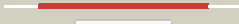



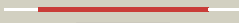



















# Phyre2

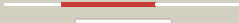

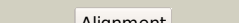
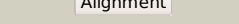
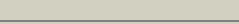

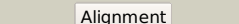
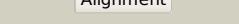

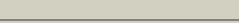

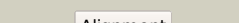
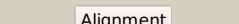

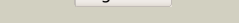






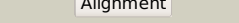

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD1758\_(cut1)\_1989049\_1989573  
 Date Fri Aug 2 13:30:36 BST 2019  
 Unique Job ID 5f5da5baec35f011

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1g66a_</a>	 Alignment		100.0	25	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Cutinase-like
2	<a href="#">d1qoza_</a>	 Alignment		100.0	23	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Cutinase-like
3	<a href="#">c4psdA_</a>	 Alignment		100.0	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> carbohydrate esterase family 5; <b>PDBTitle:</b> structure of trichoderma reesei cutinase native form.
4	<a href="#">d1cexa_</a>	 Alignment		100.0	28	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Cutinase-like
5	<a href="#">c3dd5F_</a>	 Alignment		100.0	29	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> cutinase; <b>PDBTitle:</b> glomerella cingulata e600-cutinase complex
6	<a href="#">c5x88A_</a>	 Alignment		100.0	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cutinase; <b>PDBTitle:</b> a crystal structure of cutinases from malbranchea cinnamomea
7	<a href="#">c2czqB_</a>	 Alignment		100.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cutinase-like protein; <b>PDBTitle:</b> a novel cutinase-like protein from cryptococcus sp.
8	<a href="#">c4oylC_</a>	 Alignment		100.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> cutinase; <b>PDBTitle:</b> humicola insolens cutinase in complex with monoethylphosphate
9	<a href="#">c3gbsA_</a>	 Alignment		100.0	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cutinase 1; <b>PDBTitle:</b> crystal structure of aspergillus oryzae cutinase
10	<a href="#">c3ajaA_</a>	 Alignment		100.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of msmeq_6394
11	<a href="#">c3hc7A_</a>	 Alignment		99.9	19	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> gene 12 protein; <b>PDBTitle:</b> crystal structure of lysin b from mycobacteriophage d29

12	<a href="#">c3g7nA_</a>	Alignment		97.6	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> lipase; <b>PDBTitle:</b> crystal structure of a triacylglycerol lipase from penicillium2 expansum at 1.3
13	<a href="#">c3ngmB_</a>	Alignment		97.3	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> extracellular lipase; <b>PDBTitle:</b> crystal structure of lipase from gibberella zeae
14	<a href="#">d1tcaa_</a>	Alignment		97.0	12	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
15	<a href="#">d3tgla_</a>	Alignment		96.6	15	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
16	<a href="#">c5gw8A_</a>	Alignment		96.6	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical secretory lipase (family 3); <b>PDBTitle:</b> crystal structure of a putative dag-like lipase (mgmdl2) from2 malassezia globosa
17	<a href="#">c6cl4A_</a>	Alignment		96.5	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> lipase c12; <b>PDBTitle:</b> lipc12 - lipase from metagenomics
18	<a href="#">c6qppA_</a>	Alignment		96.5	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> lipase; <b>PDBTitle:</b> rhizomucor miehei lipase propeptide complex, native
19	<a href="#">d1lgva_</a>	Alignment		96.4	17	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
20	<a href="#">d1tiba_</a>	Alignment		96.4	20	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
21	<a href="#">c5f2hA_</a>	Alignment	not modelled	96.3	18	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> 2.75 angstrom resolution crystal structure of uncharacterized protein2 from bacillus cereus atcc 10987
22	<a href="#">c3uueA_</a>	Alignment	not modelled	96.3	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> lip1, secretory lipase (family 3); <b>PDBTitle:</b> crystal structure of mono- and diacylglycerol lipase from malassezia2 globosa
23	<a href="#">d4lipd_</a>	Alignment	not modelled	96.2	26	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Bacterial lipase
24	<a href="#">d1tiaa_</a>	Alignment	not modelled	96.1	25	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
25	<a href="#">c3icvA_</a>	Alignment	not modelled	95.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> lipase b; <b>PDBTitle:</b> structural consequences of a circular permutation on lipase b from2 candida antarctica
26	<a href="#">d1cvla_</a>	Alignment	not modelled	95.9	27	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Bacterial lipase
27	<a href="#">c1mo2A_</a>	Alignment	not modelled	95.8	14	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> erythronolide synthase, modules 5 and 6; <b>PDBTitle:</b> thioesterase domain from 6-deoxyerythronolide synthase (debs te), ph2 8.5
28	<a href="#">d1mo2a_</a>	Alignment	not modelled	95.8	14	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Thioesterase domain of polypeptide, polyketide and fatty acid synthases
						<b>Fold:</b> alpha/beta-Hydrolases

