
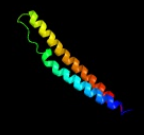

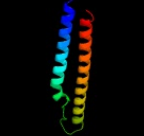

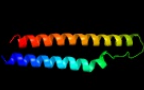







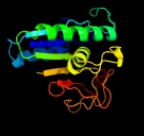








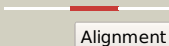










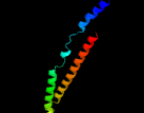

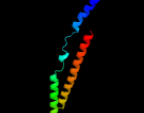




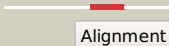
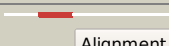


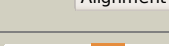
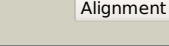
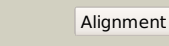
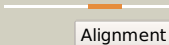


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0151c_(PE1)_177541_179307
 Date Tue Jul 23 14:50:19 BST 2019
 Unique Job ID c0269c7d7a61f10d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xf8A_	 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	34	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	34	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PE
4	c3ajaA_	 Alignment		99.8	20	PDB header: hydrolase Chain: A; PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of msmeg_6394
5	c3hc7A_	 Alignment		99.1	22	PDB header: cell adhesion Chain: A; PDB Molecule: gene 12 protein; PDBTitle: crystal structure of lysin b from mycobacteriophage d29
6	d1qoza_	 Alignment		99.1	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like
7	d1g66a_	 Alignment		99.0	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like
8	c2czaB_	 Alignment		98.7	21	PDB header: hydrolase Chain: B; PDB Molecule: cutinase-like protein; PDBTitle: a novel cutinase-like protein from cryptococcus sp.
9	d1cexa_	 Alignment		98.6	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like
10	c5x88A_	 Alignment		98.6	20	PDB header: hydrolase Chain: A; PDB Molecule: cutinase; PDBTitle: a crystal structure of cutinases from malbranchea cinnamomea
11	c3dd5F_	 Alignment		98.5	12	PDB header: hydrolase Chain: F; PDB Molecule: cutinase; PDBTitle: glomerella cingulata e600-cutinase complex

12	c3gbsA_	 Alignment		98.3	15	PDB header: hydrolase Chain: A: PDB Molecule: cutinase 1; PDBTitle: crystal structure of aspergillus oryzae cutinase
13	c4oylC_	 Alignment		98.3	16	PDB header: hydrolase Chain: C: PDB Molecule: cutinase; PDBTitle: humicola insolens cutinase in complex with monoethylphosphate
14	c4psdA_	 Alignment		98.2	17	PDB header: hydrolase Chain: A: PDB Molecule: carbohydrate esterase family 5; PDBTitle: structure of trichoderma reesei cutinase native form.
15	c5xavB_	 Alignment		93.8	13	PDB header: biosynthetic protein Chain: B: PDB Molecule: intracellular polyhydroxyalkanoate synthase; PDBTitle: structure of phac from chromobacterium sp. usm2
16	d1jmkc_	 Alignment		92.9	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
17	d2g38b1	 Alignment		92.8	12	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
18	c2g38B_	 Alignment		92.8	12	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: ppe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
19	c3icvA_	 Alignment		92.5	19	PDB header: hydrolase Chain: A: PDB Molecule: lipase b; PDBTitle: structural consequences of a circular permutation on lipase b from2 candida antartica
20	c5t6oA_	 Alignment		91.5	13	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
21	d1ei9a_	 Alignment	not modelled	91.3	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterases
22	c4xy3A_	 Alignment	not modelled	90.7	13	PDB header: protein transport Chain: A: PDB Molecule: esx-1 secretion-associated protein espb; PDBTitle: structure of esx-1 secreted protein espb
23	c5xfsB_	 Alignment	not modelled	90.5	25	PDB header: protein transport Chain: B: PDB Molecule: ppe family protein ppe15; PDBTitle: crystal structure of pe8-ppe15 in complex with espg5 from m.2 tuberculosis
24	d1tcaa_	 Alignment	not modelled	88.1	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
25	c2cbgA_	 Alignment	not modelled	84.8	19	PDB header: hydrolase Chain: A: PDB Molecule: fengycin synthetase; PDBTitle: crystal structure of the pmsf-inhibited thioesterase domain of the2 fengycin biosynthesis cluster
26	c3ds8A_	 Alignment	not modelled	81.7	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin2722 protein; PDBTitle: the crysatl structure of the gene lin2722 products from listeria2 innocua
27	d1mo2a_	 Alignment	not modelled	81.5	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
28	c1mo2A_	 Alignment	not modelled	81.5	16	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
						Fold: alpha/beta-Hydrolases

