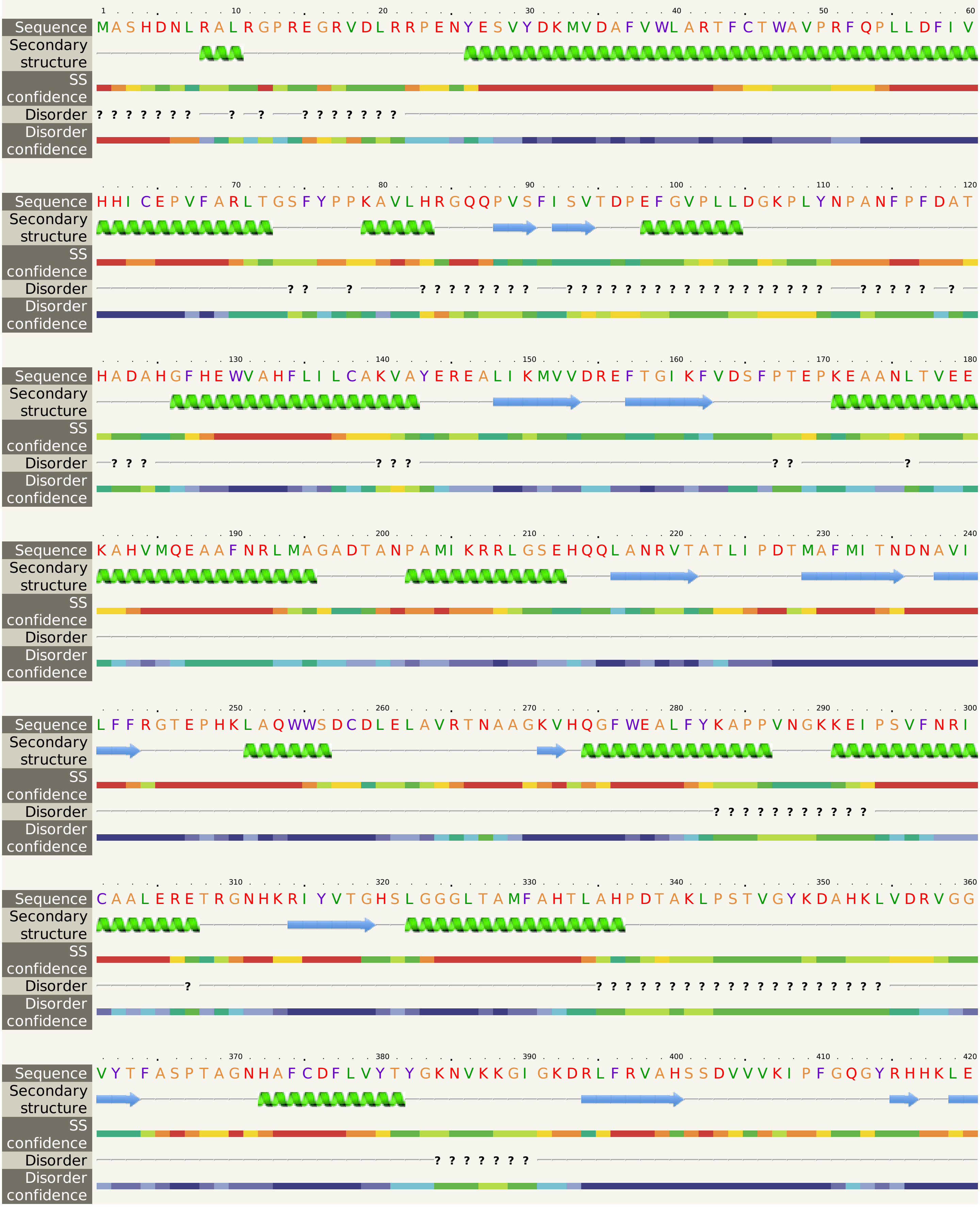
Phyre²

Email	hsiegle@gwdg.de
Description	Undefined
Date	Wed Nov 30 10:59:22 GMT 2016
Unique Job ID	6f8220dc5c148320