29	<a href="#">d1ei9a_</a>	Alignment	not modelled	95.6	19	<b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Thioesterases
30	<a href="#">c3og9A_</a>	Alignment	not modelled	95.5	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein yahd a copper inducible hydrolase; <b>PDBTitle:</b> structure of yahd with malic acid
31	<a href="#">d1ex9a_</a>	Alignment	not modelled	95.5	27	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Bacterial lipase
32	<a href="#">c3lp5A_</a>	Alignment	not modelled	95.5	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative cell surface hydrolase; <b>PDBTitle:</b> the crystal structure of the putative cell surface hydrolase from2 lactobacillus plantarum wcf51
33	<a href="#">c4gw3A_</a>	Alignment	not modelled	95.3	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative lipase; <b>PDBTitle:</b> crystal structure of the lipase from proteus mirabilis
34	<a href="#">c5xk2A_</a>	Alignment	not modelled	95.3	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> diacylglycerol lipase; <b>PDBTitle:</b> crystal structure of mono- and diacylglycerol lipase from aspergillus2 oryzae
35	<a href="#">c3o0dF_</a>	Alignment	not modelled	95.2	20	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> triacylglycerol lipase; <b>PDBTitle:</b> crystal structure of lip2 lipase from yarrowia lipolytica at 1.7 a2 resolution
36	<a href="#">d1uwca_</a>	Alignment	not modelled	95.1	24	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
37	<a href="#">c2qjwA_</a>	Alignment	not modelled	95.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein xcc1541; <b>PDBTitle:</b> crystal structure of a putative hydrolase of the alpha/beta2 superfamily (xcc1541) from xanthomonas campestris pv. campestris at3 1.35 a resolution
38	<a href="#">c3ds8A_</a>	Alignment	not modelled	94.8	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> lin2722 protein; <b>PDBTitle:</b> the crystal structure of the gene lin2722 products from listeria2 innocua
39	<a href="#">c1qgeD_</a>	Alignment	not modelled	94.8	27	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> protein (triacylglycerol hydrolase); <b>PDBTitle:</b> new crystal form of pseudomonas glumae (formerly chromobacterium2 viscosum atcc 6918) lipase
40	<a href="#">c2veoA_</a>	Alignment	not modelled	94.7	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lipase a; <b>PDBTitle:</b> x-ray structure of candida antarctica lipase a in its closed state.
41	<a href="#">c5d8mA_</a>	Alignment	not modelled	94.6	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> metagenomic carboxyl esterase mgs0156; <b>PDBTitle:</b> crystal structure of the metagenomic carboxyl esterase mgs0156
42	<a href="#">d2h1ia1</a>	Alignment	not modelled	94.5	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carboxylesterase/thioesterase 1
43	<a href="#">c2q0xA_</a>	Alignment	not modelled	94.5	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> alpha/beta hydrolase fold protein of unknown function
44	<a href="#">d1etha2</a>	Alignment	not modelled	94.4	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Pancreatic lipase, N-terminal domain
45	<a href="#">c2zyiB_</a>	Alignment	not modelled	94.3	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> lipase, putative; <b>PDBTitle:</b> a. fulgidus lipase with fatty acid fragment and calcium
46	<a href="#">c5xavB_</a>	Alignment	not modelled	94.2	11	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> intracellular polyhydroxyalkanoate synthase; <b>PDBTitle:</b> structure of phac from chromobacterium sp. usm2
47	<a href="#">c2h7xA_</a>	Alignment	not modelled	94.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> type i polyketide synthase pikaiv; <b>PDBTitle:</b> pikromycin thioesterase adduct with reduced triketide2 affinity label
48	<a href="#">c4zxiA_</a>	Alignment	not modelled	94.0	17	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> tyrocidine synthetase 3; <b>PDBTitle:</b> crystal structure of holo-ab3403 a four domain nonribosomal peptide2 synthetase bound to amp and glycine
49	<a href="#">c5t6oA_</a>	Alignment	not modelled	93.9	29	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> poly-beta-hydroxybuterate polymerase; <b>PDBTitle:</b> structure of the catalytic domain of the class i polyhydroxybutyrate2 synthase from cupriavidus necator
50	<a href="#">d1rp1a2</a>	Alignment	not modelled	93.9	21	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Pancreatic lipase, N-terminal domain
51	<a href="#">d1bu8a2</a>	Alignment	not modelled	93.8	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Pancreatic lipase, N-terminal domain
52	<a href="#">c2cbgA_</a>	Alignment	not modelled	93.5	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> fengycin synthetase; <b>PDBTitle:</b> crystal structure of the pmsf-inhibited thioesterase domain of the2 fengycin biosynthesis cluster
53	<a href="#">d2h7xa1</a>	Alignment	not modelled	93.5	20	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Thioesterase domain of polypeptide, polyketide and fatty acid synthases
54	<a href="#">d3b5ea1</a>	Alignment	not modelled	93.5	13	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carboxylesterase/thioesterase 1
55	<a href="#">d1hpla2</a>	Alignment	not modelled	93.5	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Pancreatic lipase, N-terminal domain

