

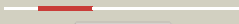
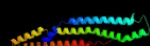

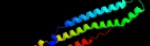

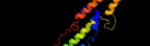

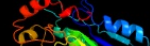

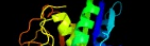



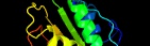








Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1800_(PPE28)_2039460_2041427
Date	Fri Aug 2 13:30:41 BST 2019
Unique Job ID	84a3ed8263c81929

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsB_	 Alignment		100.0	51	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	31	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	31	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
4	c4xy3A_	 Alignment		100.0	16	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		99.7	16	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of msmeg_6394
6	d1qoza_	 Alignment		99.1	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like
7	d1g66a_	 Alignment		99.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like
8	c3hc7A_	 Alignment		99.0	19	PDB header: cell adhesion Chain: A: PDB Molecule: gene 12 protein; PDBTitle: crystal structure of lysin b from mycobacteriophage d29
9	c2czaB_	 Alignment		98.7	21	PDB header: hydrolase Chain: B: PDB Molecule: cutinase-like protein; PDBTitle: a novel cutinase-like protein from cryptococcus sp.
10	d1cexa_	 Alignment		98.5	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like
11	c5x88A_	 Alignment		98.5	15	PDB header: hydrolase Chain: A: PDB Molecule: cutinase; PDBTitle: a crystal structure of cutinases from malbranchea cinnamomea

12	c3dd5F_	Alignment		98.4	13	PDB header: hydrolase Chain: F; PDB Molecule: cutinase; PDBTitle: glomerella cingulata e600-cutinase complex
13	c4oylC_	Alignment		98.3	15	PDB header: hydrolase Chain: C; PDB Molecule: cutinase; PDBTitle: humicola insolens cutinase in complex with monoethylphosphate
14	c3gbsA_	Alignment		98.2	14	PDB header: hydrolase Chain: A; PDB Molecule: cutinase 1; PDBTitle: crystal structure of aspergillus oryzae cutinase
15	c4psdA_	Alignment		98.0	14	PDB header: hydrolase Chain: A; PDB Molecule: carbohydrate esterase family 5; PDBTitle: structure of trichoderma reesei cutinase native form.
16	c4wj2A_	Alignment		98.0	18	PDB header: unknown function Chain: A; PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
17	c2vs0B_	Alignment		97.3	9	PDB header: cell invasion Chain: B; PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
18	c3gvmA_	Alignment		97.0	9	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		97.0	13	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	c3zbhC_	Alignment		96.9	13	PDB header: unknown function Chain: C; PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
21	d1wa8a1	Alignment	not modelled	95.9	16	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
22	c5xavB_	Alignment	not modelled	94.8	17	PDB header: biosynthetic protein Chain: B; PDB Molecule: intracellular polyhydroxyalkanoate synthase; PDBTitle: structure of phac from chromobacterium sp. usm2
23	c5t6oA_	Alignment	not modelled	94.4	28	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	c4lwsB_	Alignment	not modelled	93.5	13	PDB header: unknown function Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
25	d1ei9a_	Alignment	not modelled	93.5	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterases
26	c4lwsA_	Alignment	not modelled	93.5	18	PDB header: unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
27	d1wa8b1	Alignment	not modelled	93.3	18	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
28	d1jmkc_	Alignment	not modelled	92.7	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
						Fold: alpha/beta-Hydrolases

