
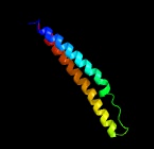

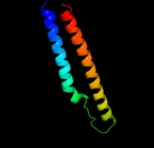
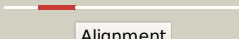
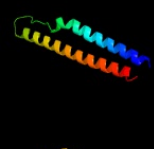
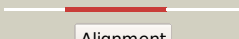

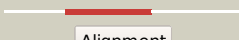






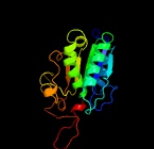























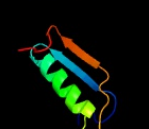

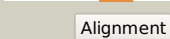



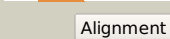
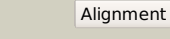




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0159c_(PE3)_187431_188837
Date	Tue Jul 23 14:50:21 BST 2019
Unique Job ID	e650fdf70558c1dd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5xfsA_</a>	 Alignment		100.0	42	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> pe family protein pe8; <b>PDBTitle:</b> crystal structure of pe8-ppe15 in complex with esp95 from m.2 tuberculosis
2	<a href="#">d2g38a1</a>	 Alignment		100.0	35	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> PE/PPE dimer-like <b>Family:</b> PE
3	<a href="#">c2g38A_</a>	 Alignment		100.0	35	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> pe family protein; <b>PDBTitle:</b> a pe/ppe protein complex from mycobacterium tuberculosis
4	<a href="#">c3ajaA_</a>	 Alignment		99.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of msmeg_6394
5	<a href="#">d1qoza_</a>	 Alignment		99.6	19	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Cutinase-like
6	<a href="#">d1g66a_</a>	 Alignment		99.6	17	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Cutinase-like
7	<a href="#">c3hc7A_</a>	 Alignment		99.5	21	<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
8	<a href="#">c2czaB_</a>	 Alignment		99.5	20	<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.
9	<a href="#">d1cexa_</a>	 Alignment		99.3	18	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Cutinase-like
10	<a href="#">c3dd5F_</a>	 Alignment		99.3	19	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> cutinase; <b>PDBTitle:</b> glomerella cingulata e600-cutinase complex
11	<a href="#">c5x88A_</a>	 Alignment		99.2	20	<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

12	<a href="#">c3gbsA_</a>	 Alignment		99.2	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cutinase 1; <b>PDBTitle:</b> crystal structure of aspergillus oryzae cutinase
13	<a href="#">c4psdA_</a>	 Alignment		99.2	19	<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.
14	<a href="#">c4oylC_</a>	 Alignment		99.1	15	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> cutinase; <b>PDBTitle:</b> humicola insolens cutinase in complex with mono-ethylphosphate
15	<a href="#">c3icvA_</a>	 Alignment		93.9	14	<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
16	<a href="#">d1tcaa_</a>	 Alignment		92.7	17	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
17	<a href="#">c5xavB_</a>	 Alignment		92.5	12	<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
18	<a href="#">d1ei9a_</a>	 Alignment		92.4	12	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Thioesterases
19	<a href="#">c4nfbB_</a>	 Alignment		91.1	19	<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
20	<a href="#">d1jmkc_</a>	 Alignment		90.3	21	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Thioesterase domain of polypeptide, polyketide and fatty acid synthases
21	<a href="#">c5t6oA_</a>	 Alignment	not modelled	89.4	15	<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
22	<a href="#">c2cbgA_</a>	 Alignment	not modelled	87.7	19	<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
23	<a href="#">c5d8mA_</a>	 Alignment	not modelled	85.6	15	<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
24	<a href="#">c2g38B_</a>	 Alignment	not modelled	85.0	6	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> ppe family protein; <b>PDBTitle:</b> a pe/pppe protein complex from mycobacterium tuberculosis
25	<a href="#">d2g38b1</a>	 Alignment	not modelled	85.0	6	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> PE/PPE dimer-like <b>Family:</b> PPE
26	<a href="#">c4wj2A_</a>	 Alignment	not modelled	84.3	14	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> antigen mtb48; <b>PDBTitle:</b> mycobacterial protein
27	<a href="#">d3b5ea1</a>	 Alignment	not modelled	84.1	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carboxylesterase/thioesterase 1
28	<a href="#">d3tglA_</a>	 Alignment	not modelled	83.8	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
		 Alignment				<b>PDB header:</b> transferase

