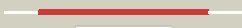



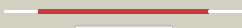




















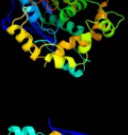




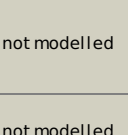


# Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P07000
Date	Wed Jan 25 15:20:12 GMT 2012
Unique Job ID	29e7ab737451bc42

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1cr6A_</a>	 Alignment		100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> epoxide hydrolase; <b>PDBTitle:</b> crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
2	<a href="#">c3jw8A_</a>	 Alignment		100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mgII protein; <b>PDBTitle:</b> crystal structure of human mono-glyceride lipase
3	<a href="#">d1hlga_</a>	 Alignment		100.0	13	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Gastric lipase
4	<a href="#">c3iliA_</a>	 Alignment		100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> homoserine o-acetyltransferase; <b>PDBTitle:</b> x-ray crystal structure of homoserine o-acetyltransferase from2 bacillus anthracis
5	<a href="#">c3hjuB_</a>	 Alignment		100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> monoglyceride lipase; <b>PDBTitle:</b> crystal structure of human monoglyceride lipase
6	<a href="#">d2b61a1</a>	 Alignment		100.0	14	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> O-acetyltransferase
7	<a href="#">c2vavL_</a>	 Alignment		100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> L: <b>PDB Molecule:</b> acetyl-coa--deacetylcephalosporin c <b>PDBTitle:</b> crystal structure of deacetylcephalosporin c2 acetyltransferase (dac-soak)
8	<a href="#">d1k8qa_</a>	 Alignment		100.0	14	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Gastric lipase
9	<a href="#">c2y6vB_</a>	 Alignment		100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> peroxisomal membrane protein lpx1; <b>PDBTitle:</b> peroxisomal alpha-beta-hydrolase lpx1 (yor084w) from2 saccharomyces cerevisiae (crystal form i)
10	<a href="#">c2cjpA_</a>	 Alignment		100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> epoxide hydrolase; <b>PDBTitle:</b> structure of potato (solanum tuberosum) epoxide hydrolase i2 (steh1)
11	<a href="#">d2vata1</a>	 Alignment		100.0	13	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> O-acetyltransferase

12	<a href="#">d2pl5a1</a>	Alignment		100.0	11	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> O-acetyltransferase
13	<a href="#">c2e3jA</a>	Alignment		100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> epoxide hydrolase ephb; <b>PDBTitle:</b> the crystal structure of epoxide hydrolase b (rv1938) from2 mycobacterium tuberculosis at 2.1 angstrom
14	<a href="#">d1b6ga</a>	Alignment		100.0	14	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloalkane dehalogenase
15	<a href="#">d1zd3a2</a>	Alignment		100.0	14	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Epoxide hydrolase
16	<a href="#">d1cr6a2</a>	Alignment		100.0	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Epoxide hydrolase
17	<a href="#">d1azwa</a>	Alignment		100.0	14	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Proline iminopeptidase-like
18	<a href="#">c2qmqA</a>	Alignment		100.0	10	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein ndr2; <b>PDBTitle:</b> crystal structure of a n-myc downstream regulated 2 protein (ndr2,2 syl2, ndr2, ai182517, au040374) from mus musculus at 1.70 a3 resolution
19	<a href="#">c3om8A</a>	Alignment		100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable hydrolase; <b>PDBTitle:</b> the crystal structure of a hydrolase from pseudomonas aeruginosa pa01
20	<a href="#">d1mtza</a>	Alignment		100.0	14	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Proline iminopeptidase-like
21	<a href="#">c3bwxA</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha/beta hydrolase; <b>PDBTitle:</b> crystal structure of an alpha/beta hydrolase (yp_496220.1) from2 novosphingobium aromaticivorans dsm 12444 at 1.50 a resolution
22	<a href="#">d1wm1a</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Proline iminopeptidase-like
23	<a href="#">c3oosA</a>	Alignment	not modelled	100.0	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha/beta hydrolase family protein; <b>PDBTitle:</b> the structure of an alpha/beta fold family hydrolase from bacillus2 anthracis str. Sterne
24	<a href="#">c2r11D</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> carboxylesterase np; <b>PDBTitle:</b> crystal structure of putative hydrolase (2632844) from2 bacillus subtilis at 1.96 a resolution
25	<a href="#">c2xuaH</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> 3-oxoadipate enol-lactonase; <b>PDBTitle:</b> crystal structure of the enol-lactonase from burkholderia2 xenovorans lb400
26	<a href="#">c2xt0A</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> haloalkane dehalogenase; <b>PDBTitle:</b> dehalogenase dppa from pleisiocystis pacifica sir-i
27	<a href="#">c2yysA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> proline iminopeptidase-related protein; <b>PDBTitle:</b> crystal structure of the proline iminopeptidase-related protein2 ttha1809 from thermus thermophilus hb8
28	<a href="#">c3qvmA</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> olei00960; <b>PDBTitle:</b> the structure of olei00960, a hydrolase from oleispira antarctica

