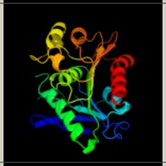
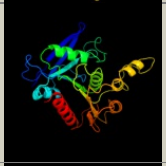
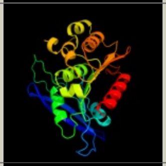
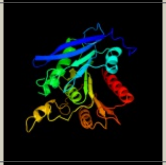
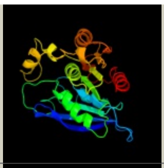
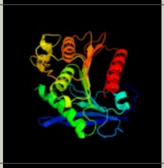
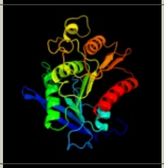
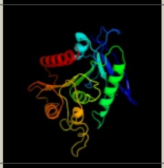
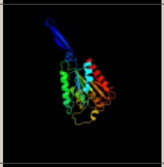
# Phyre$^2$

| | |
|---|---|
| Email | l.a.kelley@imperial.ac.uk |
| Description | P77538 |
| Date | Thu Jan 5 12:30:21 GMT 2012 |
| Unique Job ID | 3ae6baf2b4348895 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c2ecfA_ | Alignment |  | 100.0 | 19 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**dipeptidyl peptidase iv;<br>**PDBTitle:** crystal structure of dipeptidyl aminopeptidase iv from2 stenotrophomonas maltophilia |
| 2 | c3azqA_ | Alignment |  | 100.0 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**aminopeptidase;<br>**PDBTitle:** crystal structure of puromycin hydrolase s511a mutant complexed with2 pgg |
| 3 | c2hu7A_ | Alignment |  | 100.0 | 20 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**acylamino-acid-releasing enzyme;<br>**PDBTitle:** binding of inhibitors by acylaminoacyl peptidase |
| 4 | c2eepA_ | Alignment |  | 100.0 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**dipeptidyl aminopeptidase iv, putative;<br>**PDBTitle:** prolyl tripeptidyl aminopeptidase complexed with an inhibitor |
| 5 | c1z68A_ | Alignment |  | 100.0 | 16 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**fibroblast activation protein, alpha subunit;<br>**PDBTitle:** crystal structure of human fibroblast activation protein alpha |
| 6 | c2g5tA_ | Alignment |  | 100.0 | 18 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**dipeptidyl peptidase 4;<br>**PDBTitle:** crystal structure of human dipeptidyl peptidase iv (dppiv)2 complexed with cyanopyrrolidine (c5-pro-pro) inhibitor 21ag |
| 7 | c2qtbB_ | Alignment |  | 100.0 | 19 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**dipeptidyl peptidase 4;<br>**PDBTitle:** human dipeptidyl peptidase iv/cd26 in complex with a 4-aryl2 cyclohexylalanine inhibitor |
| 8 | d1l7aa_ | Alignment |  | 100.0 | 20 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Acetyl xylan esterase-like |
| 9 | c1qfmA_ | Alignment |  | 100.0 | 16 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**protein (prolyl oligopeptidase);<br>**PDBTitle:** prolyl oligopeptidase from porcine muscle |
| 10 | c2wtmC_ | Alignment |  | 100.0 | 20 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**est1e;<br>**PDBTitle:** est1e from butyrivibrio proteoclasticus |
| 11 | d1qfma2 | Alignment |  | 100.0 | 17 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Prolyl oligopeptidase, C-terminal domain |

| | | | | | | |
|---|---|---|---|---|---|---|
| 12 | c2hdwB_ | Alignment |  | 100.0 | 23 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**hypothetical protein pa2218;<br>**PDBTitle:** crystal structure of hypothetical protein pa2218 from pseudomonas2 aeruginosa |
| 13 | d1vlqa_ | Alignment |  | 100.0 | 20 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Acetyl xylan esterase-like |
| 14 | c3fcyB_ | Alignment |  | 100.0 | 19 | **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 |
| 15 | c2bklB_ | Alignment |  | 100.0 | 16 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**prolyl endopeptidase;<br>**PDBTitle:** structural and mechanistic analysis of two prolyl2 endopeptidases: role of inter-domain dynamics in3 catalysis and specificity |
| 16 | c3qm1A_ | Alignment |  | 100.0 | 21 | **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 |
| 17 | c2xe4A_ | Alignment |  | 100.0 | 15 | **PDB header:**hydrolase/inhibitor<br>**Chain:** A: **PDB Molecule:**oligopeptidase b;<br>**PDBTitle:** structure of oligopeptidase b from leishmania major |
| 18 | c1xfdD_ | Alignment |  | 100.0 | 16 | **PDB header:**membrane protein<br>**Chain:** D: **PDB Molecule:**dipeptidyl aminopeptidase-like protein 6;<br>**PDBTitle:** structure of a human a-type potassium channel accelerating factor2 dppx, a member of the dipeptidyl aminopeptidase family |
| 19 | c3ksrA_ | Alignment |  | 100.0 | 15 | **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 |
