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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1tcaa_	 Alignment		97.9	25	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
2	c3icvA_	 Alignment		97.7	25	PDB header: hydrolase Chain: A; PDB Molecule: lipase b; PDBTitle: structural consequences of a circular permutation on lipase b from2 candida antarctica
3	c5x88A_	 Alignment		97.7	17	PDB header: hydrolase Chain: A; PDB Molecule: cutinase; PDBTitle: a crystal structure of cutinases from malbranchea cinnamomea
4	d1cexa_	 Alignment		97.7	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like
5	c3dd5F_	 Alignment		97.6	14	PDB header: hydrolase Chain: F; PDB Molecule: cutinase; PDBTitle: glomerella cingulata e600-cutinase complex
6	c3gbsA_	 Alignment		97.5	16	PDB header: hydrolase Chain: A; PDB Molecule: cutinase 1; PDBTitle: crystal structure of aspergillus oryzae cutinase
7	d1ei9a_	 Alignment		97.5	11	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterases
8	d1qoza_	 Alignment		97.4	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like
9	c3lp5A_	 Alignment		97.3	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 wcf51
10	d1g66a_	 Alignment		97.1	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like
11	d1ispA_	 Alignment		97.1	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase

12	c3bdvB_	Alignment		96.9	21	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein duf1234; PDBTitle: crystal structure of a putative yden-like hydrolase (eca3091) from2 pectobacterium atrosepticum scri1043 at 1.66 a resolution
13	c3ajaA_	Alignment		96.9	20	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of msmeg_6394
14	d1tiaa_	Alignment		96.8	23	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
15	d1ex9a_	Alignment		96.8	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
16	d1tiba_	Alignment		96.7	24	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
17	d2h1a1	Alignment		96.6	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
18	c6cl4A_	Alignment		96.6	22	PDB header: hydrolase Chain: A: PDB Molecule: lipase c12; PDBTitle: lipc12 - lipase from metagenomics
19	c4gw3A_	Alignment		96.5	18	PDB header: hydrolase Chain: A: PDB Molecule: putative lipase; PDBTitle: crystal structure of the lipase from proteus mirabilis
20	c4psdA_	Alignment		96.5	18	PDB header: hydrolase Chain: A: PDB Molecule: carbohydrate esterase family 5; PDBTitle: structure of trichoderma reesei cutinase native form.
21	c3ds8A_	Alignment	not modelled	96.5	27	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin2722 protein; PDBTitle: the crysatl structure of the gene lin2722 products from listeria2 innocua
22	c5gw8A_	Alignment	not modelled	96.5	14	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical secretory lipase (family 3); PDBTitle: crystal structure of a putative dag-like lipase (mgmdl2) from2 malassezia globosa
23	c2yijA_	Alignment	not modelled	96.4	18	PDB header: hydrolase Chain: A: PDB Molecule: phospholipase a1-iigamma; PDBTitle: crystal structure of phospholipase a1
24	c3uuuA_	Alignment	not modelled	96.4	14	PDB header: hydrolase Chain: A: PDB Molecule: lip1, secretory lipase (family 3); PDBTitle: crystal structure of mono- and diacylglycerol lipase from malassezia2 globosa
25	d1uwca_	Alignment	not modelled	96.3	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
26	c5xk2A_	Alignment	not modelled	96.3	20	PDB header: hydrolase Chain: A: PDB Molecule: diacylglycerol lipase; PDBTitle: crystal structure of mono- and diacylglycerol lipase from aspergillus2 oryzae
27	c2rauA_	Alignment	not modelled	96.2	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
28	c3o0dF_	Alignment	not modelled	96.2	18	PDB header: hydrolase Chain: F: PDB Molecule: triacylglycerol lipase; PDBTitle: crystal structure of lip2 lipase from yarrowia lipolytica at 1.7 a2 resolution
29	c1ggsD	Alignment	not modelled	96.1	19	PDB header: hydrolase Chain: D: PDB Molecule: protein (triacylglycerol hydrolase);

