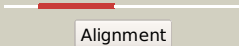


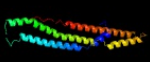

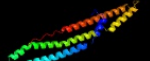

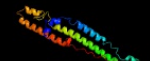
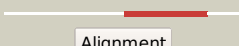

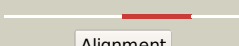

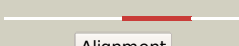








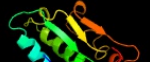


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3539_(PPE63)_3978238_3979677
 Date Fri Aug 9 18:20:21 BST 2019
 Unique Job ID 29b96611acc0f8e7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsB_	 Alignment		100.0	53	PDB header: protein transport Chain: B: PDB Molecule: ppe family protein ppe15; PDBTitle: crystal structure of pe8-ppe15 in complex with esp95 from m.2 tuberculosis
2	c2g38B_	 Alignment		100.0	33	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: ppe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
3	d2g38b1	 Alignment		100.0	33	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
4	c4xy3A_	 Alignment		100.0	17	PDB header: protein transport Chain: A: PDB Molecule: esx-1 secretion-associated protein espb; PDBTitle: structure of esx-1 secreted protein espb
5	c3ajaA_	 Alignment		99.8	13	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of msmeg_6394
6	d1qoza_	 Alignment		99.4	22	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like
7	d1g66a_	 Alignment		99.4	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like
8	c3hc7A_	 Alignment		99.2	17	PDB header: cell adhesion Chain: A: PDB Molecule: gene 12 protein; PDBTitle: crystal structure of lysin b from mycobacteriophage d29
9	c2czaB_	 Alignment		99.0	20	PDB header: hydrolase Chain: B: PDB Molecule: cutinase-like protein; PDBTitle: a novel cutinase-like protein from cryptococcus sp.
10	d1cexa_	 Alignment		98.9	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like
11	c3dd5F_	 Alignment		98.9	15	PDB header: hydrolase Chain: F: PDB Molecule: cutinase; PDBTitle: glomerella cingulata e600-cutinase complex

12	c5x88A_	Alignment		98.7	17	PDB header: hydrolase Chain: A; PDB Molecule: cutinase; PDBTitle: a crystal structure of cutinases from malbranchea cinnamomea
13	c3gbsA_	Alignment		98.7	14	PDB header: hydrolase Chain: A; PDB Molecule: cutinase 1; PDBTitle: crystal structure of aspergillus oryzae cutinase
14	c4psdA_	Alignment		98.6	28	PDB header: hydrolase Chain: A; PDB Molecule: carbohydrate esterase family 5; PDBTitle: structure of trichoderma reesei cutinase native form.
15	c4oylC_	Alignment		98.6	14	PDB header: hydrolase Chain: C; PDB Molecule: cutinase; PDBTitle: humicola insolens cutinase in complex with mono-ethylphosphate
16	c4wj2A_	Alignment		98.1	16	PDB header: unknown function Chain: A; PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
17	c2vs0B_	Alignment		97.5	14	PDB header: cell invasion Chain: B; PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
18	c3gvmA_	Alignment		97.2	15	PDB header: viral protein Chain: A; PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
19	c4iogD_	Alignment		97.2	15	PDB header: unknown function Chain: D; PDB Molecule: secreted protein esxb; PDBTitle: the crystal structure of a secreted protein esxb (wild-type, in p212 space group) from bacillus anthracis str. sterne
20	c3zbcC_	Alignment		97.1	18	PDB header: unknown function Chain: C; PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
21	d1wa8a1	Alignment	not modelled	96.2	15	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
22	c5xavB_	Alignment	not modelled	95.5	9	PDB header: biosynthetic protein Chain: B; PDB Molecule: intracellular polyhydroxyalkanoate synthase; PDBTitle: structure of phac from chromobacterium sp. usm2
23	c5t6oA_	Alignment	not modelled	95.3	17	PDB header: biosynthetic protein Chain: A; PDB Molecule: poly-beta-hydroxybuterate polymerase; PDBTitle: structure of the catalytic domain of the class i polyhydroxybutyrate2 synthase from cupriavidus necator
24	d1tcaa_	Alignment	not modelled	94.8	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
25	c4lwsA_	Alignment	not modelled	94.8	18	PDB header: unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
26	c4lwsB_	Alignment	not modelled	94.6	14	PDB header: unknown function Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
27	c3ds8A_	Alignment	not modelled	94.5	14	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: lin2722 protein; PDBTitle: the crysatl structure of the gene lin2722 products from listeria2 innocua
28	d1wa8b1	Alignment	not modelled	94.4	14	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
						Fold: alpha/beta-Hydrolases