29	<a href="#">c3u1tA</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dmma haloalkane dehalogenase; <b>PDBTitle:</b> haloalkane dehalogenase, dmma, of marine microbial origin
30	<a href="#">c3v48B</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative aminoacrylate hydrolase rtdt; <b>PDBTitle:</b> crystal structure of the putative alpha/beta hydrolase rtdt from 2 e.coli
31	<a href="#">c1y37A</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> fluoroacetate dehalogenase; <b>PDBTitle:</b> structure of fluoroacetate dehalogenase from burkholderia sp. fa1
32	<a href="#">d1q0ra</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Aclacinomycin methylesterase RdmC
33	<a href="#">d1a8qa</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloperoxidase
34	<a href="#">d1ehya</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Epoxide hydrolase
35	<a href="#">c2q0xA</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> alpha/beta hydrolase fold protein of unknown function
36	<a href="#">d1qo7a</a>	Alignment	not modelled	100.0	12	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Epoxide hydrolase
37	<a href="#">d1a8sa</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloperoxidase
38	<a href="#">d1c4xa</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carbon-carbon bond hydrolase
39	<a href="#">c3kdaB</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cftr inhibitory factor (cif); <b>PDBTitle:</b> crystal structure of the cftr inhibitory factor cif with the h269a2 mutation
40	<a href="#">c3h04A</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> the crystal structure of the protein with unknown function from 2 staphylococcus aureus subsp. aureus mu50
41	<a href="#">c1zoiC</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> crystal structure of a stereoselective esterase from 2 pseudomonas putida ifo12996
42	<a href="#">d1hkha</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloperoxidase
43	<a href="#">c3e3aA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> possible peroxidase bpoc; <b>PDBTitle:</b> the structure of rv0554 from mycobacterium tuberculosis
44	<a href="#">c3e0xB</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> lipase-esterase related protein; <b>PDBTitle:</b> the crystal structure of a lipase-esterase related protein2 from clostridium acetobutylicum atcc 824
45	<a href="#">c3kxpD</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> alpha-(n-acetylaminomethylene)succinic acid <b>PDBTitle:</b> crystal structure of e-2-(acetamidomethylene)succinate2 hydrolase
46	<a href="#">d1mj5a</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloalkane dehalogenase
47	<a href="#">c3fsgC</a>	Alignment	not modelled	100.0	10	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> alpha/beta superfamily hydrolase; <b>PDBTitle:</b> crystal structure of alpha/beta superfamily hydrolase from oenococcus2 oeni psu-1
48	<a href="#">d1va4a</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloperoxidase
49	<a href="#">c2wj4B</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 1h-3-hydroxy-4-oxoquinaldine 2,4-dioxygenase; <b>PDBTitle:</b> 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
50	<a href="#">d1a88a</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloperoxidase
51	<a href="#">d1brta</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloperoxidase
52	<a href="#">c2rauA</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative esterase; <b>PDBTitle:</b> crystal structure of a putative lipase (np_343859.1) from sulfobolus2 solfataricus at 1.85 a resolution
53	<a href="#">d1uk8a</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carbon-carbon bond hydrolase
54	<a href="#">c3nwoA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> proline iminopeptidase; <b>PDBTitle:</b> crystal structure of proline iminopeptidase