29	d1tcaa_	Alignment	not modelled	91.0	10	Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
30	c3ds8A_	Alignment	not modelled	89.4	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin2722 protein; PDBTitle: the crysatl structure of the gene lin2722 products from listeria2 innocua
31	c4i0xA_	Alignment	not modelled	88.6	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: esat-6-like protein mab_3112; PDBTitle: crystal structure of the mycobacterum abscessus esxef (mab_3112-2 mab_3113) complex
32	c3lp5A_	Alignment	not modelled	84.8	21	PDB header: hydrolase Chain: A: PDB Molecule: putative cell surface hydrolase; PDBTitle: the crystal structure of the putative cell surface hydrolase from2 lactobacillus plantarum wcf51
33	d3b5ea1	Alignment	not modelled	81.2	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
34	d3t gla_	Alignment	not modelled	80.7	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
35	c2kg7B_	Alignment	not modelled	80.5	14	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
36	c4h0cA_	Alignment	not modelled	79.9	17	PDB header: hydrolase Chain: A: PDB Molecule: phospholipase/carboxylesterase; PDBTitle: crystal structure of phospholipase/carboxylesterase from dyadobacter2 fermentans dsm 18053
37	c6qppA_	Alignment	not modelled	79.7	20	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: rhizomucor miehei lipase propeptide complex, native
38	d1mo2a_	Alignment	not modelled	78.9	22	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
39	c1mo2A_	Alignment	not modelled	78.9	22	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
40	c4n fuB_	Alignment	not modelled	78.6	16	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
41	c2vsqA_	Alignment	not modelled	76.4	15	PDB header: ligase Chain: A: PDB Molecule: surfactin synthetase subunit 3; PDBTitle: structure of surfactin a synthetase c (srfa-c), a nonribosomal peptide2 synthetase termination module
42	d1lspa_	Alignment	not modelled	76.0	11	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
43	d2h7xa1	Alignment	not modelled	75.7	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
44	c2cbgA_	Alignment	not modelled	74.7	18	PDB header: hydrolase Chain: A: PDB Molecule: fengycin synthetase; PDBTitle: crystal structure of the pmsf-inhibited thioesterase domain of the2 fengycin biosynthesis cluster
45	c3og9A_	Alignment	not modelled	71.3	11	PDB header: hydrolase Chain: A: PDB Molecule: protein yahd a copper inducible hydrolase; PDBTitle: structure of yahd with malic acid
46	c3icvA_	Alignment	not modelled	70.5	8	PDB header: hydrolase Chain: A: PDB Molecule: lipase b; PDBTitle: structural consequences of a circular permutation on lipase b from2 candida antarctica
47	c4rvqA_	Alignment	not modelled	70.1	24	PDB header: transferase Chain: A: PDB Molecule: d-mycarose 3-c-methyltransferase; PDBTitle: crystal structure of mtmc in complex with sam and tdp
48	c4zxiA_	Alignment	not modelled	69.2	9	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
49	d2r8ba1	Alignment	not modelled	67.7	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
50	c2r8bA_	Alignment	not modelled	67.1	16	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
51	d2h1ia1	Alignment	not modelled	65.9	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
52	c4f21G_	Alignment	not modelled	65.2	22	PDB header: hydrolase/hydrolase inhibitor Chain: G: PDB Molecule: carboxylesterase/phospholipase family protein; PDBTitle: crystal structure of carboxylesterase/phospholipase family protein2 from francisella tularensis
53	c3lcrA_	Alignment	not modelled	63.8	16	PDB header: hydrolase Chain: A: PDB Molecule: tautomycetin biosynthetic pks; PDBTitle: thioesterase from tautomycetin biosynthetic pathway
54	c4eziA_	Alignment	not modelled	63.2	10	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

