignment | not modelled | 100.0 | 22 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase |
| 28 | c2o7vA_ | Alignment | not modelled | 100.0 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: cxe carboxylesterase; PDBTitle: carboxylesterase aecxe1 from actinidia eriantha covalently inhibited2 by paraoxon PDB header: hydrolase |

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|----|-------------------------|-----------|--------------|-------|----|--|
| 29 | c3qh4A | Alignment | not modelled | 100.0 | 21 | Chain: A: PDB Molecule: esterase lipw; PDBTitle: crystal structure of esterase lipw from mycobacterium marinum |
| 30 | c3aikB | Alignment | not modelled | 100.0 | 20 | PDB header: hydrolase Chain: B: PDB Molecule: 303aa long hypothetical esterase; PDBTitle: crystal structure of a hsl-like carboxylesterase from sulfobolus2 tokodaii |
| 31 | c4wy5A | Alignment | not modelled | 100.0 | 20 | PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: structural analysis of two fungal esterases from rhizomucor miehei2 explaining their substrate specificity |
| 32 | c5l2pD | Alignment | not modelled | 100.0 | 19 | PDB header: hydrolase Chain: D: PDB Molecule: arylesterase; PDBTitle: structure of arylesterase |
| 33 | d1jkma | Alignment | not modelled | 100.0 | 19 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase |
| 34 | c5oljA | Alignment | not modelled | 100.0 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl peptidase iv; PDBTitle: crystal structure of porphyromonas gingivalis dipeptidyl peptidase 4 |
| 35 | c2ecfA | Alignment | not modelled | 100.0 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl peptidase iv; PDBTitle: crystal structure of dipeptidyl aminopeptidase iv from2 stentrophomonas maltophilia |
| 36 | c4zrsA | Alignment | not modelled | 100.0 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of a cloned feruloyl esterase from a soil2 metagenomic library |
| 37 | c3azqA | Alignment | not modelled | 100.0 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase; PDBTitle: crystal structure of puromycin hydrolase s511a mutant complexed with2 pgg |
| 38 | c4n5iX | Alignment | not modelled | 100.0 | 20 | PDB header: hydrolase Chain: X: PDB Molecule: esterase/lipase; PDBTitle: crystal structure of a c8-c4 sn3 inhibited esterase b from2 lactobacillus rhamnosis |
| 39 | c5l8sD | Alignment | not modelled | 100.0 | 18 | PDB header: hydrolase Chain: D: PDB Molecule: amino acyl peptidase; PDBTitle: the crystal structure of a cold-adapted acylaminoacyl peptidase2 reveals a novel quaternary architecture based on the arm-exchange3 mechanism |
| 40 | c4hxgl | Alignment | not modelled | 100.0 | 11 | PDB header: hydrolase Chain: J: PDB Molecule: putative uncharacterized protein ph0594; PDBTitle: pyrococcus horikoshii acylaminoacyl peptidase (orthorhombic crystal2 form) |
| 41 | c1z68A | Alignment | not modelled | 100.0 | 13 | PDB header: lyase Chain: A: PDB Molecule: fibroblast activation protein, alpha subunit; PDBTitle: crystal structure of human fibroblast activation protein alpha |
| 42 | c5yznA | Alignment | not modelled | 100.0 | 15 | PDB header: hydrolase Chain: A: PDB Molecule: acyl-peptide hydrolase, putative; PDBTitle: crystal structure of s9 peptidase (active form) from deinococcus2 radiodurans r1 |
| 43 | c2qtbB | Alignment | not modelled | 100.0 | 13 | PDB header: hydrolase Chain: B: PDB Molecule: dipeptidyl peptidase 4; PDBTitle: human dipeptidyl peptidase iv/cd26 in complex with a 4-aryl2 cyclohexylalanine inhibitor |
| 44 | c2q5tA | Alignment | not modelled | 100.0 | 13 | PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl peptidase 4; PDBTitle: crystal structure of human dipeptidyl peptidase iv (dppiv) complexed2 with cyanopyrrolidine (c5-pro-pro) inhibitor 21ag |