56	<a href="#">c2rauA</a>	 Alignment	not modelled	93.5	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative esterase; <b>PDBTitle:</b> crystal structure of a putative lipase (np_343859.1) from <i>sulfolobus2 solfataricus</i> at 1.85 a resolution
57	<a href="#">d1jmkc</a>	 Alignment	not modelled	93.4	20	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Thioesterase domain of polypeptide, polyketide and fatty acid synthases
58	<a href="#">d2r8ba1</a>	 Alignment	not modelled	93.4	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carboxylesterase/thioesterase 1
59	<a href="#">d1ispa</a>	 Alignment	not modelled	93.4	15	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Bacterial lipase
60	<a href="#">c2r8ba</a>	 Alignment	not modelled	93.4	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein atu2452; <b>PDBTitle:</b> the crystal structure of the protein atu2452 of unknown function from <i>2 agrobacterium tumefaciens</i> str. c58
61	<a href="#">d1lpbb2</a>	 Alignment	not modelled	93.1	18	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Pancreatic lipase, N-terminal domain
62	<a href="#">d1gpla2</a>	 Alignment	not modelled	92.9	17	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Pancreatic lipase, N-terminal domain
63	<a href="#">c2vijA</a>	 Alignment	not modelled	92.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phospholipase a1-iigamma; <b>PDBTitle:</b> crystal structure of phospholipase a1
64	<a href="#">c5h6bA</a>	 Alignment	not modelled	92.8	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative secreted lipase; <b>PDBTitle:</b> crystal structure of a thermostable lipase from marine <i>streptomyces</i>
65	<a href="#">c3lcrA</a>	 Alignment	not modelled	92.8	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tautomycetin biosynthetic pks; <b>PDBTitle:</b> thioesterase from tautomycetin biosynthetic pathway
66	<a href="#">c4qnnC</a>	 Alignment	not modelled	92.4	20	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> phospholipase a 1 from hornet( <i>vespa basalis</i> ) venom; <b>PDBTitle:</b> crystal structure of phospholipase a 1 from hornet( <i>vespa basalis</i> )2 venom
67	<a href="#">c2pvsB</a>	 Alignment	not modelled	91.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> pancreatic lipase-related protein 2; <b>PDBTitle:</b> structure of human pancreatic lipase related protein 22 mutant n336q
68	<a href="#">c1gplA</a>	 Alignment	not modelled	91.4	17	<b>PDB header:</b> serine esterase <b>Chain:</b> A: <b>PDB Molecule:</b> rp2 lipase; <b>PDBTitle:</b> rp2 lipase
69	<a href="#">c6e7kB</a>	 Alignment	not modelled	91.3	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> lipoprotein lipase; <b>PDBTitle:</b> structure of the lipoprotein lipase gpibp1 complex that mediates2 plasma triglyceride hydrolysis