55	c4qnnC	Alignment	not modelled	63.1	16	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
56	d1tiaa	Alignment	not modelled	61.6	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
57	c2veoA	Alignment	not modelled	60.3	23	PDB header: hydrolase Chain: A: PDB Molecule: lipase a; PDBTitle: x-ray structure of candida antarctica lipase a in its closed state.
58	c5xk2A	Alignment	not modelled	59.8	20	PDB header: hydrolase Chain: A: PDB Molecule: diacylglycerol lipase; PDBTitle: crystal structure of mono- and diacylglycerol lipase from aspergillus2 oryzae
59	d1lgva	Alignment	not modelled	59.5	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
60	c2zyiB	Alignment	not modelled	57.6	9	PDB header: hydrolase Chain: B: PDB Molecule: lipase, putative; PDBTitle: a. fulgidus lipase with fatty acid fragment and calcium
61	c3p3dA	Alignment	not modelled	57.1	26	PDB header: nuclear protein Chain: A: PDB Molecule: nucleoporin 53; PDBTitle: crystal structure of the nup53 rrm domain from pichia guilliermondii
62	c5d8mA	Alignment	not modelled	56.2	8	PDB header: hydrolase Chain: A: PDB Molecule: metagenomic carboxyl esterase mgs0156; PDBTitle: crystal structure of the metagenomic carboxyl esterase mgs0156
63	c2h7xA	Alignment	not modelled	56.1	17	PDB header: hydrolase Chain: A: PDB Molecule: type i polyketide synthase pikaiv; PDBTitle: pikromycin thioesterase adduct with reduced triketide2 affinity label
64	c3ndjA	Alignment	not modelled	55.5	17	PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: x-ray structure of a c-3'-methyltransferase in complex with s-2 adenosyl-l-homocysteine and sugar product
65	c2qjwA	Alignment	not modelled	53.5	19	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
66	c6n8eA	Alignment	not modelled	51.7	13	PDB header: hydrolase Chain: A: PDB Molecule: holo-obif1; PDBTitle: crystal structure of holo-obif1, a five domain nonribosomal peptide2 synthetase from burkholderia diffusa
67	d1lpbb2	Alignment	not modelled	51.5	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
68	c5uazB	Alignment	not modelled	50.6	22	PDB header: protein transport Chain: B: PDB Molecule: nucleoporin nup53; PDBTitle: crystal structure of the yeast nucleoporin
69	d1bu8a2	Alignment	not modelled	50.1	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
70	c6cl4A	Alignment	not modelled	48.6	18	PDB header: hydrolase Chain: A: PDB Molecule: lipase c12; PDBTitle: lipc12 - lipase from metagenomics
71	c4i0xl	Alignment	not modelled	48.0	23	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
72	c4xjvA	Alignment	not modelled	47.2	21	PDB header: hydrolase Chain: A: PDB Molecule: s-acyl fatty acid synthase thioesterase, medium chain; PDBTitle: crystal structure of human thioesterase 2
73	d1xkta	Alignment	not modelled	45.3	26	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
74	c2vtvA	Alignment	not modelled	44.8	14	PDB header: hydrolase Chain: A: PDB Molecule: phb depolymerase phaz7; PDBTitle: phaz7 depolymerase from paucimonas lemoignei
75	c5gw8A	Alignment	not modelled	44.3	19	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
76	c2oryA	Alignment	not modelled	41.2	18	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: crystal structure of m37 lipase
77	c3h2iA	Alignment	not modelled	40.0	13	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
78	c3g7nA	Alignment	not modelled	39.6	14	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: crystal structure of a triacylglycerol lipase from penicillium2 expansum at 1.3
79	c4fleA	Alignment	not modelled	39.1	20	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of the esterase yqia (ye3661) from yersinia2 enterocolitica, northeast structural genomics consortium target yer85
80	c2h1iA	Alignment	not modelled	38.8	17	PDB header: hydrolase Chain: A: PDB Molecule: carboxylesterase;