| 45 | c2hu7A | Alignment | not modelled | 100.0 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: acylamino-acid-releasing enzyme; PDBTitle: binding of inhibitors by acylaminoacyl peptidase |
| 46 | c2eepA | Alignment | not modelled | 100.0 | 13 | PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl aminopeptidase iv, putative; PDBTitle: prolyl tripeptidyl aminopeptidase complexed with an inhibitor |
| 47 | c3bxpA | Alignment | not modelled | 100.0 | 15 | PDB header: hydrolase Chain: A: PDB Molecule: putative lipase/esterase; PDBTitle: crystal structure of a putative carboxylesterase (lp_2923) from2 lactobacillus plantarum wcfs1 at 1.70 a resolution |
| 48 | c4wjilB | Alignment | not modelled | 100.0 | 11 | PDB header: membrane protein Chain: B: PDB Molecule: inactive dipeptidyl peptidase 10; PDBTitle: structure of human dipeptidyl peptidase 10 (dppy): a modulator of2 neuronal kv4 channels |
| 49 | c6eoqC | Alignment | not modelled | 100.0 | 15 | PDB header: hydrolase Chain: C: PDB Molecule: dipeptidyl peptidase 9; PDBTitle: dpp9 - apo |
| 50 | c6eosB | Alignment | not modelled | 100.0 | 12 | PDB header: hydrolase Chain: B: PDB Molecule: dipeptidyl peptidase 8; PDBTitle: dpp8 - apo, space group 19 |
| 51 | c4q1vA | Alignment | not modelled | 100.0 | 14 | PDB header: hydrolase Chain: A: PDB Molecule: putative dipeptidyl aminopeptidase iv; PDBTitle: crystal structure of a putative dipeptidyl aminopeptidase iv2 (bacova_01349) from bacteroides ovatus atcc 8483 at 2.48 a resolution |
| 52 | c1xfD | Alignment | not modelled | 100.0 | 10 | PDB header: membrane protein Chain: D: PDB Molecule: dipeptidyl aminopeptidase-like protein 6; PDBTitle: structure of a human a-type potassium channel accelerating factor2 dppx, a member of the dipeptidyl aminopeptidase family |
| 53 | c5t88B | Alignment | not modelled | 100.0 | 16 | PDB header: hydrolase Chain: B: PDB Molecule: prolyl endopeptidase; PDBTitle: prolyl oligopeptidase from pyrococcus furiosus |
| 54 | c5jrlC | Alignment | not modelled | 100.0 | 15 | PDB header: hydrolase Chain: C: PDB Molecule: dipeptidyl aminopeptidases/acylaminoacyl-peptidases-like |

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| | | | | | | PDBTitle: crystal structure of the shpingopyxin i lasso peptide isopeptidase2 spi-isop (native) |
| 55 | c6eotG_ | Alignment | not modelled | 100.0 | 12 | PDB header: hydrolase Chain: G: PDB Molecule: dipeptidyl peptidase 8; PDBTitle: dpp8 - slrflyeg, space group 19 |
| 56 | c6eorD_ | Alignment | not modelled | 100.0 | 14 | PDB header: hydrolase Chain: D: PDB Molecule: dipeptidyl peptidase 9; PDBTitle: dpp9 - 1g244 |
| 57 | c5txeA_ | Alignment | not modelled | 100.0 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: atxe2; PDBTitle: atxe2 isopeptidase - s527a variant with astexin3-dc4 bound |
| 58 | c2qruA_ | Alignment | not modelled | 100.0 | 18 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an alpha/beta hydrolase superfamily protein from2 enterococcus faecalis |
| 59 | c4q3kB_ | Alignment | not modelled | 100.0 | 25 | PDB header: hydrolase Chain: B: PDB Molecule: mgs-m1; PDBTitle: crystal structure of acetyl ester-xyloside bifunctional enzyme from a2 medee basin deep-sea metagenome library |
| 60 | c1qfma_ | Alignment | not modelled | 100.0 | 15 | PDB header: hydrolase Chain: A: PDB Molecule: protein (prolyl oligopeptidase); PDBTitle: prolyl oligopeptidase from porcine muscle |
| 61 | c6a6oA_ | Alignment | not modelled | 100.0 | 14 | PDB header: hydrolase Chain: A: PDB Molecule: esterase/lipase-like protein; PDBTitle: crystal structure of acetyl ester-xyloside bifunctional hydrolase from2 caldicellulosiruptor lactoaceticus |
