

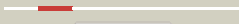


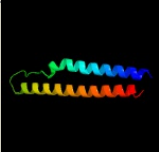







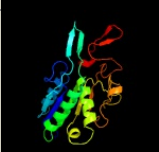









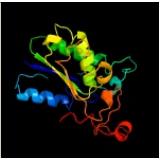





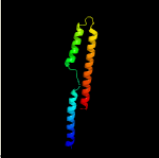

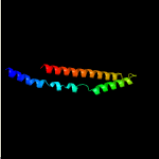

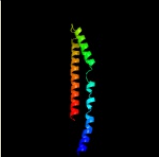

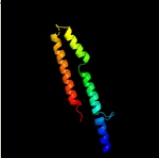






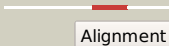



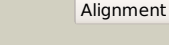
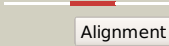


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0160c_(PE4)_188929_190437
 Date Tue Jul 23 14:50:21 BST 2019
 Unique Job ID 4a53373ae227f984

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsA_	 Alignment		100.0	47	PDB header: protein transport Chain: A; PDB Molecule: pe family protein pe8; PDBTitle: crystal structure of pe8-ppe15 in complex with esp95 from m.2 tuberculosis
2	c2g38A_	 Alignment		100.0	29	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: pe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
3	d2g38a1	 Alignment		100.0	29	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PE
4	c3ajaA_	 Alignment		99.9	19	PDB header: hydrolase Chain: A; PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of msmeg_6394
5	d1qoza_	 Alignment		99.6	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like
6	d1g66a_	 Alignment		99.5	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like
7	c2czqB_	 Alignment		99.5	20	PDB header: hydrolase Chain: B; PDB Molecule: cutinase-like protein; PDBTitle: a novel cutinase-like protein from cryptococcus sp.
8	c3hc7A_	 Alignment		99.4	18	PDB header: cell adhesion Chain: A; PDB Molecule: gene 12 protein; PDBTitle: crystal structure of lysin b from mycobacteriophage d29
9	d1cexa_	 Alignment		99.2	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like
10	c3dd5F_	 Alignment		99.2	16	PDB header: hydrolase Chain: F; PDB Molecule: cutinase; PDBTitle: glomerella cingulata e600-cutinase complex
11	c5x88A_	 Alignment		99.1	19	PDB header: hydrolase Chain: A; PDB Molecule: cutinase; PDBTitle: a crystal structure of cutinases from malbranchea cinnamomea

12	c3gbsA_	 Alignment		99.1	18	PDB header: hydrolase Chain: A: PDB Molecule: cutinase 1; PDBTitle: crystal structure of aspergillus oryzae cutinase
13	c4psdA_	 Alignment		98.9	17	PDB header: hydrolase Chain: A: PDB Molecule: carbohydrate esterase family 5; PDBTitle: structure of trichoderma reesei cutinase native form.
14	c4oylC_	 Alignment		98.9	18	PDB header: hydrolase Chain: C: PDB Molecule: cutinase; PDBTitle: humicola insolens cutinase in complex with monoethylphosphate
15	c5xfsB_	 Alignment		98.6	21	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
16	d2g38b1	 Alignment		98.6	10	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
17	c2g38B_	 Alignment		98.6	10	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: ppe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
18	c4xy3A_	 Alignment		98.3	13	PDB header: protein transport Chain: A: PDB Molecule: esx-1 secretion-associated protein espb; PDBTitle: structure of esx-1 secreted protein espb
19	c3icvA_	 Alignment		95.5	13	PDB header: hydrolase Chain: A: PDB Molecule: lipase b; PDBTitle: structural consequences of a circular permutation on lipase b from2 candida antarctica
20	c5xavB_	 Alignment		94.7	23	PDB header: biosynthetic protein Chain: B: PDB Molecule: intracellular polyhydroxyalkanoate synthase; PDBTitle: structure of phac from chromobacterium sp. usm2
21	d1ei9a_	 Alignment	not modelled	94.4	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterases
22	c5t6oA_	 Alignment	not modelled	94.4	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
23	d1tcaa_	 Alignment	not modelled	94.1	10	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
24	d1ispa_	 Alignment	not modelled	91.9	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
25	c3ds8A_	 Alignment	not modelled	91.2	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin2722 protein; PDBTitle: the crysatl structure of the gene lin2722 products from listeria2 innocua
26	c4nfbB_	 Alignment	not modelled	90.4	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
27	c3og9A_	 Alignment	not modelled	90.0	11	PDB header: hydrolase Chain: A: PDB Molecule: protein yahd a copper inducible hydrolase; PDBTitle: structure of yahd with malic acid
28	c2zyiB_	 Alignment	not modelled	90.0	22	PDB header: hydrolase Chain: B: PDB Molecule: lipase, putative; PDBTitle: a. fulgidus lipase with fatty acid fragment and calcium