						PDBTitle: crystal structure of the bacillus cereus carboxylesterase
81	c5h3bA_	Alignment	not modelled	38.8	9	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein hi_1552; PDBTitle: crystal structure of semet-biog from haemophilus influenzae at 1.492 angstroms resolution
82	c3uuuA_	Alignment	not modelled	37.7	19	PDB header: hydrolase Chain: A: PDB Molecule: lip1, secretory lipase (family 3); PDBTitle: crystal structure of mono- and diacylglycerol lipase from malassezia2 globosa
83	d1tiba_	Alignment	not modelled	37.2	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
84	d1gpla2	Alignment	not modelled	37.1	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
85	c2q0xA_	Alignment	not modelled	36.1	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: alpha/beta hydrolase fold protein of unknown function
86	c5d6oB_	Alignment	not modelled	35.5	17	PDB header: transferase Chain: B: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: orthorhombic crystal structure of an acetylerster hydrolase from2 corynebacterium glutamicum
87	d1uxoa_	Alignment	not modelled	33.4	7	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: YdeN-like
88	c5f2hA_	Alignment	not modelled	33.2	13	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
89	d1etha2	Alignment	not modelled	32.5	9	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
90	c2qs9A_	Alignment	not modelled	32.3	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
91	d1hpla2	Alignment	not modelled	31.9	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
92	c4x91C_	Alignment	not modelled	30.9	14	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)
93	c4nfuA_	Alignment	not modelled	30.0	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
94	d1cvla_	Alignment	not modelled	29.5	23	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
95	d1uwca_	Alignment	not modelled	28.9	23	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
96	d1rp1a2	Alignment	not modelled	28.6	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
97	c3qmwD_	Alignment	not modelled	28.0	18	PDB header: hydrolase Chain: D: PDB Molecule: thioesterase; PDBTitle: redj with peg molecule bound in the active site
98	c2m4mA_	Alignment	not modelled	27.7	32	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: solution structure of the rrm domain of the hypothetical protein2 cagl0m09691g from candida glabrata
99	d2hw4a1	Alignment	not modelled	27.7	31	Fold: PHP14-like Superfamily: PHP14-like Family: janus/Ocnus
100	c2rauA_	Alignment	not modelled	27.1	5	PDB header: hydrolase Chain: A: PDB Molecule: putative esterase; PDBTitle: crystal structure of a putative lipase (np_343859.1) from sulfolobus2 solfataricus at 1.85 a resolution
101	c3flaB_	Alignment	not modelled	26.5	18	PDB header: hydrolase Chain: B: PDB Molecule: rifr; PDBTitle: rifr - type ii thioesterase from rifamycin nrps/pks biosynthetic2 pathway - form 1
102	c2hw4A_	Alignment	not modelled	26.0	31	PDB header: structural genomics, hydrolase Chain: A: PDB Molecule: 14 kda phosphohistidine phosphatase; PDBTitle: crystal structure of human phosphohistidine phosphatase
103	c2y6vB_	Alignment	not modelled	25.9	10	PDB header: hydrolase Chain: B: PDB Molecule: peroxisomal membrane protein lpx1; PDBTitle: peroxisomal alpha-beta-hydrolase lpx1 (yor084w) from saccharomyces2 cerevisiae (crystal form i)
104	c2w6cX_	Alignment	not modelled	24.9	19	PDB header: hydrolase Chain: X: PDB Molecule: acetylcholinesterase; PDBTitle: ache in complex with a bis-(-)-nor-meptazinol derivative
105	c3h4zC_	Alignment	not modelled	23.7	16	PDB header: allergen Chain: C: PDB Molecule: maltose-binding periplasmic protein fused with allergen PDBTitle: crystal structure of an mbp-der p 7 fusion protein
106	c5synB_	Alignment	not modelled	23.2	17	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: acyl-protein thioesterase 2; PDBTitle: cocrystal structure of the human acyl protein thioesterase 2 with an2 isoform-selective inhibitor, ml349
						PDB header: hydrolase

107	c5h6bA_	Alignment	not modelled	23.1	16	Chain: A: PDB Molecule: putative secreted lipase; PDBTitle: crystal structure of a thermostable lipase from marine streptomyces
108	c2pvsB_	Alignment	not modelled	23.0	24	PDB header: hydrolase Chain: B: PDB Molecule: pancreatic lipase-related protein 2; PDBTitle: structure of human pancreatic lipase related protein 22 mutant n336q
109	d1k8qa_	Alignment	not modelled	22.3	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Gastric lipase
110	c4qwwA_	Alignment	not modelled	21.5	26	PDB header: hydrolase/immune system Chain: A: PDB Molecule: acetylcholinesterase; PDBTitle: crystal structure of the fab410-bfache complex
111	d1dx4a_	Alignment	not modelled	21.2	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like
112	c4fhzA_	Alignment	not modelled	20.9	11	PDB header: hydrolase Chain: A: PDB Molecule: phospholipase/carboxylesterase; PDBTitle: crystal structure of a carboxyl esterase at 2.0 angstrom resolution
113	c3bdvB_	Alignment	not modelled	20.7	13	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein duf1234; PDBTitle: crystal structure of a putative yden-like hydrolase (eca3091) from2 pectobacterium atrosepticum scri1043 at 1.66 a resolution
114	c1qgeD_	Alignment	not modelled	20.6	22	PDB header: hydrolase Chain: D: PDB Molecule: protein (triacylglycerol hydrolase); PDBTitle: new crystal form of pseudomonas glumae (formerly chromobacterium2 viscosum atcc 6918) lipase
115	d1ea5a_	Alignment	not modelled	20.6	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like
116	c3o0dF_	Alignment	not modelled	20.6	20	PDB header: hydrolase Chain: F: PDB Molecule: triacylglycerol lipase; PDBTitle: crystal structure of lip2 lipase from yarrowia lipolytica at 1.7 a2 resolution
117	d1ji3a_	Alignment	not modelled	20.2	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase