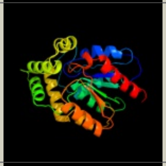
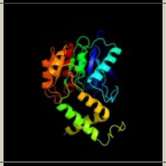
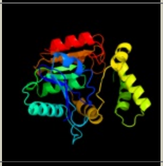
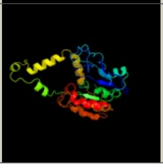
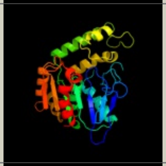
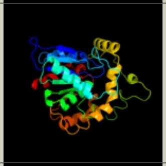
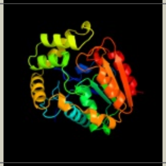
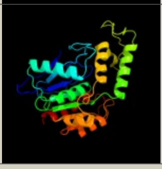
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P75895
Date	Thu Jan 5 12:15:46 GMT 2012
Unique Job ID	c61568e18a7a3907

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3v48B_	Alignment		100.0	98	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative aminoacrylate hydrolase rutd; **PDBTitle:** crystal structure of the putative alpha/beta hydrolase rutd from2 e.coli
2	c1cr6A_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**epoxide hydrolase; **PDBTitle:** crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
3	c2qmqA_	Alignment		100.0	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**protein ndrg2; **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
4	c2r11D_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**carboxylesterase np; **PDBTitle:** crystal structure of putative hydrolase (2632844) from2 bacillus subtilis at 1.96 a resolution
5	c2xmzA_	Alignment		100.0	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hydrolase, alpha/beta hydrolase fold family; **PDBTitle:** structure of menh from s. aureus
6	c2wj4B_	Alignment		100.0	10	**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
7	c2vavL_	Alignment		100.0	16	**PDB header:**transferase **Chain:** L: **PDB Molecule:**acetyl-coa--deacetylcephalosporin c **PDBTitle:** crystal structure of deacetylcephalosporin c2 acetyltransferase (dac-soak)
8	c3oosA_	Alignment		100.0	16	**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
9	c3om8A_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable hydrolase; **PDBTitle:** the crystal structure of a hydrolase from pseudomonas aeruginosa pa01
10	c3qvmA_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**olei00960; **PDBTitle:** the structure of olei00960, a hydrolase from oleispira antarctica
11	c3i1iA_	Alignment		100.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**homoserine o-acetyltransferase; **PDBTitle:** x-ray crystal structure of homoserine o-acetyltransferase from2 bacillus anthracis

12	c2y6vB_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**peroxisomal membrane protein lpx1; **PDBTitle:** peroxisomal alpha-beta-hydrolase lpx1 (yor084w) from2 saccharomyces cerevisiae (crystal form i)
13	c2xuaH_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**3-oxoadipate enol-lactonase; **PDBTitle:** crystal structure of the enol-lactonase from burkholderia2 xenovorans lb400
14	d2b61a1	Alignment		100.0	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**O-acetyltransferase
15	c3kdaB_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cftr inhibitory factor (cif); **PDBTitle:** crystal structure of the cftr inhibitory factor cif with the h269a2 mutation
16	c2e3jA_	Alignment		100.0	22	**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
17	d2rhwa1	Alignment		100.0	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carbon-carbon bond hydrolase
18	c3fsgC_	Alignment		100.0	13	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**alpha/beta superfamily hydrolase; **PDBTitle:** crystal structure of alpha/beta superfamily hydrolase from oenococcus2 oeni psu-1
19	d1c4xa_	Alignment		100.0	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carbon-carbon bond hydrolase
20	d2vata1	Alignment		100.0	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**O-acetyltransferase
21	d1e89a_	Alignment	not modelled	100.0	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Hydroxynitrile lyase-like
22	c3kxpD_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**alpha-(n-acetylaminomethylene)succinic acid **PDBTitle:** crystal structure of e-2-(acetamidomethylene)succinate2 hydrolase
23	d1uk8a_	Alignment	not modelled	100.0	18	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carbon-carbon bond hydrolase
24	c3e3aA_	Alignment	not modelled	100.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**possible peroxidase bpoc; **PDBTitle:** the structure of rv0554 from mycobacterium tuberculosis
25	d1b6ga_	Alignment	not modelled	100.0	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Haloalkane dehalogenase
26	c1u2eA_	Alignment	not modelled	100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**2-hydroxy-6-ketonona-2,4-dienedioic acid **PDBTitle:** crystal structure of the c-c bond hydrolase mhpc
27	d1m33a_	Alignment	not modelled	100.0	20	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Biotin biosynthesis protein BioH
28	c3ibtA_	Alignment	not modelled	100.0	10	**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)

29	d1ehya_	Alignment	not modelled	100.0	20	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Epoxide hydrolase
30	c3bwxA_	Alignment	not modelled	100.0	14	**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