29	d2h1ia1	Alignment	not modelled	87.4	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
30	c2q0xA	Alignment	not modelled	86.9	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: alpha/beta hydrolase fold protein of unknown function
31	c5d8mA	Alignment	not modelled	85.9	14	PDB header: hydrolase Chain: A: PDB Molecule: metagenomic carboxyl esterase mgs0156; PDBTitle: crystal structure of the metagenomic carboxyl esterase mgs0156
32	c4qnnC	Alignment	not modelled	85.5	13	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
33	c3lp5A	Alignment	not modelled	84.2	16	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
34	d2r8ba1	Alignment	not modelled	84.1	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
35	c4rvgA	Alignment	not modelled	82.4	23	PDB header: transferase Chain: A: PDB Molecule: d-mycarose 3-c-methyltransferase; PDBTitle: crystal structure of mtmc in complex with sam and tdp
36	d2h7xa1	Alignment	not modelled	78.9	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
37	c2r8bA	Alignment	not modelled	78.9	13	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
38	c4eziA	Alignment	not modelled	78.0	13	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
39	d3b5ea1	Alignment	not modelled	77.4	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
40	d1mo2a	Alignment	not modelled	77.3	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
41	c1mo2A	Alignment	not modelled	77.3	17	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
42	c5f2hA	Alignment	not modelled	76.8	10	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
43	c2h7xA	Alignment	not modelled	74.7	18	PDB header: hydrolase Chain: A: PDB Molecule: type i polyketide synthase pikaiv; PDBTitle: pikromycin thioesterase adduct with reduced triketide2 affinity label
44	c6cl4A	Alignment	not modelled	74.3	16	PDB header: hydrolase Chain: A: PDB Molecule: lipase c12; PDBTitle: lipc12 - lipase from metagenomics
45	d1jmkc	Alignment	not modelled	73.8	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
46	d3t gla	Alignment	not modelled	73.8	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
47	c3lcrA	Alignment	not modelled	73.4	19	PDB header: hydrolase Chain: A: PDB Molecule: tautomycetin biosynthetic pks; PDBTitle: thioesterase from tautomycetin biosynthetic pathway
48	d1letha2	Alignment	not modelled	72.5	10	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
49	c4x91C	Alignment	not modelled	72.0	12	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)
50	d1lpbb2	Alignment	not modelled	70.9	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
51	d1bu8a2	Alignment	not modelled	70.8	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
52	c4x96B	Alignment	not modelled	70.8	14	PDB header: transferase Chain: B: PDB Molecule: phosphatidylcholine-sterol acyltransferase; PDBTitle: low resolution crystal structure of lecithin:cholesterol2 acyltransferase (lcat; residues 21-397)
53	c4r1dA	Alignment	not modelled	70.1	16	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of tle4-tli4 complex
54	d1tiaa	Alignment	not modelled	68.1	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases PDB header: transferase

