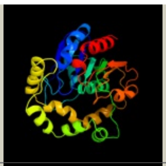
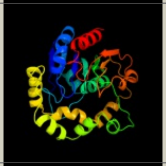
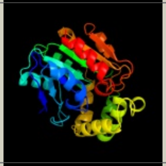
# Phyre$^2$

| | |
|---|---|
| Email | l.a.kelley@imperial.ac.uk |
| Description | P13001 |
| Date | Thu Jan 5 11:33:21 GMT 2012 |
| Unique Job ID | e98fdc2a292b391e |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | d1m33a_ | Alignment |  | 100.0 | 97 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Biotin biosynthesis protein BioH |
| 2 | c1cr6A_ | Alignment |  | 100.0 | 19 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**epoxide hydrolase;<br>**PDBTitle:** crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor |
| 3 | c1u2eA_ | Alignment |  | 100.0 | 22 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**2-hydroxy-6-ketonona-2,4-dienedioic acid<br>**PDBTitle:** crystal structure of the c-c bond hydrolase mhpc |
| 4 | d2rhwa1 | Alignment |  | 100.0 | 19 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Carbon-carbon bond hydrolase |
| 5 | c3kdaB_ | Alignment |  | 100.0 | 15 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**cftr inhibitory factor (cif);<br>**PDBTitle:** crystal structure of the cftr inhibitory factor cif with the h269a2 mutation |
| 6 | c1wprA_ | Alignment |  | 100.0 | 15 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**sigma factor sigb regulation protein rsbq;<br>**PDBTitle:** crystal structure of rsbq inhibited by pmsf |
| 7 | c3qvmA_ | Alignment |  | 100.0 | 18 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**olei00960;<br>**PDBTitle:** the structure of olei00960, a hydrolase from oleispira antarctica |
| 8 | d1ehya_ | Alignment |  | 100.0 | 16 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Epoxide hydrolase |
| 9 | c3oosA_ | Alignment |  | 100.0 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**alpha/beta hydrolase family protein;<br>**PDBTitle:** the structure of an alpha/beta fold family hydrolase from bacillus2 anthracis str. sterne |
| 10 | c3e3aA_ | Alignment |  | 100.0 | 16 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**possible peroxidase bpoc;<br>**PDBTitle:** the structure of rv0554 from mycobacterium tuberculosis |
| 11 | c3om8A_ | Alignment |  | 100.0 | 18 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**probable hydrolase;<br>**PDBTitle:** the crystal structure of a hydrolase from pseudomonas aeruginosa pa01 |

| | | | | | | |
|---|---|---|---|---|---|---|
| 12 | d1zd3a2 | Alignment |  | 100.0 | 16 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Epoxide hydrolase |
| 13 | d1cr6a2 | Alignment |  | 100.0 | 19 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Epoxide hydrolase |
| 14 | d1hkha_ | Alignment |  | 100.0 | 18 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Haloperoxidase |
| 15 | c2wj4B_ | Alignment |  | 100.0 | 13 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**1h-3-hydroxy-4-oxoquinaldine 2,4-dioxygenase;<br>**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 |
| 16 | c2xuaH_ | Alignment |  | 100.0 | 16 | **PDB header:**hydrolase<br>**Chain:** H: **PDB Molecule:**3-oxoadipate enol-lactonase;<br>**PDBTitle:** crystal structure of the enol-lactonase from burkholderia2 xenovorans lb400 |
| 17 | d1va4a_ | Alignment |  | 100.0 | 23 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Haloperoxidase |
| 18 | c3fsgC_ | Alignment |  | 100.0 | 14 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**alpha/beta superfamily hydrolase;<br>**PDBTitle:** crystal structure of alpha/beta superfamily hydrolase from oenococcus2 oeni psu-1 |
| 19 | c2qmqA_ | Alignment |  | 100.0 | 14 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**protein ndrg2;<br>**PDBTitle:** crystal structure of a n-myc downstream regulated 2 protein (ndrg2,2 syld, ndr2, ai182517, au040374) from mus musculus at 1.70 a3 resolution |
| 20 | c2cjpA_ | Alignment |  | 100.0 | 18 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**epoxide hydrolase;<br>**PDBTitle:** structure of potato (solanum tuberosum) epoxide hydrolase i2 (steh1) |