70	<a href="#">c4eziA</a>	 Alignment	not modelled	90.7	21	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative hydrolase (lpg1103) from <i>legionella2 pneumophila</i> subsp. <i>pneumophila</i> str. philadelphia 1 at 1.15 a3 resolution
71	<a href="#">c2h1iA</a>	 Alignment	not modelled	90.7	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> carboxylesterase; <b>PDBTitle:</b> crystal structure of the <i>bacillus cereus</i> carboxylesterase
72	<a href="#">c1hplB</a>	 Alignment	not modelled	90.2	16	<b>PDB header:</b> hydrolase(carboxylic esterase) <b>Chain:</b> B: <b>PDB Molecule:</b> lipase; <b>PDBTitle:</b> horse pancreatic lipase. the crystal structure at 2.3 angstroms2 resolution
73	<a href="#">c4nfuB</a>	 Alignment	not modelled	90.0	14	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> senescence-associated carboxylesterase 101; <b>PDBTitle:</b> structure of the central plant immunity signaling node eds1 in complex2 with its interaction partner sag101
74	<a href="#">c2pplA</a>	 Alignment	not modelled	90.0	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pancreatic lipase-related protein 1; <b>PDBTitle:</b> human pancreatic lipase-related protein 1
75	<a href="#">c3fleB</a>	 Alignment	not modelled	90.0	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> se_1780 protein; <b>PDBTitle:</b> se_1780 protein of unknown function from <i>staphylococcus epidermidis</i> .
76	<a href="#">c4f21G</a>	 Alignment	not modelled	89.7	14	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> G: <b>PDB Molecule:</b> carboxylesterase/phospholipase family protein; <b>PDBTitle:</b> crystal structure of carboxylesterase/phospholipase family protein2 from <i>francisella tularensis</i>
77	<a href="#">c6gupB</a>	 Alignment	not modelled	89.5	10	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> siderophore biosynthesis lipase/esterase, putative; <b>PDBTitle:</b> siderophore hydrolase estb from <i>aspergillus fumigatus</i>
78	<a href="#">d1k8qa</a>	 Alignment	not modelled	88.7	17	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Gastric lipase
79	<a href="#">c4nfuA</a>	Alignment	not modelled	88.0	18	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> eds1; <b>PDBTitle:</b> structure of the central plant immunity signaling node eds1 in complex2 with its interaction partner sag101
80	<a href="#">c2vavL</a>	Alignment	not modelled	87.0	12	<b>PDB header:</b> transferase <b>Chain:</b> L: <b>PDB Molecule:</b> acetyl-coa--deacetylcephalosporin c acetyltransferase; <b>PDBTitle:</b> crystal structure of deacetylcephalosporin c acetyltransferase (dac-2 soak)