| 20 | c2jbwB_ | Alignment |  | 100.0 | 18 | **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. |
| 21 | d2jbwa1 | Alignment | not modelled | 100.0 | 16 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**2,6-dihydropseudooxynicotine hydrolase-like |
| 22 | d1hlga_ | Alignment | not modelled | 100.0 | 17 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Gastric lipase |
| 23 | d1k8qa_ | Alignment | not modelled | 100.0 | 16 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Gastric lipase |
| 24 | c3jw8A_ | Alignment | not modelled | 100.0 | 19 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**mgll protein;<br>**PDBTitle:** crystal structure of human mono-glyceride lipase |
| 25 | d2fuka1 | Alignment | not modelled | 100.0 | 21 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Atu1826-like |
| 26 | c3fnbB_ | Alignment | not modelled | 100.0 | 20 | **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 |
| 27 | c3iumA_ | Alignment | not modelled | 100.0 | 16 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**prolyl endopeptidase;<br>**PDBTitle:** appep_wtx opened state |
| 28 | c3hjuB_ | Alignment | not modelled | 100.0 | 17 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**monoglyceride lipase;<br>**PDBTitle:** crystal structure of human monoglyceride lipase |
| 29 | c3mveB_ | Alignment | not modelled | 99.9 | 14 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**upf0255 protein vv1_0328; |

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
|  |  |  |  |  |  | **PDBTitle:** crystal structure of a novel pyruvate decarboxylase |
| 30 | d2hu7a2 | Alignment | not modelled | 99.9 | 18 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Acylamino-acid-releasing enzyme, C-terminal donain |
| 31 | d1orva2 | Alignment | not modelled | 99.9 | 15 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**DPP6 catalytic domain-like |
| 32 | c1cr6A_ | Alignment | not modelled | 99.9 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**epoxide hydrolase;<br>**PDBTitle:** crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor |
| 33 | c3h04A_ | Alignment | not modelled | 99.9 | 17 | **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 |
| 34 | c3llcA_ | Alignment | not modelled | 99.9 | 20 | **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 |
| 35 | d2bgra2 | Alignment | not modelled | 99.9 | 15 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**DPP6 catalytic domain-like |
| 36 | d2i3da1 | Alignment | not modelled | 99.9 | 21 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Atu1826-like |
| 37 | c2i3dA_ | Alignment | not modelled | 99.9 | 21 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**hypothetical protein atu1826;<br>**PDBTitle:** crystal structure of protein of unknown function atu1826, a putative2 alpha/beta hydrolase from agrobacterium tumefaciens |
| 38 | c3trdA_ | Alignment | not modelled | 99.9 | 19 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**alpha/beta hydrolase;<br>**PDBTitle:** structure of an alpha-beta serine hydrolase homologue from coxiella2 burnetii |
| 39 | c1yr2A_ | Alignment | not modelled | 99.9 | 14 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**prolyl oligopeptidase;<br>**PDBTitle:** structural and mechanistic analysis of two prolyl endopeptidases: role2 of inter-domain dynamics in catalysis and specificity |
| 40 | d1ju3a2 | Alignment | not modelled | 99.9 | 15 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**PepX catalytic domain-like |
| 41 | c3f67A_ | Alignment | not modelled | 99.9 | 14 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**putative dienelactone hydrolase;<br>**PDBTitle:** crystal structure of putative dienelactone hydrolase from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578 |
| 42 | d1a8qa_ | Alignment | not modelled | 99.9 | 19 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Haloperoxidase |
| 43 | c2o2gA_ | Alignment | not modelled | 99.9 | 19 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**dienelactone hydrolase;<br>**PDBTitle:** crystal structure of dienelactone hydrolase (yp_324580.1) from2 anabaena variabilis atcc 29413 at 1.92 a resolution |
| 44 | d1b6ga_ | Alignment | not modelled | 99.9 | 18 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Haloalkane dehalogenase |