| 21 | c2vavL_ | Alignment | not modelled | 100.0 | 11 | **PDB header:**transferase<br>**Chain:** L: **PDB Molecule:**acetyl-coa--deacetylcephalosporin c<br>**PDBTitle:** crystal structure of deacetylcephalosporin c2 acetyltransferase (dac-soak) |
| 22 | c3ibtA_ | Alignment | not modelled | 100.0 | 11 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**1h-3-hydroxy-4-oxoquinoline 2,4-dioxygenase;<br>**PDBTitle:** structure of 1h-3-hydroxy-4-oxoquinoline 2,4-dioxygenase (qdo) |
| 23 | d1brta_ | Alignment | not modelled | 100.0 | 18 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Haloperoxidase |
| 24 | c3kxpD_ | Alignment | not modelled | 100.0 | 19 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**alpha-(n-acetylaminomethylene)succinic acid<br>**PDBTitle:** crystal structure of e-2-(acetamidomethylene)succinate2 hydrolase |
| 25 | d1c4xa_ | Alignment | not modelled | 100.0 | 19 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Carbon-carbon bond hydrolase |
| 26 | c3u1tA_ | Alignment | not modelled | 100.0 | 18 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**dmma haloalkane dehalogenase;<br>**PDBTitle:** haloalkane dehalogenase, dmma, of marine microbial origin |
| 27 | c2xmzA_ | Alignment | not modelled | 100.0 | 15 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**hydrolase, alpha/beta hydrolase fold family;<br>**PDBTitle:** structure of menh from s. aureus |
| 28 | d1b6ga_ | Alignment | not modelled | 100.0 | 12 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Haloalkane dehalogenase |

| | | | | | | |
|---|---|---|---|---|---|---|
| 29 | c3a2nF_ | Alignment | not modelled | 100.0 | 15 | **PDB header:**hydrolase<br>**Chain:** F: **PDB Molecule:**haloalkane dehalogenase;<br>**PDBTitle:** crystal structure of dbja (wild type type ii p21) |
| 30 | d1q0ra_ | Alignment | not modelled | 100.0 | 18 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Aclacinomycin methylesterase RdmC |
| 31 | d1a8qa_ | Alignment | not modelled | 100.0 | 16 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Haloperoxidase |
| 32 | c3v48B_ | Alignment | not modelled | 100.0 | 20 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**putative aminoacrylate hydrolase rutd;<br>**PDBTitle:** crystal structure of the putative alpha/beta hydrolase rutd from2 e.coli |
| 33 | c2vf2A_ | Alignment | not modelled | 100.0 | 19 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate<br>**PDBTitle:** x-ray crystal structure of hsad from mycobacterium2 tuberculosis |
| 34 | c2y6vB_ | Alignment | not modelled | 100.0 | 14 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**peroxisomal membrane protein lpx1;<br>**PDBTitle:** peroxisomal alpha-beta-hydrolase lpx1 (yor084w) from2 saccharomyces cerevisiae (crystal form i) |
| 35 | c2e3jA_ | Alignment | not modelled | 100.0 | 20 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**epoxide hydrolase ephb;<br>**PDBTitle:** the crystal structure of epoxide hydrolase b (rv1938) from2 mycobacterium tuberculosis at 2.1 angstrom |
| 36 | d1r3da_ | Alignment | not modelled | 100.0 | 16 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Hypothetical protein VC1974 |
| 37 | d1bn7a_ | Alignment | not modelled | 100.0 | 15 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Haloalkane dehalogenase |
| 38 | d1uk8a_ | Alignment | not modelled | 100.0 | 19 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Carbon-carbon bond hydrolase |
| 39 | d2vata1 | Alignment | not modelled | 100.0 | 12 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**O-acetyltransferase |
| 40 | c3fobA_ | Alignment | not modelled | 100.0 | 19 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**bromoperoxidase;<br>**PDBTitle:** crystal structure of bromoperoxidase from bacillus anthracis |
| 41 | d1a8sa_ | Alignment | not modelled | 100.0 | 19 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Haloperoxidase |
| 42 | d1mj5a_ | Alignment | not modelled | 100.0 | 17 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Haloalkane dehalogenase |
