



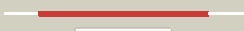








# Phyre2

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Description	RVBD1984c_cfp21_2227916_2228569
Date	Mon Aug 5 13:25:08 BST 2019
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4psdA_</a>	 Alignment		100.0	35	<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.
2	<a href="#">d1cexa_</a>	 Alignment		100.0	24	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Cutinase-like
3	<a href="#">d1g66a_</a>	 Alignment		100.0	30	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Cutinase-like
4	<a href="#">d1qoza_</a>	 Alignment		100.0	32	<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	28	<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="#">c2czqB_</a>	 Alignment		100.0	28	<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.
7	<a href="#">c5x88A_</a>	 Alignment		100.0	32	<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
8	<a href="#">c3gbsA_</a>	 Alignment		100.0	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> cutinase 1; <b>PDBTitle:</b> crystal structure of aspergillus oryzae cutinase
9	<a href="#">c4oylC_</a>	 Alignment		100.0	30	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> cutinase; <b>PDBTitle:</b> humicola insolens cutinase in complex with monoethylphosphate
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		100.0	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		98.2	19	<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		98.2	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="#">c6qppA_</a>	Alignment		98.2	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lipase; <b>PDBTitle:</b> rhizomucor miehei lipase propeptide complex, native
15	<a href="#">d1tcaa_</a>	Alignment		97.9	14	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
16	<a href="#">d3tgla_</a>	Alignment		97.9	19	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
17	<a href="#">c3icvA_</a>	Alignment		97.8	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
18	<a href="#">d1lgva_</a>	Alignment		97.7	19	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
19	<a href="#">d1ei9a_</a>	Alignment		97.7	15	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Thioesterases
20	<a href="#">d1uwca_</a>	Alignment		97.7	25	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
21	<a href="#">d1tiba_</a>	Alignment	not modelled	97.5	19	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
22	<a href="#">c3o0dF_</a>	Alignment	not modelled	97.5	22	<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
23	<a href="#">c5xk2A_</a>	Alignment	not modelled	97.5	16	<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
24	<a href="#">c2q0xA_</a>	Alignment	not modelled	97.3	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
25	<a href="#">c5gw8A_</a>	Alignment	not modelled	97.3	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
26	<a href="#">c3uuuA_</a>	Alignment	not modelled	97.2	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
27	<a href="#">d1ispa_</a>	Alignment	not modelled	97.1	19	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Bacterial lipase
28	<a href="#">c3lp5A_</a>	Alignment	not modelled	97.1	15	<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
						<b>Fold:</b> alpha/beta-Hydrolases

29	<a href="#">d1gp1a2</a>	Alignment	not modelled	97.0	11	<b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Pancreatic lipase, N-terminal domain
30	<a href="#">d1mo2a_</a>	Alignment	not modelled	97.0	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
31	<a href="#">c1mo2A_</a>	Alignment	not modelled	97.0	17	<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
32	<a href="#">c5d8mA_</a>	Alignment	not modelled	96.9	22	<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="#">c6e7kB_</a>	Alignment	not modelled	96.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> lipoprotein lipase; <b>PDBTitle:</b> structure of the lipoprotein lipase gpibhp1 complex that mediates2 plasma triglyceride hydrolysis
34	<a href="#">d1etha2</a>	Alignment	not modelled	96.9	12	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Pancreatic lipase, N-terminal domain
35	<a href="#">c6c14A_</a>	Alignment	not modelled	96.8	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lipase c12; <b>PDBTitle:</b> lipc12 - lipase from metagenomics
36	<a href="#">d1lpbb2</a>	Alignment	not modelled	96.8	11	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Pancreatic lipase, N-terminal domain
37	<a href="#">d1rp1a2</a>	Alignment	not modelled	96.7	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Pancreatic lipase, N-terminal domain
38	<a href="#">d1bu8a2</a>	Alignment	not modelled	96.7	12	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Pancreatic lipase, N-terminal domain
39	<a href="#">d1tiaa_</a>	Alignment	not modelled	96.6	25	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
40	<a href="#">d1hpla2</a>	Alignment	not modelled	96.6	8	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Pancreatic lipase, N-terminal domain
41	<a href="#">c1gp1A_</a>	Alignment	not modelled	96.6	9	<b>PDB header:</b> serine esterase <b>Chain:</b> A: <b>PDB Molecule:</b> rp2 lipase; <b>PDBTitle:</b> rp2 lipase
42	<a href="#">c2pplA_</a>	Alignment	not modelled	96.5	17	<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
43	<a href="#">d1ex9a_</a>	Alignment	not modelled	96.5	20	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Bacterial lipase
44	<a href="#">d4lipd_</a>	Alignment	not modelled	96.5	25	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Bacterial lipase
45	<a href="#">c3ds8A_</a>	Alignment	not modelled	96.5	11	<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
46	<a href="#">c1hplB_</a>	Alignment	not modelled	96.4	10	<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
47	<a href="#">c5h6bA_</a>	Alignment	not modelled	96.4	19	<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
48	<a href="#">c2zyiB_</a>	Alignment	not modelled	96.4	18	<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
49	<a href="#">d1cv1a_</a>	Alignment	not modelled	96.4	24	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Bacterial lipase
50	<a href="#">c5xavB_</a>	Alignment	not modelled	96.4	6	<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
51	<a href="#">c2h7xA_</a>	Alignment	not modelled	96.4	14	<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
52	<a href="#">c4x96B_</a>	Alignment	not modelled	96.3	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)
53	<a href="#">c5t6oA_</a>	Alignment	not modelled	96.3	16	<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
54	<a href="#">d2h7xa1</a>	Alignment	not modelled	96.3	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
55	<a href="#">c5f2hA_</a>	Alignment	not modelled	96.3	16	<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