						mycobacterium smegmatis
55	<a href="#">c3l80A_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein smu.1393c; <b>PDBTitle:</b> crystal structure of smu.1393c from streptococcus mutans ua159
56	<a href="#">c3qitB_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> polyketide synthase; <b>PDBTitle:</b> thioesterase domain from curacin biosynthetic pathway
57	<a href="#">d1bn7a_</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloalkane dehalogenase
58	<a href="#">d1m33a_</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Biotin biosynthesis protein BioH
59	<a href="#">c3a2nF_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> haloalkane dehalogenase; <b>PDBTitle:</b> crystal structure of dbja (wild type type ii p21)
60	<a href="#">c2xmzA_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrolase, alpha/beta hydrolase fold family; <b>PDBTitle:</b> structure of menh from s. aureus
61	<a href="#">d2rhwa1</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carbon-carbon bond hydrolase
62	<a href="#">c3ibtA_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 1h-3-hydroxy-4-oxoquinoline 2,4-dioxygenase; <b>PDBTitle:</b> structure of 1h-3-hydroxy-4-oxoquinoline 2,4-dioxygenase (qdo)
63	<a href="#">c3c5wP_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> P: <b>PDB Molecule:</b> pp2a-specific methylesterase pme-1; <b>PDBTitle:</b> complex between pp2a-specific methylesterase pme-1 and pp2a core2 enzyme
64	<a href="#">c3qyiB_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> alr0039 protein; <b>PDBTitle:</b> crystal structure of alr0039, a putative alpha/beta hydrolase from2 nostoc sp pcc 7120.
65	<a href="#">c2hu7A_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> acylamino-acid-releasing enzyme; <b>PDBTitle:</b> binding of inhibitors by acylaminoacyl peptidase
66	<a href="#">c2vf2A_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate <b>PDBTitle:</b> x-ray crystal structure of hsd from mycobacterium2 tuberculosis
67	<a href="#">c1u2eA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-hydroxy-6-ketonona-2,4-dienedioic acid <b>PDBTitle:</b> crystal structure of the c-c bond hydrolase mhpc
68	<a href="#">c2hdwB_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein pa2218; <b>PDBTitle:</b> crystal structure of hypothetical protein pa2218 from pseudomonas2 aeruginosa
69	<a href="#">d3c70a1</a>	Alignment	not modelled	100.0	11	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Hydroxynitrile lyase-like
70	<a href="#">c2qvbA_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> haloalkane dehalogenase 3; <b>PDBTitle:</b> crystal structure of haloalkane dehalogenase rv2579 from mycobacterium2 tuberculosis
71	<a href="#">d1xkla_</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Hydroxynitrile lyase-like
72	<a href="#">c3r3xA_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> fluoroacetate dehalogenase; <b>PDBTitle:</b> crystal structure of the fluoroacetate dehalogenase rpa1163 -2 asp110asn/bromoacetate
73	<a href="#">d1e89a_</a>	Alignment	not modelled	100.0	12	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Hydroxynitrile lyase-like
74	<a href="#">c3fobA_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> bromoperoxidase; <b>PDBTitle:</b> crystal structure of bromoperoxidase from bacillus anthracis
75	<a href="#">c2wtmC_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> est1e; <b>PDBTitle:</b> est1e from butyrivibrio proteoclasticus
76	<a href="#">c3dyvA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase d; <b>PDBTitle:</b> snapshots of esterase d from lactobacillus rhamnosus:2 insights into a rotation driven catalytic mechanism
77	<a href="#">c3p2mA_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> possible hydrolase; <b>PDBTitle:</b> crystal structure of a novel esterase rv0045c from mycobacterium2 tuberculosis
78	<a href="#">c3r0vA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha/beta hydrolase fold protein; <b>PDBTitle:</b> the crystal structure of an alpha/beta hydrolase from sphaerobacter2 thermophilus dsm 20745.
79	<a href="#">c3dqzB_</a>	Alignment	not modelled	100.0	9	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-hydroxynitrile lyase-like protein; <b>PDBTitle:</b> structure of the hydroxynitrile lyase from arabidopsis2 thaliana
80	<a href="#">c1wnrA_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> sigma factor sigb regulation protein