29	c1qgeU_	Alignment	not modelled	96.1	19	PDBTitle: new crystal form of pseudomonas glumae (formerly chromobacterium2 viscosum atcc 6918) lipase PDB header: hydrolase
30	c4oylC_	Alignment	not modelled	96.0	17	Chain: C: PDB Molecule: cutinase; PDBTitle: humicola insolens cutinase in complex with mono-ethylphosphate
31	c3ngmB_	Alignment	not modelled	96.0	22	PDB header: hydrolase Chain: B: PDB Molecule: extracellular lipase; PDBTitle: crystal structure of lipase from gibberella zeae
32	d1cvla_	Alignment	not modelled	96.0	27	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
33	c2y6vB_	Alignment	not modelled	96.0	15	PDB header: hydrolase Chain: B: PDB Molecule: peroxisomal membrane protein lpx1; PDBTitle: peroxisomal alpha-beta-hydrolase lpx1 (yor084w) from saccharomyces2 cerevisiae (crystal form i)
34	c4x91C_	Alignment	not modelled	95.9	18	PDB header: transferase Chain: C: PDB Molecule: group xv phospholipase a2; PDBTitle: crystal structure of lysosomal phospholipase a2 in complex with2 isopropyl dodec-11-enylfluorophosphonate (idfp)
35	d1rp1a2	Alignment	not modelled	95.8	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
36	c2vavL_	Alignment	not modelled	95.7	13	PDB header: transferase Chain: L: PDB Molecule: acetyl-coa--deacetylcephalosporin c acetyltransferase; PDBTitle: crystal structure of deacetylcephalosporin c acetyltransferase (dac-2 soak)
37	d1lpbb2	Alignment	not modelled	95.6	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
38	d1pjaa_	Alignment	not modelled	95.6	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterases
39	c1pjaA_	Alignment	not modelled	95.6	18	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)
40	c1cr6A_	Alignment	not modelled	95.5	17	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
41	c4nfuB_	Alignment	not modelled	95.5	13	PDB header: signaling protein Chain: B: PDB Molecule: senescence-associated carboxylesterase 101; PDBTitle: structure of the central plant immunity signaling node eds1 in complex2 with its interaction partner sag101
42	d4lipd_	Alignment	not modelled	95.4	27	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
43	c3g7nA_	Alignment	not modelled	95.4	15	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: crystal structure of a triacylglycerol lipase from penicillium2 expansum at 1.3
44	d1gpla2	Alignment	not modelled	95.4	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
45	c2zyiB_	Alignment	not modelled	95.4	18	PDB header: hydrolase Chain: B: PDB Molecule: lipase, putative; PDBTitle: a. fulgidus lipase with fatty acid fragment and calcium
46	d1bu8a2	Alignment	not modelled	95.3	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
47	c4x96B_	Alignment	not modelled	95.3	19	PDB header: transferase Chain: B: PDB Molecule: phosphatidylcholine-sterol acyltransferase; PDBTitle: low resolution crystal structure of lecithin:cholesterol2 acyltransferase (lcat; residues 21-397)
48	c3i28A_	Alignment	not modelled	95.2	19	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase 2; PDBTitle: crystal structure of soluble epoxide hydrolase
49	c5h6bA_	Alignment	not modelled	95.0	19	PDB header: hydrolase Chain: A: PDB Molecule: putative secreted lipase; PDBTitle: crystal structure of a thermostable lipase from marine streptomyces
50	c4qnnC_	Alignment	not modelled	95.0	19	PDB header: hydrolase Chain: C: PDB Molecule: phospholipase a 1 from hornet(vespa basalis) venom; PDBTitle: crystal structure of phospholipase a 1 from hornet(vespa basalis)2 venom
51	c5f2hA_	Alignment	not modelled	94.9	17	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: 2.75 angstrom resolution crystal structure of uncharacterized protein2 from bacillus cereus atcc 10987
52	d3b5ea1	Alignment	not modelled	94.9	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
53	c2czqB_	Alignment	not modelled	94.8	22	PDB header: hydrolase Chain: B: PDB Molecule: cutinase-like protein; PDBTitle: a novel cutinase-like protein from cryptococcus sp.