| 62 | c3bjrA_ | Alignment | not modelled | 100.0 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: putative carboxylesterase; PDBTitle: crystal structure of a putative carboxylesterase (lp_1002) from2 lactobacillus plantarum wcf51 at 2.09 a resolution |
| 63 | c2bkIB_ | Alignment | not modelled | 100.0 | 21 | PDB header: hydrolase Chain: B: PDB Molecule: prolyl endopeptidase; PDBTitle: structural and mechanistic analysis of two prolyl2 endopeptidases: role of inter-domain dynamics in3 catalysis and specificity |
| 64 | c3hIkB_ | Alignment | not modelled | 100.0 | 19 | PDB header: hydrolase Chain: B: PDB Molecule: acyl-coenzyme a thioesterase 2, mitochondrial; PDBTitle: crystal structure of human mitochondrial acyl-coa thioesterase (acot2) |
| 65 | c3hxkB_ | Alignment | not modelled | 100.0 | 19 | PDB header: hydrolase Chain: B: PDB Molecule: sugar hydrolase; PDBTitle: crystal structure of a sugar hydrolase (yeeb) from lactococcus lactis,2 northeast structural genomics consortium target kr108 |
| 66 | c4bp9A_ | Alignment | not modelled | 100.0 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: oligopeptidase b; PDBTitle: oligopeptidase b from trypanosoma brucei with covalently bound2 antipain - closed form |
| 67 | c2xe4A_ | Alignment | not modelled | 100.0 | 15 | PDB header: hydrolase/inhibitor Chain: A: PDB Molecule: oligopeptidase b; PDBTitle: structure of oligopeptidase b from leishmania major |
| 68 | c3k2iA_ | Alignment | not modelled | 100.0 | 20 | PDB header: hydrolase Chain: A: PDB Molecule: acyl-coenzyme a thioesterase 4; PDBTitle: human acyl-coenzyme a thioesterase 4 |
| 69 | c5n4dA_ | Alignment | not modelled | 100.0 | 15 | PDB header: hydrolase Chain: A: PDB Molecule: prolyl oligopeptidase; PDBTitle: prolyl oligopeptidase b from galerina marginata bound to 25mer2 macrocyclization substrate - d661a mutant |
| 70 | d1qfma2 | Alignment | not modelled | 100.0 | 14 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Prolyl oligopeptidase, C-terminal domain |
| 71 | c4hvtA_ | Alignment | not modelled | 100.0 | 15 | PDB header: hydrolase Chain: A: PDB Molecule: post-proline cleaving enzyme; PDBTitle: structure of a post-proline cleaving enzyme from rickettsia typhi |
| 72 | c4e14A_ | Alignment | not modelled | 100.0 | 12 | PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: kynurenine formamidase; PDBTitle: crystal structure of kynurenine formamidase conjugated with2 phenylmethylsulfonyl fluoride |
| 73 | c3iumA_ | Alignment | not modelled | 100.0 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: prolyl endopeptidase; PDBTitle: appep_wtx opened state |
| 74 | c1yr2A_ | Alignment | not modelled | 100.0 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: prolyl oligopeptidase; PDBTitle: structural and mechanistic analysis of two prolyl endopeptidases: role2 of inter-domain dynamics in catalysis and specificity |
| 75 | c5aoaA_ | Alignment | not modelled | 100.0 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: the structure of a novel thermophilic esterase from the planctomycetes2 species, thermogutta terrifontis, est2-propionate bound |
| 76 | d2pbla1 | Alignment | not modelled | 100.0 | 15 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase |
| 77 | d2hu7a2 | Alignment | not modelled | 100.0 | 17 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acylamino-acid-releasing enzyme, C-terminal donain |
| 78 | c5uzwD_ | Alignment | not modelled | 100.0 | 13 | PDB header: lyase Chain: D: PDB Molecule: peptide cyclase 1; PDBTitle: pcy1 g696insertion variant in complex with follower peptide and the2 covalent inhibitor zpp |
| 79 | c3h04A_ | Alignment | not modelled | 100.0 | 15 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of the protein with unknown function |

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| | | | | | | from2 staphylococcus aureus subsp. aureus mu50 |