80	<a href="#">c1wpiA</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> hydrolase <b>PDBTitle:</b> crystal structure of rsbq inhibited by pmsf
81	<a href="#">c3bdiA</a>	Alignment	not modelled	100.0	23	<b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ta0194; <b>PDBTitle:</b> crystal structure of predicted cib-like hydrolase (np_393672.1) from2 thermoplasma acidophilum at 1.45 a resolution
82	<a href="#">c3llcA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative hydrolase; <b>PDBTitle:</b> crystal structure of putative hydrolase (yp_002548124.1) from2 agrobacterium vitis s4 at 1.80 a resolution
83	<a href="#">c2pseA</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> renilla-luciferin 2-monoxygenase; <b>PDBTitle:</b> crystal structures of the luciferase and green fluorescent2 protein from renilla reniformis
84	<a href="#">d1imja</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Ccg1/TafII250-interacting factor B (Cib)
85	<a href="#">c2ockA</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> valacyclovir hydrolase; <b>PDBTitle:</b> crystal structure of valacyclovir hydrolase d123n mutant
86	<a href="#">c3gzjB</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> polyneuridine-aldehyde esterase; <b>PDBTitle:</b> crystal structure of polyneuridine aldehyde esterase2 complexed with 16-epi-velliosimine
87	<a href="#">c1jliA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> meta cleavage compound hydrolase; <b>PDBTitle:</b> crystal structure of a his-tagged serine hydrolase involved2 in the carbazole degradation (carc enzyme)
88	<a href="#">d1jlia</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carbon-carbon bond hydrolase
89	<a href="#">c3bf7B</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> esterase ybff; <b>PDBTitle:</b> 1.1 resolution structure of ybff, a new esterase from2 escherichia coli: a unique substrate-binding crevice3 generated by domain arrangement
90	<a href="#">d1r3da</a>	Alignment	not modelled	100.0	10	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Hypothetical protein VC1974
91	<a href="#">c3qm1A</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cinnamoyl esterase; <b>PDBTitle:</b> crystal structure of the lactobacillus johnsonii cinnamoyl esterase2 lj0536 s106a mutant in complex with ethylferulate, form ii
92	<a href="#">d1l7aa</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Acetyl xylan esterase-like
93	<a href="#">d1tqha</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carboxylesterase/lipase
94	<a href="#">c2jwbB</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 2,6-dihydroxy-pseudo-oxynicotine hydrolase; <b>PDBTitle:</b> crystal structure of the 2,6-dihydroxy-pseudo-oxynicotine2 hydrolase.
95	<a href="#">c3flaB</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> rifr; <b>PDBTitle:</b> rifr - type ii thioesterase from rifamycin nrps/pks biosynthetic2 pathway - form 1
96	<a href="#">c1pjaA</a>	Alignment	not modelled	99.9	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> palmitoyl-protein thioesterase 2 precursor; <b>PDBTitle:</b> the crystal structure of palmitoyl protein thioesterase-2 reveals the2 basis for divergent substrate specificities of the two lysosomal3 thioesterases (ppt1 and ppt2)
97	<a href="#">d1pjaa</a>	Alignment	not modelled	99.9	9	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Thioesterases
98	<a href="#">c2o2gA</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dienelactone hydrolase; <b>PDBTitle:</b> crystal structure of dienelactone hydrolase (yp_324580.1) from2 anabaena variabilis atcc 29413 at 1.92 a resolution
99	<a href="#">c3fleB</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> se_1780 protein; <b>PDBTitle:</b> se_1780 protein of unknown function from staphylococcus epidermidis.
100	<a href="#">d2jba1</a>	Alignment	not modelled	99.9	18	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> 2,6-dihydropseudooxynicotine hydrolase-like
101	<a href="#">c3mveB</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> upf0255 protein vv1_0328; <b>PDBTitle:</b> crystal structure of a novel pyruvate decarboxylase
102	<a href="#">c3fnbB</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> acylaminoacyl peptidase smu_737; <b>PDBTitle:</b> crystal structure of acylaminoacyl peptidase smu_737 from2 streptococcus mutans ua159
103	<a href="#">c3azqA</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> aminopeptidase; <b>PDBTitle:</b> crystal structure of puromycin hydrolase s511a mutant complexed with2 pgg
104	<a href="#">c2ecfA</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dipeptidyl peptidase iv; <b>PDBTitle:</b> crystal structure of dipeptidyl aminopeptidase iv from2 stentrophomonas maltophilia <b>PDB header:</b> hydrolase