| 45 | d1mtza_ | Alignment | not modelled | 99.9 | 18 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Proline iminopeptidase-like |
| 46 | c3k2iA_ | Alignment | not modelled | 99.9 | 18 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**acyl-coenzyme a thioesterase 4;<br>**PDBTitle:** human acyl-coenzyme a thioesterase 4 |
| 47 | c3hlkB_ | Alignment | not modelled | 99.9 | 18 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**acyl-coenzyme a thioesterase 2, mitochondrial;<br>**PDBTitle:** crystal structure of human mitochondrial acyl-coa2 thioesterase (acot2) |
| 48 | d1dina_ | Alignment | not modelled | 99.9 | 19 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Dienelactone hydrolase |
| 49 | c3dyvA_ | Alignment | not modelled | 99.9 | 11 | **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 |
| 50 | d1brta_ | Alignment | not modelled | 99.9 | 17 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Haloperoxidase |
| 51 | d1xfda2 | Alignment | not modelled | 99.9 | 17 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**DPP6 catalytic domain-like |
| 52 | d1cr6a2 | Alignment | not modelled | 99.9 | 17 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Epoxide hydrolase |
| 53 | c1zoiC_ | Alignment | not modelled | 99.9 | 21 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**esterase;<br>**PDBTitle:** crystal structure of a stereoselective esterase from2 pseudomonas putida ifo12996 |
| 54 | d1a8sa_ | Alignment | not modelled | 99.9 | 24 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Haloperoxidase |
| 55 | d1zd3a2 | Alignment | not modelled | 99.9 | 19 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Epoxide hydrolase |

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
| 56 | c3bxpA_ | Alignment | not modelled | 99.9 | 14 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**putative lipase/esterase;<br>**PDBTitle:** crystal structure of a putative carboxylesterase (lp_2923) from2 lactobacillus plantarum wcfs1 at 1.70 a resolution |
| 57 | d1va4a_ | Alignment | not modelled | 99.9 | 20 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Haloperoxidase |
| 58 | c2xt0A_ | Alignment | not modelled | 99.9 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**haloalkane dehalogenase;<br>**PDBTitle:** dehalogenase dppa from plesiocystis pacifica sir-i |
| 59 | d1tqha_ | Alignment | not modelled | 99.9 | 20 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Carboxylesterase/lipase |
| 60 | d1a88a_ | Alignment | not modelled | 99.9 | 18 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Haloperoxidase |
| 61 | c2vavL_ | Alignment | not modelled | 99.9 | 14 | **PDB header:**transferase<br>**Chain:** L: **PDB Molecule:**acetyl-coa--deacetylcephalosporin c<br>**PDBTitle:** crystal structure of deacetylcephalosporin c2 acetyltransferase (dac-soak) |
| 62 | c3i1iA_ | Alignment | not modelled | 99.9 | 16 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**homoserine o-acetyltransferase;<br>**PDBTitle:** x-ray crystal structure of homoserine o-acetyltransferase from2 bacillus anthracis |
| 63 | c3doiA_ | Alignment | not modelled | 99.9 | 16 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**esterase;<br>**PDBTitle:** crystal structure of a thermostable esterase complex with2 paraoxon |
| 64 | c3om8A_ | Alignment | not modelled | 99.9 | 18 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**probable hydrolase;<br>**PDBTitle:** the crystal structure of a hydrolase from pseudomonas aeruginosa pa01 |
| 65 | c3bwxA_ | Alignment | not modelled | 99.9 | 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 |
| 66 | c2e3jA_ | Alignment | not modelled | 99.9 | 18 | **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 |
| 67 | d1ehya_ | Alignment | not modelled | 99.9 | 15 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Epoxide hydrolase |
| 68 | c3v48B_ | Alignment | not modelled | 99.9 | 15 | **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 |
| 69 | d1q0ra_ | Alignment | not modelled | 99.9 | 20 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Aclacinomycin methylesterase RdmC |
| 70 | d1ufoa_ | Alignment | not modelled | 99.9 | 18 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Hypothetical protein TT1662 |
