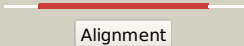

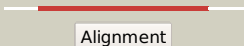

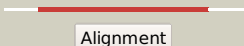







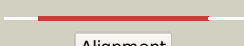




















Phyre2

| | |
|------------------|---------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD0272c (-)_328575_329708 |
| Date | Tue Jul 23 14:50:33 BST 2019 |
| Unique Job ID | 24f8b465a036e9ff |

Detailed template
information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|---|
| 1 | c3i28A_ |  |  | 100.0 | 16 | PDB header: hydrolase Chain: A; PDB Molecule: epoxide hydrolase 2; PDBTitle: crystal structure of soluble epoxide hydrolase |
| 2 | c1cr6A_ |  |  | 100.0 | 15 | PDB header: hydrolase Chain: A; PDB Molecule: epoxide hydrolase; PDBTitle: crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor |
| 3 | c4d9jl_ |  |  | 100.0 | 15 | PDB header: de novo protein Chain: I; PDB Molecule: designed 16nm tetrahedral protein cage containing non-haem PDBTitle: structure of a 16 nm protein cage designed by fusing symmetric2 oligomeric domains |
| 4 | d2b61a1 |  |  | 100.0 | 13 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase |
| 5 | c3i1iA_ |  |  | 100.0 | 10 | PDB header: transferase Chain: A; PDB Molecule: homoserine o-acetyltransferase; PDBTitle: x-ray crystal structure of homoserine o-acetyltransferase from2 bacillus anthracis |
| 6 | d1k8qa_ |  |  | 100.0 | 15 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Gastric lipase |
| 7 | c2vavL_ |  |  | 100.0 | 13 | PDB header: transferase Chain: L; PDB Molecule: acetyl-coa--deacetylcephalosporin c acetyltransferase; PDBTitle: crystal structure of deacetylcephalosporin c acetyltransferase (dac-2 soak) |
| 8 | c5w8pA_ |  |  | 100.0 | 13 | PDB header: transferase Chain: A; PDB Molecule: homoserine o-acetyltransferase; PDBTitle: homoserine transacetylase meta from mycobacterium abscessus |
| 9 | c4qloA_ |  |  | 100.0 | 14 | PDB header: transferase Chain: A; PDB Molecule: homoserine o-acetyltransferase; PDBTitle: crystal structure of homoserine o-acetyltransferase from2 staphylococcus aureus |
| 10 | c5d6oB_ |  |  | 100.0 | 11 | PDB header: transferase Chain: B; PDB Molecule: homoserine o-acetyltransferase; PDBTitle: orthorhombic crystal structure of an acetylerster hydrolase from2 corynebacterium glutamicum |
| 11 | c5xmdA_ |  |  | 100.0 | 15 | PDB header: hydrolase Chain: A; PDB Molecule: epoxide hydrolase a; PDBTitle: crystal structure of epoxide hydrolase vreh1 from vigna radiata |

| | | | | | | |
|----|-------------------------|-----------|---|-------|----|--|
| 12 | c5jkjA | Alignment |  | 100.0 | 14 | PDB header: hydrolase Chain: A: PDB Molecule: esterase e22; PDBTitle: crystal structure of esterase e22 I374d mutant |
| 13 | c4qlaA | Alignment |  | 100.0 | 10 | PDB header: hydrolase Chain: A: PDB Molecule: juvenile hormone epoxide hydrolase; PDBTitle: crystal structure of juvenile hormone epoxide hydrolase from the2 silkworm bombyx mori |
| 14 | c2e3jA | Alignment |  | 100.0 | 10 | PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase ephb; PDBTitle: the crystal structure of epoxide hydrolase b (rv1938) from2 mycobacterium tuberculosis at 2.1 angstrom |
| 15 | d1hlga | Alignment |  | 100.0 | 14 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Gastric lipase |
| 16 | c3vvIA | Alignment |  | 100.0 | 14 | PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: crystal structure of l-serine-o-acetyltransferase found in d-2 cycloserine biosynthetic pathway |