Secondary structure and disorder prediction



1 MASHDNLRALRGPREGRVDLRRPENYESVYDKMVDAFVWLARTFCTWAVPRFQPLLDFIV 60

61 HHICEPVFARLTGSFYPPKAVLHRGQQPVSFISVTDPEFGVPLLDGKPLYNPANFPFDAT 120

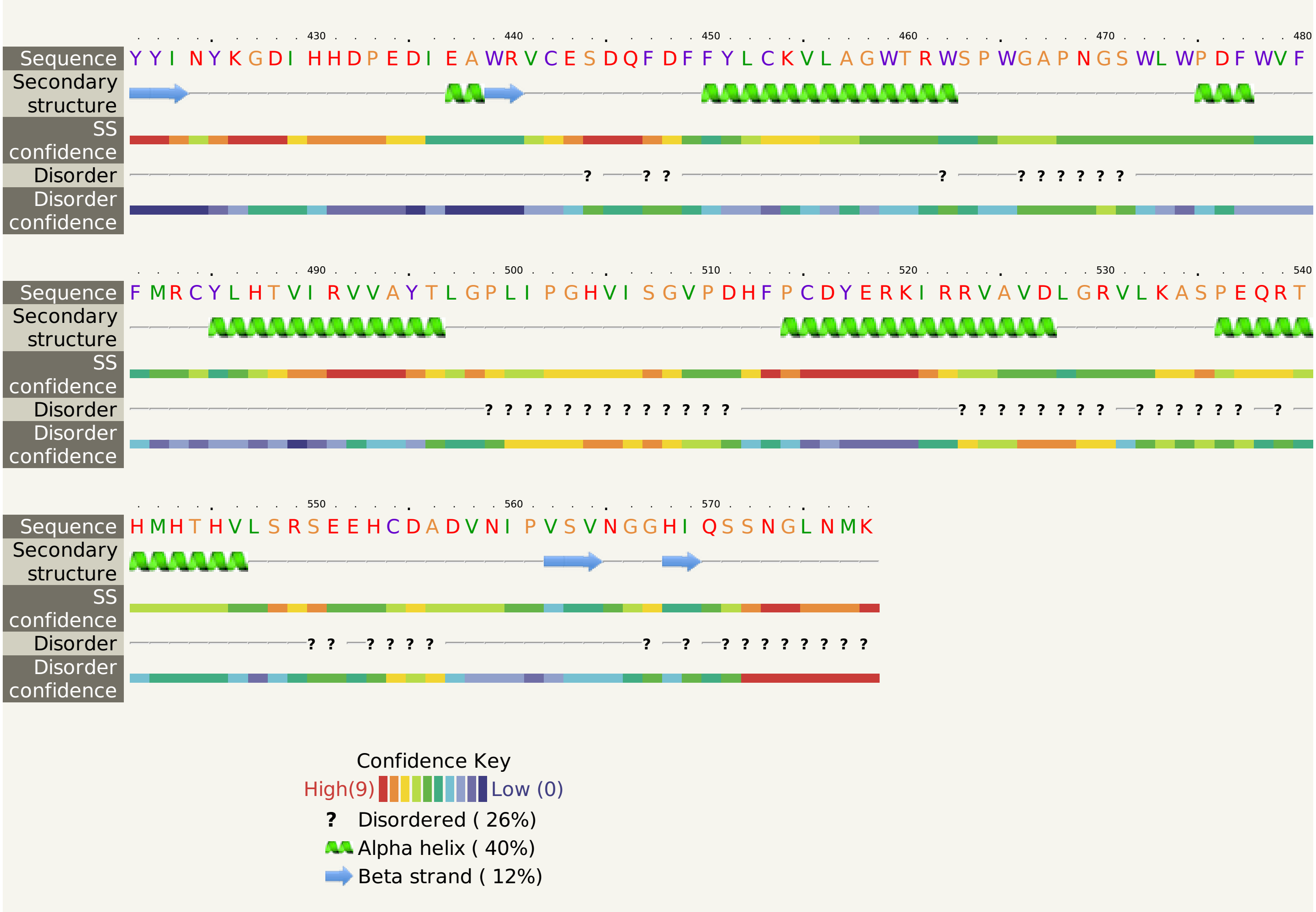
121 HADAHGFHEWVAHFLILCAKVAYEREALIKMVVDREFTGIKFVDSFPTEPKEAANLTVEE 180

181 KAHVMQEAAFNRLMAGADTANPAMIKRRLGSEHQQLANRVTATLIPDTMAFMITNDNAVI 240

241 LFFRGTEPHKLAQWWSDCDLELAVRTNAAGKVHQGFWEALFYKAPPVNGKKEIPSVFNRI 300

301 CAALERETRGNHKRIYVTGHSLGGGLTAMFAHTLAHPDTAKLPSTVGYKDAHKLVDRVGG 360

361 VYTFASPTAGNHAFCDFLVYTYGKNVKKGIGKDRLFRVAHSSDVVVKIPFGQGYRHHKLE 420


430
440
450
460
470
480
Sequence
YYINYKGDIHHDPEDIEAWRVCESDQFDFFYLCKVLAGWTRWSPWGAPNGSWLWPDFWVF
Secondary structure
SS confidence
Disorder
? ? ? ? ? ? ? ? ? ?
Disorder confidence
490
500
510
520
530
540
Sequence
FMRCYLHTVIRVVAYTLGPLIPGHVISGVPDHFPCDYERKIRRVAVDLGRVLKASPEQRT
Secondary structure
SS confidence
Disorder
? ?
Disorder confidence
550
560
570
Sequence
HMHTHVLSRSEEHCDADVNIPVSVNGGHIQSSNGLNMK
Secondary structure
SS confidence
Disorder
? ? ? ? ? ? ? ? ? ? ? ? ? ? ? ? ? ?
Disorder confidence
Confidence Key
High(9)
Low (0)
? Disordered (26%)
Alpha helix (40%)
Beta strand (12%)

Phyre^2

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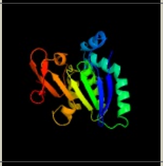
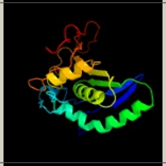
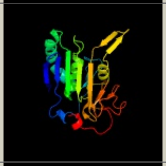
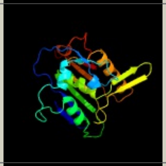
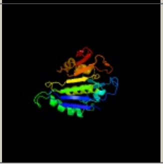
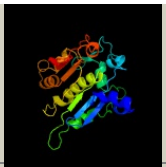
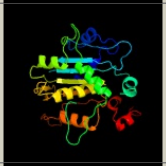
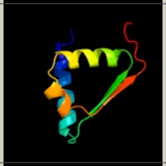
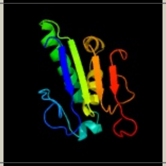
