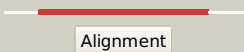

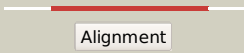



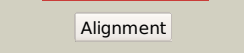



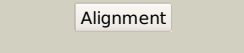

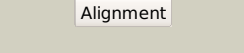



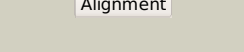

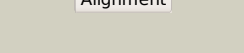

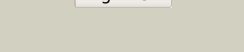



Phyre2

| | |
|---------------|------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD0519c_(-)_611175_612077 |
| Date | Fri Jul 26 01:50:06 BST 2019 |
| Unique Job ID | a9451995f5f89c4f |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|---|
| 1 | c3c8dA_ |  Alignment |  | 100.0 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: enterochelin esterase; PDBTitle: crystal structure of the enterobactin esterase fes from2 shigella flexneri in the presence of 2,3-di-hydroxy-n-3 benzoyl-glycine |
| 2 | d3c8da2 |  Alignment |  | 100.0 | 19 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase |
| 3 | c4h18D_ |  Alignment |  | 100.0 | 17 | PDB header: transferase Chain: D: PDB Molecule: cmt1; PDBTitle: three dimensional structure of corynomycoloyl tranferase c |
| 4 | d1jjfa_ |  Alignment |  | 100.0 | 19 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase |
| 5 | c1wb4A_ |  Alignment |  | 100.0 | 14 | PDB header: hydrolase Chain: A: PDB Molecule: endo-1,4-beta-xylanase y; PDBTitle: s954a mutant of the feruloyl esterase module from2 clostridium thermocellum complexed with sinapinate |
| 6 | c5cxcC_ |  Alignment |  | 100.0 | 17 | 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 |
| 7 | c3i6yA_ |  Alignment |  | 100.0 | 20 | PDB header: hydrolase Chain: A: PDB Molecule: esterase apc40077; PDBTitle: structure of an esterase from the oil-degrading bacterium oleispira2 antarctica |
| 8 | c4b6gA_ |  Alignment |  | 100.0 | 20 | PDB header: hydrolase Chain: A: PDB Molecule: putative esterase; PDBTitle: the crystal structure of the neisserial esterase d. |
| 9 | d1dqza_ |  Alignment |  | 100.0 | 20 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Mycobacterial antigens |
| 10 | c3e4dD_ |  Alignment |  | 100.0 | 17 | PDB header: hydrolase Chain: D: PDB Molecule: esterase d; PDBTitle: structural and kinetic study of an s-formylglutathione hydrolase from2 agrobacterium tumefaciens |
| 11 | c2uz0B_ |  Alignment |  | 100.0 | 22 | 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 |