29	d1ei9a_	Alignment	not modelled	94.2	11	Superfamily: alpha/beta-Hydrolases Family: Thioesterases
30	c3icvA_	Alignment	not modelled	93.8	20	PDB header: hydrolase Chain: A: PDB Molecule: lipase b; PDBTitle: structural consequences of a circular permutation on lipase b from2 candida antarctica
31	c4i0xA_	Alignment	not modelled	92.9	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: esat-6-like protein mab_3112; PDBTitle: crystal structure of the mycobacterium abscessus esxf (mab_3112-2 mab_3113) complex
32	c3lp5A_	Alignment	not modelled	92.4	14	PDB header: hydrolase Chain: A: PDB Molecule: putative cell surface hydrolase; PDBTitle: the crystal structure of the putative cell surface hydrolase from2 lactobacillus plantarum wcfs1
33	c4nfbB_	Alignment	not modelled	92.3	17	PDB header: signaling protein Chain: B: PDB Molecule: senescence-associated carboxylesterase 101; PDBTitle: structure of the central plant immunity signaling node eds1 in complex2 with its interaction partner sag101
34	d1jmkc_	Alignment	not modelled	91.8	10	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
35	c1mo2A_	Alignment	not modelled	90.9	18	PDB header: transferase Chain: A: PDB Molecule: erythronolide synthase, modules 5 and 6; PDBTitle: thioesterase domain from 6-deoxyerythronolide synthase (debs te), ph2 8.5
36	d1mo2a_	Alignment	not modelled	90.9	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
37	c3lcrA_	Alignment	not modelled	88.5	20	PDB header: hydrolase Chain: A: PDB Molecule: tautomycin biosynthetic pks; PDBTitle: thioesterase from tautomycin biosynthetic pathway
38	c2vtvA_	Alignment	not modelled	88.3	27	PDB header: hydrolase Chain: A: PDB Molecule: phb depolymerase phaz7; PDBTitle: phaz7 depolymerase from paucimonas lemoignei
39	c6qppA_	Alignment	not modelled	88.3	22	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: rhizomucor miehei lipase propeptide complex, native
40	d3t gla_	Alignment	not modelled	87.8	22	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
41	d2h7xa1	Alignment	not modelled	87.6	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
42	c5d8mA_	Alignment	not modelled	87.1	15	PDB header: hydrolase Chain: A: PDB Molecule: metagenomic carboxyl esterase mgs0156; PDBTitle: crystal structure of the metagenomic carboxyl esterase mgs0156
43	c4qnnC_	Alignment	not modelled	86.8	6	PDB header: hydrolase Chain: C: PDB Molecule: phospholipase a 1 from hornet(vespa basalis) venom; PDBTitle: crystal structure of phospholipase a 1 from hornet(vespa basalis)2 venom
44	d1ispa_	Alignment	not modelled	86.4	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
45	c3og9A_	Alignment	not modelled	85.9	9	PDB header: hydrolase Chain: A: PDB Molecule: protein yahd a copper inducible hydrolase; PDBTitle: structure of yahd with malic acid
46	c2kg7B_	Alignment	not modelled	84.9	16	PDB header: unknown function Chain: B: PDB Molecule: esat-6-like protein esxh; PDBTitle: structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
47	c6e6uA_	Alignment	not modelled	82.1	18	PDB header: biosynthetic protein Chain: A: PDB Molecule: dieckmann cyclase, ncmc; PDBTitle: variant c89s of dieckmann cyclase, ncmc
48	c4h0cA_	Alignment	not modelled	81.9	19	PDB header: hydrolase Chain: A: PDB Molecule: phospholipase/carboxylesterase; PDBTitle: crystal structure of phospholipase/carboxylesterase from dyadobacter2 fermentans dsm 18053
49	c4x96B_	Alignment	not modelled	81.6	23	PDB header: transferase Chain: B: PDB Molecule: phosphatidylcholine-sterol acyltransferase; PDBTitle: low resolution crystal structure of lecithin:cholesterol2 acyltransferase (lcat; residues 21-397)
50	d3b5ea1	Alignment	not modelled	81.1	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
51	c4x91C_	Alignment	not modelled	80.3	25	PDB header: transferase Chain: C: PDB Molecule: group xv phospholipase a2; PDBTitle: crystal structure of lysosomal phospholipase a2 in complex with2 isopropyl dodec-11-enylfluorophosphonate (idfp)
52	c2h7xA_	Alignment	not modelled	80.1	20	PDB header: hydrolase Chain: A: PDB Molecule: type i polyketide synthase pikaiv; PDBTitle: pikromycin thioesterase adduct with reduced triketide2 affinity label
53	d1lgya_	Alignment	not modelled	78.5	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
54	c5f2hA_	Alignment	not modelled	77.8	19	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: 2.75 angstrom resolution crystal structure of uncharacterized protein2 from bacillus cereus atcc 10987
						Fold: alpha/beta-Hydrolases