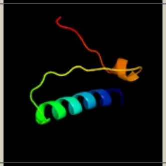
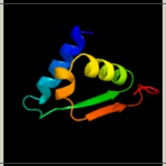
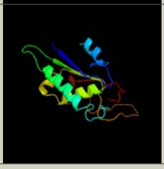
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3o0dF_	Alignment		100.0	29	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**triacylglycerol lipase; **PDBTitle:** crystal structure of lip2 lipase from yarrowia lipolytica at 1.7 a2 resolution
2	c3uueA_	Alignment		100.0	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lip1, secretory lipase (family 3); **PDBTitle:** crystal structure of mono- and diacylglycerol lipase from malassezia2 globosa
3	c3ngmB_	Alignment		100.0	29	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**extracellular lipase; **PDBTitle:** crystal structure of lipase from gibberella zeae
4	d1uwca_	Alignment		100.0	29	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
5	d1tiaa_	Alignment		100.0	30	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
6	c3g7nA_	Alignment		100.0	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipase; **PDBTitle:** crystal structure of a triacylglycerol lipase from penicillium2 expansum at 1.3
7	d1tiba_	Alignment		100.0	25	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
8	d3tgla_	Alignment		100.0	30	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
9	d1lgya_	Alignment		100.0	27	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
10	c2yijA_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phospholipase a1-iigamma; **PDBTitle:** crystal structure of phospholipase a1
11	c4nfuB_	Alignment		100.0	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