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|----|-------------------------|-----------|--------------|-------|----|--|
| 12 | d1pv1a_ | Alignment | | 100.0 | 17 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hypothetical esterase YJL068C |
| 13 | c3fcxA_ | Alignment | | 100.0 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: s-formylglutathione hydrolase; PDBTitle: crystal structure of human esterase d |
| 14 | d1f0na_ | Alignment | | 100.0 | 17 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Mycobacterial antigens |
| 15 | d1wb4a1 | Alignment | | 100.0 | 14 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase |
| 16 | d1r88a_ | Alignment | | 100.0 | 17 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Mycobacterial antigens |
| 17 | c3ls2D_ | Alignment | | 100.0 | 20 | PDB header: hydrolase Chain: D: PDB Molecule: s-formylglutathione hydrolase; PDBTitle: crystal structure of an s-formylglutathione hydrolase from2 pseudoalteromonas haloplanktis tac125 |
| 18 | d1sfra_ | Alignment | | 100.0 | 16 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Mycobacterial antigens |
| 19 | c4rgyA_ | Alignment | | 100.0 | 25 | 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 |
| 20 | c5oljA_ | Alignment | | 100.0 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl peptidase iv; PDBTitle: crystal structure of porphyromonas gingivalis dipeptidyl peptidase 4 |
| 21 | c4rotA_ | Alignment | not modelled | 100.0 | 21 | PDB header: hydrolase Chain: A: PDB Molecule: esterase a; PDBTitle: crystal structure of esterase a from streptococcus pyogenes |
| 22 | c5volA_ | Alignment | not modelled | 100.0 | 21 | PDB header: hydrolase Chain: A: PDB Molecule: putative esterase; PDBTitle: bacint_04212 ferulic acid esterase |
| 23 | c1z68A_ | Alignment | not modelled | 100.0 | 15 | PDB header: lyase Chain: A: PDB Molecule: fibroblast activation protein, alpha subunit; PDBTitle: crystal structure of human fibroblast activation protein alpha |
| 24 | c2ecfA_ | Alignment | not modelled | 100.0 | 20 | PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl peptidase iv; PDBTitle: crystal structure of dipeptidyl aminopeptidase iv from2 stentrophomonas maltophilia |
| 25 | c4wjlB_ | Alignment | not modelled | 100.0 | 15 | 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 |
| 26 | c2qtB_ | Alignment | not modelled | 100.0 | 16 | PDB header: hydrolase Chain: B: PDB Molecule: dipeptidyl peptidase 4; PDBTitle: human dipeptidyl peptidase iv/cd26 in complex with a 4-aryl2 cyclohexylalanine inhibitor |
| 27 | c2g5tA_ | Alignment | not modelled | 100.0 | 14 | 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 |
| 28 | 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 |