55	c3ndjA_	Alignment	not modelled	67.4	22	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
56	c4xjvA_	Alignment	not modelled	67.1	25	PDB header: hydrolase Chain: A; PDB Molecule: s-acyl fatty acid synthase thioesterase, medium chain; PDBTitle: crystal structure of human thioesterase 2
57	c4h0cA_	Alignment	not modelled	65.2	19	PDB header: hydrolase Chain: A; PDB Molecule: phospholipase/carboxylesterase; PDBTitle: crystal structure of phospholipase/carboxylesterase from dyadobacter2 fermentans dsm 18053
58	c2veoA_	Alignment	not modelled	64.9	23	PDB header: hydrolase Chain: A; PDB Molecule: lipase a; PDBTitle: x-ray structure of candida antarctica lipase a in its closed state.
59	c1qgeD_	Alignment	not modelled	64.6	17	PDB header: hydrolase Chain: D; PDB Molecule: protein (triacylglycerol hydrolase); PDBTitle: new crystal form of pseudomonas glumae (formerly chromobacterium2 viscosum atcc 6918) lipase
60	d1rplA2	Alignment	not modelled	62.9	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
61	d1cvla_	Alignment	not modelled	62.6	25	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
62	c2h1iA_	Alignment	not modelled	62.4	17	PDB header: hydrolase Chain: A; PDB Molecule: carboxylesterase; PDBTitle: crystal structure of the bacillus cereus carboxylesterase
63	c3d0kA_	Alignment	not modelled	62.2	13	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
64	d1hpla2	Alignment	not modelled	58.4	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
65	c6qppA_	Alignment	not modelled	58.3	14	PDB header: hydrolase Chain: A; PDB Molecule: lipase; PDBTitle: rhizomucor miehei lipase propeptide complex, native
66	d1ex9a_	Alignment	not modelled	57.0	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
67	d1pjaa_	Alignment	not modelled	56.8	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterases
68	c1pjaA_	Alignment	not modelled	56.8	13	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)
69	d1ji3a_	Alignment	not modelled	55.2	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
70	c3gvmA_	Alignment	not modelled	54.1	11	PDB header: viral protein Chain: A; PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
71	d1lgva_	Alignment	not modelled	54.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
72	c3fleB_	Alignment	not modelled	53.6	10	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: se_1780 protein; PDBTitle: se_1780 protein of unknown function from staphylococcus epidermidis.
73	c3h2iA_	Alignment	not modelled	53.6	19	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
74	c5xk2A_	Alignment	not modelled	53.5	16	PDB header: hydrolase Chain: A; PDB Molecule: diacylglycerol lipase; PDBTitle: crystal structure of mono- and diacylglycerol lipase from aspergillus2 oryzae
75	c4fleA_	Alignment	not modelled	53.2	11	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
76	d1gpla2	Alignment	not modelled	52.5	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
77	c2oryA_	Alignment	not modelled	52.4	17	PDB header: hydrolase Chain: A; PDB Molecule: lipase; PDBTitle: crystal structure of m37 lipase
78	c2yijA_	Alignment	not modelled	51.5	14	PDB header: hydrolase Chain: A; PDB Molecule: phospholipase a1-iigamma; PDBTitle: crystal structure of phospholipase a1
79	c3flaB_	Alignment	not modelled	51.3	13	PDB header: hydrolase Chain: B; PDB Molecule: rifr; PDBTitle: rifr - type ii thioesterase from rifamycin nrps/pks biosynthetic2 pathway - form 1
80	c3p3dA_	Alignment	not modelled	51.2	27	PDB header: nuclear protein Chain: A; PDB Molecule: nucleoporin 53; PDBTitle: crystal structure of the nup53 rrm domain from pichia guilliermondii

