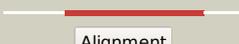
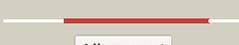


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0963c_(-)_1075301_1076101
Date	Wed Jul 31 22:05:02 BST 2019
Unique Job ID	289b8f7fbf47e077

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1tcaa_	 Alignment		97.9	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
2	c3icvA_	 Alignment		97.6	17	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		97.4	15	PDB header: hydrolase Chain: A; PDB Molecule: cutinase; PDBTitle: a crystal structure of cutinases from malbranchea cinnamomea
4	d1ei9a_	 Alignment		97.4	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterases
5	c3gbsA_	 Alignment		97.4	16	PDB header: hydrolase Chain: A; PDB Molecule: cutinase 1; PDBTitle: crystal structure of aspergillus oryzae cutinase
6	d1ex9a_	 Alignment		97.3	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
7	c4psdA_	 Alignment		97.2	19	PDB header: hydrolase Chain: A; PDB Molecule: carbohydrate esterase family 5; PDBTitle: structure of trichoderma reesei cutinase native form.
8	c4gw3A_	 Alignment		97.0	13	PDB header: hydrolase Chain: A; PDB Molecule: putative lipase; PDBTitle: crystal structure of the lipase from proteus mirabilis
9	c3bdvB_	 Alignment		97.0	22	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
10	d1g66a_	 Alignment		97.0	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like
11	c3dd5F_	 Alignment		97.0	13	PDB header: hydrolase Chain: F; PDB Molecule: cutinase; PDBTitle: glomerella cingulata e600-cutinase complex

12	d1cexa_	Alignment		97.0	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like
13	c4x91C_	Alignment		96.9	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)
14	d1cvla_	Alignment		96.8	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
15	d1qoza_	Alignment		96.8	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like
16	c3uuuA_	Alignment		96.8	19	PDB header: hydrolase Chain: A: PDB Molecule: lip1, secretory lipase (family 3); PDBTitle: crystal structure of mono- and diacylglycerol lipase from malassezia2 globosa
17	c3lp5A_	Alignment		96.8	19	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
18	d1tiaa_	Alignment		96.7	23	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
19	c6cl4A_	Alignment		96.7	18	PDB header: hydrolase Chain: A: PDB Molecule: lipase c12; PDBTitle: lipc12 - lipase from metagenomics
20	d1ispa_	Alignment		96.7	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
21	c5gw8A_	Alignment	not modelled	96.6	19	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
22	c4x96B_	Alignment	not modelled	96.6	15	PDB header: transferase Chain: B: PDB Molecule: phosphatidylcholine-sterol acyltransferase; PDBTitle: low resolution crystal structure of lecithin:cholesterol2 acyltransferase (lcat; residues 21-397)
23	d1bu8a2	Alignment	not modelled	96.5	10	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
24	c3ds8A_	Alignment	not modelled	96.5	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin2722 protein; PDBTitle: the crysatl structure of the gene lin2722 products from listeria2 innocua
25	d1rp1a2	Alignment	not modelled	96.3	10	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
26	d1etha2	Alignment	not modelled	96.2	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
27	c2vavL_	Alignment	not modelled	96.0	18	PDB header: transferase Chain: L: PDB Molecule: acetyl-coa--deacetylcephalosporin c acetyltransferase; PDBTitle: crystal structure of deacetylcephalosporin c acetyltransferase (dac-2 soak)
28	d1uwca_	Alignment	not modelled	96.0	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases

29	c1cr6A_	Alignment	not modelled	96.0	14	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
30	c1gplA_	Alignment	not modelled	96.0	11	PDB header: serine esterase Chain: A: PDB Molecule: rp2 lipase; PDBTitle: rp2 lipase
31	d1lpbb2	Alignment	not modelled	95.9	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
32	d1gpla2	Alignment	not modelled	95.9	11	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
33	c1qgeD_	Alignment	not modelled	95.9	17	PDB header: hydrolase Chain: D: PDB Molecule: protein (triacylglycerol hydrolase); PDBTitle: new crystal form of pseudomonas glumae (formerly chromobacterium2 viscosum atcc 6918) lipase
34	c2pvsB_	Alignment	not modelled	95.9	12	PDB header: hydrolase Chain: B: PDB Molecule: pancreatic lipase-related protein 2; PDBTitle: structure of human pancreatic lipase related protein 22 mutant n336q
35	d1hpla2	Alignment	not modelled	95.8	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
36	c3ajaA_	Alignment	not modelled	95.7	15	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of msmeg_6394
37	c5xk2A_	Alignment	not modelled	95.7	20	PDB header: hydrolase Chain: A: PDB Molecule: diacylglycerol lipase; PDBTitle: crystal structure of mono- and diacylglycerol lipase from aspergillus2 oryzae
38	c2y6vB_	Alignment	not modelled	95.7	16	PDB header: hydrolase Chain: B: PDB Molecule: peroxisomal membrane protein lpx1; PDBTitle: peroxisomal alpha-beta-hydrolase lpx1 (yor084w) from saccharomyces2 cerevisiae (crystal form i)
39	c3i28A_	Alignment	not modelled	95.6	14	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase 2; PDBTitle: crystal structure of soluble epoxide hydrolase
40	c2zyiB_	Alignment	not modelled	95.6	17	PDB header: hydrolase Chain: B: PDB Molecule: lipase, putative; PDBTitle: a. fulgidus lipase with fatty acid fragment and calcium
41	c2q0xA_	Alignment	not modelled	95.6	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: alpha/beta hydrolase fold protein of unknown function
42	d4lipd_	Alignment	not modelled	95.6	25	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
43	c4qnnC_	Alignment	not modelled	95.6	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
44	c2vtvA_	Alignment	not modelled	95.6	16	PDB header: hydrolase Chain: A: PDB Molecule: phb depolymerase phaz7; PDBTitle: phaz7 depolymerase from paucimonas lemoignei
45	c3vvlA_	Alignment	not modelled	95.5	13	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
46	c5h6bA_	Alignment	not modelled	95.5	16	PDB header: hydrolase Chain: A: PDB Molecule: putative secreted lipase; PDBTitle: crystal structure of a thermostable lipase from marine streptomyces
47	c2h1iA_	Alignment	not modelled	95.5	13	PDB header: hydrolase Chain: A: PDB Molecule: carboxylesterase; PDBTitle: crystal structure of the bacillus cereus carboxylesterase
48	c5f2hA_	Alignment	not modelled	95.4	13	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
49	c3o0dF_	Alignment	not modelled	95.4	18	PDB header: hydrolase Chain: F: PDB Molecule: triacylglycerol lipase; PDBTitle: crystal structure of lip2 lipase from yarrowia lipolytica at 1.7 a2 resolution
50	c1mo2A_	Alignment	not modelled	95.4	20	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
51	d1mo2a_	Alignment	not modelled	95.4	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
52	c4qloA_	Alignment	not modelled	95.3	18	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: crystal structure of homoserine o-acetyltransferase from2 staphylococcus aureus
53	c1hplB_	Alignment	not modelled	95.3	11	PDB header: hydrolase(carboxylic esterase) Chain: B: PDB Molecule: lipase; PDBTitle: horse pancreatic lipase. the crystal structure at 2.3 angstroms2 resolution
54	c3og9A_	Alignment	not modelled	95.3	17	PDB header: hydrolase Chain: A: PDB Molecule: protein yahd a copper inducible hydrolase; PDBTitle: structure of yahd with malic acid
						PDB header: hydrolase