12	c4nfuA_	Alignment		100.0	22	**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
13	c2oryA_	Alignment		100.0	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipase; **PDBTitle:** crystal structure of m37 lipase
14	c4x96B_	Alignment		96.7	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphatidylcholine-sterol acyltransferase; **PDBTitle:** low resolution crystal structure of lecithin:cholesterol2 acyltransferase (lcat; residues 21-397)
15	c4x91C_	Alignment		96.5	16	**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)
16	c4psdA_	Alignment		95.9	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**carbohydrate esterase family 5; **PDBTitle:** structure of trichoderma reesei cutinase native form.
17	c4z8zA_	Alignment		95.7	17	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the hypothetical protein from ruminiclostridium2 thermocellum atcc 27405
18	c3lp5A_	Alignment		95.6	28	**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
19	c2zyiB_	Alignment		95.5	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lipase, putative; **PDBTitle:** a. fulgidus lipase with fatty acid fragment and calcium
20	d1cexa_	Alignment		95.3	19	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Cutinase-like
21	c4r1dA_	Alignment	not modelled	94.9	22	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of tle4-tli4 complex
22	c5f2hA_	Alignment	not modelled	94.9	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
23	c3ds8A_	Alignment	not modelled	94.9	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin2722 protein; **PDBTitle:** the crysatl structure of the gene lin2722 products from listeria2 innocua
24	d1uxoa_	Alignment	not modelled	94.8	22	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**YdeN-like
25	d1cvla_	Alignment	not modelled	94.5	31	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Bacterial lipase
26	d1ex9a_	Alignment	not modelled	94.4	24	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Bacterial lipase
27	c4qnnC_	Alignment	not modelled	94.3	17	**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
28	d1ispa_	Alignment	not modelled	94.3	19	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Bacterial lipase
						PDB header:hydrolase

29	c3d0kA_	Alignment	not modelled	94.2	21	**Chain:** A: **PDB Molecule:**putative poly(3-hydroxybutyrate) depolymerase lpqc; **PDBTitle:** crystal structure of the lpqc, poly(3-hydroxybutyrate) depolymerase2 from bordetella parapertussis
30	d1tcaa_	Alignment	not modelled	94.2	21	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
31	c2h7xA_	Alignment	not modelled	94.0	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**type i polyketide synthase pikaiv; **PDBTitle:** pikromycin thioesterase adduct with reduced triketide2 affinity label
32	d1sfra_	Alignment	not modelled	94.0	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Mycobacterial antigens
33	c4gw3A_	Alignment	not modelled	93.9	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative lipase; **PDBTitle:** crystal structure of the lipase from proteus mirabilis
34	d2h1ia1	Alignment	not modelled	93.8	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase/thioesterase 1
35	c3fleB_	Alignment	not modelled	93.8	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**se_1780 protein; **PDBTitle:** se_1780 protein of unknown function from staphylococcus epidermidis.
36	d2jbwa1	Alignment	not modelled	93.8	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**2,6-dihydropseudooxynicotine hydrolase-like
37	d2h7xa1	Alignment	not modelled	93.8	23	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Thioesterase domain of polypeptide, polyketide and fatty acid synthases
38	c2h1iA_	Alignment	not modelled	93.7	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**carboxylesterase; **PDBTitle:** crystal structure of the bacillus cereus carboxylesterase
39	c1pjaA_	Alignment	not modelled	93.7	11	**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)
40	d1pjaa_	Alignment	not modelled	93.7	11	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Thioesterases
41	c2y6vB_	Alignment	not modelled	93.6	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**peroxisomal membrane protein lpx1; **PDBTitle:** peroxisomal alpha-beta-hydrolase lpx1 (yor084w) from2 saccharomyces cerevisiae (crystal form i)
42	d1ei9a_	Alignment	not modelled	93.6	19	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Thioesterases
43	c2rauA_	Alignment	not modelled	93.5	18	**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
44	c3lcrA_	Alignment	not modelled	93.5	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tautomycetin biosynthetic pks; **PDBTitle:** thioesterase from tautomycetin biosynthhetic pathway
45	c1qgeD_	Alignment	not modelled	93.4	22	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**protein (triacylglycerol hydrolase); **PDBTitle:** new crystal form of pseudomonas glumae (formerly chromobacterium2 viscosum atcc 6918) lipase
46	d1r88a_	Alignment	not modelled	93.0	8	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Mycobacterial antigens
47	c3mveB_	Alignment	not modelled	93.0	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**upf0255 protein vv1_0328; **PDBTitle:** crystal structure of a novel pyruvate decarboxylase
48	c1mo2A_	Alignment	not modelled	93.0	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**erythronolide synthase, modules 5 and 6; **PDBTitle:** thioesterase domain from 6-deoxyerythronolide synthase2 (debs te), ph 8.5
49	d1mo2a_	Alignment	not modelled	93.0	25	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Thioesterase domain of polypeptide, polyketide and fatty acid synthases
50	c2jbwB_	Alignment	not modelled	92.9	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**2,6-dihydroxy-pseudo-oxynicotine hydrolase; **PDBTitle:** crystal structure of the 2,6-dihydroxy-pseudo-oxynicotine2 hydrolase.
51	c4fleA_	Alignment	not modelled	92.7	15	**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
52	c3bdvB_	Alignment	not modelled	92.7	22	**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
53	d3b5ea1	Alignment	not modelled	92.6	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase/thioesterase 1
54	d1k8qa_	Alignment	not modelled	92.5	22	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases

						Family: Gastric lipase
55	d1xkta_	Alignment	not modelled	92.5	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Thioesterase domain of polypeptide, polyketide and fatty acid synthases
56	d4lipd_	Alignment	not modelled	92.4	30	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Bacterial lipase
57	c3picB_	Alignment	not modelled	92.4	31	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cip2; **PDBTitle:** glucuronoyl esterase catalytic domain (cip2_ge) from hypocrea jecorina
58	c2qruA_	Alignment	not modelled	92.4	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an alpha/beta hydrolase superfamily protein from2 enterococcus faecalis
59	d1lpbb2	Alignment	not modelled	92.3	18	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Pancreatic lipase, N-terminal domain
60	c3l80A_	Alignment	not modelled	92.2	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein smu.1393c; **PDBTitle:** crystal structure of smu.1393c from streptococcus mutans ua159
61	d1hlga_	Alignment	not modelled	92.0	24	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Gastric lipase
62	d1bu8a2	Alignment	not modelled	91.8	21	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Pancreatic lipase, N-terminal domain
63	c2vavL_	Alignment	not modelled	91.7	20	**PDB header:**transferase **Chain:** L: **PDB Molecule:**acetyl-coa--deacetylcephalosporin c **PDBTitle:** crystal structure of deacetylcephalosporin c2 acetyltransferase (dac-soak)
64	c2veoA_	Alignment	not modelled	91.6	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipase a; **PDBTitle:** x-ray structure of candida antarctica lipase a in its closed state.
65	c4h0cA_	Alignment	not modelled	91.6	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phospholipase/carboxylesterase; **PDBTitle:** crystal structure of phospholipase/carboxylesterase from dyadobacter2 fermentans dsm 18053
66	c3h2iA_	Alignment	not modelled	91.5	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
67	c3wlaA_	Alignment	not modelled	91.5	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**oxidized polyvinyl alcohol hydrolase; **PDBTitle:** crystal structure of soph native
68	d1f0na_	Alignment	not modelled	91.4	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Mycobacterial antigens
69	c3i28A_	Alignment	not modelled	91.4	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**epoxide hydrolase 2; **PDBTitle:** crystal structure of soluble epoxide hydrolase
70	c2cbgA_	Alignment	not modelled	91.4	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**fengycin synthetase; **PDBTitle:** crystal structure of the pmsf-inhibited thioesterase domain2 of the fengycin biosynthesis cluster
71	d1g66a_	Alignment	not modelled	91.2	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Cutinase-like
72	c4eziA_	Alignment	not modelled	91.2	24	**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
73	c3k2iA_	Alignment	not modelled	91.1	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acyl-coenzyme a thioesterase 4; **PDBTitle:** human acyl-coenzyme a thioesterase 4
74	d1gpla2	Alignment	not modelled	91.0	22	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Pancreatic lipase, N-terminal domain
75	c3ajaA_	Alignment	not modelled	90.9	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of msmeg_6394
76	c4ao6A_	Alignment	not modelled	90.8	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase; **PDBTitle:** native structure of a novel cold-adapted esterase from an2 arctic intertidal metagenomic library
77	c3fcxA_	Alignment	not modelled	90.8	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**s-formylglutathione hydrolase; **PDBTitle:** crystal structure of human esterase d
78	c3wydA_	Alignment	not modelled	90.8	35	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lc-est1c; **PDBTitle:** c-terminal esterase domain of lc-est1
79	c3og9A_	Alignment	not modelled	90.8	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein yahd a copper inducible hydrolase; **PDBTitle:** structure of yahd with malic acid
80	c3g8yA_	Alignment	not modelled	90.8	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**susd/ragb-associated esterase-like protein; **PDBTitle:** crystal structure of a putative hydrolase (bvu_4111) from bacteroides2 vulgatus atcc 8482 at 1.90 a resolution