| 80 | c5uw7B | Alignment | not modelled | 100.0 | 12 | PDB header: lyase Chain: B: PDB Molecule: peptide cyclase 1; PDBTitle: pcy1 y481f variant in complex with follower peptide |
| 81 | d1vkha | Alignment | not modelled | 100.0 | 16 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Putative serine hydrolase Ydr428c |
| 82 | d1xfda2 | Alignment | not modelled | 100.0 | 10 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like |
| 83 | d2bgra2 | Alignment | not modelled | 99.9 | 13 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like |
| 84 | d1orva2 | Alignment | not modelled | 99.9 | 13 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like |
| 85 | c4zi5A | Alignment | not modelled | 99.9 | 15 | PDB header: hydrolase Chain: A: PDB Molecule: p91; PDBTitle: crystal structure of dienelactone hydrolase-like promiscuous2 phosphotriesterase p91 from metagenomic libraries |
| 86 | d2i3da1 | Alignment | not modelled | 99.9 | 18 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Atu1826-like |
| 87 | c2i3dA | Alignment | not modelled | 99.9 | 18 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein atu1826; PDBTitle: crystal structure of protein of unknown function atu1826, a putative2 alpha/beta hydrolase from agrobacterium tumefaciens |
| 88 | d1dina | Alignment | not modelled | 99.9 | 15 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Dienelactone hydrolase |
| 89 | c3fnbB | Alignment | not modelled | 99.9 | 13 | PDB header: hydrolase Chain: B: PDB Molecule: acylaminoacyl peptidase smu_737; PDBTitle: crystal structure of acylaminoacyl peptidase smu_737 from2 streptococcus mutans ua159 |
| 90 | c2o2gA | Alignment | not modelled | 99.9 | 21 | PDB header: hydrolase Chain: A: PDB Molecule: dienelactone hydrolase; PDBTitle: crystal structure of dienelactone hydrolase (yp_324580.1) from2 anabaena variabilis atcc 29413 at 1.92 a resolution |
| 91 | c3i6yA | Alignment | not modelled | 99.9 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: esterase apc40077; PDBTitle: structure of an esterase from the oil-degrading bacterium oleispira2 antarctica |
| 92 | c5f2hA | Alignment | not modelled | 99.9 | 13 | 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 |
| 93 | d1ju3a2 | Alignment | not modelled | 99.9 | 13 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PepX catalytic domain-like |
| 94 | c4zv9E | Alignment | not modelled | 99.9 | 23 | PDB header: structural genomics, unknown function Chain: E: PDB Molecule: uncharacterized protein; PDBTitle: 2.00 angstrom resolution crystal structure of an uncharacterized2 protein from escherichia coli o157:h7 str. sakai |
| 95 | c3f67A | Alignment | not modelled | 99.9 | 21 | PDB header: hydrolase Chain: A: PDB Molecule: putative dienelactone hydrolase; PDBTitle: crystal structure of putative dienelactone hydrolase from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578 |
| 96 | c4b6gA | Alignment | not modelled | 99.9 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: putative esterase; PDBTitle: the crystal structure of the neisserial esterase d. |
| 97 | c3doiA | Alignment | not modelled | 99.9 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of a thermostable esterase complex with2 paraoxon |
| 98 | d1sfra | Alignment | not modelled | 99.9 | 15 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Mycobacterial antigens |
| 99 | c3fcxA | Alignment | not modelled | 99.9 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: s-formylglutathione hydrolase; PDBTitle: crystal structure of human esterase d |
| 100 | c5vola | Alignment | not modelled | 99.9 | 15 | PDB header: hydrolase Chain: A: PDB Molecule: putative esterase; PDBTitle: bacint_04212 ferulic acid esterase |
