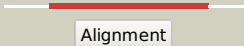

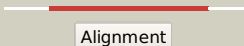

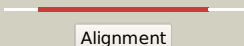







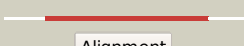











Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3452_cut4_3873631_3874311
 Date Fri Aug 9 18:20:12 BST 2019
 Unique Job ID 56f7122c0aa1e0fc

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1qoza_	 Alignment		100.0	31	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like
2	d1g66a_	 Alignment		100.0	31	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like
3	c4psdA_	 Alignment		100.0	32	PDB header: hydrolase Chain: A; PDB Molecule: carbohydrate esterase family 5; PDBTitle: structure of trichoderma reesei cutinase native form.
4	d1cexa_	 Alignment		100.0	29	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like
5	c3dd5F_	 Alignment		100.0	27	PDB header: hydrolase Chain: F; PDB Molecule: cutinase; PDBTitle: glomerella cingulata e600-cutinase complex
6	c5x88A_	 Alignment		100.0	28	PDB header: hydrolase Chain: A; PDB Molecule: cutinase; PDBTitle: a crystal structure of cutinases from malbranchea cinnamomea
7	c2czqB_	 Alignment		100.0	27	PDB header: hydrolase Chain: B; PDB Molecule: cutinase-like protein; PDBTitle: a novel cutinase-like protein from cryptococcus sp.
8	c3gbsA_	 Alignment		100.0	26	PDB header: hydrolase Chain: A; PDB Molecule: cutinase 1; PDBTitle: crystal structure of aspergillus oryzae cutinase
9	c4oylC_	 Alignment		100.0	29	PDB header: hydrolase Chain: C; PDB Molecule: cutinase; PDBTitle: humicola insolens cutinase in complex with monoethylphosphate
10	c3ajaA_	 Alignment		100.0	26	PDB header: hydrolase Chain: A; PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of msmeq_6394
11	c3hc7A_	 Alignment		100.0	24	PDB header: cell adhesion Chain: A; PDB Molecule: gene 12 protein; PDBTitle: crystal structure of lysin b from mycobacteriophage d29

12	c3g7nA_	Alignment		98.3	14	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: crystal structure of a triacylglycerol lipase from penicillium2 expansum at 1.3
13	c3ngmB_	Alignment		98.2	18	PDB header: hydrolase Chain: B: PDB Molecule: extracellular lipase; PDBTitle: crystal structure of lipase from gibberella zeae
14	d1uwca_	Alignment		97.9	22	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
15	c5xk2A_	Alignment		97.8	17	PDB header: hydrolase Chain: A: PDB Molecule: diacylglycerol lipase; PDBTitle: crystal structure of mono- and diacylglycerol lipase from aspergillus2 oryzae
16	d3tgla_	Alignment		97.7	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
17	c6qppA_	Alignment		97.6	13	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: rhizomucor miehei lipase propeptide complex, native
18	d1tiba_	Alignment		97.5	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
19	d1tcaa_	Alignment		97.5	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
20	c3icvA_	Alignment		97.4	12	PDB header: hydrolase Chain: A: PDB Molecule: lipase b; PDBTitle: structural consequences of a circular permutation on lipase b from2 candida antarctica
21	c2zyiB_	Alignment	not modelled	96.9	15	PDB header: hydrolase Chain: B: PDB Molecule: lipase, putative; PDBTitle: a. fulgidus lipase with fatty acid fragment and calcium
22	d1ei9a_	Alignment	not modelled	96.9	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterases
23	c5f2hA_	Alignment	not modelled	96.9	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
24	c3lp5A_	Alignment	not modelled	96.9	16	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
25	c5gw8A_	Alignment	not modelled	96.8	25	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
26	d1lgya_	Alignment	not modelled	96.7	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
27	c2q0xA_	Alignment	not modelled	96.7	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: alpha/beta hydrolase fold protein of unknown function
28	c3uuuA_	Alignment	not modelled	96.5	21	PDB header: hydrolase Chain: A: PDB Molecule: lip1, secretory lipase (family 3); PDBTitle: crystal structure of mono- and diacylglycerol lipase from malassezia2 globosa
						Fold: alpha/beta-Hydrolases