29	<a href="#">c1mo2A_</a>	Alignment	not modelled	83.6	18	<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
30	<a href="#">d1mo2a_</a>	Alignment	not modelled	83.6	18	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Thioesterase domain of polypeptide, polyketide and fatty acid synthases
31	<a href="#">c3ds8A_</a>	Alignment	not modelled	83.4	14	<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
32	<a href="#">c2zyiB_</a>	Alignment	not modelled	82.7	15	<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
33	<a href="#">c3og9A_</a>	Alignment	not modelled	81.4	23	<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
34	<a href="#">c4qnnC_</a>	Alignment	not modelled	81.0	10	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> phospholipase a 1 from hornet(vespa basalis) venom; <b>PDBTitle:</b> crystal structure of phospholipase a 1 from hornet(vespa basalis)2 venom
35	<a href="#">c2oryA_</a>	Alignment	not modelled	80.4	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lipase; <b>PDBTitle:</b> crystal structure of m37 lipase
36	<a href="#">c4h0cA_</a>	Alignment	not modelled	76.9	19	<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
37	<a href="#">c3gvmA_</a>	Alignment	not modelled	76.9	15	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein sag1039; <b>PDBTitle:</b> structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
38	<a href="#">d2h1ia1</a>	Alignment	not modelled	75.7	18	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carboxylesterase/thioesterase 1
39	<a href="#">d1wa8a1</a>	Alignment	not modelled	74.0	20	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
40	<a href="#">c4xjvA_</a>	Alignment	not modelled	72.8	15	<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
41	<a href="#">c3lp5A_</a>	Alignment	not modelled	72.6	17	<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
42	<a href="#">c2qs9A_</a>	Alignment	not modelled	72.2	18	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> retinoblastoma-binding protein 9; <b>PDBTitle:</b> crystal structure of the human retinoblastoma-binding2 protein 9 (rbbp-9). nesg target hr2978
43	<a href="#">d1etha2</a>	Alignment	not modelled	71.9	13	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Pancreatic lipase, N-terminal domain
44	<a href="#">d1tiaa_</a>	Alignment	not modelled	70.4	18	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
45	<a href="#">c2q0xA_</a>	Alignment	not modelled	67.8	14	<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
46	<a href="#">c4x96B_</a>	Alignment	not modelled	67.2	20	<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)
47	<a href="#">c5f2hA_</a>	Alignment	not modelled	66.3	17	<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
48	<a href="#">d1bu8a2</a>	Alignment	not modelled	65.7	15	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Pancreatic lipase, N-terminal domain
49	<a href="#">c4x91C_</a>	Alignment	not modelled	65.1	23	<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)
50	<a href="#">c6cl4A_</a>	Alignment	not modelled	64.5	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lipase c12; <b>PDBTitle:</b> lipc12 - lipase from metagenomics
51	<a href="#">c2vijA_</a>	Alignment	not modelled	64.3	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phospholipase a1-iigamma; <b>PDBTitle:</b> crystal structure of phospholipase a1
52	<a href="#">c4f21G_</a>	Alignment	not modelled	64.0	19	<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 francisella tularensis
53	<a href="#">c5xk2A_</a>	Alignment	not modelled	63.9	15	<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
54	<a href="#">c5gw8A_</a>	Alignment	not modelled	62.1	17	<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
						<b>Fold:</b> alpha/beta-Hydrolases