81	<a href="#">d1vkha_</a>	Alignment	not modelled	86.2	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Putative serine hydrolase Ydr428c
82	<a href="#">c2orvA_</a>	Alignment	not modelled	86.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lipase; <b>PDBTitle:</b> crystal structure of m37 lipase
83	<a href="#">c4h0cA_</a>	Alignment	not modelled	85.8	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phospholipase/carboxylesterase; <b>PDBTitle:</b> crystal structure of phospholipase/carboxylesterase from dyadobacter2 fermentans dsm 18053
84	<a href="#">c1rp1A_</a>	Alignment	not modelled	85.8	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pancreatic lipase related protein 1; <b>PDBTitle:</b> dog pancreatic lipase related protein 1
85	<a href="#">c2vsqA_</a>	Alignment	not modelled	85.4	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> surfactin synthetase subunit 3; <b>PDBTitle:</b> structure of surfactin a synthetase c (srfa-c), a nonribosomal peptide2 synthetase termination module
86	<a href="#">c3bdvB_</a>	Alignment	not modelled	84.6	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein duf1234; <b>PDBTitle:</b> crystal structure of a putative yden-like hydrolase (eca3091) from2 pectobacterium atrosepticum scri1043 at 1.66 a resolution
87	<a href="#">c5ugzA_</a>	Alignment	not modelled	84.6	8	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative thioesterase; <b>PDBTitle:</b> crystal structure of clbq from the colibactin nrps/pks pathway
88	<a href="#">c4fleA_</a>	Alignment	not modelled	84.4	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> crystal structure of the esterase yqia (ye3661) from yersinia2 enterocolitica, northeast structural genomics consortium target yer85
89	<a href="#">d1xkta_</a>	Alignment	not modelled	84.4	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Thioesterase domain of polypeptide, polyketide and fatty acid synthases
90	<a href="#">c3flaB_</a>	Alignment	not modelled	84.2	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> rifr; <b>PDBTitle:</b> rifr - type ii thioesterase from rifamycin nrps/pks biosynthetic2 pathway - form 1
91	<a href="#">c4xjvA_</a>	Alignment	not modelled	84.1	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> s-acyl fatty acid synthase thioesterase, medium chain; <b>PDBTitle:</b> crystal structure of human thioesterase 2
92	<a href="#">c3h04A_</a>	Alignment	not modelled	84.0	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> the crystal structure of the protein with unknown function from2 staphylococcus aureus subsp. aureus mu50
93	<a href="#">c3h2iA_</a>	Alignment	not modelled	83.7	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> crystal structure of n228w mutant of the rice cell wall2 degrading esterase lipa from xanthomonas oryzae
94	<a href="#">d1hlga_</a>	Alignment	not modelled	82.6	21	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Gastric lipase
95	<a href="#">c3ilsA_</a>	Alignment	not modelled	81.3	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> afatoxin biosynthesis polyketide synthase; <b>PDBTitle:</b> the thioesterase domain from pksa
96	<a href="#">c3l80A_</a>	Alignment	not modelled	79.8	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein smu.1393c; <b>PDBTitle:</b> crystal structure of smu.1393c from streptococcus mutans ua159
97	<a href="#">c3qmwD_</a>	Alignment	not modelled	79.6	17	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> thioesterase; <b>PDBTitle:</b> redj with peg molecule bound in the active site
98	<a href="#">c5ja2A_</a>	Alignment	not modelled	78.6	14	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> enterobactin synthase component f; <b>PDBTitle:</b> entf, a terminal nonribosomal peptide synthetase module bound to the2 non-native mbth-like protein pa2412
99	<a href="#">c2qrUA_</a>	Alignment	not modelled	78.5	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of an alpha/beta hydrolase superfamily protein from2 enterococcus faecalis
100	<a href="#">d1luxoa_</a>	Alignment	not modelled	78.5	10	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> YdeN-like
101	<a href="#">c5ah0B_</a>	Alignment	not modelled	76.0	9	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> lipase; <b>PDBTitle:</b> structure of lipase 1 from pelosinus fermentans
102	<a href="#">c2fx5A_</a>	Alignment	not modelled	75.7	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lipase; <b>PDBTitle:</b> pseudomonas mendocina lipase
103	<a href="#">d1pjaa_</a>	Alignment	not modelled	74.3	10	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Thioesterases
104	<a href="#">c1pjaA_</a>	Alignment	not modelled	74.3	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> palmitoyl-protein thioesterase 2 precursor; <b>PDBTitle:</b> the crystal structure of palmitoyl protein thioesterase-2 reveals the2 basis for divergent substrate specificities of the two lysosomal3 thioesterases (ppt1 and ppt2)
105	<a href="#">c3trdA_</a>	Alignment	not modelled	73.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha/beta hydrolase; <b>PDBTitle:</b> structure of an alpha-beta serine hydrolase homologue from coxiella2 burnetii
106	<a href="#">d2nn6i2</a>	Alignment	not modelled	72.8	23	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Ribosomal L27 protein-like