56	<a href="#">c2veoA</a>	Alignment	not modelled	96.2	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.
57	<a href="#">c1rp1A</a>	Alignment	not modelled	96.2	14	<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
58	<a href="#">c6e6uA</a>	Alignment	not modelled	96.2	11	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> dieckmann cyclase, ncmc; <b>PDBTitle:</b> variant c89s of dieckmann cyclase, ncmc
59	<a href="#">c2pvsB</a>	Alignment	not modelled	96.1	10	<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
60	<a href="#">c4x91C</a>	Alignment	not modelled	96.1	22	<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 with 2 isopropyl dodec-11-enylfluorophosphonate (idfp)
61	<a href="#">c4eziA</a>	Alignment	not modelled	96.1	18	<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
62	<a href="#">d2r8ba1</a>	Alignment	not modelled	96.0	14	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carboxylesterase/thioesterase 1
63	<a href="#">c3lcrA</a>	Alignment	not modelled	96.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tautomycetin biosynthetic pks; <b>PDBTitle:</b> thioesterase from tautomycetin biosynthetic pathway
64	<a href="#">c2qjwA</a>	Alignment	not modelled	96.0	12	<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 at 3 1.35 a resolution
65	<a href="#">c4zxiA</a>	Alignment	not modelled	95.9	14	<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
66	<a href="#">c3og9A</a>	Alignment	not modelled	95.9	14	<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
67	<a href="#">c2r8bA</a>	Alignment	not modelled	95.9	13	<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 2 agrobacterium tumefaciens str. c58
68	<a href="#">d1jmkc</a>	Alignment	not modelled	95.9	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
69	<a href="#">c4qnnC</a>	Alignment	not modelled	95.9	16	<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
70	<a href="#">c4gw3A</a>	Alignment	not modelled	95.8	17	<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
71	<a href="#">d2h1ia1</a>	Alignment	not modelled	95.8	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carboxylesterase/thioesterase 1
72	<a href="#">c2cbgA</a>	Alignment	not modelled	95.7	20	<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 the 2 fengycin biosynthesis cluster
73	<a href="#">d3b5ea1</a>	Alignment	not modelled	95.6	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carboxylesterase/thioesterase 1
74	<a href="#">c1qgeD</a>	Alignment	not modelled	95.5	23	<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
75	<a href="#">c2rauA</a>	Alignment	not modelled	95.5	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 sulfobolus2 solfataricus at 1.85 a resolution
76	<a href="#">d1pjaa</a>	Alignment	not modelled	94.9	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Thioesterases
77	<a href="#">c1pjaA</a>	Alignment	not modelled	94.9	16	<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 the 2 basis for divergent substrate specificities of the two lysosomal 3 thioesterases (ppt1 and ppt2)
78	<a href="#">c3h2ia</a>	Alignment	not modelled	93.9	22	<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 wall 2 degrading esterase lipa from xanthomonas oryzae
79	<a href="#">c4nfbB</a>	Alignment	not modelled	93.8	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 complex 2 with its interaction partner sag101
80	<a href="#">c4h0cA</a>	Alignment	not modelled	93.3	15	<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 <b>PDB header:</b> hydrolase/hydrolase inhibitor