29	d1ispa_	Alignment	not modelled	96.4	18	Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
30	c6e6uA	Alignment	not modelled	96.4	16	PDB header: biosynthetic protein Chain: A: PDB Molecule: dieckmann cyclase, ncmc; PDBTitle: variant c89s of dieckmann cyclase, ncmc
31	d1tiaa_	Alignment	not modelled	96.3	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
32	d2h1ia1	Alignment	not modelled	96.3	23	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
33	c6e7kB_	Alignment	not modelled	96.3	14	PDB header: hydrolase Chain: B: PDB Molecule: lipoprotein lipase; PDBTitle: structure of the lipoprotein lipase gpibp1 complex that mediates2 plasma triglyceride hydrolysis
34	c3og9A_	Alignment	not modelled	96.3	16	PDB header: hydrolase Chain: A: PDB Molecule: protein yahd a copper inducible hydrolase; PDBTitle: structure of yahd with malic acid
35	c2qjwA_	Alignment	not modelled	96.3	16	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
36	c3ds8A_	Alignment	not modelled	96.3	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin2722 protein; PDBTitle: the crysatl structure of the gene lin2722 products from listeria2 innocua
37	d1mo2a_	Alignment	not modelled	96.2	11	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
38	c1mo2A_	Alignment	not modelled	96.2	11	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
39	d1etha2	Alignment	not modelled	96.2	11	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
40	c2r8bA_	Alignment	not modelled	96.2	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atu2452; PDBTitle: the crystal structure of the protein atu2452 of unknown function from2 agrobacterium tumefaciens str. c58
41	c1hplB_	Alignment	not modelled	96.1	12	PDB header: hydrolase(carboxylic esterase) Chain: B: PDB Molecule: lipase; PDBTitle: horse pancreatic lipase. the crystal structure at 2.3 angstroms2 resolution
42	c2oryA_	Alignment	not modelled	96.1	14	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: crystal structure of m37 lipase
43	c2pvsB_	Alignment	not modelled	96.0	11	PDB header: hydrolase Chain: B: PDB Molecule: pancreatic lipase-related protein 2; PDBTitle: structure of human pancreatic lipase related protein 22 mutant n336q
44	c3o0dF_	Alignment	not modelled	96.0	19	PDB header: hydrolase Chain: F: PDB Molecule: triacylglycerol lipase; PDBTitle: crystal structure of lip2 lipase from yarrowia lipolytica at 1.7 a2 resolution
45	d4lipd_	Alignment	not modelled	96.0	24	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
46	d1gpla2	Alignment	not modelled	95.9	11	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
47	d3b5ea1	Alignment	not modelled	95.9	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
48	c4zxiA_	Alignment	not modelled	95.9	16	PDB header: biosynthetic protein Chain: A: PDB Molecule: tyrocidine synthetase 3; PDBTitle: crystal structure of holo-ab3403 a four domain nonribosomal peptide2 synthetase bound to amp and glycine
49	c6cl4A_	Alignment	not modelled	95.9	17	PDB header: hydrolase Chain: A: PDB Molecule: lipase c12; PDBTitle: lipc12 - lipase from metagenomics
50	d1hpla2	Alignment	not modelled	95.8	11	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
51	c4f21G_	Alignment	not modelled	95.7	13	PDB header: hydrolase/hydrolase inhibitor Chain: G: PDB Molecule: carboxylesterase/phospholipase family protein; PDBTitle: crystal structure of carboxylesterase/phospholipase family protein2 from francisella tularensis
52	d1lpbb2	Alignment	not modelled	95.7	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
53	d1cvla_	Alignment	not modelled	95.7	25	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
54	c5xavB_	Alignment	not modelled	95.6	4	PDB header: biosynthetic protein Chain: B: PDB Molecule: intracellular polyhydroxyalkanoate synthase; PDBTitle: structure of phac from chromobacterium sp. usm2
55	c5d8mA_	Alignment	not modelled	95.6	18	PDB header: hydrolase Chain: A: PDB Molecule: metagenomic carboxyl esterase mgs0156; PDBTitle: crystal structure of the metagenomic carboxyl esterase

						mgs0156
56	c2rauA_	Alignment	not modelled	95.4	15	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
57	d2r8ba1	Alignment	not modelled	95.4	22	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
58	c5t6oA_	Alignment	not modelled	95.3	14	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
59	d1bu8a2	Alignment	not modelled	95.3	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
60	c1gplA_	Alignment	not modelled	95.3	13	PDB header: serine esterase Chain: A: PDB Molecule: rp2 lipase; PDBTitle: rp2 lipase
61	c2veoA_	Alignment	not modelled	95.2	20	PDB header: hydrolase Chain: A: PDB Molecule: lipase a; PDBTitle: x-ray structure of candida antarctica lipase a in its closed state.
62	c1qgeD_	Alignment	not modelled	95.2	22	PDB header: hydrolase Chain: D: PDB Molecule: protein (triacylglycerol hydrolase); PDBTitle: new crystal form of pseudomonas glumae (formerly chromobacterium2 viscosum atcc 6918) lipase
63	d1ex9a_	Alignment	not modelled	95.2	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
64	d1rp1a2	Alignment	not modelled	95.1	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
65	c5h6bA_	Alignment	not modelled	95.0	20	PDB header: hydrolase Chain: A: PDB Molecule: putative secreted lipase; PDBTitle: crystal structure of a thermostable lipase from marine streptomyces
66	c2pplA_	Alignment	not modelled	95.0	17	PDB header: hydrolase Chain: A: PDB Molecule: pancreatic lipase-related protein 1; PDBTitle: human pancreatic lipase-related protein 1
67	c4qnnC_	Alignment	not modelled	94.9	14	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
68	c4gw3A_	Alignment	not modelled	94.6	21	PDB header: hydrolase Chain: A: PDB Molecule: putative lipase; PDBTitle: crystal structure of the lipase from proteus mirabilis
69	c4h0cA_	Alignment	not modelled	94.5	18	PDB header: hydrolase Chain: A: PDB Molecule: phospholipase/carboxylesterase; PDBTitle: crystal structure of phospholipase/carboxylesterase from dyadobacter2 fermentans dsm 18053
70	c1rp1A_	Alignment	not modelled	94.4	16	PDB header: hydrolase Chain: A: PDB Molecule: pancreatic lipase related protein 1; PDBTitle: dog pancreatic lipase related protein 1
71	c2vijA_	Alignment	not modelled	94.3	12	PDB header: hydrolase Chain: A: PDB Molecule: phospholipase a1-iigamma; PDBTitle: crystal structure of phospholipase a1
72	c2h7xA_	Alignment	not modelled	94.0	24	PDB header: hydrolase Chain: A: PDB Molecule: type i polyketide synthase pikaiv; PDBTitle: pikromycin thioesterase adduct with reduced triketide2 affinity label
73	c4nfuB_	Alignment	not modelled	93.5	16	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	c4eziA_	Alignment	not modelled	93.1	22	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative hydrolase (lpg1103) from legionella2 pneumophila subsp. pneumophila str. philadelphia 1 at 1.15 a3 resolution
75	c3lcrA_	Alignment	not modelled	92.9	15	PDB header: hydrolase Chain: A: PDB Molecule: tautomycin biosynthetic pks; PDBTitle: thioesterase from tautomycin biosynthetic pathway
76	c2cbgA_	Alignment	not modelled	92.9	22	PDB header: hydrolase Chain: A: PDB Molecule: fengycin synthetase; PDBTitle: crystal structure of the pmsf-inhibited thioesterase domain of the2 fengycin biosynthesis cluster
77	c2hi1A_	Alignment	not modelled	92.7	19	PDB header: hydrolase Chain: A: PDB Molecule: carboxylesterase; PDBTitle: crystal structure of the bacillus cereus carboxylesterase
78	d1k8qa_	Alignment	not modelled	92.2	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Gastric lipase
79	d2h7xa1	Alignment	not modelled	91.9	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
80	c3bdvB_	Alignment	not modelled	91.9	20	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
						PDB header: transferase