						<b>Family:</b> ECR1 N-terminal domain-like
107	<a href="#">c2y6vB_</a>	Alignment	not modelled	71.7	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> peroxisomal membrane protein lpx1; <b>PDBTitle:</b> peroxisomal alpha-beta-hydrolase lpx1 (yor084w) from saccharomyces2 cerevisiae (crystal form i)
108	<a href="#">c4x91C_</a>	Alignment	not modelled	71.2	16	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> group xv phospholipase a2; <b>PDBTitle:</b> crystal structure of lysosomal phospholipase a2 in complex with2 isopropyl dodec-11-enylfluorophosphonate (idfp)
109	<a href="#">c4c87A_</a>	Alignment	not modelled	70.7	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> esterase lpest1 from lactobacillus plantarum wcfs1
110	<a href="#">c5x6sB_</a>	Alignment	not modelled	68.2	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> acetylxylyan esterase a; <b>PDBTitle:</b> acetyl xylan esterase from aspergillus awamori
111	<a href="#">c3mveB_</a>	Alignment	not modelled	66.7	17	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> upf0255 protein vv1_0328; <b>PDBTitle:</b> crystal structure of a novel pyruvate decarboxylase
112	<a href="#">c4x96B_</a>	Alignment	not modelled	66.2	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphatidylcholine-sterol acyltransferase; <b>PDBTitle:</b> low resolution crystal structure of lecithin:cholesterol2 acyltransferase (lcat; residues 21-397)
113	<a href="#">d1ku0a_</a>	Alignment	not modelled	64.8	10	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Bacterial lipase
114	<a href="#">d2fuka1</a>	Alignment	not modelled	64.6	22	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Atu1826-like
115	<a href="#">c4ao6A_</a>	Alignment	not modelled	63.6	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> native structure of a novel cold-adapted esterase from an2 arctic intertidal metagenomic library
116	<a href="#">d2jbwa1</a>	Alignment	not modelled	63.3	14	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> 2,6-dihydropseudooxynicotine hydrolase-like
117	<a href="#">d1ji3a_</a>	Alignment	not modelled	63.3	10	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Bacterial lipase
118	<a href="#">c3fnbB_</a>	Alignment	not modelled	62.6	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> acylaminoacyl peptidase smu_737; <b>PDBTitle:</b> crystal structure of acylaminoacyl peptidase smu_737 from2 streptococcus mutans ua159
119	<a href="#">c2ronA_</a>	Alignment	not modelled	62.3	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> surfactin synthetase thioesterase subunit; <b>PDBTitle:</b> the external thioesterase of the surfactin-synthetase
120	<a href="#">c3wiaA_</a>	Alignment	not modelled	62.2	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidized polyvinyl alcohol hydrolase; <b>PDBTitle:</b> crystal structure of soph native