55	c1rp1A_	Alignment	not modelled	95.3	11	Chain: A: PDB Molecule: pancreatic lipase related protein 1; PDBTitle: dog pancreatic lipase related protein 1
56	c3ngmB_	Alignment	not modelled	95.3	22	PDB header: hydrolase Chain: B: PDB Molecule: extracellular lipase; PDBTitle: crystal structure of lipase from gibberella zeae
57	c5w8pA_	Alignment	not modelled	95.2	14	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: homoserine transacetylase meta from mycobacterium abscessus
58	c5d8mA_	Alignment	not modelled	95.2	23	PDB header: hydrolase Chain: A: PDB Molecule: metagenomic carboxyl esterase mgs0156; PDBTitle: crystal structure of the metagenomic carboxyl esterase mgs0156
59	d1tiba_	Alignment	not modelled	95.2	24	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
60	c2yijA_	Alignment	not modelled	95.0	22	PDB header: hydrolase Chain: A: PDB Molecule: phospholipase a1-iiigamma; PDBTitle: crystal structure of phospholipase a1
61	c2rauA_	Alignment	not modelled	95.0	9	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
62	c2qmqa_	Alignment	not modelled	94.9	12	PDB header: signaling protein Chain: A: PDB Molecule: protein ndr2; 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
63	c3jyhD_	Alignment	not modelled	94.8	20	PDB header: hydrolase Chain: D: PDB Molecule: dipeptidyl-peptidase 2; PDBTitle: human dipeptidyl peptidase dpp7
64	c3ilsA_	Alignment	not modelled	94.8	14	PDB header: hydrolase Chain: A: PDB Molecule: afatoxin biosynthesis polyketide synthase; PDBTitle: the thioesterase domain from pksa
65	c5uohA_	Alignment	not modelled	94.7	29	PDB header: hydrolase Chain: A: PDB Molecule: carboxylesterase a; PDBTitle: crystal structure of hip1 (rv2224c) t466a mutant
66	d2h1ia1	Alignment	not modelled	94.7	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
67	c2czqB_	Alignment	not modelled	94.6	24	PDB header: hydrolase Chain: B: PDB Molecule: cutinase-like protein; PDBTitle: a novel cutinase-like protein from cryptococcus sp.
68	c6e7kB_	Alignment	not modelled	94.6	15	PDB header: hydrolase Chain: B: PDB Molecule: lipoprotein lipase; PDBTitle: structure of the lipoprotein lipase gpibp1 complex that mediates2 plasma triglyceride hydrolysis
69	c4oylC_	Alignment	not modelled	94.4	12	PDB header: hydrolase Chain: C: PDB Molecule: cutinase; PDBTitle: humicola insolens cutinase in complex with mono-ethylphosphate
70	c3lcrA_	Alignment	not modelled	94.4	20	PDB header: hydrolase Chain: A: PDB Molecule: tautomycetin biosynthetic pks; PDBTitle: thioesterase from tautomycetin biosynthetic pathway
71	c1pjaA_	Alignment	not modelled	94.3	19	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)
72	d1pjaa_	Alignment	not modelled	94.3	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterases
73	c4nfbB_	Alignment	not modelled	94.2	22	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
74	c3g7nA_	Alignment	not modelled	94.2	16	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: crystal structure of a triacylglycerol lipase from penicillium2 expansum at 1.3
75	d2b61a1	Alignment	not modelled	94.2	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
76	c3d0kA_	Alignment	not modelled	94.1	24	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
77	c5jkjA_	Alignment	not modelled	94.1	17	PDB header: hydrolase Chain: A: PDB Molecule: esterase e22; PDBTitle: crystal structure of esterase e22 l374d mutant
78	c31iaA_	Alignment	not modelled	94.0	15	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: x-ray crystal structure of homoserine o-acetyltransferase from2 bacillus anthracis
79	d2vata1	Alignment	not modelled	94.0	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
80	d1xkta_	Alignment	not modelled	93.9	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases

81	d1uxoa_	Alignment	not modelled	93.9	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: YdeN-like
82	c4z8zA_	Alignment	not modelled	93.7	8	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the hypothetical protein from ruminiclostridium2 thermocellum atcc 27405
83	d2pl5a1	Alignment	not modelled	93.6	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
84	c3l80A_	Alignment	not modelled	93.5	14	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein smu.1393c; PDBTitle: crystal structure of smu.1393c from streptococcus mutans ua159
85	c5d6oB_	Alignment	not modelled	93.3	11	PDB header: transferase Chain: B: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: orthorhombic crystal structure of an acetylester hydrolase from2 corynebacterium glutamicum
86	d3b5ea1	Alignment	not modelled	93.0	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
87	c5hdfB_	Alignment	not modelled	93.0	14	PDB header: hydrolase Chain: B: PDB Molecule: hydrolase; PDBTitle: hydrolase semet-stna
88	c2pplA_	Alignment	not modelled	92.7	13	PDB header: hydrolase Chain: A: PDB Molecule: pancreatic lipase-related protein 1; PDBTitle: human pancreatic lipase-related protein 1
89	c3e0xB_	Alignment	not modelled	92.7	14	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
90	c2cbgA_	Alignment	not modelled	92.6	20	PDB header: hydrolase Chain: A: PDB Molecule: fengycin synthetase; PDBTitle: crystal structure of the pmsf-inhibited thioesterase domain of the2 fengycin biosynthesis cluster
91	c5xavB_	Alignment	not modelled	92.5	15	PDB header: biosynthetic protein Chain: B: PDB Molecule: intracellular polyhydroxyalkanoate synthase; PDBTitle: structure of phac from chromobacterium sp. usm2
92	c4r1dA_	Alignment	not modelled	92.2	21	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of tle4-tli4 complex
93	c3fleB_	Alignment	not modelled	92.1	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: se_1780 protein; PDBTitle: se_1780 protein of unknown function from staphylococcus epidermidis.
94	c4qlaB_	Alignment	not modelled	91.9	14	PDB header: hydrolase Chain: B: PDB Molecule: juvenile hormone epoxide hydrolase; PDBTitle: crystal structure of juvenile hormone epoxide hydrolase from the2 silkworm bombyx mori
95	c2o2gA_	Alignment	not modelled	91.7	18	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
96	d1jmkc_	Alignment	not modelled	91.6	24	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
97	c3qvmA_	Alignment	not modelled	91.5	14	PDB header: hydrolase Chain: A: PDB Molecule: olei00960; PDBTitle: the structure of olei00960, a hydrolase from oleispira antarctica
98	c2hu7A_	Alignment	not modelled	91.5	19	PDB header: hydrolase Chain: A: PDB Molecule: acylamino-acid-releasing enzyme; PDBTitle: binding of inhibitors by acylaminoacyl peptidase
99	c4wfiA_	Alignment	not modelled	90.9	21	PDB header: hydrolase Chain: A: PDB Molecule: cutinase; PDBTitle: crystal structure of pet-degrading cutinase cut190 s226p mutant in2 ca(2+)-free state
100	c2fx5A_	Alignment	not modelled	90.8	20	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: pseudomonas mendocina lipase
101	c5t6oA_	Alignment	not modelled	90.4	20	PDB header: biosynthetic protein Chain: A: PDB Molecule: poly-beta-hydroxybuterate polymerase; PDBTitle: structure of the catalytic domain of the class i polyhydroxybutyrate2 synthase from cupriavidus necator
102	c4qlaA_	Alignment	not modelled	90.3	13	PDB header: hydrolase Chain: A: PDB Molecule: juvenile hormone epoxide hydrolase; PDBTitle: crystal structure of juvenile hormone epoxide hydrolase from the2 silkworm bombyx mori
103	c5yalA_	Alignment	not modelled	90.2	17	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: ferulic acid esterase from streptomyces cinnamoneus at 1.5 a2 resolution
104	c2jwbB_	Alignment	not modelled	90.0	13	PDB header: hydrolase Chain: B: PDB Molecule: 2,6-dihydroxy-pseudo-oxynicotine hydrolase; PDBTitle: crystal structure of the 2,6-dihydroxy-pseudo-oxynicotine hydrolase.
105	c5h3bA_	Alignment	not modelled	89.7	24	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
106	d1k8qa_	Alignment	not modelled	89.4	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Gastric lipase