| 17 | d2vata1 | Alignment |  | 100.0 | 14 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase |
| 18 | c2y6vB | Alignment |  | 100.0 | 13 | PDB header: hydrolase Chain: B: PDB Molecule: peroxisomal membrane protein lpx1; PDBTitle: peroxisomal alpha-beta-hydrolase lpx1 (yor084w) from saccharomyces2 cerevisiae (crystal form i) |
| 19 | c5uroA | Alignment |  | 100.0 | 14 | PDB header: hydrolase Chain: A: PDB Molecule: predicted protein; PDBTitle: structure of a soluble epoxide hydrolase identified in trichoderma2 reesei |
| 20 | c2cjpA | Alignment |  | 100.0 | 13 | PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: structure of potato (solanum tuberosum) epoxide hydrolase i (steh1) |
| 21 | c5f4zB | Alignment | not modelled | 100.0 | 8 | PDB header: hydrolase Chain: B: PDB Molecule: epoxide hydrolase; PDBTitle: the crystal structure of an epoxide hydrolase from streptomyces2 carzinostaticus subsp. neocarzinostaticus |
| 22 | d1zd3a2 | Alignment | not modelled | 100.0 | 15 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase |
| 23 | c5esrA | Alignment | not modelled | 100.0 | 9 | PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of haloalkane dehalogenase (dcca) from caulobacter2 crescentus |
| 24 | d1cr6a2 | Alignment | not modelled | 100.0 | 13 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase |
| 25 | d1b6ga | Alignment | not modelled | 100.0 | 14 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloalkane dehalogenase |
| 26 | c4i19A | Alignment | not modelled | 100.0 | 11 | PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: the crystal structure of an epoxide hydrolase from streptomyces2 carzinostaticus subsp. neocarzinostaticus. |
| 27 | c4qlaB | Alignment | not modelled | 100.0 | 12 | PDB header: hydrolase Chain: B: PDB Molecule: juvenile hormone epoxide hydrolase; PDBTitle: crystal structure of juvenile hormone epoxide hydrolase from the2 silkworm bombyx mori |
| 28 | c5efzC | Alignment | not modelled | 100.0 | 12 | PDB header: hydrolase Chain: C: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: monoclinic structure of the acetyl esterase mekb |
| | | | | | | Fold: alpha/beta-Hydrolases |

| | | | | | | |
|----|-------------------------|-----------|--------------|-------|----|---|
| 29 | d2pl5a1 | Alignment | not modelled | 100.0 | 11 | Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase |
| 30 | c3fsgC | Alignment | not modelled | 100.0 | 8 | PDB header: hydrolase Chain: C: PDB Molecule: alpha/beta superfamily hydrolase; PDBTitle: crystal structure of alpha/beta superfamily hydrolase from oenococcus2 oeni psu-1 |
| 31 | c3v48B | Alignment | not modelled | 100.0 | 12 | PDB header: hydrolase Chain: B: PDB Molecule: putative aminoacrylate hydrolase rutt; PDBTitle: crystal structure of the putative alpha/beta hydrolase rutt from2 e.coli |
| 32 | c5yhpB | Alignment | not modelled | 100.0 | 12 | PDB header: hydrolase Chain: B: PDB Molecule: cold active proline iminopeptidase; PDBTitle: proline iminopeptidase from psychrophilic yeast glaciozyma antarctica |
| 33 | c4pw0A | Alignment | not modelled | 100.0 | 13 | PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase fold protein; PDBTitle: alpha/beta hydrolase fold protein from chitinophaga pinensis |
| 34 | c3jw8A | Alignment | not modelled | 100.0 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: mgll protein; PDBTitle: crystal structure of human mono-glyceride lipase |