| 43 | c2r11D_ | Alignment | not modelled | 100.0 | 16 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**carboxylesterase np;<br>**PDBTitle:** crystal structure of putative hydrolase (2632844) from2 bacillus subtilis at 1.96 a resolution |
| 44 | c2pseA_ | Alignment | not modelled | 100.0 | 16 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**renilla-luciferin 2-monooxygenase;<br>**PDBTitle:** crystal structures of the luciferase and green fluorescent2 protein from renilla reniformis |
| 45 | d2b61a1 | Alignment | not modelled | 100.0 | 16 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**O-acetyltransferase |
| 46 | d1j1ia_ | Alignment | not modelled | 100.0 | 23 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Carbon-carbon bond hydrolase |
| 47 | c1j1iA_ | Alignment | not modelled | 100.0 | 23 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**meta cleavage compound hydrolase;<br>**PDBTitle:** crystal structure of a his-tagged serine hydrolase involved2 in the carbazole degradation (carc enzyme) |
| 48 | c3i1iA_ | Alignment | not modelled | 100.0 | 15 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**homoserine o-acetyltransferase;<br>**PDBTitle:** x-ray crystal structure of homoserine o-acetyltransferase from2 bacillus anthracis |
| 49 | c2qvbA_ | Alignment | not modelled | 100.0 | 18 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**haloalkane dehalogenase 3;<br>**PDBTitle:** crystal structure of haloalkane dehalogenase rv2579 from mycobacterium2 tuberculosis |
| 50 | c2xt0A_ | Alignment | not modelled | 100.0 | 14 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**haloalkane dehalogenase;<br>**PDBTitle:** dehalogenase dppa from plesiocystis pacifica sir-i |
| 51 | c1zoiC_ | Alignment | not modelled | 100.0 | 17 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**esterase;<br>**PDBTitle:** crystal structure of a stereoselective esterase from2 pseudomonas putida ifo12996 |
| 52 | c3qyjB_ | Alignment | not modelled | 100.0 | 20 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**alr0039 protein;<br>**PDBTitle:** crystal structure of alr0039, a putative alpha/beta hydrolase from2 nostoc sp pcc 7120. |
| 53 | c2yysA_ | Alignment | not modelled | 100.0 | 17 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**proline iminopeptidase-related protein;<br>**PDBTitle:** crystal structure of the proline iminopeptidase-related protein2 ttha1809 from thermus thermophilus hb8 |
| 54 | c3e0xB_ | Alignment | not modelled | 100.0 | 19 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**lipase-esterase related protein;<br>**PDBTitle:** the crystal structure of a lipase-esterase related protein2 from clostridium acetobutylicum atcc 824 |
| | | | | | | **PDB header:**hydrolase |

| | | | | | | |
|---|---|---|---|---|---|---|
| 55 | c1y37A_ | Alignment | not modelled | 100.0 | 18 | **Chain:** A: **PDB Molecule:**fluoroacetate dehalogenase;<br>**PDBTitle:** structure of fluoroacetate dehalogenase from burkholderia sp. fa1 |
| 56 | d1mtza_ | Alignment | not modelled | 100.0 | 14 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Proline iminopeptidase-like |
| 57 | c3p2mA_ | Alignment | not modelled | 100.0 | 21 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**possible hydrolase;<br>**PDBTitle:** crystal structure of a novel esterase rv0045c from mycobacterium2 tuberculosis |
| 58 | c3r0vA_ | Alignment | not modelled | 100.0 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**alpha/beta hydrolase fold protein;<br>**PDBTitle:** the crystal structure of an alpha/beta hydrolase from sphaerobacter2 thermophilus dsm 20745. |
| 59 | c3bwxA_ | Alignment | not modelled | 100.0 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**alpha/beta hydrolase;<br>**PDBTitle:** crystal structure of an alpha/beta hydrolase (yp_496220.1) from2 novosphingobium aromaticivorans dsm 12444 at 1.50 a resolution |
| 60 | d1a88a_ | Alignment | not modelled | 100.0 | 18 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Haloperoxidase |