81	d1lfa_	Alignment	not modelled	50.6	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
82	c2cbgA_	Alignment	not modelled	49.9	13	PDB header: hydrolase Chain: A: PDB Molecule: fengycin synthetase; PDBTitle: crystal structure of the pmf-inhibited thioesterase domain of the2 fengycin biosynthesis cluster
83	c4gw3A_	Alignment	not modelled	48.9	20	PDB header: hydrolase Chain: A: PDB Molecule: putative lipase; PDBTitle: crystal structure of the lipase from proteus mirabilis
84	c5w8pA_	Alignment	not modelled	47.5	21	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: homoserine transacetylase meta from mycobacterium abscessus
85	c2qs9A_	Alignment	not modelled	46.7	15	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
86	c4f21G_	Alignment	not modelled	46.6	16	PDB header: hydrolase/hydrolase inhibitor Chain: G: PDB Molecule: carboxylesterase/phospholipase family protein; PDBTitle: crystal structure of carboxylesterase/phospholipase family protein2 from francisella tularensis
87	c2w6cX_	Alignment	not modelled	46.4	16	PDB header: hydrolase Chain: X: PDB Molecule: acetylcholinesterase; PDBTitle: ache in complex with a bis-(-)-nor-meptazinol derivative
88	c5ah0B_	Alignment	not modelled	46.2	21	PDB header: hydrolase Chain: B: PDB Molecule: lipase; PDBTitle: structure of lipase 1 from pelosinus fermentans
89	c5h6bA_	Alignment	not modelled	45.5	17	PDB header: hydrolase Chain: A: PDB Molecule: putative secreted lipase; PDBTitle: crystal structure of a thermostable lipase from marine streptomyces
90	d1uwca_	Alignment	not modelled	44.6	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
91	c5d6oB_	Alignment	not modelled	43.9	15	PDB header: transferase Chain: B: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: orthorhombic crystal structure of an acetyler hydrolase from2 corynebacterium glutamicum
92	d1ea5a_	Alignment	not modelled	43.8	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like
93	c5uazB_	Alignment	not modelled	43.3	32	PDB header: protein transport Chain: B: PDB Molecule: nucleoporin nup53; PDBTitle: crystal structure of the yeast nucleoporin
94	c5gw8A_	Alignment	not modelled	43.3	11	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
95	c4qwwA_	Alignment	not modelled	43.0	16	PDB header: hydrolase/immune system Chain: A: PDB Molecule: acetylcholinesterase; PDBTitle: crystal structure of the fab410-bfache complex
96	c3bdvB_	Alignment	not modelled	42.8	15	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
97	d1uxoa_	Alignment	not modelled	42.0	8	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: YdeN-like
98	c4fg5B_	Alignment	not modelled	41.5	16	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
99	d1k4ya_	Alignment	not modelled	41.2	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like
100	d1dx4a_	Alignment	not modelled	40.7	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like
101	d1xkta_	Alignment	not modelled	39.8	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
102	c2qjwA_	Alignment	not modelled	39.7	17	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
103	c3uuuA_	Alignment	not modelled	39.4	11	PDB header: hydrolase Chain: A: PDB Molecule: lip1, secretory lipase (family 3); PDBTitle: crystal structure of mono- and diacylglycerol lipase from malassezia2 globosa
104	d2ha2a1	Alignment	not modelled	39.4	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like
105	d1gz7a_	Alignment	not modelled	39.0	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
106	c1f8uA_	Alignment	not modelled	37.9	19	PDB header: hydrolase/toxin Chain: A: PDB Molecule: acetylcholinesterase; PDBTitle: crystal structure of mutant e202q of human acetylcholinesterase2 complexed with green mamba venom peptide

						fasciculin-ii
107	d1f8ua_	Alignment	not modelled	37.9	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like
108	d1lukca_	Alignment	not modelled	37.8	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
109	d1wa8a1	Alignment	not modelled	37.7	15	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
110	d1crla_	Alignment	not modelled	37.4	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
111	c2pvsB_	Alignment	not modelled	37.1	20	PDB header: hydrolase Chain: B: PDB Molecule: pancreatic lipase-related protein 2; PDBTitle: structure of human pancreatic lipase related protein 22 mutant n336q
112	c2vtvA_	Alignment	not modelled	36.9	7	PDB header: hydrolase Chain: A: PDB Molecule: phb depolymerase phaz7; PDBTitle: phaz7 depolymerase from paucimonas lemoignei
113	c6i2tC_	Alignment	not modelled	36.5	16	PDB header: hydrolase Chain: C: PDB Molecule: cholinesterase; PDBTitle: cryoem reconstruction of full-length, fully-glycosylated human2 butyrylcholinesterase tetramer
114	c2m4mA_	Alignment	not modelled	36.2	25	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
115	c2fj0A_	Alignment	not modelled	35.7	13	PDB header: hydrolase Chain: A: PDB Molecule: carboxylic ester hydrolase; PDBTitle: crystal structure of juvenile hormone esterase from manduca sexta,2 with otfp covalently attached
116	c4bdtA_	Alignment	not modelled	35.3	19	PDB header: hydrolase/inhibitor Chain: A: PDB Molecule: acetylcholinesterase; PDBTitle: human acetylcholinesterase in complex with huprine w and fasciculin 2
117	c3i1iA_	Alignment	not modelled	35.2	8	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: x-ray crystal structure of homoserine o-acetyltransferase from2 bacillus anthracis
118	c4zxiA_	Alignment	not modelled	33.7	13	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
119	d1tiba_	Alignment	not modelled	33.6	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
120	c1hplB_	Alignment	not modelled	32.3	14	PDB header: hydrolase(carboxylic esterase) Chain: B: PDB Molecule: lipase; PDBTitle: horse pancreatic lipase. the crystal structure at 2.3 angstroms2 resolution