29	d3b5ea1	Alignment	not modelled	80.5	18	Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
30	d2h7xa1	Alignment	not modelled	79.3	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
31	c3lp5A_	Alignment	not modelled	77.4	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
32	c3qmwD_	Alignment	not modelled	76.5	14	PDB header: hydrolase Chain: D: PDB Molecule: thioesterase; PDBTitle: redj with peg molecule bound in the active site
33	d1ispa_	Alignment	not modelled	74.4	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
34	c4xjvA_	Alignment	not modelled	73.9	21	PDB header: hydrolase Chain: A: PDB Molecule: s-acyl fatty acid synthase thioesterase, medium chain; PDBTitle: crystal structure of human thioesterase 2
35	c3lcrA_	Alignment	not modelled	71.5	13	PDB header: hydrolase Chain: A: PDB Molecule: tautomycin biosynthetic pks; PDBTitle: thioesterase from tautomycin biosynthetic pathway
36	c4h0cA_	Alignment	not modelled	71.3	15	PDB header: hydrolase Chain: A: PDB Molecule: phospholipase/carboxylesterase; PDBTitle: crystal structure of phospholipase/carboxylesterase from dyadobacter2 fermentans dsm 18053
37	c2h7xA_	Alignment	not modelled	68.7	18	PDB header: hydrolase Chain: A: PDB Molecule: type i polyketide synthase pikaiv; PDBTitle: pikromycin thioesterase adduct with reduced triketide2 affinity label
38	c3og9A_	Alignment	not modelled	67.7	10	PDB header: hydrolase Chain: A: PDB Molecule: protein yahd a copper inducible hydrolase; PDBTitle: structure of yahd with malic acid
39	d2h1ia1	Alignment	not modelled	67.0	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
40	c5f2hA_	Alignment	not modelled	65.2	21	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
41	d2r8ba1	Alignment	not modelled	64.9	9	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
42	c3ndjA_	Alignment	not modelled	63.4	15	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
43	c4nfbB_	Alignment	not modelled	63.3	19	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
44	c4r1dA_	Alignment	not modelled	63.0	11	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of tle4-tli4 complex
45	c2r8bA_	Alignment	not modelled	61.0	12	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
46	c4qnnC_	Alignment	not modelled	56.8	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
47	c3p3dA_	Alignment	not modelled	56.7	26	PDB header: nuclear protein Chain: A: PDB Molecule: nucleoporin 53; PDBTitle: crystal structure of the nup53 rrm domain from pichia guilliermondii
48	c4f21G_	Alignment	not modelled	56.2	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
49	c2zyiB_	Alignment	not modelled	53.7	21	PDB header: hydrolase Chain: B: PDB Molecule: lipase, putative; PDBTitle: a. fulgidus lipase with fatty acid fragment and calcium
50	c5uazB_	Alignment	not modelled	53.4	30	PDB header: protein transport Chain: B: PDB Molecule: nucleoporin nup53; PDBTitle: crystal structure of the yeast nucleoporin
51	c2qjwA_	Alignment	not modelled	53.3	20	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
52	c5d8mA_	Alignment	not modelled	52.3	10	PDB header: hydrolase Chain: A: PDB Molecule: metagenomic carboxyl esterase mgs0156; PDBTitle: crystal structure of the metagenomic carboxyl esterase mgs0156
53	c4x96B_	Alignment	not modelled	52.1	11	PDB header: transferase Chain: B: PDB Molecule: phosphatidylcholine-sterol acyltransferase; PDBTitle: low resolution crystal structure of lecithin:cholesterol2 acyltransferase (lcat; residues 21-397)