| 35 | c3u1tA | Alignment | not modelled | 100.0 | 11 | PDB header: hydrolase Chain: A: PDB Molecule: dmma haloalkane dehalogenase; PDBTitle: haloalkane dehalogenase, dmma, of marine microbial origin |
| 36 | c3oosA | Alignment | not modelled | 100.0 | 12 | PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase family protein; PDBTitle: the structure of an alpha/beta fold family hydrolase from bacillus2 anthracis str. Sterne |
| 37 | c3qvmA | Alignment | not modelled | 100.0 | 11 | PDB header: hydrolase Chain: A: PDB Molecule: olei00960; PDBTitle: the structure of olei00960, a hydrolase from oleispira antarctica |
| 38 | c2r11D | Alignment | not modelled | 100.0 | 11 | PDB header: hydrolase Chain: D: PDB Molecule: carboxylesterase np; PDBTitle: crystal structure of putative hydrolase (2632844) from bacillus2 subtilis at 1.96 a resolution |
| 39 | c4y7dA | Alignment | not modelled | 100.0 | 14 | PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase fold protein; PDBTitle: alpha/beta hydrolase fold protein from nakamurella multipartita |
| 40 | c2qmqA | Alignment | not modelled | 100.0 | 8 | PDB header: signaling protein Chain: A: PDB Molecule: protein ndr2; PDBTitle: crystal structure of a n-myc downstream regulated 2 protein (ndr2,2 syld, ndr2, ai182517, au040374) from mus musculus at 1.70 a3 resolution |
| 41 | c3om8A | Alignment | not modelled | 100.0 | 20 | PDB header: hydrolase Chain: A: PDB Molecule: probable hydrolase; PDBTitle: the crystal structure of a hydrolase from pseudomonas aeruginosa pa01 |
| 42 | c4f0jA | Alignment | not modelled | 100.0 | 12 | PDB header: hydrolase Chain: A: PDB Molecule: probable hydrolytic enzyme; PDBTitle: crystal structure of a probable hydrolytic enzyme (pa3053) from2 pseudomonas aeruginosa pao1 at 1.50 a resolution |
| 43 | c3kdaB | Alignment | not modelled | 100.0 | 13 | PDB header: hydrolase Chain: B: PDB Molecule: cftr inhibitory factor (cif); PDBTitle: crystal structure of the cftr inhibitory factor cif with the h269a2 mutation |
| 44 | c1y37A | Alignment | not modelled | 100.0 | 15 | PDB header: hydrolase Chain: A: PDB Molecule: fluoroacetate dehalogenase; PDBTitle: structure of fluoroacetate dehalogenase from burkholderia sp. fa1 |
| 45 | c5cw2C | Alignment | not modelled | 100.0 | 15 | PDB header: hydrolase Chain: C: PDB Molecule: putative epoxide hydrolase epha; PDBTitle: crystal structure of epoxide hydrolase a from mycobacterium2 thermoresistibile |
| 46 | c4nvrC | Alignment | not modelled | 100.0 | 12 | PDB header: transferase Chain: C: PDB Molecule: putative acyltransferase; PDBTitle: 2.22 angstrom resolution crystal structure of a putative2 acyltransferase from salmonella enterica |
| 47 | c2q0xA | Alignment | not modelled | 100.0 | 13 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: alpha/beta hydrolase fold protein of unknown function |
| 48 | c3wibB | Alignment | not modelled | 100.0 | 11 | PDB header: hydrolase Chain: B: PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of y109w mutant haloalkane dehalogenase data from2 agrobacterium tumefaciens c58 |
| 49 | c4mj3B | Alignment | not modelled | 100.0 | 13 | PDB header: hydrolase Chain: B: PDB Molecule: haloalkane dehalogenase; PDBTitle: haloalkane dehalogenase dmra from mycobacterium rhodesiae js60 |
| 50 | d1azwa | Alignment | not modelled | 100.0 | 10 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Proline iminopeptidase-like |
| 51 | c2xt0A | Alignment | not modelled | 100.0 | 11 | PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase; PDBTitle: dehalogenase dppa from plesiocystis pacifica sir-i |
| 52 | c3hjuB | Alignment | not modelled | 100.0 | 16 | PDB header: hydrolase Chain: B: PDB Molecule: monoglyceride lipase; PDBTitle: crystal structure of human monoglyceride lipase |
| 53 | c6eicA | Alignment | not modelled | 100.0 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: mycobacterium tuberculosis monoglyceride lipase; PDBTitle: crystal structure of rv0183, a monoglyceride lipase from mycobacterium2 tuberculosis |
| 54 | d1wm1a | Alignment | not modelled | 100.0 | 12 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Proline iminopeptidase-like |

| | | | | | | |
|----|------------------------|-----------|--------------|-------|----|---|
| 55 | c2xuaH | Alignment | not modelled | 100.0 | 16 | PDB header: hydrolase Chain: H: PDB Molecule: 3-oxoadipate enol-lactonase; PDBTitle: crystal structure of the eno-lactonase from burkholderia2 xenovorans lb400 |
| 56 | c6brtB | Alignment | not modelled | 100.0 | 18 | PDB header: ligase Chain: B: PDB Molecule: d3-cth-d14-d-ring; PDBTitle: f-box protein cth with hydrolase |
| 57 | c6f9oA | Alignment | not modelled | 100.0 | 10 | PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of cold-adapted haloalkane dehalogenase dpca from2 psychrobacter cryohalolentis k5 |
| 58 | d1q0ra | Alignment | not modelled | 100.0 | 13 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Aclacinomycin methylesterase RdmC |
| 59 | c5egnB | Alignment | not modelled | 100.0 | 16 | PDB header: hydrolase Chain: B: PDB Molecule: esterase; PDBTitle: est816 as an n-acyl homoserine lactone degrading enzyme |
| 60 | c3a2nF | Alignment | not modelled | 100.0 | 13 | PDB header: hydrolase Chain: F: PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of dbja (wild type type ii p21) |
| 61 | d1c4xa | Alignment | not modelled | 100.0 | 14 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase |
| 62 | d1hkha | Alignment | not modelled | 100.0 | 17 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase |
| 63 | c3e3aA | Alignment | not modelled | 100.0 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: possible peroxidase bpoc; PDBTitle: the structure of rv0554 from mycobacterium tuberculosis |
| 64 | c5mxbB | Alignment | not modelled | 100.0 | 11 | PDB header: hydrolase Chain: B: PDB Molecule: alpha/beta hydrolase; PDBTitle: haloalkane dehalogenase dmxa from marinobacter sp. elb17 possessing a2 unique catalytic residue |
| 65 | c4oseA | Alignment | not modelled | 100.0 | 12 | PDB header: hydrolase Chain: A: PDB Molecule: putative hydrolase; PDBTitle: x-ray crystal structure of a putative hydrolase from rickettsia typhi |
| 66 | c5oluA | Alignment | not modelled | 100.0 | 11 | PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase family protein; PDBTitle: the crystal structure of a highly thermostable carboxyl esterase from2 bacillus coagulans in complex with glycerol |
| 67 | c4inzB | Alignment | not modelled | 100.0 | 10 | PDB header: hydrolase Chain: B: PDB Molecule: soluble epoxide hydrolase; PDBTitle: the crystal structure of m145a mutant of an epoxide hydrolase from2 bacillus megaterium |
| 68 | c5h3hB | Alignment | not modelled | 100.0 | 16 | PDB header: hydrolase Chain: B: PDB Molecule: abhydrolase domain-containing protein; PDBTitle: esterase (eaest) from exiguobacterium antarcticum |
| 69 | c4b9aA | Alignment | not modelled | 100.0 | 13 | PDB header: hydrolase Chain: A: PDB Molecule: probable epoxide hydrolase; PDBTitle: structure of a putative epoxide hydrolase from pseudomonas2 aeruginosa. |
| 70 | c4l0cA | Alignment | not modelled | 100.0 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: deformylase; PDBTitle: crystal structure of the n-fopmylmaeamic acid deformylase nfo(s94a)2 from pseudomonas putida s16 |
| 71 | c3kxpD | Alignment | not modelled | 100.0 | 13 | PDB header: hydrolase Chain: D: PDB Molecule: alpha-(n-acetylaminomethylene)succinic acid hydrolase; PDBTitle: crystal structure of e-2-(acetamidomethylene)succinate hydrolase |
| 72 | d1qo7a | Alignment | not modelled | 100.0 | 11 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase |
| 73 | c5nfgA | Alignment | not modelled | 100.0 | 14 | PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase belonging to alpha/beta hydrolase PDBTitle: novel epoxide hydrolases belonging to the alpha/beta hydrolases2 superfamily in metagenomes from hot environments |
| 74 | d1a8qa | Alignment | not modelled | 100.0 | 14 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase |
| 75 | d1mtza | Alignment | not modelled | 100.0 | 14 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Proline iminopeptidase-like |
| 76 | d1ehya | Alignment | not modelled | 100.0 | 11 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase |
| 77 | c5hdfB | Alignment | not modelled | 100.0 | 13 | PDB header: hydrolase Chain: B: PDB Molecule: hydrolase; PDBTitle: hydrolase semet-stna |
| 78 | c3r3xA | Alignment | not modelled | 100.0 | 13 | PDB header: hydrolase Chain: A: PDB Molecule: fluoroacetate dehalogenase; PDBTitle: crystal structure of the fluoroacetate dehalogenase rpa1163 -2 asp110asn/bromoacetate |
| 79 | d1brta | Alignment | not modelled | 100.0 | 13 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase |
| 80 | c4rpcA | Alignment | not modelled | 100.0 | 11 | PDB header: hydrolase Chain: A: PDB Molecule: putative alpha/beta hydrolase; PDBTitle: crystal structure of the putative alpha/beta hydrolase family protein2 from desulfitobacterium hafniense PDB header: hydrolase |

| | | | | | | |
|-----|-------------------------|-----------|--------------|-------|----|--|
| 81 | c2rauA | Alignment | not modelled | 100.0 | 12 | Chain: A: PDB Molecule: putative esterase; PDBTitle: crystal structure of a putative lipase (np_343859.1) from sulfobolus2 solfataricus at 1.85 a resolution |
| 82 | c4uhhA | Alignment | not modelled | 100.0 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: structural studies of a thermophilic esterase from2 thermogutta terrifontis (cacodylate complex) |
| 83 | d1m33a | Alignment | not modelled | 100.0 | 11 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Biotin biosynthesis protein BioH |
| 84 | c5ng7B | Alignment | not modelled | 100.0 | 12 | PDB header: hydrolase Chain: B: PDB Molecule: epoxide hydrolase; PDBTitle: novel epoxide hydrolases belonging to the alpha/beta hydrolases2 superfamily in metagenomes from hot environments |
| 85 | c3fobA | Alignment | not modelled | 100.0 | 13 | PDB header: oxidoreductase Chain: A: PDB Molecule: bromoperoxidase; PDBTitle: crystal structure of bromoperoxidase from bacillus anthracis |
| 86 | c5w15D | Alignment | not modelled | 100.0 | 17 | PDB header: hydrolase Chain: D: PDB Molecule: alpha/beta hydrolase fold protein; PDBTitle: crystal structure of an alpha/beta hydrolase fold protein from2 burkholderia ambifaria. |
| 87 | c4zwnD | Alignment | not modelled | 100.0 | 11 | PDB header: hydrolase Chain: D: PDB Molecule: monoglyceride lipase; PDBTitle: crystal structure of a soluble variant of the monoglyceride lipase2 from saccharomyces cerevisiae |
| 88 | c5bovD | Alignment | not modelled | 100.0 | 12 | PDB header: hydrolase Chain: D: PDB Molecule: putative epoxide hydrolase protein; PDBTitle: crystal structure of a putative epoxide hydrolase (kpn_01808) from2 klebsiella pneumoniae subsp. pneumoniae mgh 78578 at 1.60 a3 resolution |
| 89 | c3e0xB | Alignment | not modelled | 100.0 | 12 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: lipase-esterase related protein; PDBTitle: the crystal structure of a lipase-esterase related protein2 from clostridium acetobutylicum atcc 824 |
| 90 | d1e89a | Alignment | not modelled | 100.0 | 13 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hydroxynitrile lyase-like |
| 91 | c4q3IC | Alignment | not modelled | 100.0 | 13 | PDB header: hydrolase Chain: C: PDB Molecule: mgs-m2; PDBTitle: crystal structure of mgs-m2, an alpha/beta hydrolase enzyme from a2 medee basin deep-sea metagenome library |
| 92 | c3wzIB | Alignment | not modelled | 100.0 | 14 | PDB header: hydrolase Chain: B: PDB Molecule: zearalenone hydrolase; PDBTitle: zen lactonase |
| 93 | c4psuA | Alignment | not modelled | 100.0 | 19 | PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase; PDBTitle: crystal structure of alpha/beta hydrolase from rhodospseudomonas2 palustris cga009 |
| 94 | d1a8sa | Alignment | not modelled | 100.0 | 14 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase |
| 95 | d1va4a | Alignment | not modelled | 100.0 | 14 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase |
| 96 | d2rhwa1 | Alignment | not modelled | 100.0 | 8 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase |
| 97 | c2wj4B | Alignment | not modelled | 100.0 | 11 | PDB header: oxidoreductase Chain: B: PDB Molecule: 1h-3-hydroxy-4-oxoquinaldine 2,4-dioxygenase; PDBTitle: crystal structure of the cofactor-devoid 1-h-3-hydroxy-4-2 oxoquinaldine 2,4-dioxygenase (hod) from arthrobacter3 nitroguajacolicus ru61a anaerobically complexed with its4 natural substrate 1-h-3-hydroxy-4-oxoquinaldine |
| 98 | d1mj5a | Alignment | not modelled | 100.0 | 11 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloalkane dehalogenase |
| 99 | c3llcA | Alignment | not modelled | 100.0 | 13 | PDB header: hydrolase Chain: A: PDB Molecule: putative hydrolase; PDBTitle: crystal structure of putative hydrolase (yp_002548124.1) from2 agrobacterium vitis s4 at 1.80 a resolution |
| 100 | c2yysA | Alignment | not modelled | 100.0 | 14 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: proline iminopeptidase-related protein; PDBTitle: crystal structure of the proline iminopeptidase-related protein2 ttha1809 from thermus thermophilus hb8 |
| 101 | d1xkla | Alignment | not modelled | 100.0 | 11 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hydroxynitrile lyase-like |
| 102 | c3bwxA | Alignment | not modelled | 100.0 | 13 | PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase; PDBTitle: crystal structure of an alpha/beta hydrolase (yp_496220.1) from2 novosphingobium aromaticivorans dsm 12444 at 1.50 a resolution |
| 103 | c1zoiC | Alignment | not modelled | 100.0 | 13 | PDB header: hydrolase Chain: C: PDB Molecule: esterase; PDBTitle: crystal structure of a stereoselective esterase from2 pseudomonas putida ifo12996 |
| 104 | c3qyjB | Alignment | not modelled | 100.0 | 12 | PDB header: hydrolase Chain: B: PDB Molecule: alr0039 protein; PDBTitle: crystal structure of alr0039, a putative alpha/beta hydrolase from2 nostoc sp pcc 7120. |
| 105 | d1uk8a | Alignment | not modelled | 100.0 | 11 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase |
| | | | | | | PDB header: hydrolase |

| | | | | | | |
|-----|-------------------------|-----------|--------------|-------|----|---|
| 106 | c1u2eA_ | Alignment | not modelled | 100.0 | 10 | Chain: A; PDB Molecule: 2-hydroxy-6-ketona-2,4-dienedioic acid PDBTitle: crystal structure of the c-c bond hydrolase mhpc |
| 107 | d3c70a1 | Alignment | not modelled | 100.0 | 11 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hydroxynitrile lyase-like |
| 108 | c3l80A_ | Alignment | not modelled | 100.0 | 10 | PDB header: hydrolase Chain: A; PDB Molecule: putative uncharacterized protein smu.1393c; PDBTitle: crystal structure of smu.1393c from streptococcus mutans ua159 |
| 109 | c3p2mA_ | Alignment | not modelled | 100.0 | 14 | PDB header: hydrolase Chain: A; PDB Molecule: possible hydrolase; PDBTitle: crystal structure of a novel esterase rv0045c from mycobacterium2 tuberculosis |
| 110 | c3ibtA_ | Alignment | not modelled | 100.0 | 9 | PDB header: oxidoreductase Chain: A; PDB Molecule: 1h-3-hydroxy-4-oxoquinoline 2,4-dioxygenase; PDBTitle: structure of 1h-3-hydroxy-4-oxoquinoline 2,4-dioxygenase (qdo) |
| 111 | d1bn7a_ | Alignment | not modelled | 100.0 | 15 | Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloalkane dehalogenase |
| 112 | c2xmzA_ | Alignment | not modelled | 100.0 | 15 | PDB header: lyase Chain: A; PDB Molecule: hydrolase, alpha/beta hydrolase fold family; PDBTitle: structure of menh from s. aureus |
| 113 | c4i3fA_ | Alignment | not modelled | 100.0 | 15 | PDB header: hydrolase Chain: A; PDB Molecule: serine hydrolase ccsp0084; PDBTitle: crystal structure of serine hydrolase ccsp0084 from the polyaromatic2 hydrocarbon (pah)-degrading bacterium cycloclasticus zankles |
| 114 | c5dnuA_ | Alignment | not modelled | 100.0 | 12 | PDB header: hydrolase Chain: A; PDB Molecule: shkai2ib; PDBTitle: crystal structure of kai2-like protein from striga (apo state 2) |
| 115 | c4rncB_ | Alignment | not modelled | 100.0 | 13 | PDB header: hydrolase Chain: B; PDB Molecule: esterase; PDBTitle: crystal structure of an esterase rhest1 from rhodococcus sp. ecu1013 |
| 116 | c3wwoA_ | Alignment | not modelled | 100.0 | 11 | PDB header: lyase Chain: A; PDB Molecule: (s)-hydroxynitrile lyase; PDBTitle: s-selective hydroxynitrile lyase from baliospermum montanum (apo1) |
| 117 | c3nwoA_ | Alignment | not modelled | 100.0 | 15 | PDB header: hydrolase Chain: A; PDB Molecule: proline iminopeptidase; PDBTitle: crystal structure of proline iminopeptidase mycobacterium smegmatis |
| 118 | c3rm3A_ | Alignment | not modelled | 100.0 | 18 | PDB header: hydrolase Chain: A; PDB Molecule: thermostable monoacylglycerol lipase; PDBTitle: crystal structure of monoacylglycerol lipase from bacillus sp. h257 |
| 119 | c3flaB_ | Alignment | not modelled | 100.0 | 17 | PDB header: hydrolase Chain: B; PDB Molecule: rifr; PDBTitle: rifr - type ii thioesterase from rifamycin nrps/pks biosynthetic2 pathway - form 1 |
| 120 | c6g75B_ | Alignment | not modelled | 100.0 | 10 | PDB header: hydrolase Chain: B; PDB Molecule: common ancestor of haloalkane dehalogenase and renilla PDBTitle: crystal structure of the common ancestor of haloalkane dehalogenases2 and renilla luciferase (anchld-rluc) |