55	d1lpbb2	Alignment	not modelled	77.5	12	Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
56	d2h1ia1	Alignment	not modelled	77.2	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
57	c3uuuA	Alignment	not modelled	75.5	14	PDB header: hydrolase Chain: A: PDB Molecule: lip1, secretory lipase (family 3); PDBTitle: crystal structure of mono- and diacylglycerol lipase from malassezia2 globosa
58	d1bu8a2	Alignment	not modelled	75.4	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
59	c2veoA	Alignment	not modelled	74.9	18	PDB header: hydrolase Chain: A: PDB Molecule: lipase a; PDBTitle: x-ray structure of candida antarctica lipase a in its closed state.
60	c4eziA	Alignment	not modelled	73.9	20	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative hydrolase (lpg1103) from legionella2 pneumophila subsp. pneumophila str. philadelphia 1 at 1.15 a3 resolution
61	d1gpla2	Alignment	not modelled	73.7	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
62	d1jj3a	Alignment	not modelled	73.2	23	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
63	c4f21G	Alignment	not modelled	72.9	14	PDB header: hydrolase/hydrolase inhibitor Chain: G: PDB Molecule: carboxylesterase/phospholipase family protein; PDBTitle: crystal structure of carboxylesterase/phospholipase family protein2 from francisella tularensis
64	c3h2iA	Alignment	not modelled	72.8	17	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of n228w mutant of the rice cell wall2 degrading esterase lipa from xanthomonas oryzae
65	c6cl4A	Alignment	not modelled	72.6	18	PDB header: hydrolase Chain: A: PDB Molecule: lipase c12; PDBTitle: lipc12 - lipase from metagenomics
66	d1etha2	Alignment	not modelled	72.6	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
67	c2cbgA	Alignment	not modelled	70.7	9	PDB header: hydrolase Chain: A: PDB Molecule: fengycin synthetase; PDBTitle: crystal structure of the pmsf-inhibited thioesterase domain of the2 fengycin biosynthesis cluster
68	c5gw8A	Alignment	not modelled	70.6	12	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical secretory lipase (family 3); PDBTitle: crystal structure of a putative dag-like lipase (mgmdl2) from2 malassezia globosa
69	c2zyiB	Alignment	not modelled	70.6	26	PDB header: hydrolase Chain: B: PDB Molecule: lipase, putative; PDBTitle: a. fulgidus lipase with fatty acid fragment and calcium
70	d1hpla2	Alignment	not modelled	69.9	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
71	d1tiaa	Alignment	not modelled	68.6	22	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
72	c3g7nA	Alignment	not modelled	68.3	20	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: crystal structure of a triacylglycerol lipase from penicillium2 expansum at 1.3
73	c5xfsA	Alignment	not modelled	68.0	24	PDB header: protein transport Chain: A: PDB Molecule: pe family protein pe8; PDBTitle: crystal structure of pe8-ppe15 in complex with esp5 from m.2 tuberculosis
74	d1xkta	Alignment	not modelled	67.8	27	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
75	c4r1dA	Alignment	not modelled	67.7	21	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of tle4-tli4 complex
76	c4xjvA	Alignment	not modelled	66.9	29	PDB header: hydrolase Chain: A: PDB Molecule: s-acyl fatty acid synthase thioesterase, medium chain; PDBTitle: crystal structure of human thioesterase 2
77	d1uxoa	Alignment	not modelled	66.5	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: YdeN-like
78	c4zxiA	Alignment	not modelled	66.3	14	PDB header: biosynthetic protein Chain: A: PDB Molecule: tyrocidine synthetase 3; PDBTitle: crystal structure of holo-ab3403 a four domain nonribosomal peptide2 synthetase bound to amp and glycine
79	c5xk2A	Alignment	not modelled	66.2	14	PDB header: hydrolase Chain: A: PDB Molecule: diacylglycerol lipase; PDBTitle: crystal structure of mono- and diacylglycerol lipase from aspergillus2 oryzae
80	c2r8bA	Alignment	not modelled	65.6	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atu2452; PDBTitle: the crystal structure of the protein atu2452 of unknown function from2 agrobacterium tumefaciens str. c58
						Fold: alpha/beta-Hydrolases