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|----|------------------------|-----------|--------------|-------|----|--|
| 29 | c5tXeA | Alignment | not modelled | 100.0 | 15 | PDB header: hydrolase Chain: A: PDB Molecule: atxe2; PDBTitle: atxe2 isopeptidase - s527a variant with astexin3-dc4 bound |
| 30 | c5l8sD | Alignment | not modelled | 100.0 | 14 | 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 |
| 31 | c1qfmA | Alignment | not modelled | 100.0 | 15 | PDB header: hydrolase Chain: A: PDB Molecule: protein (prolyl oligopeptidase); PDBTitle: prolyl oligopeptidase from porcine muscle |
| 32 | c2eepA | Alignment | not modelled | 100.0 | 14 | PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl aminopeptidase iv, putative; PDBTitle: prolyl tripeptidyl aminopeptidase complexed with an inhibitor |
| 33 | c3doiA | Alignment | not modelled | 100.0 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of a thermostable esterase complex with2 paraoxon |
| 34 | c2hu7A | Alignment | not modelled | 100.0 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: acylamino-acid-releasing enzyme; PDBTitle: binding of inhibitors by acylaminoacyl peptidase |
| 35 | c6eoqC | Alignment | not modelled | 100.0 | 18 | PDB header: hydrolase Chain: C: PDB Molecule: dipeptidyl peptidase 9; PDBTitle: dpp9 - apo |
| 36 | c6eorD | Alignment | not modelled | 100.0 | 18 | PDB header: hydrolase Chain: D: PDB Molecule: dipeptidyl peptidase 9; PDBTitle: dpp9 - 1g244 |
| 37 | c2bklB | Alignment | not modelled | 100.0 | 13 | 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 |
| 38 | c3azqA | Alignment | not modelled | 100.0 | 15 | PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase; PDBTitle: crystal structure of puromycin hydrolase s511a mutant complexed with2 pgg |
| 39 | c5jrlC | Alignment | not modelled | 100.0 | 11 | PDB header: hydrolase Chain: C: PDB Molecule: dipeptidyl aminopeptidases/acylaminoacyl-peptidases-like PDBTitle: crystal structure of the sphingopyxin i lasso peptide isopeptidase2 spi-isop (native) |
| 40 | c6eosB | Alignment | not modelled | 100.0 | 16 | PDB header: hydrolase Chain: B: PDB Molecule: dipeptidyl peptidase 8; PDBTitle: dpp8 - apo, space group 19 |
| 41 | c3iumA | Alignment | not modelled | 100.0 | 14 | PDB header: hydrolase Chain: A: PDB Molecule: prolyl endopeptidase; PDBTitle: appep_wtx opened state |
| 42 | c6eotG | Alignment | not modelled | 100.0 | 15 | PDB header: hydrolase Chain: G: PDB Molecule: dipeptidyl peptidase 8; PDBTitle: dpp8 - slrflyeg, space group 19 |
| 43 | c2xe4A | Alignment | not modelled | 99.9 | 16 | PDB header: hydrolase/inhibitor Chain: A: PDB Molecule: oligopeptidase b; PDBTitle: structure of oligopeptidase b from leishmania major |
| 44 | c4bp9A | Alignment | not modelled | 99.9 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: oligopeptidase b; PDBTitle: oligopeptidase b from trypanosoma brucei with covalently bound2 antipain - closed form |
| 45 | c5uzwD | Alignment | not modelled | 99.9 | 15 | PDB header: lyase Chain: D: PDB Molecule: peptide cyclase 1; PDBTitle: pcy1 g696insertion variant in complex with follower peptide and the2 covalent inhibitor zpp |
| 46 | c1xfD | Alignment | not modelled | 99.9 | 13 | 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 |
| 47 | c4hxgl | Alignment | not modelled | 99.9 | 14 | PDB header: hydrolase Chain: J: PDB Molecule: putative uncharacterized protein ph0594; PDBTitle: pyrococcus horikoshii acylaminoacyl peptidase (orthorhombic crystal2 form) |
| 48 | c5yznA | Alignment | not modelled | 99.9 | 13 | PDB header: hydrolase Chain: A: PDB Molecule: acyl-peptide hydrolase, putative; PDBTitle: crystal structure of s9 peptidase (active form) from deinococcus2 radiodurans r1 |
| 49 | c5n4dA | Alignment | not modelled | 99.9 | 13 | PDB header: hydrolase Chain: A: PDB Molecule: prolyl oligopeptidase; PDBTitle: prolyl oligopeptidase b from galerina marginata bound to 25mer2 macrocyclization substrate - d661a mutant |
| 50 | c6guiA | Alignment | not modelled | 99.9 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: siderophore esterase iroo-like, putative; PDBTitle: siderophore hydrolase estb mutant h267n from aspergillus fumigatus |
| 51 | c1yr2A | Alignment | not modelled | 99.9 | 14 | 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 |
| 52 | c5t88B | Alignment | not modelled | 99.9 | 15 | PDB header: hydrolase Chain: B: PDB Molecule: prolyl endopeptidase; PDBTitle: prolyl oligopeptidase from pyrococcus furiosus |
| 53 | c6qi5A | Alignment | not modelled | 99.9 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: ferric enterobactin esterase; PDBTitle: crystal structure of the ferric enterobactin esterase (pfee) from2 pseudomonas aeruginosa in complex with the tris-catechol vector |