81	c2vavL_	Alignment	not modelled	91.1	15	Chain: L: PDB Molecule: acetyl-coa--deacetylcephalosporin c acetyltransferase; PDBTitle: crystal structure of deacetylcephalosporin c acetyltransferase (dac-2 soak)
82	d1jmkc_	Alignment	not modelled	91.1	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
83	d1hlga_	Alignment	not modelled	90.6	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Gastric lipase
84	c2vsqA_	Alignment	not modelled	90.0	16	PDB header: ligase Chain: A: PDB Molecule: surfactin synthetase subunit 3; PDBTitle: structure of surfactin a synthetase c (srfa-c), a nonribosomal peptide2 synthetase termination module
85	c4x91C_	Alignment	not modelled	89.4	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)
86	c4x96B_	Alignment	not modelled	89.4	15	PDB header: transferase Chain: B: PDB Molecule: phosphatidylcholine-sterol acyltransferase; PDBTitle: low resolution crystal structure of lecithin:cholesterol2 acyltransferase (lcat; residues 21-397)
87	c3h2iA_	Alignment	not modelled	89.1	20	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
88	c4nfaA_	Alignment	not modelled	88.3	16	PDB header: signaling protein Chain: A: PDB Molecule: eds1; PDBTitle: structure of the central plant immunity signaling node eds1 in complex2 with its interaction partner sag101
89	c4c87A_	Alignment	not modelled	88.3	22	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: esterase lpest1 from lactobacillus plantarum wcfs1
90	c4ao6A_	Alignment	not modelled	87.6	20	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: native structure of a novel cold-adapted esterase from an2 arctic intertidal metagenomic library
91	c3l80A_	Alignment	not modelled	86.7	14	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein smu.1393c; PDBTitle: crystal structure of smu.1393c from streptococcus mutans ua159
92	c5ja2A_	Alignment	not modelled	86.3	18	PDB header: ligase Chain: A: PDB Molecule: enterobactin synthase component f; PDBTitle: entf, a terminal nonribosomal peptide synthetase module bound to the2 non-native mbth-like protein pa2412
93	c1pjaA_	Alignment	not modelled	85.7	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)
94	d1pjaa_	Alignment	not modelled	85.7	10	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterases
95	c6gupB_	Alignment	not modelled	85.4	13	PDB header: hydrolase Chain: B: PDB Molecule: siderophore biosynthesis lipase/esterase, putative; PDBTitle: siderophore hydrolase estb from aspergillus fumigatus
96	c5x6sB_	Alignment	not modelled	85.2	27	PDB header: hydrolase Chain: B: PDB Molecule: acetylxy lan esterase a; PDBTitle: acetyl xylan esterase from aspergillus awamori
97	c3fleB_	Alignment	not modelled	84.3	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: se_1780 protein; PDBTitle: se_1780 protein of unknown function from staphylococcus epidermidis.
98	c3h04A_	Alignment	not modelled	84.1	13	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
99	c4fleA_	Alignment	not modelled	83.2	11	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of the esterase yqia (ye3661) from yersinia2 enterocolitica, northeast structural genomics consortium target yer85
100	c2y6vB_	Alignment	not modelled	82.0	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)
101	c3qmwD_	Alignment	not modelled	81.9	13	PDB header: hydrolase Chain: D: PDB Molecule: thioesterase; PDBTitle: redj with peg molecule bound in the active site
102	c2qrUA_	Alignment	not modelled	81.5	14	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
103	c3ilsA_	Alignment	not modelled	81.2	19	PDB header: hydrolase Chain: A: PDB Molecule: afatoxin biosynthesis polyketide synthase; PDBTitle: the thioesterase domain from pksa
104	c5ugzA_	Alignment	not modelled	81.0	12	PDB header: hydrolase Chain: A: PDB Molecule: putative thioesterase; PDBTitle: crystal structure of clbq from the colibactin nrps/pks pathway
105	d2jbwa1	Alignment	not modelled	80.7	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: 2,6-dihydropseudooxynicotine hydrolase-like
106	d1xkta	Alignment	not modelled	80.1	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases

106	c1akqA_	Alignment	not modelled	89.1	41	Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
107	c5hdfB_	Alignment	not modelled	80.0	22	PDB header: hydrolase Chain: B: PDB Molecule: hydrolase; PDBTitle: hydrolase semet-stna
108	c4wfiA_	Alignment	not modelled	79.0	22	PDB header: hydrolase Chain: A: PDB Molecule: cutinase; PDBTitle: crystal structure of pet-degrading cutinase cut190 s226p mutant in2 ca(2+)-free state
109	c4xjvA_	Alignment	not modelled	78.6	16	PDB header: hydrolase Chain: A: PDB Molecule: s-acyl fatty acid synthase thioesterase, medium chain; PDBTitle: crystal structure of human thioesterase 2
110	c3fnbB_	Alignment	not modelled	77.5	19	PDB header: hydrolase Chain: B: PDB Molecule: acylaminoacyl peptidase smu_737; PDBTitle: crystal structure of acylaminoacyl peptidase smu_737 from2 streptococcus mutans ua159
111	c3visB_	Alignment	not modelled	76.8	22	PDB header: hydrolase Chain: B: PDB Molecule: esterase; PDBTitle: crystal structure of cutinase est119 from thermobifida alba ahk119
112	c3wydA_	Alignment	not modelled	76.1	18	PDB header: hydrolase Chain: A: PDB Molecule: lc-est1c; PDBTitle: c-terminal esterase domain of lc-est1
113	d1ji3a_	Alignment	not modelled	75.6	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
114	c3flaB_	Alignment	not modelled	73.2	18	PDB header: hydrolase Chain: B: PDB Molecule: rifr; PDBTitle: rifr - type ii thioesterase from rifamycin nrps/pks biosynthetic2 pathway - form 1
115	c1cr6A_	Alignment	not modelled	73.2	13	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
116	c5ah0B_	Alignment	not modelled	73.1	14	PDB header: hydrolase Chain: B: PDB Molecule: lipase; PDBTitle: structure of lipase 1 from pelosinus fermentans
117	c4pf1D_	Alignment	not modelled	73.1	21	PDB header: hydrolase Chain: D: PDB Molecule: peptidase s15/coce/nond; PDBTitle: crystal structure of aminopeptidase from marine sediment archaeon2 thaumarchaeota archaeon
118	c2jwbB_	Alignment	not modelled	73.0	17	PDB header: hydrolase Chain: B: PDB Molecule: 2,6-dihydroxy-pseudo-oxynicotine hydrolase; PDBTitle: crystal structure of the 2,6-dihydroxy-pseudo-oxynicotine hydrolase.
119	c2b9vB_	Alignment	not modelled	72.6	16	PDB header: hydrolase Chain: B: PDB Molecule: alpha-amino acid ester hydrolase; PDBTitle: acetobacter turbidans alpha-amino acid ester hydrolase
120	c3hkB_	Alignment	not modelled	70.9	16	PDB header: hydrolase Chain: B: PDB Molecule: acyl-coenzyme a thioesterase 2, mitochondrial; PDBTitle: crystal structure of human mitochondrial acyl-coa thioesterase (acot2)