| 61 | c3bf7B_ | Alignment | not modelled | 100.0 | 16 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**esterase ybff;<br>**PDBTitle:** 1.1 resolution structure of ybff, a new esterase from2 escherichia coli: a unique substrate-binding crevice3 generated by domain arrangement |
| 62 | d1azwa_ | Alignment | not modelled | 100.0 | 19 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Proline iminopeptidase-like |
| 63 | c3r3xA_ | Alignment | not modelled | 100.0 | 21 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**fluoroacetate dehalogenase;<br>**PDBTitle:** crystal structure of the fluoroacetate dehalogenase rpa1163 -2 asp110asn/bromoacetate |
| 64 | d1xkla_ | Alignment | not modelled | 100.0 | 16 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Hydroxynitrile lyase-like |
| 65 | d1wm1a_ | Alignment | not modelled | 100.0 | 21 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Proline iminopeptidase-like |
| 66 | c3nwoA_ | Alignment | not modelled | 100.0 | 18 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**proline iminopeptidase;<br>**PDBTitle:** crystal structure of proline iminopeptidase mycobacterium smegmatis |
| 67 | c2ockA_ | Alignment | not modelled | 100.0 | 22 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**valacyclovir hydrolase;<br>**PDBTitle:** crystal structure of valacyclovir hydrolase d123n mutant |
| 68 | c3l80A_ | Alignment | not modelled | 100.0 | 12 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**putative uncharacterized protein smu.1393c;<br>**PDBTitle:** crystal structure of smu.1393c from streptococcus mutans ua159 |
| 69 | d2pl5a1 | Alignment | not modelled | 99.9 | 15 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**O-acetyltransferase |
| 70 | c3dqzB_ | Alignment | not modelled | 99.9 | 14 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**alpha-hydroxynitrile lyase-like protein;<br>**PDBTitle:** structure of the hydroxynitrile lyase from arabidopsis2 thaliana |
| 71 | d1e89a_ | Alignment | not modelled | 99.9 | 13 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Hydroxynitrile lyase-like |
| 72 | d3c70a1 | Alignment | not modelled | 99.9 | 14 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Hydroxynitrile lyase-like |
| 73 | d1qo7a_ | Alignment | not modelled | 99.9 | 13 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Epoxide hydrolase |
| 74 | c3gzjB_ | Alignment | not modelled | 99.9 | 16 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**polyneuridine-aldehyde esterase;<br>**PDBTitle:** crystal structure of polyneuridine aldehyde esterase2 complexed with 16-epi-vellosimine |
| 75 | c3qitB_ | Alignment | not modelled | 99.9 | 14 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**polyketide synthase;<br>**PDBTitle:** thioesterase domain from curacin biosynthetic pathway |
| 76 | c3jw8A_ | Alignment | not modelled | 99.9 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**mgll protein;<br>**PDBTitle:** crystal structure of human mono-glyceride lipase |
| 77 | c3c5wP_ | Alignment | not modelled | 99.9 | 16 | **PDB header:**hydrolase<br>**Chain:** P: **PDB Molecule:**pp2a-specific methylesterase pme-1;<br>**PDBTitle:** complex between pp2a-specific methylesterase pme-1 and pp2a core2 enzyme |
| 78 | c3hjuB_ | Alignment | not modelled | 99.9 | 15 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**monoglyceride lipase;<br>**PDBTitle:** crystal structure of human monoglyceride lipase |
| 79 | c3flaB_ | Alignment | not modelled | 99.9 | 13 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**rifr;<br>**PDBTitle:** rifr - type ii thioesterase from rifamycin nrps/pks biosynthetic2 pathway - form 1 |
| 80 | c2ronA_ | Alignment | not modelled | 99.9 | 13 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**surfactin synthetase thioesterase subunit;<br>**PDBTitle:** the external thioesterase of the surfactin-synthetase |
| | | | | | | **Fold:**alpha/beta-Hydrolases |

| | | | | | | |
|---|---|---|---|---|---|---|
| 81 | d1imja_ | Alignment | not modelled | 99.9 | 25 | **Superfamily:**alpha/beta-Hydrolases<br>**Family:**Ccg1/TafII250-interacting factor B (Cib) |