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|----|-------------------------|-----------|--------------|------|----|--|
| 54 | c5x6sB | Alignment | not modelled | 99.9 | 16 | PDB header: hydrolase Chain: B: PDB Molecule: acetyl xylan esterase a; PDBTitle: acetyl xylan esterase from aspergillus awamori |
| 55 | d2h1ia1 | Alignment | not modelled | 99.9 | 17 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1 |
| 56 | c4hvtA | Alignment | not modelled | 99.9 | 13 | PDB header: hydrolase Chain: A: PDB Molecule: post-proline cleaving enzyme; PDBTitle: structure of a post-proline cleaving enzyme from rickettsia typhi |
| 57 | c3wiaA | Alignment | not modelled | 99.9 | 20 | PDB header: hydrolase Chain: A: PDB Molecule: oxidized polyvinyl alcohol hydrolase; PDBTitle: crystal structure of soph native |
| 58 | d3b5ea1 | Alignment | not modelled | 99.9 | 17 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1 |
| 59 | c5f2hA | Alignment | not modelled | 99.9 | 14 | 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 |
| 60 | c6gunB | Alignment | not modelled | 99.9 | 15 | PDB header: hydrolase Chain: B: PDB Molecule: estb from aspergillus nidulans; PDBTitle: siderophore hydrolase estb from aspergillus nidulans |
| 61 | c6guoC | Alignment | not modelled | 99.9 | 14 | PDB header: hydrolase Chain: C: PDB Molecule: putative siderophore-degrading esterase (eurofung); PDBTitle: siderophore hydrolase esta from aspergillus nidulans |
| 62 | c3wydA | Alignment | not modelled | 99.9 | 21 | PDB header: hydrolase Chain: A: PDB Molecule: lc-est1c; PDBTitle: c-terminal esterase domain of lc-est1 |
| 63 | d2gzsa1 | Alignment | not modelled | 99.9 | 14 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: IroE-like |
| 64 | c5uw7B | Alignment | not modelled | 99.9 | 13 | PDB header: lyase Chain: B: PDB Molecule: peptide cyclase 1; PDBTitle: pcy1 y481f variant in complex with follower peptide |
| 65 | c2qm0B | Alignment | not modelled | 99.9 | 12 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: bes; PDBTitle: crystal structure of bes protein from bacillus cereus |
| 66 | c3og9A | Alignment | not modelled | 99.9 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: protein yahd a copper inducible hydrolase; PDBTitle: structure of yahd with malic acid |
| 67 | c2h1iA | Alignment | not modelled | 99.9 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: carboxylesterase; PDBTitle: crystal structure of the bacillus cereus carboxylesterase |
| 68 | c2r8bA | Alignment | not modelled | 99.9 | 16 | 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 |
| 69 | d2jba1 | Alignment | not modelled | 99.9 | 15 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: 2,6-dihydropseudooxynicotine hydrolase-like |
| 70 | c2jbaB | Alignment | not modelled | 99.9 | 15 | PDB header: hydrolase Chain: B: PDB Molecule: 2,6-dihydroxy-pseudo-oxynicotine hydrolase; PDBTitle: crystal structure of the 2,6-dihydroxy-pseudo-oxynicotine hydrolase. |
| 71 | c2o7vA | Alignment | not modelled | 99.9 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: cxe carboxylesterase; PDBTitle: carboxylesterase aecxe1 from actinidia eriantha covalently inhibited2 by paraoxon |
| 72 | d2r8ba1 | Alignment | not modelled | 99.9 | 16 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1 |
| 73 | c3gffA | Alignment | not modelled | 99.9 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: iroe-like serine hydrolase; PDBTitle: crystal structure of iroe-like serine hydrolase (np_718593.1) from2 shewanella oneidensis at 2.12 a resolution |
| 74 | c3d0kA | Alignment | not modelled | 99.9 | 21 | 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 |
| 75 | c4h0cA | Alignment | not modelled | 99.9 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: phospholipase/carboxylesterase; PDBTitle: crystal structure of phospholipase/carboxylesterase from dyadobacter2 fermentans dsm 18053 |
| 76 | c2o2gA | Alignment | not modelled | 99.9 | 17 | 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 |
| 77 | d1ju3a2 | Alignment | not modelled | 99.9 | 17 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PepX catalytic domain-like |
| 78 | d1qfma2 | Alignment | not modelled | 99.9 | 13 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Prolyl oligopeptidase, C-terminal domain |
| 79 | d1orva2 | Alignment | not modelled | 99.9 | 13 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like |
| | | | | | | PDB header: hydrolase |