54	c4zxiA_	Alignment	not modelled	51.6	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
55	d1bu8a2	Alignment	not modelled	50.2	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
56	c4gw3A	Alignment	not modelled	50.1	16	PDB header: hydrolase Chain: A; PDB Molecule: putative lipase; PDBTitle: crystal structure of the lipase from proteus mirabilis
57	c2vsqA	Alignment	not modelled	49.9	18	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
58	c3gvmA	Alignment	not modelled	49.7	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
59	d1xkta	Alignment	not modelled	49.5	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
60	c4x91C	Alignment	not modelled	49.0	9	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)
61	d1pjaa	Alignment	not modelled	47.5	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterases
62	c1pjaA	Alignment	not modelled	47.5	14	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)
63	c4eziA	Alignment	not modelled	47.0	12	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
64	c4rvqA	Alignment	not modelled	46.0	15	PDB header: transferase Chain: A; PDB Molecule: d-mycarose 3-c-methyltransferase; PDBTitle: crystal structure of mtmc in complex with sam and tdp
65	d1lppb2	Alignment	not modelled	44.8	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
66	c3flaB	Alignment	not modelled	42.6	15	PDB header: hydrolase Chain: B; PDB Molecule: riifr; PDBTitle: riifr - type ii thioesterase from rifamycin nrps/pks biosynthetic2 pathway - form 1
67	c2m4mA	Alignment	not modelled	41.6	27	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
68	c3ilsA	Alignment	not modelled	39.4	13	PDB header: hydrolase Chain: A; PDB Molecule: afatoxin biosynthesis polyketide synthase; PDBTitle: the thioesterase domain from pksa
69	c6cl4A	Alignment	not modelled	39.4	9	PDB header: hydrolase Chain: A; PDB Molecule: lipase c12; PDBTitle: lipc12 - lipase from metagenomics
70	c2qs9A	Alignment	not modelled	39.0	13	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
71	c3h2iA	Alignment	not modelled	38.9	15	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
72	c2h1iA	Alignment	not modelled	38.3	27	PDB header: hydrolase Chain: A; PDB Molecule: carboxylesterase; PDBTitle: crystal structure of the bacillus cereus carboxylesterase
73	c5h3bA	Alignment	not modelled	38.2	19	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
74	c2oryA	Alignment	not modelled	36.8	16	PDB header: hydrolase Chain: A; PDB Molecule: lipase; PDBTitle: crystal structure of m37 lipase
75	c2q0xA	Alignment	not modelled	34.9	11	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: alpha/beta hydrolase fold protein of unknown function
76	c2ronA	Alignment	not modelled	34.1	15	PDB header: hydrolase Chain: A; PDB Molecule: surfactin synthetase thioesterase subunit; PDBTitle: the external thioesterase of the surfactin-synthetase
77	c4fleA	Alignment	not modelled	34.0	16	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
78	d1etha2	Alignment	not modelled	32.0	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
79	d3t gla	Alignment	not modelled	30.6	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
80	c2w6cX	Alignment	not modelled	30.6	19	PDB header: hydrolase Chain: X; PDB Molecule: acetylcholinesterase; PDBTitle: ache in complex with a bis-(-)-nor-meptazinol derivative

