
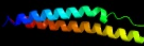






















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1430_(PE16)_1606392_1607978
Date	Wed Jul 31 22:05:54 BST 2019
Unique Job ID	c962ddce6185cf75

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5xfsA_</a>	 Alignment		99.9	50	<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		99.9	26	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> PE/PPE dimer-like <b>Family:</b> PE
3	<a href="#">c2g38A_</a>	 Alignment		99.9	26	<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	20	<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		99.4	18	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Cutinase-like
6	<a href="#">d1g66a_</a>	 Alignment		99.4	18	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Cutinase-like
7	<a href="#">c3hc7A_</a>	 Alignment		99.3	20	<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		99.2	21	<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="#">c3dd5F_</a>	 Alignment		99.1	14	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> cutinase; <b>PDBTitle:</b> glomerella cingulata e600-cutinase complex
10	<a href="#">d1cexa_</a>	 Alignment		99.0	12	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Cutinase-like
11	<a href="#">c5x88A_</a>	 Alignment		99.0	17	<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="#">c4oylC_</a>	Alignment		98.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> cutinase; <b>PDBTitle:</b> humicola insolens cutinase in complex with monoethylphosphate
13	<a href="#">c3gbsA_</a>	Alignment		98.7	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cutinase 1; <b>PDBTitle:</b> crystal structure of aspergillus oryzae cutinase
14	<a href="#">c4psdA_</a>	Alignment		98.7	16	<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.
15	<a href="#">c1mo2A_</a>	Alignment		95.5	15	<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
16	<a href="#">d1mo2a_</a>	Alignment		95.5	15	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Thioesterase domain of polypeptide, polyketide and fatty acid synthases
17	<a href="#">c3icvA_</a>	Alignment		95.4	23	<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
18	<a href="#">d1tcaa_</a>	Alignment		94.5	23	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
19	<a href="#">c5xavB_</a>	Alignment		94.4	14	<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
20	<a href="#">c5xfsB_</a>	Alignment		94.4	21	<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
21	<a href="#">d2g38b1</a>	Alignment	not modelled	93.8	6	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> PE/PPE dimer-like <b>Family:</b> PPE
22	<a href="#">c2g38B_</a>	Alignment	not modelled	93.8	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/ppe protein complex from mycobacterium tuberculosis
23	<a href="#">d1jmkc_</a>	Alignment	not modelled	93.6	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
24	<a href="#">c5t6oA_</a>	Alignment	not modelled	93.1	22	<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
25	<a href="#">d1ei9a_</a>	Alignment	not modelled	92.8	17	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Thioesterases
26	<a href="#">c4xy3A_</a>	Alignment	not modelled	91.7	6	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> esx-1 secretion-associated protein espb; <b>PDBTitle:</b> structure of esx-1 secreted protein espb
27	<a href="#">c3ds8A_</a>	Alignment	not modelled	90.1	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> lin2722 protein; <b>PDBTitle:</b> the crysatl structure of the gene lin2722 products from listeria2 innocua
28	<a href="#">c4nfb_</a>	Alignment	not modelled	89.4	22	<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

29	<a href="#">c3lp5A</a>	Alignment	not modelled	87.8	24	<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
30	<a href="#">d3b5ea1</a>	Alignment	not modelled	86.3	18	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carboxylesterase/thioesterase 1
31	<a href="#">c2cbgA</a>	Alignment	not modelled	85.2	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
32	<a href="#">c5d8mA</a>	Alignment	not modelled	84.7	19	<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
33	<a href="#">d1lspa</a>	Alignment	not modelled	84.2	15	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Bacterial lipase
34	<a href="#">c4h0cA</a>	Alignment	not modelled	83.9	18	<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
35	<a href="#">c2vsqA</a>	Alignment	not modelled	83.7	13	<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
36	<a href="#">c2zyiB</a>	Alignment	not modelled	82.3	22	<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
37	<a href="#">c3lcrA</a>	Alignment	not modelled	81.6	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tautomycin biosynthetic pks; <b>PDBTitle:</b> thioesterase from tautomycin biosynthetic pathway
38	<a href="#">d2h1ia1</a>	Alignment	not modelled	80.3	25	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carboxylesterase/thioesterase 1
39	<a href="#">c2oryA</a>	Alignment	not modelled	80.2	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lipase; <b>PDBTitle:</b> crystal structure of m37 lipase
40	<a href="#">d3tqla</a>	Alignment	not modelled	79.1	18	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
41	<a href="#">c5f2hA</a>	Alignment	not modelled	77.7	22	<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
42	<a href="#">c6qppA</a>	Alignment	not modelled	77.1	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lipase; <b>PDBTitle:</b> rhizomucor miehei lipase propeptide complex, native
43	<a href="#">c2h7xA</a>	Alignment	not modelled	76.4	28	<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
44	<a href="#">d2h7xa1</a>	Alignment	not modelled	75.7	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
45	<a href="#">c2veoA</a>	Alignment	not modelled	75.6	22	<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.
46	<a href="#">c4xjvA</a>	Alignment	not modelled	74.0	19	<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
47	<a href="#">c4r1dA</a>	Alignment	not modelled	73.3	20	<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
48	<a href="#">c4qnnC</a>	Alignment	not modelled	72.9	18	<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
49	<a href="#">c5xk2A</a>	Alignment	not modelled	72.0	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
50	<a href="#">c3uuuA</a>	Alignment	not modelled	71.7	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
51	<a href="#">c3og9A</a>	Alignment	not modelled	71.6	11	<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
52	<a href="#">c4f21G</a>	Alignment	not modelled	71.4	28	<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="#">c4zxiA</a>	Alignment	not modelled	69.7	13	<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
54	<a href="#">c5gw8A</a>	Alignment	not modelled	67.0	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