| 82 | d1tqha_ | Alignment | not modelled | 99.9 | 16 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Carboxylesterase/lipase |
| 83 | d1hlga_ | Alignment | not modelled | 99.9 | 17 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Gastric lipase |
| 84 | c3dyvA_ | Alignment | not modelled | 99.9 | 19 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**esterase d;<br>**PDBTitle:** snapshots of esterase d from lactobacillus rhamnosus:2 insights into a rotation driven catalytic mechanism |
| 85 | c3bdiA_ | Alignment | not modelled | 99.9 | 22 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**uncharacterized protein ta0194;<br>**PDBTitle:** crystal structure of predicted cib-like hydrolase (np_393672.1) from2 thermoplasma acidophilum at 1.45 a resolution |
| 86 | d1k8qa_ | Alignment | not modelled | 99.9 | 16 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Gastric lipase |
| 87 | c3h04A_ | Alignment | not modelled | 99.9 | 13 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** the crystal structure of the protein with unknown function from2 staphylococcus aureus subsp. aureus mu50 |
| 88 | d1pjaa_ | Alignment | not modelled | 99.9 | 15 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Thioesterases |
| 89 | c1pjaA_ | Alignment | not modelled | 99.9 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**palmitoyl-protein thioesterase 2 precursor;<br>**PDBTitle:** the crystal structure of palmitoyl protein thioesterase-2 reveals the2 basis for divergent substrate specificities of the two lysosomal3 thioesterases (ppt1 and ppt2) |
| 90 | c3qm1A_ | Alignment | not modelled | 99.9 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**cinnamoyl esterase;<br>**PDBTitle:** crystal structure of the lactobacillus johnsonii cinnamoyl esterase2 lj0536 s106a mutant in complex with ethylferulate, form ii |
| 91 | d1xkta_ | Alignment | not modelled | 99.9 | 11 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Thioesterase domain of polypeptide, polyketide and fatty acid synthases |
| 92 | c3fcyB_ | Alignment | not modelled | 99.9 | 11 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**xylan esterase 1;<br>**PDBTitle:** crystal structure of acetyl xylan esterase 1 from2 thermoanaerobacterium sp. jw/sl ys485 |
| 93 | c3llcA_ | Alignment | not modelled | 99.9 | 16 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**putative hydrolase;<br>**PDBTitle:** crystal structure of putative hydrolase (yp_002548124.1) from2 agrobacterium vitis s4 at 1.80 a resolution |
| 94 | c2q0xA_ | Alignment | not modelled | 99.9 | 8 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** alpha/beta hydrolase fold protein of unknown function |
| 95 | c3qmwD_ | Alignment | not modelled | 99.9 | 15 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**thioesterase;<br>**PDBTitle:** redj with peg molecule bound in the active site |
| 96 | c2px6A_ | Alignment | not modelled | 99.9 | 10 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**thioesterase domain;<br>**PDBTitle:** crystal structure of the thioesterase domain of human fatty2 acid synthase inhibited by orlistat |
| 97 | c3lcrA_ | Alignment | not modelled | 99.8 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**tautomycetin biosynthetic pks;<br>**PDBTitle:** thioesterase from tautomycetin biosynthhetic pathway |
| 98 | c2wtmC_ | Alignment | not modelled | 99.8 | 13 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**est1e;<br>**PDBTitle:** est1e from butyrivibrio proteoclasticus |
| 99 | d1l7aa_ | Alignment | not modelled | 99.8 | 15 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Acetyl xylan esterase-like |
| 100 | c2hdwB_ | Alignment | not modelled | 99.8 | 10 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**hypothetical protein pa2218;<br>**PDBTitle:** crystal structure of hypothetical protein pa2218 from pseudomonas2 aeruginosa |
| 101 | c3fleB_ | Alignment | not modelled | 99.8 | 14 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**se_1780 protein;<br>**PDBTitle:** se_1780 protein of unknown function from staphylococcus epidermidis. |
| 102 | d1uxoa_ | Alignment | not modelled | 99.8 | 13 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**YdeN-like |
| 103 | d1qlwa_ | Alignment | not modelled | 99.8 | 14 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**A novel bacterial esterase |
| 104 | d1ufoa_ | Alignment | not modelled | 99.8 | 19 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Hypothetical protein TT1662 |
| 105 | c2qs9A_ | Alignment | not modelled | 99.8 | 17 | **PDB header:**structural protein<br>**Chain:** A: **PDB Molecule:**retinoblastoma-binding protein 9;<br>**PDBTitle:** crystal structure of the human retinoblastoma-binding2 protein 9 (rbbp-9). nesg target hr2978 |
| 106 | c2qruA_ | Alignment | not modelled | 99.8 | 12 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** crystal structure of an alpha/beta hydrolase superfamily protein from2 enterococcus faecalis |

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
| 107 | c3fnbB_ | Alignment | not modelled | 99.8 | 15 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**acylaminoacyl peptidase smu_737;<br>**PDBTitle:** crystal structure of acylaminoacyl peptidase smu_737 from2 streptococcus mutans ua159 |
| 108 | c3mveB_ | Alignment | not modelled | 99.8 | 11 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**upf0255 protein vv1_0328;<br>**PDBTitle:** crystal structure of a novel pyruvate decarboxylase |
| 109 | d1ex9a_ | Alignment | not modelled | 99.8 | 15 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Bacterial lipase |
| 110 | c2h7xA_ | Alignment | not modelled | 99.8 | 16 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**type i polyketide synthase pikaiv;<br>**PDBTitle:** pikromycin thioesterase adduct with reduced triketide2 affinity label |
| 111 | c3ksrA_ | Alignment | not modelled | 99.8 | 16 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**putative serine hydrolase;<br>**PDBTitle:** crystal structure of a putative serine hydrolase (xcc3885) from2 xanthomonas campestris pv. campestris at 2.69 a resolution |
| 112 | c3ilsA_ | Alignment | not modelled | 99.8 | 10 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**aflatoxin biosynthesis polyketide synthase;<br>**PDBTitle:** the thioesterase domain from pksa |
| 113 | d2h7xa1 | Alignment | not modelled | 99.7 | 17 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Thioesterase domain of polypeptide, polyketide and fatty acid synthases |
| 114 | c2rauA_ | Alignment | not modelled | 99.7 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**putative esterase;<br>**PDBTitle:** crystal structure of a putative lipase (np_343859.1) from sulfolobus2 solfataricus at 1.85 a resolution |
| 115 | c2qjwA_ | Alignment | not modelled | 99.7 | 23 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**uncharacterized protein xcc1541;<br>**PDBTitle:** crystal structure of a putative hydrolase of the alpha/beta2 superfamily (xcc1541) from xanthomonas campestris pv. campestris at3 1.35 a resolution |
| 116 | d1vlqa_ | Alignment | not modelled | 99.7 | 19 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Acetyl xylan esterase-like |
| 117 | c2jbwB_ | Alignment | not modelled | 99.7 | 19 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**2,6-dihydroxy-pseudo-oxynicotine hydrolase;<br>**PDBTitle:** crystal structure of the 2,6-dihydroxy-pseudo-oxynicotine2 hydrolase. |
| 118 | c3lp5A_ | Alignment | not modelled | 99.7 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**putative cell surface hydrolase;<br>**PDBTitle:** the crystal structure of the putative cell surface hydrolase from2 lactobacillus plantarum wcfs1 |
| 119 | c1mo2A_ | Alignment | not modelled | 99.7 | 14 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**erythronolide synthase, modules 5 and 6;<br>**PDBTitle:** thioesterase domain from 6-deoxyerythronolide synthase2 (debs te), ph 8.5 |
| 120 | d1mo2a_ | Alignment | not modelled | 99.7 | 14 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Thioesterase domain of polypeptide, polyketide and fatty acid synthases |