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|-----|-------------------------|-----------|--------------|------|----|--|
| 80 | c5hc4A_ | Alignment | not modelled | 99.9 | 15 | Chain: A: PDB Molecule: lipolytic enzyme; PDBTitle: structure of esterase est22 |
| 81 | c3mveB_ | Alignment | not modelled | 99.9 | 12 | PDB header: lyase Chain: B: PDB Molecule: upf0255 protein vw1_0328; PDBTitle: crystal structure of a novel pyruvate decarboxylase |
| 82 | c4fhzA_ | Alignment | not modelled | 99.9 | 21 | PDB header: hydrolase Chain: A: PDB Molecule: phospholipase/carboxylesterase; PDBTitle: crystal structure of a carboxyl esterase at 2.0 angstrom resolution |
| 83 | c1l7qA_ | Alignment | not modelled | 99.9 | 14 | PDB header: hydrolase Chain: A: PDB Molecule: cocaine esterase; PDBTitle: ser117ala mutant of bacterial cocaine esterase coce |
| 84 | d2bgra2 | Alignment | not modelled | 99.9 | 13 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like |
| 85 | c3k2iA_ | Alignment | not modelled | 99.9 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: acyl-coenzyme a thioesterase 4; PDBTitle: human acyl-coenzyme a thioesterase 4 |
| 86 | c3ed1E_ | Alignment | not modelled | 99.9 | 16 | PDB header: hydrolase receptor Chain: E: PDB Molecule: gibberellin receptor gid1; PDBTitle: crystal structure of rice gid1 complexed with ga3 |
| 87 | c4ao6A_ | Alignment | not modelled | 99.8 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: native structure of a novel cold-adapted esterase from an2 arctic intertidal metagenomic library |
| 88 | c4f21G_ | Alignment | not modelled | 99.8 | 15 | PDB header: hydrolase/hydrolase inhibitor Chain: G: PDB Molecule: carboxylesterase/phospholipase family protein; PDBTitle: crystal structure of carboxylesterase/phospholipase family protein2 from francisella tularensis |
| 89 | c5g59A_ | Alignment | not modelled | 99.8 | 16 | PDB header: structural protein Chain: A: PDB Molecule: esterase; PDBTitle: structure of the pyrococcus furiosus esterase pf2001 with space group2 p3121 |
| 90 | d2hu7a2 | Alignment | not modelled | 99.8 | 14 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acylamino-acid-releasing enzyme, C-terminal donain |
| 91 | c3h1kB_ | Alignment | not modelled | 99.8 | 18 | PDB header: hydrolase Chain: B: PDB Molecule: acyl-coenzyme a thioesterase 2, mitochondrial; PDBTitle: crystal structure of human mitochondrial acyl-coa thioesterase (acot2) |
| 92 | c4zrsA_ | Alignment | not modelled | 99.8 | 14 | PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of a cloned feruloyl esterase from a soil2 metagenomic library |
| 93 | c3fnbB_ | Alignment | not modelled | 99.8 | 12 | PDB header: hydrolase Chain: B: PDB Molecule: acylaminoacyl peptidase smu_737; PDBTitle: crystal structure of acylaminoacyl peptidase smu_737 from2 streptococcus mutans ua159 |
| 94 | c6gocA_ | Alignment | not modelled | 99.8 | 15 | PDB header: carbohydrate Chain: A: PDB Molecule: duf3826 domain-containing protein; PDBTitle: methylesterase bt1017 |
| 95 | c4zi5A_ | Alignment | not modelled | 99.8 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: p91; PDBTitle: crystal structure of dienelactone hydrolase-like promiscuous2 phosphotriesterase p91 from metagenomic libraries |
| 96 | d1xfda2 | Alignment | not modelled | 99.8 | 16 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like |
| 97 | c3ga7A_ | Alignment | not modelled | 99.8 | 13 | PDB header: hydrolase Chain: A: PDB Molecule: acetyl esterase; PDBTitle: 1.55 angstrom crystal structure of an acetyl esterase from salmonella2 typhimurium |
| 98 | d1jkma_ | Alignment | not modelled | 99.8 | 16 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase |
| 99 | c6avwA_ | Alignment | not modelled | 99.8 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: carboxylesterase sober1; PDBTitle: crystal structure of arabidopsis thaliana sober1 l63a |
| 100 | c2zshA_ | Alignment | not modelled | 99.8 | 15 | 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 |
| 101 | c4q82A_ | Alignment | not modelled | 99.8 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: phospholipase/carboxylesterase; PDBTitle: crystal structure of phospholipase/carboxylesterase from haliangium2 ochraceum |
| 102 | c3bxpA_ | Alignment | not modelled | 99.8 | 11 | 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 |
| 103 | c2hdwB_ | Alignment | not modelled | 99.8 | 13 | PDB header: hydrolase Chain: B: PDB Molecule: hypothetical protein pa2218; PDBTitle: crystal structure of hypothetical protein pa2218 from pseudomonas2 aeruginosa |
| 104 | d2b9va2 | Alignment | not modelled | 99.8 | 17 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PepX catalytic domain-like |
| 105 | d1l7aa_ | Alignment | not modelled | 99.8 | 15 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetyl xylan esterase-like |
| 106 | c3ih3A_ | Alignment | not modelled | 99.8 | 15 | PDB header: hydrolase Chain: A: PDB Molecule: coce/nond family hydrolase; |