81	<a href="#">c4f21G_</a>	Alignment	not modelled	93.2	14	<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
82	<a href="#">c2y6vB_</a>	Alignment	not modelled	93.2	16	<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)
83	<a href="#">c2vsgA_</a>	Alignment	not modelled	93.1	14	<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
84	<a href="#">c3flaB_</a>	Alignment	not modelled	93.0	17	<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
85	<a href="#">c3bdvB_</a>	Alignment	not modelled	92.9	19	<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
86	<a href="#">c2vavL_</a>	Alignment	not modelled	92.8	10	<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)
87	<a href="#">c5hdfB_</a>	Alignment	not modelled	92.5	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hydrolase; <b>PDBTitle:</b> hydrolase semet-stna
88	<a href="#">c3fleB_</a>	Alignment	not modelled	92.4	8	<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.
89	<a href="#">c4c87A_</a>	Alignment	not modelled	92.4	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> esterase lpest1 from lactobacillus plantarum wcfs1
90	<a href="#">c2yjiA_</a>	Alignment	not modelled	92.4	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phospholipase a1-iigamma; <b>PDBTitle:</b> crystal structure of phospholipase a1
91	<a href="#">c5ugzA_</a>	Alignment	not modelled	91.9	13	<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
92	<a href="#">c2oryA_</a>	Alignment	not modelled	91.8	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lipase; <b>PDBTitle:</b> crystal structure of m37 lipase
93	<a href="#">d1k8qa_</a>	Alignment	not modelled	91.7	17	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Gastric lipase
94	<a href="#">c5ah0B_</a>	Alignment	not modelled	91.4	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> lipase; <b>PDBTitle:</b> structure of lipase 1 from pelosinus fermentans
95	<a href="#">c3mveB_</a>	Alignment	not modelled	91.3	14	<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
96	<a href="#">d1xkta_</a>	Alignment	not modelled	91.2	22	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Thioesterase domain of polypeptide, polyketide and fatty acid synthases
97	<a href="#">c2h1iA_</a>	Alignment	not modelled	91.2	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> carboxylesterase; <b>PDBTitle:</b> crystal structure of the bacillus cereus carboxylesterase
98	<a href="#">c3ilsA_</a>	Alignment	not modelled	91.2	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
99	<a href="#">c3qmwD_</a>	Alignment	not modelled	90.9	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
100	<a href="#">d1hlga_</a>	Alignment	not modelled	90.9	21	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Gastric lipase
101	<a href="#">c3l80A_</a>	Alignment	not modelled	90.6	15	<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
102	<a href="#">c3qvmA_</a>	Alignment	not modelled	89.4	8	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> olei00960; <b>PDBTitle:</b> the structure of olei00960, a hydrolase from oleispira antarctica
103	<a href="#">c4nfuA_</a>	Alignment	not modelled	88.5	23	<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
104	<a href="#">d1ji3a_</a>	Alignment	not modelled	88.3	21	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Bacterial lipase
105	<a href="#">c5x6sB_</a>	Alignment	not modelled	87.8	18	<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
106	<a href="#">c4wfiA_</a>	Alignment	not modelled	87.8	16	<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

107	<a href="#">c4eb0A_</a>	Alignment	not modelled	87.2	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lcc; <b>PDBTitle:</b> crystal structure of leaf-branch compost bacterial cutinase homolog
108	<a href="#">c2h1hB_</a>	Alignment	not modelled	86.7	18	<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
109	<a href="#">c3fnbB_</a>	Alignment	not modelled	86.4	14	<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
110	<a href="#">c4ao6A_</a>	Alignment	not modelled	86.3	15	<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
111	<a href="#">d1ku0a_</a>	Alignment	not modelled	86.0	18	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Bacterial lipase
112	<a href="#">c5w8pA_</a>	Alignment	not modelled	85.9	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> homoserine o-acetyltransferase; <b>PDBTitle:</b> homoserine transacetylase meta from mycobacterium abscessus
113	<a href="#">c5ah1A_</a>	Alignment	not modelled	85.9	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> triacylglycerol lipase; <b>PDBTitle:</b> structure of esta from clostridium botulinum
114	<a href="#">c4r1dA_</a>	Alignment	not modelled	85.4	23	<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
115	<a href="#">c3i28A_</a>	Alignment	not modelled	84.8	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> epoxide hydrolase 2; <b>PDBTitle:</b> crystal structure of soluble epoxide hydrolase
116	<a href="#">c3h1kB_</a>	Alignment	not modelled	84.7	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> acyl-coenzyme a thioesterase 2, mitochondrial; <b>PDBTitle:</b> crystal structure of human mitochondrial acyl-coa thioesterase (acot2)
117	<a href="#">c3visB_</a>	Alignment	not modelled	84.3	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> crystal structure of cutinase est119 from thermobifida alba ahk119
118	<a href="#">c2r11D_</a>	Alignment	not modelled	84.1	16	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> carboxylesterase np; <b>PDBTitle:</b> crystal structure of putative hydrolase (2632844) from bacillus2 subtilis at 1.96 a resolution
119	<a href="#">c4xjvA_</a>	Alignment	not modelled	84.1	7	<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
120	<a href="#">c2ronA_</a>	Alignment	not modelled	83.3	12	<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