54	c3jyhD_	Alignment	not modelled	94.8	25	PDB header: hydrolase Chain: D: PDB Molecule: dipeptidyl-peptidase 2; PDBTitle: human dipeptidyl peptidase dpp7
						PDB header: hydrolase

55	c2vtvA_	Alignment	not modelled	94.7	16	Chain: A: PDB Molecule: phb depolymerase phaz7; PDBTitle: phaz7 depolymerase from paucimonas lemoignei
56	c5w8pA_	Alignment	not modelled	94.7	17	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: homoserine transacetylase meta from mycobacterium abscessus
57	c4r1dA_	Alignment	not modelled	94.7	17	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of tle4-tli4 complex
58	d1etha2	Alignment	not modelled	94.6	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
59	d3tgla_	Alignment	not modelled	94.6	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
60	c2pvsB_	Alignment	not modelled	94.5	11	PDB header: hydrolase Chain: B: PDB Molecule: pancreatic lipase-related protein 2; PDBTitle: structure of human pancreatic lipase related protein 22 mutant n336q
61	c1gplA_	Alignment	not modelled	94.5	15	PDB header: serine esterase Chain: A: PDB Molecule: rp2 lipase; PDBTitle: rp2 lipase
62	c2h1iA_	Alignment	not modelled	94.5	18	PDB header: hydrolase Chain: A: PDB Molecule: carboxylesterase; PDBTitle: crystal structure of the bacillus cereus carboxylesterase
63	c2pplA_	Alignment	not modelled	94.5	18	PDB header: hydrolase Chain: A: PDB Molecule: pancreatic lipase-related protein 1; PDBTitle: human pancreatic lipase-related protein 1
64	c2q0xA_	Alignment	not modelled	94.4	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: alpha/beta hydrolase fold protein of unknown function
65	d1mo2a_	Alignment	not modelled	94.4	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
66	c1mo2A_	Alignment	not modelled	94.4	18	PDB header: transferase Chain: A: PDB Molecule: erythronolide synthase, modules 5 and 6; PDBTitle: thioesterase domain from 6-deoxyerythronolide synthase (debs te), ph2 8.5
67	c3vvvA_	Alignment	not modelled	94.3	9	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: crystal structure of l-serine-o-acetyltransferase found in d-2 cycloserine biosynthetic pathway
68	c1hplB_	Alignment	not modelled	94.2	15	PDB header: hydrolase(carboxylic esterase) Chain: B: PDB Molecule: lipase; PDBTitle: horse pancreatic lipase. the crystal structure at 2.3 angstroms2 resolution
69	d1hpla2	Alignment	not modelled	94.2	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
70	c3og9A_	Alignment	not modelled	93.9	14	PDB header: hydrolase Chain: A: PDB Molecule: protein yahd a copper inducible hydrolase; PDBTitle: structure of yahd with malic acid
71	c5jkjA_	Alignment	not modelled	93.8	19	PDB header: hydrolase Chain: A: PDB Molecule: esterase e22; PDBTitle: crystal structure of esterase e22 l374d mutant
72	c3lcrA_	Alignment	not modelled	93.6	15	PDB header: hydrolase Chain: A: PDB Molecule: tautomycetin biosynthetic pks; PDBTitle: thioesterase from tautomycetin biosynthetic pathway
73	c1rp1A_	Alignment	not modelled	93.6	16	PDB header: hydrolase Chain: A: PDB Molecule: pancreatic lipase related protein 1; PDBTitle: dog pancreatic lipase related protein 1
74	c4qloA_	Alignment	not modelled	93.6	19	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: crystal structure of homoserine o-acetyltransferase from2 staphylococcus aureus
75	d2vata1	Alignment	not modelled	93.5	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
76	d1ku0a_	Alignment	not modelled	93.5	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
77	d1xkta_	Alignment	not modelled	93.4	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