31	c3bf7B_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**esterase ybff; **PDBTitle:** 1.1 resolution structure of ybff, a new esterase from2 escherichia coli: a unique substrate-binding crevice3 generated by domain arrangement
32	c2cjpA_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**epoxide hydrolase; **PDBTitle:** structure of potato (solanum tuberosum) epoxide hydrolase i2 (steh1)
33	d1xkla_	Alignment	not modelled	100.0	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Hydroxynitrile lyase-like
34	d1zd3a2	Alignment	not modelled	100.0	19	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Epoxide hydrolase
35	d1cr6a2	Alignment	not modelled	100.0	19	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Epoxide hydrolase
36	c3u1tA_	Alignment	not modelled	100.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dmma haloalkane dehalogenase; **PDBTitle:** haloalkane dehalogenase, dmma, of marine microbial origin
37	d1brta_	Alignment	not modelled	100.0	20	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Haloperoxidase
38	c1wprA_	Alignment	not modelled	100.0	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**sigma factor sigb regulation protein rsbq; **PDBTitle:** crystal structure of rsbq inhibited by pmsf
39	d3c70a1	Alignment	not modelled	100.0	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Hydroxynitrile lyase-like
40	d2pl5a1	Alignment	not modelled	100.0	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**O-acetyltransferase
41	c2pseA_	Alignment	not modelled	100.0	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**renilla-luciferin 2-monooxygenase; **PDBTitle:** crystal structures of the luciferase and green fluorescent2 protein from renilla reniformis
42	c3a2nF_	Alignment	not modelled	100.0	14	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**haloalkane dehalogenase; **PDBTitle:** crystal structure of dbja (wild type type ii p21)
43	c2vf2A_	Alignment	not modelled	100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate **PDBTitle:** x-ray crystal structure of hsad from mycobacterium2 tuberculosis
44	d1mtza_	Alignment	not modelled	100.0	19	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Proline iminopeptidase-like
45	c2xt0A_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**haloalkane dehalogenase; **PDBTitle:** dehalogenase dppa from plesiocystis pacifica sir-i
46	c3e0xB_	Alignment	not modelled	100.0	15	**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
47	d1hkha_	Alignment	not modelled	100.0	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Haloperoxidase
48	c2yysA_	Alignment	not modelled	100.0	17	**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
49	c3dqzB_	Alignment	not modelled	100.0	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**alpha-hydroxynitrile lyase-like protein; **PDBTitle:** structure of the hydroxynitrile lyase from arabidopsis2 thaliana
50	d1a8sa_	Alignment	not modelled	100.0	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Haloperoxidase
51	c1y37A_	Alignment	not modelled	100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**fluoroacetate dehalogenase; **PDBTitle:** structure of fluoroacetate dehalogenase from burkholderia sp. fa1
52	c3fobA_	Alignment	not modelled	100.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**bromoperoxidase; **PDBTitle:** crystal structure of bromoperoxidase from bacillus anthracis
53	d1q0ra_	Alignment	not modelled	100.0	20	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Aclacinomycin methylesterase RdmC
54	d1a8qa_	Alignment	not modelled	100.0	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Haloperoxidase

55	d1va4a_	Alignment	not modelled	100.0	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Haloperoxidase
56	c1zoiC_	Alignment	not modelled	100.0	21	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**esterase; **PDBTitle:** crystal structure of a stereoselective esterase from2 pseudomonas putida ifo12996
57	d1bn7a_	Alignment	not modelled	100.0	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Haloalkane dehalogenase
58	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
59	d1azwa_	Alignment	not modelled	100.0	19	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Proline iminopeptidase-like
60	c3p2mA_	Alignment	not modelled	100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**possible hydrolase; **PDBTitle:** crystal structure of a novel esterase rv0045c from mycobacterium2 tuberculosis
61	d1j1ia_	Alignment	not modelled	100.0	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carbon-carbon bond hydrolase
62	c1j1iA_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**meta cleavage compound hydrolase; **PDBTitle:** crystal structure of a his-tagged serine hydrolase involved2 in the carbazole degradation (carc enzyme)
63	d1a88a_	Alignment	not modelled	100.0	19	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Haloperoxidase
64	c3qyjB_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alr0039 protein; **PDBTitle:** crystal structure of alr0039, a putative alpha/beta hydrolase from2 nostoc sp pcc 7120.