105	<a href="#">c3ksrA_</a>	Alignment	not modelled	99.9	19	<b>Chain:</b> A: <b>PDB Molecule:</b> putative serine hydrolase; <b>PDBTitle:</b> crystal structure of a putative serine hydrolase (xcc3885) from2 xanthomonas campestris pv. campestris at 2.69 a resolution
106	<a href="#">c2ronA_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> surfactin synthetase thioesterase subunit; <b>PDBTitle:</b> the external thioesterase of the surfactin-synthetase
107	<a href="#">c3lp5A_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative cell surface hydrolase; <b>PDBTitle:</b> the crystal structure of the putative cell surface hydrolase from2 lactobacillus plantarum wcf51
108	<a href="#">d1lfoa_</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Hypothetical protein TT1662
109	<a href="#">d1xkta_</a>	Alignment	not modelled	99.9	11	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Thioesterase domain of polypeptide, polyketide and fatty acid synthases
110	<a href="#">d1ju3a2</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> PepX catalytic domain-like
111	<a href="#">c2g5tA_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dipeptidyl peptidase 4; <b>PDBTitle:</b> crystal structure of human dipeptidyl peptidase iv (dppi)2 complexed with cyanopyrrolidine (c5-pro-pro) inhibitor 21ag
112	<a href="#">c2qrUA_</a>	Alignment	not modelled	99.9	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of an alpha/beta hydrolase superfamily protein from2 enterococcus faecalis
113	<a href="#">c2qtbB_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dipeptidyl peptidase 4; <b>PDBTitle:</b> human dipeptidyl peptidase iv/cd26 in complex with a 4-aryl2 cyclohexylalanine inhibitor
114	<a href="#">c2eepA_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dipeptidyl aminopeptidase iv, putative; <b>PDBTitle:</b> prolyl tripeptidyl aminopeptidase complexed with an inhibitor
115	<a href="#">c3fcyB_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> xylan esterase 1; <b>PDBTitle:</b> crystal structure of acetyl xylan esterase 1 from2 thermoanaerobacterium sp. jw/sl ys485
116	<a href="#">c1z68A_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> fibroblast activation protein, alpha subunit; <b>PDBTitle:</b> crystal structure of human fibroblast activation protein alpha
117	<a href="#">c3k2iA_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-coenzyme a thioesterase 4; <b>PDBTitle:</b> human acyl-coenzyme a thioesterase 4
118	<a href="#">d1ex9a_</a>	Alignment	not modelled	99.9	9	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Bacterial lipase
119	<a href="#">d1uxoa_</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> YdeN-like
120	<a href="#">c3h1kB_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> acyl-coenzyme a thioesterase 2, mitochondrial; <b>PDBTitle:</b> crystal structure of human mitochondrial acyl-coa2 thioesterase (acot2)