81	d2r8ba1	Alignment	not modelled	65.5	15	Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
82	d1cvla_	Alignment	not modelled	65.4	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
83	d1rpl2	Alignment	not modelled	65.0	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
84	c2qjwA_	Alignment	not modelled	64.1	37	PDB header: hydrolase Chain: A; PDB Molecule: uncharacterized protein xcc1541; PDBTitle: crystal structure of a putative hydrolase of the alpha/beta2 superfamily (xcc1541) from xanthomonas campestris pv. campestris at3 1.35 a resolution
85	c2g38A_	Alignment	not modelled	63.1	19	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: pe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
86	d2g38a1	Alignment	not modelled	63.1	19	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PE
87	c3qmwD_	Alignment	not modelled	63.0	12	PDB header: hydrolase Chain: D; PDB Molecule: thioesterase; PDBTitle: redj with peg molecule bound in the active site
88	d1ex9a_	Alignment	not modelled	62.9	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
89	c3fleB_	Alignment	not modelled	62.9	17	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: se_1780 protein; PDBTitle: se_1780 protein of unknown function from staphylococcus epidermidis.
90	d1tiba_	Alignment	not modelled	62.3	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
91	c2pvsB_	Alignment	not modelled	62.2	20	PDB header: hydrolase Chain: B; PDB Molecule: pancreatic lipase-related protein 2; PDBTitle: structure of human pancreatic lipase related protein 22 mutant n336q
92	c2hihB_	Alignment	not modelled	62.0	25	PDB header: hydrolase Chain: B; PDB Molecule: lipase 46 kda form; PDBTitle: crystal structure of staphylococcus hyicus lipase
93	c4gw3A_	Alignment	not modelled	61.9	17	PDB header: hydrolase Chain: A; PDB Molecule: putative lipase; PDBTitle: crystal structure of the lipase from proteus mirabilis
94	c4nfuA_	Alignment	not modelled	59.9	13	PDB header: signaling protein Chain: A; PDB Molecule: eds1; PDBTitle: structure of the central plant immunity signaling node eds1 in complex2 with its interaction partner sag101
95	c6n8eA_	Alignment	not modelled	59.4	18	PDB header: hydrolase Chain: A; PDB Molecule: holo-obif1; PDBTitle: crystal structure of holo-obif1, a five domain nonribosomal peptide2 synthetase from burkholderia diffusa
96	d1uwca_	Alignment	not modelled	59.4	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
97	c3p3dA_	Alignment	not modelled	58.7	22	PDB header: nuclear protein Chain: A; PDB Molecule: nucleoporin 53; PDBTitle: crystal structure of the nup53 rrm domain from pichia guilliermondii
98	c2qs9A_	Alignment	not modelled	58.4	11	PDB header: structural protein Chain: A; PDB Molecule: retinoblastoma-binding protein 9; PDBTitle: crystal structure of the human retinoblastoma-binding2 protein 9 (rbbp-9). nesg target hr2978
99	c2vijA_	Alignment	not modelled	57.8	16	PDB header: hydrolase Chain: A; PDB Molecule: phospholipase a1-iigamma; PDBTitle: crystal structure of phospholipase a1
100	c2pplA_	Alignment	not modelled	57.5	13	PDB header: hydrolase Chain: A; PDB Molecule: pancreatic lipase-related protein 1; PDBTitle: human pancreatic lipase-related protein 1
101	c1hplB_	Alignment	not modelled	56.9	16	PDB header: hydrolase(carboxylic esterase) Chain: B; PDB Molecule: lipase; PDBTitle: horse pancreatic lipase. the crystal structure at 2.3 angstroms2 resolution
102	c2y6vB_	Alignment	not modelled	56.7	16	PDB header: hydrolase Chain: B; PDB Molecule: peroxisomal membrane protein lpx1; PDBTitle: peroxisomal alpha-beta-hydrolase lpx1 (yor084w) from saccharomyces2 cerevisiae (crystal form i)
103	c2oryA_	Alignment	not modelled	56.5	20	PDB header: hydrolase Chain: A; PDB Molecule: lipase; PDBTitle: crystal structure of m37 lipase
104	c6e7kB_	Alignment	not modelled	55.8	12	PDB header: hydrolase Chain: B; PDB Molecule: lipoprotein lipase; PDBTitle: structure of the lipoprotein lipase gpihbp1 complex that mediates2 plasma triglyceride hydrolysis
105	c2w6cX_	Alignment	not modelled	55.5	23	PDB header: hydrolase Chain: X; PDB Molecule: acetylcholinesterase; PDBTitle: ache in complex with a bis-(-)-nor-meptazinol derivative
106	c5h6bA_	Alignment	not modelled	53.8	15	PDB header: hydrolase Chain: A; PDB Molecule: putative secreted lipase; PDBTitle: crystal structure of a thermostable lipase from marine streptomyces
107	c3flaB_	Alignment	not modelled	53.0	13	PDB header: hydrolase Chain: B; PDB Molecule: rifr; PDBTitle: rifr - type ii thioesterase from rifamycin nrps/pks

