



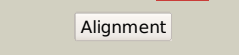

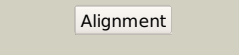

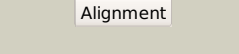

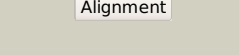

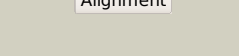

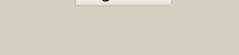





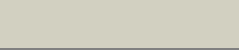



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2079 (-) _2335363_2337333
Date	Mon Aug 5 13:25:19 BST 2019
Unique Job ID	24f3ecaacd5ec4ec

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1tcaa_</a>	 Alignment		97.6	11	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
2	<a href="#">c3icvA_</a>	 Alignment		97.4	12	<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
3	<a href="#">d1tiaa_</a>	 Alignment		97.2	15	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
4	<a href="#">d1ei9a_</a>	 Alignment		97.1	10	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Thioesterases
5	<a href="#">d1cexa_</a>	 Alignment		97.0	14	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Cutinase-like
6	<a href="#">c3gbsA_</a>	 Alignment		97.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cutinase 1; <b>PDBTitle:</b> crystal structure of aspergillus oryzae cutinase
7	<a href="#">c5xk2A_</a>	 Alignment		96.9	18	<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
8	<a href="#">c4gw3A_</a>	 Alignment		96.9	14	<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
9	<a href="#">d1ispa_</a>	 Alignment		96.9	15	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Bacterial lipase
10	<a href="#">d1ex9a_</a>	 Alignment		96.9	20	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Bacterial lipase
11	<a href="#">c4psdA_</a>	 Alignment		96.9	22	<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.

12	<a href="#">c5x88A_</a>	Alignment		96.8	13	<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
13	<a href="#">d1cvla_</a>	Alignment		96.8	18	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Bacterial lipase
14	<a href="#">c3bdvB_</a>	Alignment		96.7	20	<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
15	<a href="#">c3lp5A_</a>	Alignment		96.6	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 wcfs1
16	<a href="#">c2vavL_</a>	Alignment		96.6	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)
17	<a href="#">c1gp1A_</a>	Alignment		96.6	21	<b>PDB header:</b> serine esterase <b>Chain:</b> A: <b>PDB Molecule:</b> rp2 lipase; <b>PDBTitle:</b> rp2 lipase
18	<a href="#">d1bu8a2</a>	Alignment		96.5	22	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Pancreatic lipase, N-terminal domain
19	<a href="#">c2yija_</a>	Alignment		96.5	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phospholipase a1-iigamma; <b>PDBTitle:</b> crystal structure of phospholipase a1
20	<a href="#">d1tiba_</a>	Alignment		96.5	17	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
21	<a href="#">d2h1ia1</a>	Alignment	not modelled	96.5	19	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carboxylesterase/thioesterase 1
22	<a href="#">d1gp1a2</a>	Alignment	not modelled	96.5	21	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Pancreatic lipase, N-terminal domain
23	<a href="#">c3dd5F_</a>	Alignment	not modelled	96.5	11	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> cutinase; <b>PDBTitle:</b> glomerella cingulata e600-cutinase complex
24	<a href="#">d1qoza_</a>	Alignment	not modelled	96.5	24	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Cutinase-like
25	<a href="#">c1qgeD_</a>	Alignment	not modelled	96.4	17	<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
26	<a href="#">d1g66a_</a>	Alignment	not modelled	96.4	19	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Cutinase-like
27	<a href="#">c6cl4A_</a>	Alignment	not modelled	96.3	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lipase c12; <b>PDBTitle:</b> lipc12 - lipase from metagenomics
28	<a href="#">c3ajaA_</a>	Alignment	not modelled	96.2	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
29	<a href="#">d1etha2</a>	Alignment	not modelled	96.2	21	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases

						<b>Family:</b> Pancreatic lipase, N-terminal domain
30	<a href="#">c3l80A_</a>	Alignment	not modelled	96.2	16	<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
31	<a href="#">d1lpbb2</a>	Alignment	not modelled	96.2	22	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Pancreatic lipase, N-terminal domain
32	<a href="#">c1cr6A_</a>	Alignment	not modelled	96.1	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> epoxide hydrolase; <b>PDBTitle:</b> crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
33	<a href="#">d1rpl2</a>	Alignment	not modelled	96.0	20	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Pancreatic lipase, N-terminal domain
34	<a href="#">c3ds8A_</a>	Alignment	not modelled	95.8	16	<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
35	<a href="#">c5gw8A_</a>	Alignment	not modelled	95.7	19	<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
36	<a href="#">d1hpla2</a>	Alignment	not modelled	95.6	21	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Pancreatic lipase, N-terminal domain
37	<a href="#">c2pvsB_</a>	Alignment	not modelled	95.6	21	<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
38	<a href="#">c3i28A_</a>	Alignment	not modelled	95.6	19	<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
39	<a href="#">d4lipd_</a>	Alignment	not modelled	95.5	18	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Bacterial lipase
40	<a href="#">c3g7nA_</a>	Alignment	not modelled	95.5	12	<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
41	<a href="#">c2rauA_</a>	Alignment	not modelled	95.4	13	<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 sulfobolbus2 solfataricus at 1.85 a resolution
42	<a href="#">c1hplB_</a>	Alignment	not modelled	95.4	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
43	<a href="#">c2czqB_</a>	Alignment	not modelled	95.3	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.
44	<a href="#">c2q0xA_</a>	Alignment	not modelled	95.2	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
45	<a href="#">c2qmqA_</a>	Alignment	not modelled	95.1	11	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein ndr2; <b>PDBTitle:</b> crystal structure of a n-myc downstream regulated 2 protein (ndrg2,2 syld, ndr2, ai182517, au040374) from mus musculus at 1.70 a3 resolution
46	<a href="#">c3uuuA_</a>	Alignment	not modelled	95.1	15	<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
47	<a href="#">c4qnnC_</a>	Alignment	not modelled	95.0	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
48	<a href="#">c4x91C_</a>	Alignment	not modelled	95.0	19	<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)
49	<a href="#">c3o0dF_</a>	Alignment	not modelled	95.0	15	<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
50	<a href="#">c4qloA_</a>	Alignment	not modelled	95.0	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> homoserine o-acetyltransferase; <b>PDBTitle:</b> crystal structure of homoserine o-acetyltransferase from2 staphylococcus aureus
51	<a href="#">c3ngmB_</a>	Alignment	not modelled	95.0	22	<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
52	<a href="#">d1lgva_</a>	Alignment	not modelled	94.9	12	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
53	<a href="#">c5f2hA_</a>	Alignment	not modelled	94.8	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
54	<a href="#">c4nfbB_</a>	Alignment	not modelled	94.8	13	<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