65	c3gzjB_	Alignment	not modelled	100.0	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**polyneuridine-aldehyde esterase; **PDBTitle:** crystal structure of polyneuridine aldehyde esterase2 complexed with 16-epi-vellosimine
66	c3flaB_	Alignment	not modelled	100.0	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**rifr; **PDBTitle:** rifr - type ii thioesterase from rifamycin nrps/pks biosynthetic2 pathway - form 1
67	c3r3xA_	Alignment	not modelled	100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**fluoroacetate dehalogenase; **PDBTitle:** crystal structure of the fluoroacetate dehalogenase rpa1163 -2 asp110asn/bromoacetate
68	d1mj5a_	Alignment	not modelled	100.0	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Haloalkane dehalogenase
69	d1qo7a_	Alignment	not modelled	100.0	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Epoxide hydrolase
70	d1wm1a_	Alignment	not modelled	100.0	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Proline iminopeptidase-like
71	c3nwoA_	Alignment	not modelled	100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**proline iminopeptidase; **PDBTitle:** crystal structure of proline iminopeptidase mycobacterium smegmatis
72	c3jw8A_	Alignment	not modelled	100.0	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mgll protein; **PDBTitle:** crystal structure of human mono-glyceride lipase
73	d1r3da_	Alignment	not modelled	100.0	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Hypothetical protein VC1974
74	c3r0vA_	Alignment	not modelled	100.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha/beta hydrolase fold protein; **PDBTitle:** the crystal structure of an alpha/beta hydrolase from sphaerobacter2 thermophilus dsm 20745.
75	c2qvbA_	Alignment	not modelled	100.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**haloalkane dehalogenase 3; **PDBTitle:** crystal structure of haloalkane dehalogenase rv2579 from mycobacterium2 tuberculosis
76	d1k8qa_	Alignment	not modelled	100.0	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Gastric lipase
77	c3hjuB_	Alignment	not modelled	100.0	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**monoglyceride lipase; **PDBTitle:** crystal structure of human monoglyceride lipase
78	d1hlga_	Alignment	not modelled	100.0	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Gastric lipase
79	c2ronA_	Alignment	not modelled	100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**surfactin synthetase thioesterase subunit; **PDBTitle:** the external thioesterase of the surfactin-synthetase
80	c3c5wP_	Alignment	not modelled	100.0	18	**PDB header:**hydrolase **Chain:** P: **PDB Molecule:**pp2a-specific methylesterase pme-1; **PDBTitle:** complex between pp2a-specific methylesterase pme-1 and pp2a core2 enzyme
81	c3qitB_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**polyketide synthase;

						PDBTitle: thioesterase domain from curacin biosynthetic pathway
82	c2ockA_	Alignment	not modelled	100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**valacyclovir hydrolase; **PDBTitle:** crystal structure of valacyclovir hydrolase d123n mutant
83	c3bdiA_	Alignment	not modelled	100.0	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized protein ta0194; **PDBTitle:** crystal structure of predicted cib-like hydrolase (np_393672.1) from2 thermoplasma acidophilum at 1.45 a resolution
84	d1tqha_	Alignment	not modelled	100.0	20	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase/lipase
85	d1imja_	Alignment	not modelled	100.0	22	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Ccg1/TafII250-interacting factor B (Cib)
86	c3h04A_	Alignment	not modelled	100.0	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of the protein with unknown function from2 staphylococcus aureus subsp. aureus mu50
87	c3dyvA_	Alignment	not modelled	100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase d; **PDBTitle:** snapshots of esterase d from lactobacillus rhamnosus:2 insights into a rotation driven catalytic mechanism
88	c2q0xA_	Alignment	not modelled	100.0	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** alpha/beta hydrolase fold protein of unknown function
89	c1pjaA_	Alignment	not modelled	100.0	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**palmitoyl-protein thioesterase 2 precursor; **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	d1pjaa_	Alignment	not modelled	100.0	10	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Thioesterases
91	c3llcA_	Alignment	not modelled	100.0	17	**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
92	c3qmwD_	Alignment	not modelled	100.0	19	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**thioesterase; **PDBTitle:** redj with peg molecule bound in the active site
93	c3ilsA_	Alignment	not modelled	100.0	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aflatoxin biosynthesis polyketide synthase; **PDBTitle:** the thioesterase domain from pksa
94	c3qm1A_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cinnamoyl esterase; **PDBTitle:** crystal structure of the lactobacillus johnsonii cinnamoyl esterase2 lj0536 s106a mutant in complex with ethylferulate, form ii
95	d1xkta_	Alignment	not modelled	100.0	12	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Thioesterase domain of polypeptide, polyketide and fatty acid synthases
96	c3lcrA_	Alignment	not modelled	100.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tautomycetin biosynthetic pks; **PDBTitle:** thioesterase from tautomycetin biosynthhetic pathway
97	c2wtmC_	Alignment	not modelled	99.9	17	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**est1e; **PDBTitle:** est1e from butyrivibrio proteoclasticus
98	c3fleB_	Alignment	not modelled	99.9	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**se_1780 protein; **PDBTitle:** se_1780 protein of unknown function from staphylococcus epidermidis.