| 71 | c2cjpA_ | Alignment | not modelled | 99.9 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**epoxide hydrolase;<br>**PDBTitle:** structure of potato (solanum tuberosum) epoxide hydrolase i2 (steh1) |
| 72 | c2y6vB_ | Alignment | not modelled | 99.9 | 17 | **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) |
| 73 | d1wm1a_ | Alignment | not modelled | 99.9 | 18 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Proline iminopeptidase-like |
| 74 | d2vata1 | Alignment | not modelled | 99.9 | 13 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**O-acetyltransferase |
| 75 | d1azwa_ | Alignment | not modelled | 99.9 | 20 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Proline iminopeptidase-like |
| 76 | c2r11D_ | Alignment | not modelled | 99.9 | 14 | **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 |
| 77 | c2yysA_ | Alignment | not modelled | 99.9 | 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 |
| 78 | c3ib3A_ | Alignment | not modelled | 99.9 | 16 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**coce/nond family hydrolase;<br>**PDBTitle:** crystal structure of sacol2612 - coce/nond family hydrolase from2 staphylococcus aureus |
| 79 | c2xuaH_ | Alignment | not modelled | 99.9 | 21 | **PDB header:**hydrolase<br>**Chain:** H: **PDB Molecule:**3-oxoadipate enol-lactonase;<br>**PDBTitle:** crystal structure of the enol-lactonase from burkholderia2 xenovorans lb400 |
| 80 | c3hxkB_ | Alignment | not modelled | 99.9 | 16 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**sugar hydrolase;<br>**PDBTitle:** crystal structure of a sugar hydrolase (yeeb) from2 lactococcus lactis, northeast structural genomics3 consortium target kr108 |
| 81 | c3u1tA_ | Alignment | not modelled | 99.9 | 16 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**dmma haloalkane dehalogenase;<br>**PDBTitle:** haloalkane dehalogenase, dmma, of marine microbial |

| | | | | | | |
|---|---|---|---|---|---|---|
| | | | | | | origin |
| 82 | c3dqzB_ | Alignment | not modelled | 99.9 | 16 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**alpha-hydroxynitrile lyase-like protein;<br>**PDBTitle:** structure of the hydroxynitrile lyase from arabidopsis2 thaliana |
| 83 | c3fobA_ | Alignment | not modelled | 99.9 | 22 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**bromoperoxidase;<br>**PDBTitle:** crystal structure of bromoperoxidase from bacillus anthracis |
| 84 | c2ockA_ | Alignment | not modelled | 99.9 | 21 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**valacyclovir hydrolase;<br>**PDBTitle:** crystal structure of valacyclovir hydrolase d123n mutant |
| 85 | c3qvmA_ | Alignment | not modelled | 99.9 | 16 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**olei00960;<br>**PDBTitle:** the structure of olei00960, a hydrolase from oleispira antarctica |
| 86 | c1l7qA_ | Alignment | not modelled | 99.9 | 16 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**cocaine esterase;<br>**PDBTitle:** ser117ala mutant of bacterial cocaine esterase coce |
| 87 | c3oosA_ | Alignment | not modelled | 99.9 | 14 | **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 |
| 88 | d1e89a_ | Alignment | not modelled | 99.9 | 15 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Hydroxynitrile lyase-like |
| 89 | d1hkha_ | Alignment | not modelled | 99.9 | 16 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Haloperoxidase |
| 90 | d3c70a1 | Alignment | not modelled | 99.9 | 16 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Hydroxynitrile lyase-like |
| 91 | c2vf2A_ | Alignment | not modelled | 99.9 | 18 | **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 |
| 92 | c2c7bA_ | Alignment | not modelled | 99.9 | 13 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**carboxylesterase;<br>**PDBTitle:** the crystal structure of este1, a new thermophilic and2 thermostable carboxylesterase cloned from a metagenomic3 library |
| 93 | d1c4xa_ | Alignment | not modelled | 99.9 | 17 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Carbon-carbon bond hydrolase |
| 94 | d2b61a1 | Alignment | not modelled | 99.9 | 14 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**O-acetyltransferase |