78	c2o2gA_	Alignment	not modelled	93.4	12	PDB header: hydrolase Chain: A: PDB Molecule: dienelactone hydrolase; PDBTitle: crystal structure of dienelactone hydrolase (yp_324580.1) from2 anabaena variabilis atcc 29413 at 1.92 a resolution
79	c3ilsA_	Alignment	not modelled	93.3	17	PDB header: hydrolase Chain: A: PDB Molecule: afatoxin biosynthesis polyketide synthase; PDBTitle: the thioesterase domain from pksa
80	d2b61a1	Alignment	not modelled	93.2	25	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
81	d2pl5a1	Alignment	not modelled	93.2	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
						PDB header: hydrolase

82	c5d8mA	Alignment	not modelled	93.1	22	Chain: A: PDB Molecule: metagenomic carboxyl esterase mgs015b; PDBTitle: crystal structure of the metagenomic carboxyl esterase mgs0156
83	c3liiA	Alignment	not modelled	93.1	11	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: x-ray crystal structure of homoserine o-acetyltransferase from2 bacillus anthracis
84	d1gya	Alignment	not modelled	92.9	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
85	c6qppA	Alignment	not modelled	92.7	18	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: rhizomucor miehei lipase propeptide complex, native
86	c5d6oB	Alignment	not modelled	92.7	11	PDB header: transferase Chain: B: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: orthorhombic crystal structure of an acylester hydrolase from2 corynebacterium glutamicum
87	c5uohA	Alignment	not modelled	92.7	20	PDB header: hydrolase Chain: A: PDB Molecule: carboxylesterase a; PDBTitle: crystal structure of hip1 (rv2224c) t466a mutant
88	c2qmqA	Alignment	not modelled	92.6	15	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
89	c6e7kB	Alignment	not modelled	92.3	17	PDB header: hydrolase Chain: B: PDB Molecule: lipoprotein lipase; PDBTitle: structure of the lipoprotein lipase gpibp1 complex that mediates2 plasma triglyceride hydrolysis
90	d1uxoa	Alignment	not modelled	92.2	23	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: YdeN-like
91	c3l80A	Alignment	not modelled	92.1	15	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein smu.1393c; PDBTitle: crystal structure of smu.1393c from streptococcus mutans ua159
92	c3fleB	Alignment	not modelled	92.1	18	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: se_1780 protein; PDBTitle: se_1780 protein of unknown function from staphylococcus epidermidis.
93	c3d0kA	Alignment	not modelled	91.0	22	PDB header: hydrolase Chain: A: PDB Molecule: putative poly(3-hydroxybutyrate) depolymerase lpqc; PDBTitle: crystal structure of the lpqc, poly(3-hydroxybutyrate) depolymerase2 from bordetella parapertussis
94	d2h7xa1	Alignment	not modelled	90.9	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
95	c5x6sB	Alignment	not modelled	90.8	10	PDB header: hydrolase Chain: B: PDB Molecule: acetylxytan esterase a; PDBTitle: acetyl xylan esterase from aspergillus awamori
96	c2cbgA	Alignment	not modelled	90.8	14	PDB header: hydrolase Chain: A: PDB Molecule: fengycin synthetase; PDBTitle: crystal structure of the pmsf-inhibited thioesterase domain of the2 fengycin biosynthesis cluster
97	c3qmwD	Alignment	not modelled	90.8	28	PDB header: hydrolase Chain: D: PDB Molecule: thioesterase; PDBTitle: redj with peg molecule bound in the active site
98	c6e6uA	Alignment	not modelled	90.6	16	PDB header: biosynthetic protein Chain: A: PDB Molecule: dieckmann cyclase, ncmc; PDBTitle: variant c89s of dieckmann cyclase, ncmc
99	c1l7qA	Alignment	not modelled	90.5	13	PDB header: hydrolase Chain: A: PDB Molecule: cocaine esterase; PDBTitle: ser117ala mutant of bacterial cocaine esterase coce