107	c5f4zB_	Alignment	not modelled	89.3	11	PDB header: hydrolase Chain: B: PDB Molecule: epoxide hydrolase; PDBTitle: the crystal structure of an epoxide hydrolase from streptomyces2 carzinostaticus subsp. neocarzinostaticus
108	c4l0cA_	Alignment	not modelled	89.1	19	PDB header: hydrolase Chain: A: PDB Molecule: deformylase; PDBTitle: crystal structure of the n-fopmylmaeamic acid deformylase nfo(s94a)2 from pseudomonas putida s16
109	c3k2iA_	Alignment	not modelled	89.0	17	PDB header: hydrolase Chain: A: PDB Molecule: acyl-coenzyme a thioesterase 4; PDBTitle: human acyl-coenzyme a thioesterase 4
110	c3qmwD_	Alignment	not modelled	88.7	17	PDB header: hydrolase Chain: D: PDB Molecule: thioesterase; PDBTitle: redj with peg molecule bound in the active site
111	c4i19A_	Alignment	not modelled	88.6	12	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: the crystal structure of an epoxide hydrolase from streptomyces2 carzinostaticus subsp. neocarzinostaticus.
112	d3tglA_	Alignment	not modelled	88.6	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
113	c2qjwA_	Alignment	not modelled	88.2	17	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
114	c5xg0A_	Alignment	not modelled	87.9	19	PDB header: hydrolase Chain: A: PDB Molecule: poly(ethylene terephthalate) hydrolase; PDBTitle: crystal structure of a novel pet hydrolase from ideonella sakaiensis2 201-f6
115	c1l7qA_	Alignment	not modelled	87.8	10	PDB header: hydrolase Chain: A: PDB Molecule: cocaine esterase; PDBTitle: ser117ala mutant of bacterial cocaine esterase coce
116	c3h1kB_	Alignment	not modelled	87.7	16	PDB header: hydrolase Chain: B: PDB Molecule: acyl-coenzyme a thioesterase 2, mitochondrial; PDBTitle: crystal structure of human mitochondrial acyl-coa thioesterase (acot2)
117	d2r8ba1	Alignment	not modelled	87.7	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
118	d1mpxa2	Alignment	not modelled	87.6	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PepX catalytic domain-like
119	c5oljA_	Alignment	not modelled	87.4	19	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl peptidase iv; PDBTitle: crystal structure of porphyromonas gingivalis dipeptidyl peptidase 4
120	c6guoC_	Alignment	not modelled	87.0	33	PDB header: hydrolase Chain: C: PDB Molecule: putative siderophore-degrading esterase (eurofung); PDBTitle: siderophore hydrolase esta from aspergillus nidulans