| 95 | c3h2iA_ | Alignment | not modelled | 99.9 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**esterase;<br>**PDBTitle:** crystal structure of n228w mutant of the rice cell wall2 degrading esterase lipa from xanthomonas oryzae |
| 96 | c3bdiA_ | Alignment | not modelled | 99.9 | 19 | **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 |
| 97 | d1jkma_ | Alignment | not modelled | 99.9 | 13 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Carboxylesterase |
| 98 | c3nwoA_ | Alignment | not modelled | 99.9 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**proline iminopeptidase;<br>**PDBTitle:** crystal structure of proline iminopeptidase mycobacterium smegmatis |
| 99 | d1uxoa_ | Alignment | not modelled | 99.9 | 14 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**YdeN-like |
| 100 | c3kdaB_ | Alignment | not modelled | 99.9 | 18 | **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 |
| 101 | d2rhwa1 | Alignment | not modelled | 99.9 | 19 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Carbon-carbon bond hydrolase |
| 102 | d1fj2a_ | Alignment | not modelled | 99.9 | 16 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Carboxylesterase/thioesterase 1 |
| 103 | d1xkla_ | Alignment | not modelled | 99.9 | 18 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Hydroxynitrile lyase-like |
| 104 | c3ed1E_ | Alignment | not modelled | 99.9 | 13 | **PDB header:**hydrolase receptor<br>**Chain:** E: **PDB Molecule:**gibberellin receptor gid1;<br>**PDBTitle:** crystal structure of rice gid1 complexed with ga3 |
| 105 | c2qruA_ | Alignment | not modelled | 99.9 | 17 | **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 |
| 106 | c2qmqA_ | Alignment | not modelled | 99.9 | 12 | **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 |
| 107 | c3kxpD_ | Alignment | not modelled | 99.9 | 17 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**alpha-(n-acetylaminomethylene)succinic acid |

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
|  |  |  |  |  |  | **PDBTitle:** crystal structure of e-2-(acetamidomethylene)succinate2 hydrolase |
| 108 | c1u2eA_ | Alignment | not modelled | 99.9 | 16 | **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 |
| 109 | c3r0vA_ | Alignment | not modelled | 99.9 | 18 | **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. |
| 110 | c2wirB_ | Alignment | not modelled | 99.9 | 14 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**alpha/beta hydrolase fold-3 domain protein;<br>**PDBTitle:** hyperthermophilic esterase from the archeon pyrobaculum2 calidifontis |
| 111 | c3e0xB_ | Alignment | not modelled | 99.9 | 21 | **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 |
| 112 | d1uk8a_ | Alignment | not modelled | 99.9 | 18 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Carbon-carbon bond hydrolase |
| 113 | c3ga7A_ | Alignment | not modelled | 99.9 | 14 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**acetyl esterase;<br>**PDBTitle:** 1.55 angstrom crystal structure of an acetyl esterase from salmonella2 typhimurium |
| 114 | c3p2mA_ | Alignment | not modelled | 99.9 | 13 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**possible hydrolase;<br>**PDBTitle:** crystal structure of a novel esterase rv0045c from mycobacterium2 tuberculosis |
| 115 | c2wj4B_ | Alignment | not modelled | 99.9 | 14 | **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 |
| 116 | c2q0xA_ | Alignment | not modelled | 99.9 | 12 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** alpha/beta hydrolase fold protein of unknown function |
| 117 | c3aikB_ | Alignment | not modelled | 99.9 | 12 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**303aa long hypothetical esterase;<br>**PDBTitle:** crystal structure of a hsl-like carboxylesterase from sulfolobus2 tokodaii |
| 118 | c2b9vB_ | Alignment | not modelled | 99.9 | 17 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**alpha-amino acid ester hydrolase;<br>**PDBTitle:** acetobacter turbidans alpha-amino acid ester hydrolase |
| 119 | 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 |
| 120 | d1jfra_ | Alignment | not modelled | 99.9 | 18 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Lipase |