81	d1hpla2	Alignment	not modelled	30.5	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
82	c5d6oB	Alignment	not modelled	27.8	13	PDB header: transferase Chain: B: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: orthorhombic crystal structure of an acetyester hydrolase from <i>Corynebacterium glutamicum</i>
83	d1gpla2	Alignment	not modelled	27.8	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
84	c5xk2A	Alignment	not modelled	26.2	20	PDB header: hydrolase Chain: A: PDB Molecule: diacylglycerol lipase; PDBTitle: crystal structure of mono- and diacylglycerol lipase from <i>Aspergillus oryzae</i>
85	c3onjA	Alignment	not modelled	25.8	26	PDB header: protein transport Chain: A: PDB Molecule: t-snare vti1; PDBTitle: crystal structure of yeast vti1p_habc domain
86	c4be4A	Alignment	not modelled	25.1	19	PDB header: hydrolase Chain: A: PDB Molecule: sterol esterase; PDBTitle: closed conformation of <i>O. piceae</i> sterol esterase
87	d1dx4a	Alignment	not modelled	24.8	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like
88	d1ex9a	Alignment	not modelled	24.3	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
89	c3ke2A	Alignment	not modelled	24.1	45	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein yp_928783.1; PDBTitle: crystal structure of a duf2131 family protein (sama_2911) from <i>Shewanella amazonensis sb2b</i> at 2.50 Å resolution
90	c4wj2A	Alignment	not modelled	23.8	14	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
91	c4fg5B	Alignment	not modelled	22.9	23	PDB header: hydrolase Chain: B: PDB Molecule: e3 alpha-esterase-7 carboxylesterase; PDBTitle: crystal structure of the alpha-esterase-7 carboxylesterase, e3, from <i>Lucilia cuprina</i>
92	c2y6vB	Alignment	not modelled	22.7	13	PDB header: hydrolase Chain: B: PDB Molecule: peroxisomal membrane protein lpx1; PDBTitle: peroxisomal alpha-beta-hydrolase lpx1 (yor084w) from <i>Saccharomyces cerevisiae</i> (crystal form i)
93	c4nfaA	Alignment	not modelled	22.7	11	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	c5h6bA	Alignment	not modelled	22.6	15	PDB header: hydrolase Chain: A: PDB Molecule: putative secreted lipase; PDBTitle: crystal structure of a thermostable lipase from marine <i>Streptomyces</i>
95	d1nda2	Alignment	not modelled	22.4	25	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase
96	d1ea5a	Alignment	not modelled	22.0	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like
97	d1f0la3	Alignment	not modelled	21.9	43	Fold: Toxins' membrane translocation domains Superfamily: Diphtheria toxin, middle domain Family: Diphtheria toxin, middle domain
98	c2veoA	Alignment	not modelled	21.6	13	PDB header: hydrolase Chain: A: PDB Molecule: lipase a; PDBTitle: x-ray structure of <i>Candida antarctica</i> lipase a in its closed state.
99	d1nm8a2	Alignment	not modelled	21.3	25	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase
100	c2fj0A	Alignment	not modelled	21.2	16	PDB header: hydrolase Chain: A: PDB Molecule: carboxylic ester hydrolase; PDBTitle: crystal structure of juvenile hormone esterase from <i>Manduca sexta</i> , 2 with otfp covalently attached
101	c6i2tC	Alignment	not modelled	21.2	29	PDB header: hydrolase Chain: C: PDB Molecule: cholinesterase; PDBTitle: cryoem reconstruction of full-length, fully-glycosylated human2 butyrylcholinesterase tetramer
102	c6ba8A	Alignment	not modelled	21.1	13	PDB header: hydrolase Chain: A: PDB Molecule: iron acquisition yersiniabactin synthesis enzyme, ybtt; PDBTitle: ybtt - type ii thioesterase from yersiniabactin nrps/pks biosynthetic2 pathway
103	d1tiaa	Alignment	not modelled	21.0	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
104	d1pov1	Alignment	not modelled	21.0	38	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
105	c3uuuA	Alignment	not modelled	20.6	16	PDB header: hydrolase Chain: A: PDB Molecule: lip1, secretory lipase (family 3); PDBTitle: crystal structure of mono- and diacylglycerol lipase from <i>Malassezia globosa</i>