99	c3fcyB_	Alignment	not modelled	99.9	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**xylan esterase 1; **PDBTitle:** crystal structure of acetyl xylan esterase 1 from2 thermoanaerobacterium sp. jw/sl ys485
100	d1l7aa_	Alignment	not modelled	99.9	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetyl xylan esterase-like
101	c2hdwB_	Alignment	not modelled	99.9	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hypothetical protein pa2218; **PDBTitle:** crystal structure of hypothetical protein pa2218 from pseudomonas2 aeruginosa
102	c2px6A_	Alignment	not modelled	99.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thioesterase domain; **PDBTitle:** crystal structure of the thioesterase domain of human fatty2 acid synthase inhibited by orlistat
103	c2h7xA_	Alignment	not modelled	99.9	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**type i polyketide synthase pikaiv; **PDBTitle:** pikromycin thioesterase adduct with reduced triketide2 affinity label
104	d2h7xa1	Alignment	not modelled	99.9	18	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Thioesterase domain of polypeptide, polyketide and fatty acid synthases
105	d1qlwa_	Alignment	not modelled	99.9	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**A novel bacterial esterase
106	c3fnbB_	Alignment	not modelled	99.9	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**acylaminoacyl peptidase smu_737; **PDBTitle:** crystal structure of acylaminoacyl peptidase smu_737 from2 streptococcus mutans ua159

107	d1ex9a_	Alignment	not modelled	99.9	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Bacterial lipase
108	c2jbwB_	Alignment	not modelled	99.9	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**2,6-dihydroxy-pseudo-oxynicotine hydrolase; **PDBTitle:** crystal structure of the 2,6-dihydroxy-pseudo-oxynicotine2 hydrolase.
109	c2qruA_	Alignment	not modelled	99.9	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an alpha/beta hydrolase superfamily protein from2 enterococcus faecalis
110	c2rauA_	Alignment	not modelled	99.9	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative esterase; **PDBTitle:** crystal structure of a putative lipase (np_343859.1) from sulfolobus2 solfataricus at 1.85 a resolution
111	d1ufoa_	Alignment	not modelled	99.9	21	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Hypothetical protein TT1662
112	c3mveB_	Alignment	not modelled	99.9	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**upf0255 protein vv1_0328; **PDBTitle:** crystal structure of a novel pyruvate decarboxylase
113	c3ksrA_	Alignment	not modelled	99.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative serine hydrolase; **PDBTitle:** crystal structure of a putative serine hydrolase (xcc3885) from2 xanthomonas campestris pv. campestris at 2.69 a resolution
114	d2jbwa1	Alignment	not modelled	99.9	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**2,6-dihydropseudooxynicotine hydrolase-like
115	c1mo2A_	Alignment	not modelled	99.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**erythronolide synthase, modules 5 and 6; **PDBTitle:** thioesterase domain from 6-deoxyerythronolide synthase2 (debs te), ph 8.5
116	d1mo2a_	Alignment	not modelled	99.9	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Thioesterase domain of polypeptide, polyketide and fatty acid synthases
117	d1uxoa_	Alignment	not modelled	99.9	18	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**YdeN-like
118	d1ispa_	Alignment	not modelled	99.9	18	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Bacterial lipase
119	c2qs9A_	Alignment	not modelled	99.9	17	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**retinoblastoma-binding protein 9; **PDBTitle:** crystal structure of the human retinoblastoma-binding2 protein 9 (rbbp-9). nesg target hr2978
120	c3lp5A_	Alignment	not modelled	99.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative cell surface hydrolase; **PDBTitle:** the crystal structure of the putative cell surface hydrolase from2 lactobacillus plantarum wcfs1