| 101 | c5g59A | Alignment | not modelled | 99.9 | 13 | PDB header: structural protein Chain: A: PDB Molecule: esterase; PDBTitle: structure of the pyrococcus furiosus esterase pf2001 with space group2 p3121 |
| 102 | c3d0kA | Alignment | not modelled | 99.9 | 13 | 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 |
| 103 | c3e4dD | Alignment | not modelled | 99.9 | 17 | PDB header: hydrolase Chain: D: PDB Molecule: esterase d; PDBTitle: structural and kinetic study of an s-formylglutathione hydrolase from2 agrobacterium tumefaciens |
| 104 | d2jbwa1 | Alignment | not modelled | 99.9 | 13 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: 2,6-dihydropseudooxynicotine hydrolase-like |
| 105 | c4eziA | Alignment | not modelled | 99.9 | 16 | 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 |

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| 106 | d1l7aa_ | Alignment | not modelled | 99.9 | 15 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetyl xylan esterase-like |
| 107 | c4h18D_ | Alignment | not modelled | 99.9 | 10 | PDB header: transferase Chain: D: PDB Molecule: cmt1; PDBTitle: three dimensional structure of corynomycoloyl tranferase c |
| 108 | c2jbwB_ | Alignment | not modelled | 99.9 | 13 | PDB header: hydrolase Chain: B: PDB Molecule: 2,6-dihydroxy-pseudo-oxynicotine hydrolase; PDBTitle: crystal structure of the 2,6-dihydroxy-pseudo-oxynicotine hydrolase. |
| 109 | c3ls2D_ | Alignment | not modelled | 99.9 | 17 | PDB header: hydrolase Chain: D: PDB Molecule: s-formylglutathione hydrolase; PDBTitle: crystal structure of an s-formylglutathione hydrolase from2 pseudoalteromonas haloplanktis tac125 |
| 110 | c2uz0B_ | Alignment | not modelled | 99.9 | 12 | PDB header: hydrolase Chain: B: PDB Molecule: tributyryn esterase; PDBTitle: the crystal crystal structure of the esta protein, a2 virulence factor esta protein from streptococcus pneumonia |
| 111 | c3ksrA_ | Alignment | not modelled | 99.9 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: putative serine hydrolase; PDBTitle: crystal structure of a putative serine hydrolase (xcc3885) from2 xanthomonas campestris pv. campestris at 2.69 a resolution |
| 112 | c1l7qA_ | Alignment | not modelled | 99.9 | 12 | PDB header: hydrolase Chain: A: PDB Molecule: cocaine esterase; PDBTitle: ser117ala mutant of bacterial cocaine esterase coce |
| 113 | c5cxcC_ | Alignment | not modelled | 99.9 | 14 | PDB header: hydrolase Chain: C: PDB Molecule: ferulic acid esterase, amce1/fae1a; PDBTitle: structure of a ce1 ferulic acid esterase, amce1/fae1a, from2 anaeromyces mucronatus in complex with ferulic acid |
| 114 | c3mveB_ | Alignment | not modelled | 99.9 | 11 | PDB header: lyase Chain: B: PDB Molecule: upf0255 protein vv1_0328; PDBTitle: crystal structure of a novel pyruvate decarboxylase |
| 115 | d1qe3a_ | Alignment | not modelled | 99.9 | 17 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like |
| 116 | c5x6sB_ | Alignment | not modelled | 99.9 | 13 | PDB header: hydrolase Chain: B: PDB Molecule: acetyl xylan esterase a; PDBTitle: acetyl xylan esterase from aspergillus awamori |
| 117 | c3wydA_ | Alignment | not modelled | 99.9 | 22 | PDB header: hydrolase Chain: A: PDB Molecule: lc-est1c; PDBTitle: c-terminal esterase domain of lc-est1 |
| 118 | d2fuka1 | Alignment | not modelled | 99.9 | 19 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Atu1826-like |
| 119 | c4rgyA_ | Alignment | not modelled | 99.9 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: structural and functional analysis of a low-temperature-active2 alkaline esterase from south china sea marine sediment microbial3 metagenomic library |
| 120 | c2b9vB_ | Alignment | not modelled | 99.9 | 11 | PDB header: hydrolase Chain: B: PDB Molecule: alpha-amino acid ester hydrolase; PDBTitle: acetobacter turbidans alpha-amino acid ester hydrolase |