55	<a href="#">d2r8ba1</a>	Alignment	not modelled	60.6	12	<b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carboxylesterase/thioesterase 1
56	<a href="#">c2pvsB</a>	Alignment	not modelled	59.9	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
57	<a href="#">c3zbhC</a>	Alignment	not modelled	59.7	17	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> esxa; <b>PDBTitle:</b> geobacillus thermodenitrificans esxa crystal form i
58	<a href="#">d1lgya</a>	Alignment	not modelled	57.5	19	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
59	<a href="#">c2vsaA</a>	Alignment	not modelled	55.9	18	<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
60	<a href="#">d1lppb2</a>	Alignment	not modelled	55.3	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Pancreatic lipase, N-terminal domain
61	<a href="#">d1rpa2</a>	Alignment	not modelled	54.4	18	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Pancreatic lipase, N-terminal domain
62	<a href="#">c2r8bA</a>	Alignment	not modelled	53.2	14	<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 from2 agrobacterium tumefaciens str. c58
63	<a href="#">c4zxiA</a>	Alignment	not modelled	52.8	16	<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
64	<a href="#">c4gw3A</a>	Alignment	not modelled	52.2	24	<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
65	<a href="#">c6qppA</a>	Alignment	not modelled	52.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lipase; <b>PDBTitle:</b> rhizomucor miehei lipase propeptide complex, native
66	<a href="#">c4r1dA</a>	Alignment	not modelled	51.8	18	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> the crystal structure of tle4-tli4 complex
67	<a href="#">c5xfsB</a>	Alignment	not modelled	51.3	17	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> ppe family protein ppe15; <b>PDBTitle:</b> crystal structure of pe8-ppe15 in complex with esp5 from m.2 tuberculosis
68	<a href="#">c4nfaA</a>	Alignment	not modelled	51.1	12	<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
69	<a href="#">c4iogD</a>	Alignment	not modelled	50.7	13	<b>PDB header:</b> unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> secreted protein esxb; <b>PDBTitle:</b> the crystal structure of a secreted protein esxb (wild-type, in p212 space group) from bacillus anthracis str. sterne
70	<a href="#">d1luxoa</a>	Alignment	not modelled	49.3	8	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> YdeN-like
71	<a href="#">c4eziA</a>	Alignment	not modelled	49.1	11	<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 legionella2 pneumophila subsp. pneumophila str. philadelphia 1 at 1.15 a3 resolution
72	<a href="#">c2qjwA</a>	Alignment	not modelled	49.0	20	<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
73	<a href="#">d1gpla2</a>	Alignment	not modelled	48.3	19	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Pancreatic lipase, N-terminal domain
74	<a href="#">c3bdvB</a>	Alignment	not modelled	47.0	14	<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
75	<a href="#">c3p3dA</a>	Alignment	not modelled	45.8	26	<b>PDB header:</b> nuclear protein <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoporin 53; <b>PDBTitle:</b> crystal structure of the nup53 rrm domain from pichia guilliermondii
76	<a href="#">c3uueA</a>	Alignment	not modelled	45.8	18	<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
77	<a href="#">d1ispa</a>	Alignment	not modelled	45.5	12	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Bacterial lipase
78	<a href="#">c3g7nA</a>	Alignment	not modelled	45.1	13	<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
79	<a href="#">d1hpla2</a>	Alignment	not modelled	44.5	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Pancreatic lipase, N-terminal domain
80	<a href="#">c3lcrA</a>	Alignment	not modelled	44.3	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tautomycin biosynthetic pks; <b>PDBTitle:</b> thioesterase from tautomycin biosynthetic pathway
						<b>PDB header:</b> hydrolase

81	<a href="#">c2h1IA_</a>	Alignment	not modelled	42.8	18	<b>Chain:</b> A: <b>PDB Molecule:</b> carboxylesterase; <b>PDBTitle:</b> crystal structure of the bacillus cereus carboxylesterase
82	<a href="#">d1tiba_</a>	Alignment	not modelled	42.0	19	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
83	<a href="#">c6e7kB_</a>	Alignment	not modelled	40.5	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> lipoprotein lipase; <b>PDBTitle:</b> structure of the lipoprotein lipase gp1hbp1 complex that mediates2 plasma triglyceride hydrolysis
84	<a href="#">c5h3bA_</a>	Alignment	not modelled	39.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein hi_1552; <b>PDBTitle:</b> crystal structure of semet-biog from haemophilus influenzae at 1.492 angstroms resolution
85	<a href="#">c5uazB_</a>	Alignment	not modelled	38.2	22	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> nucleoporin nup53; <b>PDBTitle:</b> crystal structure of the yeast nucleoporin
86	<a href="#">c3flaB_</a>	Alignment	not modelled	37.5	13	<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
87	<a href="#">c2w6cX_</a>	Alignment	not modelled	34.6	23	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> acetylcholinesterase; <b>PDBTitle:</b> ache in complex with a bis-(-)-nor-meptazinol derivative
88	<a href="#">c1qgeD_</a>	Alignment	not modelled	34.2	18	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> protein (triaclylglycerol hydrolase); <b>PDBTitle:</b> new crystal form of pseudomonas glumae (formerly chromobacterium2 viscosum atcc 6918) lipase
89	<a href="#">d1uwca_</a>	Alignment	not modelled	34.0	18	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
90	<a href="#">d1cvla_</a>	Alignment	not modelled	33.5	21	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Bacterial lipase
91	<a href="#">d2h7xa1</a>	Alignment	not modelled	33.3	19	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Thioesterase domain of polypeptide, polyketide and fatty acid synthases
92	<a href="#">c3h2iA_</a>	Alignment	not modelled	33.2	18	<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
93	<a href="#">d1xkta_</a>	Alignment	not modelled	33.2	17	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Thioesterase domain of polypeptide, polyketide and fatty acid synthases
94	<a href="#">c4rvga_</a>	Alignment	not modelled	33.0	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> d-mycarose 3-c-methyltransferase; <b>PDBTitle:</b> crystal structure of mtmc in complex with sam and tdp
95	<a href="#">c2vtvA_</a>	Alignment	not modelled	31.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phb depolymerase phaz7; <b>PDBTitle:</b> phaz7 depolymerase from paucimonas lemoignei
96	<a href="#">c1hplB_</a>	Alignment	not modelled	31.7	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
97	<a href="#">c2vs0B_</a>	Alignment	not modelled	31.3	14	<b>PDB header:</b> cell invasion <b>Chain:</b> B: <b>PDB Molecule:</b> virulence factor esxa; <b>PDBTitle:</b> structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
98	<a href="#">c4fg5B_</a>	Alignment	not modelled	30.8	26	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> e3 alpha-esterase-7 caboxylesterase; <b>PDBTitle:</b> crystal structure of the alpha-esterase-7 carboxylesterase, e3, from2 lucilia cuprina
99	<a href="#">c5d6oB_</a>	Alignment	not modelled	30.8	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> homoserine o-acetyltransferase; <b>PDBTitle:</b> orthorhombic crystal structure of an acylester hydrolase from2 corynebacterium glutamicum
100	<a href="#">c3qmwD_</a>	Alignment	not modelled	30.6	16	<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
101	<a href="#">c3ilsA_</a>	Alignment	not modelled	30.4	16	<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
102	<a href="#">c4fleA_</a>	Alignment	not modelled	29.2	17	<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
103	<a href="#">c4lwsA_</a>	Alignment	not modelled	28.7	15	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> esxa : esxb (semet) hetero-dimer from thermomonospora curvata
104	<a href="#">c4qwwA_</a>	Alignment	not modelled	27.3	32	<b>PDB header:</b> hydrolase/immune system <b>Chain:</b> A: <b>PDB Molecule:</b> acetylcholinesterase; <b>PDBTitle:</b> crystal structure of the fab410-bfache complex
105	<a href="#">c1pjaA_</a>	Alignment	not modelled	26.9	12	<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)
106	<a href="#">d1pjaa_</a>	Alignment	not modelled	26.9	12	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Thioesterases
						<b>Fold:</b> alpha/beta-Hydrolases

107	<a href="#">d1ea5a_</a>	Alignment	not modelled	25.5	22	<b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Acetylcholinesterase-like
108	<a href="#">c1f8uA_</a>	Alignment	not modelled	25.4	23	<b>PDB header:</b> hydrolase/toxin <b>Chain:</b> A; <b>PDB Molecule:</b> acetylcholinesterase; <b>PDBTitle:</b> crystal structure of mutant e202q of human acetylcholinesterase2 complexed with green mamba venom peptide fasciculin-ii
109	<a href="#">d1f8ua_</a>	Alignment	not modelled	25.4	23	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Acetylcholinesterase-like
110	<a href="#">c2veoA_</a>	Alignment	not modelled	25.4	20	<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.
111	<a href="#">d2ha2a1</a>	Alignment	not modelled	24.9	29	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Acetylcholinesterase-like
112	<a href="#">c1gplA_</a>	Alignment	not modelled	23.6	19	<b>PDB header:</b> serine esterase <b>Chain:</b> A; <b>PDB Molecule:</b> rp2 lipase; <b>PDBTitle:</b> rp2 lipase
113	<a href="#">d1lghb_</a>	Alignment	not modelled	23.5	31	<b>Fold:</b> Light-harvesting complex subunits <b>Superfamily:</b> Light-harvesting complex subunits <b>Family:</b> Light-harvesting complex subunits
114	<a href="#">c3i80A_</a>	Alignment	not modelled	23.0	10	<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
115	<a href="#">c5a2gB_</a>	Alignment	not modelled	22.8	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> carboxylic ester hydrolase; <b>PDBTitle:</b> an esterase from anaerobic clostridium hathewayi can2 hydrolyze aliphatic aromatic polyesters
116	<a href="#">c3h4zC_</a>	Alignment	not modelled	22.7	16	<b>PDB header:</b> allergen <b>Chain:</b> C; <b>PDB Molecule:</b> maltose-binding periplasmic protein fused with allergen <b>PDBTitle:</b> crystal structure of an mbp-der p 7 fusion protein
117	<a href="#">c3ngmB_</a>	Alignment	not modelled	21.8	24	<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
118	<a href="#">c2h7xA_</a>	Alignment	not modelled	21.2	21	<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
119	<a href="#">c2y6vB_</a>	Alignment	not modelled	21.1	17	<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)
120	<a href="#">c2pplA_</a>	Alignment	not modelled	20.7	22	<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