55	<a href="#">c4oylC_</a>	Alignment	not modelled	94.7	12	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> cutinase; <b>PDBTitle:</b> humicola insolens cutinase in complex with monoethylphosphate
56	<a href="#">c3ilsA_</a>	Alignment	not modelled	94.7	11	<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
57	<a href="#">c2y6vB_</a>	Alignment	not modelled	94.6	15	<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)
58	<a href="#">c2zyiB_</a>	Alignment	not modelled	94.5	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
59	<a href="#">d1uwca_</a>	Alignment	not modelled	94.4	17	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
60	<a href="#">c2o2gA_</a>	Alignment	not modelled	94.3	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dienelactone hydrolase; <b>PDBTitle:</b> crystal structure of dienelactone hydrolase (yp_324580.1) from2 anabaena variabilis atcc 29413 at 1.92 a resolution
61	<a href="#">c1rp1A_</a>	Alignment	not modelled	94.2	20	<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
62	<a href="#">c1mo2A_</a>	Alignment	not modelled	94.1	20	<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
63	<a href="#">d1mo2a_</a>	Alignment	not modelled	94.1	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
64	<a href="#">c2r11D_</a>	Alignment	not modelled	94.0	18	<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
65	<a href="#">d3tglA_</a>	Alignment	not modelled	94.0	18	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
66	<a href="#">c2h1iA_</a>	Alignment	not modelled	93.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> carboxylesterase; <b>PDBTitle:</b> crystal structure of the bacillus cereus carboxylesterase
67	<a href="#">c4x96B_</a>	Alignment	not modelled	93.8	19	<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)
68	<a href="#">c3vvlA_</a>	Alignment	not modelled	93.8	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> homoserine o-acetyltransferase; <b>PDBTitle:</b> crystal structure of l-serine-o-acetyltransferase found in d-2 cycloserine biosynthetic pathway
69	<a href="#">c3lcrA_</a>	Alignment	not modelled	93.7	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tautomycetin biosynthetic pks; <b>PDBTitle:</b> thioesterase from tautomycetin biosynthetic pathway
70	<a href="#">c3d0kA_</a>	Alignment	not modelled	93.7	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative poly(3-hydroxybutyrate) depolymerase lppc; <b>PDBTitle:</b> crystal structure of the lppc, poly(3-hydroxybutyrate) depolymerase2 from bordetella parapertussis
71	<a href="#">c3jyhD_</a>	Alignment	not modelled	93.6	19	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> dipeptidyl-peptidase 2; <b>PDBTitle:</b> human dipeptidyl peptidase dpp7
72	<a href="#">c6qppA_</a>	Alignment	not modelled	93.6	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lipase; <b>PDBTitle:</b> rhizomucor miehei lipase propeptide complex, native
73	<a href="#">d3b5ea1</a>	Alignment	not modelled	93.6	24	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carboxylesterase/thioesterase 1
74	<a href="#">c5w8pA_</a>	Alignment	not modelled	93.6	21	<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
75	<a href="#">c3v48B_</a>	Alignment	not modelled	93.4	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative aminoacrylate hydrolase rtdt; <b>PDBTitle:</b> crystal structure of the putative alpha/beta hydrolase rtdt from2 e.coli
76	<a href="#">c2pplA_</a>	Alignment	not modelled	93.2	18	<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
77	<a href="#">c5h6bA_</a>	Alignment	not modelled	93.0	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
78	<a href="#">c3e0xB_</a>	Alignment	not modelled	92.9	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> lipase-esterase related protein; <b>PDBTitle:</b> the crystal structure of a lipase-esterase related protein2 from clostridium acetobutylicum atcc 824
79	<a href="#">c2fx5A_</a>	Alignment	not modelled	92.9	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lipase; <b>PDBTitle:</b> pseudomonas mendocina lipase
80	<a href="#">c1pjaA_</a>	Alignment	not modelled	92.8	13	<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)