						biosynthetic2 pathway - form 1
108	c1gplA_	Alignment	not modelled	53.0	15	PDB header: serine esterase Chain: A: PDB Molecule: rp2 lipase; PDBTitle: rp2 lipase
109	c4i0xl_	Alignment	not modelled	52.6	19	PDB header: structural genomics, unknown function Chain: J: PDB Molecule: esat-6-like protein mab_3113; PDBTitle: crystal structure of the mycobacterium abscessus esxf (mab_3112-2 mab_3113) complex
110	c3d0kA_	Alignment	not modelled	52.2	16	PDB header: hydrolase Chain: A: PDB Molecule: putative poly(3-hydroxybutyrate) depolymerase lpqc; PDBTitle: crystal structure of the lpqc, poly(3-hydroxybutyrate) depolymerase2 from bordetella parapertussis
111	c5uazB_	Alignment	not modelled	52.1	9	PDB header: protein transport Chain: B: PDB Molecule: nucleoporin nup53; PDBTitle: crystal structure of the yeast nucleoporin
112	c1pjaA_	Alignment	not modelled	50.0	15	PDB header: hydrolase Chain: A: PDB Molecule: palmitoyl-protein thioesterase 2 precursor; PDBTitle: the crystal structure of palmitoyl protein thioesterase-2 reveals the2 basis for divergent substrate specificities of the two lysosomal3 thioesterases (ppt1 and ppt2)
113	d1pjaa_	Alignment	not modelled	50.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterases
114	c3ilsA_	Alignment	not modelled	49.3	17	PDB header: hydrolase Chain: A: PDB Molecule: afatoxin biosynthesis polyketide synthase; PDBTitle: the thioesterase domain from pksa
115	c5d6oB_	Alignment	not modelled	48.5	11	PDB header: transferase Chain: B: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: orthorhombic crystal structure of an acetyler hydrolyase from2 corynebacterium glutamicum
116	d1ea5a_	Alignment	not modelled	48.2	22	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like
117	c4fg5B_	Alignment	not modelled	47.9	19	PDB header: hydrolase Chain: B: PDB Molecule: e3 alpha-esterase-7 caboxylesterase; PDBTitle: crystal structure of the alpha-esterase-7 carboxylesterase, e3, from2 lucilia cuprina
118	c4qwwA_	Alignment	not modelled	47.8	29	PDB header: hydrolase/immune system Chain: A: PDB Molecule: acetylcholinesterase; PDBTitle: crystal structure of the fab410-bfache complex
119	c1gqeD_	Alignment	not modelled	47.7	20	PDB header: hydrolase Chain: D: PDB Molecule: protein (triacylglycerol hydrolase); PDBTitle: new crystal form of pseudomonas glumae (formerly chromobacterium2 viscosum atcc 6918) lipase
120	c6i2tC_	Alignment	not modelled	47.4	26	PDB header: hydrolase Chain: C: PDB Molecule: cholinesterase; PDBTitle: cryoem reconstruction of full-length, fully-glycosylated human2 butyrylcholinesterase tetramer