55	<a href="#">c2vtvA</a>	Alignment	not modelled	66.7	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phb depolymerase phaz7; <b>PDBTitle:</b> phaz7 depolymerase from paucimonas lemoignei
56	<a href="#">c4eziA</a>	Alignment	not modelled	65.8	12	<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
57	<a href="#">d2r8ba1</a>	Alignment	not modelled	65.1	19	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carboxylesterase/thioesterase 1
58	<a href="#">c4x96B</a>	Alignment	not modelled	64.0	21	<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)
59	<a href="#">d1etha2</a>	Alignment	not modelled	63.7	23	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Pancreatic lipase, N-terminal domain
60	<a href="#">c2r8bA</a>	Alignment	not modelled	63.0	15	<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
61	<a href="#">c3h2iA</a>	Alignment	not modelled	62.3	16	<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
62	<a href="#">c1pjaA</a>	Alignment	not modelled	61.5	14	<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)
63	<a href="#">d1pjaa</a>	Alignment	not modelled	61.5	14	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Thioesterases
64	<a href="#">c2yijA</a>	Alignment	not modelled	60.7	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phospholipase a1-iigamma; <b>PDBTitle:</b> crystal structure of phospholipase a1
65	<a href="#">c6c14A</a>	Alignment	not modelled	59.3	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lipase c12; <b>PDBTitle:</b> lipc12 - lipase from metagenomics
66	<a href="#">c6n8eA</a>	Alignment	not modelled	58.5	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> holo-obif1; <b>PDBTitle:</b> crystal structure of holo-obif1, a five domain nonribosomal peptide2 synthetase from burkholderia diffusa
67	<a href="#">c4x91C</a>	Alignment	not modelled	58.4	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)
68	<a href="#">c2qjwA</a>	Alignment	not modelled	58.0	26	<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
69	<a href="#">c3p3dA</a>	Alignment	not modelled	57.8	13	<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
70	<a href="#">d1lpbb2</a>	Alignment	not modelled	57.8	23	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Pancreatic lipase, N-terminal domain
71	<a href="#">d1tiaa</a>	Alignment	not modelled	57.4	22	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
72	<a href="#">c1qgeD</a>	Alignment	not modelled	57.4	29	<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
73	<a href="#">d1uxoa</a>	Alignment	not modelled	56.9	11	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> YdeN-like
74	<a href="#">d1bu8a2</a>	Alignment	not modelled	55.8	24	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Pancreatic lipase, N-terminal domain
75	<a href="#">c3bdvB</a>	Alignment	not modelled	55.7	16	<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
76	<a href="#">c4gw3A</a>	Alignment	not modelled	54.3	22	<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
77	<a href="#">c4nfuA</a>	Alignment	not modelled	53.7	17	<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
78	<a href="#">d1xkta</a>	Alignment	not modelled	53.7	27	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Thioesterase domain of polypeptide, polyketide and fatty acid synthases
79	<a href="#">c5uazB</a>	Alignment	not modelled	51.7	17	<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
80	<a href="#">d1uwca</a>	Alignment	not modelled	51.4	20	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases

81	<a href="#">d1hpla2</a>	Alignment	not modelled	50.4	21	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Pancreatic lipase, N-terminal domain
82	<a href="#">d1gp1a2</a>	Alignment	not modelled	50.2	26	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Pancreatic lipase, N-terminal domain
83	<a href="#">c2q0xA</a>	Alignment	not modelled	48.2	15	<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
84	<a href="#">c3g7nA</a>	Alignment	not modelled	48.0	17	<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
85	<a href="#">c2h1iA</a>	Alignment	not modelled	47.2	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> carboxylesterase; <b>PDBTitle:</b> crystal structure of the bacillus cereus carboxylesterase
86	<a href="#">d1cv1a</a>	Alignment	not modelled	46.3	22	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Bacterial lipase
87	<a href="#">c2h1hB</a>	Alignment	not modelled	46.3	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> lipase 46 kda form; <b>PDBTitle:</b> crystal structure of staphylococcus hyicus lipase
88	<a href="#">d1t1ba</a>	Alignment	not modelled	44.5	23	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
89	<a href="#">c6fvjB</a>	Alignment	not modelled	44.4	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> thioesterase; <b>PDBTitle:</b> tesa a major thioesterase from mycobacterium tuberculosis
90	<a href="#">c3flaB</a>	Alignment	not modelled	42.7	10	<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="#">c3fleB</a>	Alignment	not modelled	42.4	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 staphylococcus epidermidis.
92	<a href="#">d1lgva</a>	Alignment	not modelled	42.0	27	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
93	<a href="#">c4fleA</a>	Alignment	not modelled	41.3	24	<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
94	<a href="#">c3qmwD</a>	Alignment	not modelled	39.2	14	<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
95	<a href="#">c2w6cX</a>	Alignment	not modelled	38.6	19	<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
96	<a href="#">c2m4mA</a>	Alignment	not modelled	37.5	22	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> solution structure of the rrm domain of the hypothetical protein2 cagl0m09691g from candida glabrata
97	<a href="#">c2pvsB</a>	Alignment	not modelled	37.2	34	<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
98	<a href="#">c4rvgA</a>	Alignment	not modelled	37.1	19	<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
99	<a href="#">c3ndjA</a>	Alignment	not modelled	36.9	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase; <b>PDBTitle:</b> x-ray structure of a c-3'-methyltransferase in complex with s-2 adenosyl-l-homocysteine and sugar product
100	<a href="#">c5h3bA</a>	Alignment	not modelled	36.6	22	<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
101	<a href="#">d1rp1a2</a>	Alignment	not modelled	36.6	19	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Pancreatic lipase, N-terminal domain
102	<a href="#">c2qs9A</a>	Alignment	not modelled	36.2	14	<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
103	<a href="#">c4qwwA</a>	Alignment	not modelled	35.8	23	<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
104	<a href="#">c5h6bA</a>	Alignment	not modelled	34.4	16	<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 streptomyces
105	<a href="#">c3gvmA</a>	Alignment	not modelled	34.2	12	<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
106	<a href="#">c2y6vB</a>	Alignment	not modelled	34.1	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)
						<b>PDB header:</b> hydrolase

107	<a href="#">c3o0dF_</a>	Alignment	not modelled	32.4	22	<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
108	<a href="#">c4fg5B_</a>	Alignment	not modelled	32.4	19	<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
109	<a href="#">c2rauA_</a>	Alignment	not modelled	31.8	9	<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 sulfobolbus solfataricus at 1.85 a resolution
110	<a href="#">d1ea5a_</a>	Alignment	not modelled	30.5	19	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Acetylcholinesterase-like
111	<a href="#">c5d6oB_</a>	Alignment	not modelled	30.4	15	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> homoserine o-acetyltransferase; <b>PDBTitle:</b> orthorhombic crystal structure of an acetyler hydrolase from2 corynebacterium glutamicum
112	<a href="#">c1hplB_</a>	Alignment	not modelled	29.5	21	<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
113	<a href="#">c2pplA_</a>	Alignment	not modelled	28.0	20	<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
114	<a href="#">c2ronA_</a>	Alignment	not modelled	27.3	15	<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
115	<a href="#">d1ku0a_</a>	Alignment	not modelled	27.2	18	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Bacterial lipase
116	<a href="#">c5x6sB_</a>	Alignment	not modelled	26.6	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> acetylxytan esterase a; <b>PDBTitle:</b> acetyl xylan esterase from aspergillus awamori
117	<a href="#">d1ex9a_</a>	Alignment	not modelled	26.4	14	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Bacterial lipase
118	<a href="#">c3ngmB_</a>	Alignment	not modelled	26.4	27	<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
119	<a href="#">c4wfiA_</a>	Alignment	not modelled	25.5	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> cutinase; <b>PDBTitle:</b> crystal structure of pet-degrading cutinase cut190 s226p mutant in2 ca(2+)-free state
120	<a href="#">c6e7kB_</a>	Alignment	not modelled	25.4	20	<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