100	c5yalA	Alignment	not modelled	90.4	15	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: ferulic acid esterase from streptomyces cinnamoneus at 1.5 a2 resolution
101	c4l0cA	Alignment	not modelled	89.9	16	PDB header: hydrolase Chain: A: PDB Molecule: deformylase; PDBTitle: crystal structure of the n-fopmylmaaleamic acid deformylase nfo(s94a)2 from pseudomonas putida s16
102	c5xavB	Alignment	not modelled	89.9	17	PDB header: biosynthetic protein Chain: B: PDB Molecule: intracellular polyhydroxyalkanoate synthase; PDBTitle: structure of phac from chromobacterium sp. usm2
103	c2hihB	Alignment	not modelled	89.8	25	PDB header: hydrolase Chain: B: PDB Molecule: lipase 46 kda form; PDBTitle: crystal structure of staphylococcus hyicus lipase
104	c2oryA	Alignment	not modelled	89.7	16	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: crystal structure of m37 lipase
105	c2hu7A	Alignment	not modelled	89.5	22	PDB header: hydrolase Chain: A: PDB Molecule: acylamino-acid-releasing enzyme; PDBTitle: binding of inhibitors by acylaminoacyl peptidase
106	c4qlaB	Alignment	not modelled	89.2	10	PDB header: hydrolase Chain: B: PDB Molecule: juvenile hormone epoxide hydrolase; PDBTitle: crystal structure of juvenile hormone epoxide hydrolase from the2 silkworm bombyx mori
107	c3qvmA	Alignment	not modelled	89.2	16	PDB header: hydrolase Chain: A: PDB Molecule: olei00960; PDBTitle: the structure of olei00960, a hydrolase from oleispira antarctica PDB header: hydrolase

108	c6guiA_	Alignment	not modelled	89.1	33	Chain: A: PDB Molecule: siderophore esterase iroe-like, putative; PDBTitle: siderophore hydrolase estb mutant h267n from aspergillus fumigatus
109	c5h3bA_	Alignment	not modelled	89.0	17	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein hi_1552; PDBTitle: crystal structure of semet-biog from haemophilus influenzae at 1.492 angstroms resolution
110	c2qs9A_	Alignment	not modelled	88.9	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
111	d1jmkc_	Alignment	not modelled	88.1	25	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
112	d1mpxa2	Alignment	not modelled	87.7	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PepX catalytic domain-like
113	d1ji3a_	Alignment	not modelled	87.6	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
114	c3h2iA_	Alignment	not modelled	87.3	16	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of n228w mutant of the rice cell wall2 degrading esterase lipa from xanthomonas oryzae
115	c5ah0B_	Alignment	not modelled	86.9	29	PDB header: hydrolase Chain: B: PDB Molecule: lipase; PDBTitle: structure of lipase 1 from pelosinus fermentans
116	c2b9vB_	Alignment	not modelled	86.6	15	PDB header: hydrolase Chain: B: PDB Molecule: alpha-amino acid ester hydrolase; PDBTitle: acetobacter turbidans alpha-amino acid ester hydrolase
117	d1k8qa_	Alignment	not modelled	86.6	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Gastric lipase
118	c2qjwA_	Alignment	not modelled	86.6	11	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein xcc1541; PDBTitle: crystal structure of a putative hydrolase of the alpha/beta2 superfamily (xcc1541) from xanthomonas campestris pv. campestris at3 1.35 a resolution
119	c4pf1D_	Alignment	not modelled	86.2	13	PDB header: hydrolase Chain: D: PDB Molecule: peptidase s15/coce/nond; PDBTitle: crystal structure of aminopeptidase from marine sediment archaeon2 thaumarchaeota archaeon
120	c4z8zA_	Alignment	not modelled	86.1	13	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the hypothetical protein from ruminiclostridium2 thermocellum atcc 27405