81	<a href="#">d1pjaa_</a>	Alignment	not modelled	92.8	13	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Thioesterases
82	<a href="#">c5uoha_</a>	Alignment	not modelled	92.7	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> carboxylesterase a; <b>PDBTitle:</b> crystal structure of hip1 (rv2224c) t466a mutant
83	<a href="#">c3qvmA_</a>	Alignment	not modelled	92.7	15	<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
84	<a href="#">c3i1iA_</a>	Alignment	not modelled	92.6	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> homoserine o-acetyltransferase; <b>PDBTitle:</b> x-ray crystal structure of homoserine o-acetyltransferase from2 bacillus anthracis
85	<a href="#">d1xkta_</a>	Alignment	not modelled	92.5	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
86	<a href="#">d2vata1</a>	Alignment	not modelled	92.5	23	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> O-acetyltransferase
87	<a href="#">d1uxoa_</a>	Alignment	not modelled	92.5	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> YdeN-like
88	<a href="#">c2cbgA_</a>	Alignment	not modelled	92.4	18	<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
89	<a href="#">d2b61a1</a>	Alignment	not modelled	92.4	15	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> O-acetyltransferase
90	<a href="#">c5ijkA_</a>	Alignment	not modelled	92.3	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase e22; <b>PDBTitle:</b> crystal structure of esterase e22 I374d mutant
91	<a href="#">d2pl5a1</a>	Alignment	not modelled	92.0	18	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> O-acetyltransferase
92	<a href="#">c5d8mA_</a>	Alignment	not modelled	91.4	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
93	<a href="#">c5hdfB_</a>	Alignment	not modelled	91.3	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hydrolase; <b>PDBTitle:</b> hydrolase semet-stna
94	<a href="#">c6e6uA_</a>	Alignment	not modelled	91.2	16	<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
95	<a href="#">c2hu7A_</a>	Alignment	not modelled	91.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> acylamino-acid-releasing enzyme; <b>PDBTitle:</b> binding of inhibitors by acylaminoacyl peptidase
96	<a href="#">c3qmwD_</a>	Alignment	not modelled	90.7	13	<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
97	<a href="#">c6gupB_</a>	Alignment	not modelled	90.7	14	<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 aspergillus fumigatus
98	<a href="#">c3og9A_</a>	Alignment	not modelled	90.6	18	<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
99	<a href="#">c3fleB_</a>	Alignment	not modelled	90.3	20	<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.
100	<a href="#">d1jmkc_</a>	Alignment	not modelled	90.2	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
101	<a href="#">c5x6sB_</a>	Alignment	not modelled	90.1	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> acetyl/xylan esterase a; <b>PDBTitle:</b> acetyl xylan esterase from aspergillus awamori
102	<a href="#">c4i0cA_</a>	Alignment	not modelled	90.1	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> deformylase; <b>PDBTitle:</b> crystal structure of the n-fopmylmaleamic acid deformylase nfo(s94a)2 from pseudomonas putida s16
103	<a href="#">c2qs9A_</a>	Alignment	not modelled	90.0	16	<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
104	<a href="#">c4wfiA_</a>	Alignment	not modelled	89.9	19	<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
105	<a href="#">c5yala_</a>	Alignment	not modelled	89.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> ferulic acid esterase from streptomyces cinnamoneus at 1.5 a2 resolution
106	<a href="#">c6e7kB_</a>	Alignment	not modelled	89.5	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> lipoprotein lipase; <b>PDBTitle:</b> structure of the lipoprotein lipase gpihbp1 complex that mediates2 plasma triglyceride hydrolysis
107	<a href="#">c5jrlC_</a>	Alignment	not modelled	89.3	24	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> dipeptidyl aminopeptidases/acylaminoacyl-peptidases-like

						<b>PDBTitle:</b> crystal structure of the sphingopyxin i lasso peptide isopeptidase2 spi-isop (native)
108	<a href="#">c3flaB_</a>	Alignment	not modelled	89.2	16	<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
109	<a href="#">c2xuaH_</a>	Alignment	not modelled	88.8	14	<b>PDB header:</b> hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> 3-oxoadipate enol-lactonase; <b>PDBTitle:</b> crystal structure of the enol-lactonase from burkholderia2 xenovorans lb400
110	<a href="#">c3doiA_</a>	Alignment	not modelled	88.6	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> crystal structure of a thermostable esterase complex with2 paraoxon
111	<a href="#">c3azqA_</a>	Alignment	not modelled	88.4	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> aminopeptidase; <b>PDBTitle:</b> crystal structure of puromycin hydrolase s511a mutant complexed with2 pgg
112	<a href="#">d1mpxa2</a>	Alignment	not modelled	88.3	19	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> PepX catalytic domain-like
113	<a href="#">c4r1dA_</a>	Alignment	not modelled	88.3	24	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> the crystal structure of tie4-tli4 complex
114	<a href="#">c2qjwA_</a>	Alignment	not modelled	88.1	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
115	<a href="#">c5h3bA_</a>	Alignment	not modelled	88.0	18	<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
116	<a href="#">c1l7qA_</a>	Alignment	not modelled	87.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cocaine esterase; <b>PDBTitle:</b> ser117ala mutant of bacterial cocaine esterase coce
117	<a href="#">c5xavB_</a>	Alignment	not modelled	87.2	18	<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
118	<a href="#">c3iumA_</a>	Alignment	not modelled	87.1	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> prolyl endopeptidase; <b>PDBTitle:</b> appep_wtx opened state
119	<a href="#">c4g4gA_</a>	Alignment	not modelled	87.1	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-o-methyl-glucuronoyl methylesterase; <b>PDBTitle:</b> crystal structure of recombinant glucuronoyl esterase from2 sporotrichum thermophile determined at 1.55 a resolution
120	<a href="#">c4z8zA_</a>	Alignment	not modelled	87.0	8	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of the hypothetical protein from ruminiclostridium2 thermocellum atcc 27405