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|-----|-------------------------|-----------|--------------|------|----|---|
| 106 | c3b2A_ | Alignment | not modelled | 99.8 | 13 | PDBTitle: crystal structure of sacI2612 - coce/nond family hydrolase from2 staphylococcus aureus PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterised protein coch_1243 from2 capnocytophaga ochracea dsm 7271 |
| 107 | c4w9rA_ | Alignment | not modelled | 99.8 | 13 | PDB header: hydrolase Chain: B: PDB Molecule: alpha-amino acid ester hydrolase; PDBTitle: acetobacter turbidans alpha-amino acid ester hydrolase |
| 108 | c2b9vB_ | Alignment | not modelled | 99.8 | 15 | PDB header: hydrolase Chain: C: PDB Molecule: est1e; PDBTitle: est1e from butyrivibrio proteoclasticus |
| 109 | c2wtmC_ | Alignment | not modelled | 99.8 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: poly(ethylene terephthalate) hydrolase; PDBTitle: crystal structure of a novel pet hydrolase from ideonella sakaiensis2 201-f6 |
| 110 | c5xg0A_ | Alignment | not modelled | 99.8 | 18 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Gastric lipase |
| 111 | d1hlga_ | Alignment | not modelled | 99.8 | 17 | PDB header: hydrolase Chain: B: PDB Molecule: esterase; PDBTitle: crystal structure of esterase pe8 |
| 112 | c5dwdB_ | Alignment | not modelled | 99.8 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: the structure of a novel thermophilic esterase from the planctomycetes2 species, thermogutta terrfontis, est2-propionate bound |
| 113 | c5aoaA_ | Alignment | not modelled | 99.8 | 11 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetyl xylan esterase-like |
| 114 | d1vlqa_ | Alignment | not modelled | 99.8 | 15 | PDB header: hydrolase Chain: A: PDB Molecule: putative carboxylesterase; PDBTitle: crystal structure of a putative carboxylesterase (lp_1002) from2 lactobacillus plantarum wcfs1 at 2.09 a resolution |
| 115 | c3bjrA_ | Alignment | not modelled | 99.8 | 13 | PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: acyl-protein thioesterase 2; PDBTitle: cocrystal structure of the human acyl protein thioesterase 2 with an2 isoform-selective inhibitor, ml349 |
| 116 | c5synB_ | Alignment | not modelled | 99.8 | 17 | PDB header: hydrolase Chain: A: PDB Molecule: lcc; PDBTitle: crystal structure of leaf-branch compost bacterial cutinase homolog |
| 117 | c4eb0A_ | Alignment | not modelled | 99.8 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: lysophospholipase-like protein 1; PDBTitle: crystal structure analysis of human lypl1 |
| 118 | c3u0vA_ | Alignment | not modelled | 99.8 | 20 | 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 |
| 119 | c5jd5A_ | Alignment | not modelled | 99.8 | 18 | PDB header: hydrolase Chain: D: PDB Molecule: peptidase s15/coce/nond; PDBTitle: crystal structure of aminopeptidase from marine sediment archaeon2 thaumarchaeota archaeon |
| 120 | c4pf1D_ | Alignment | not modelled | 99.8 | 14 | |