81	c4g4gA_	Alignment	not modelled	90.7	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**4-o-methyl-glucuronoyl methylesterase; **PDBTitle:** crystal structure of recombinant glucuronoyl esterase from2 sporotrichum thermophile determined at 1.55 a resolution
82	c3h04A_	Alignment	not modelled	90.6	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of the protein with unknown function from2 staphylococcus aureus subsp. aureus mu50
83	c3fnbB_	Alignment	not modelled	90.5	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**acylaminoacyl peptidase smu_737; **PDBTitle:** crystal structure of acylaminoacyl peptidase smu_737 from2 streptococcus mutans ua159
84	d1dqza_	Alignment	not modelled	90.4	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Mycobacterial antigens
85	c3qmwD_	Alignment	not modelled	90.3	28	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**thioesterase; **PDBTitle:** redj with peg molecule bound in the active site
86	c3gbsA_	Alignment	not modelled	90.3	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cutinase 1; **PDBTitle:** crystal structure of aspergillus oryzae cutinase
87	c2qs9A_	Alignment	not modelled	90.1	19	**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
88	d1qoza_	Alignment	not modelled	90.1	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Cutinase-like
89	c2q0xA_	Alignment	not modelled	90.0	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** alpha/beta hydrolase fold protein of unknown function
90	c3flaB_	Alignment	not modelled	90.0	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**rifr; **PDBTitle:** rifr - type ii thioesterase from rifamycin nrps/pks biosynthetic2 pathway - form 1
91	c2r8bA_	Alignment	not modelled	90.0	11	**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
92	c2czqB_	Alignment	not modelled	89.9	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cutinase-like protein; **PDBTitle:** a novel cutinase-like protein from cryptococcus sp.
93	c2qjwA_	Alignment	not modelled	89.7	18	**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
94	c3dd5F_	Alignment	not modelled	89.6	19	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**cutinase; **PDBTitle:** glomerella cingulata e600-cutinase complex
95	c4xjvA_	Alignment	not modelled	89.2	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**s-acyl fatty acid synthase thioesterase, medium chain; **PDBTitle:** crystal structure of human thioesterase 2
96	d1etha2	Alignment	not modelled	89.2	18	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Pancreatic lipase, N-terminal domain
97	c3hlkB_	Alignment	not modelled	89.1	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**acyl-coenzyme a thioesterase 2, mitochondrial; **PDBTitle:** crystal structure of human mitochondrial acyl-coa2 thioesterase (acot2)
98	c3d59B_	Alignment	not modelled	88.8	35	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**platelet-activating factor acetylhydrolase; **PDBTitle:** crystal structure of human plasma platelet activating2 factor acetylhydrolase
99	d1rp1a2	Alignment	not modelled	88.8	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Pancreatic lipase, N-terminal domain
100	c1cr6A_	Alignment	not modelled	88.6	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**epoxide hydrolase; **PDBTitle:** crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
101	d2r8ba1	Alignment	not modelled	88.6	11	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase/thioesterase 1
102	c4eb0A_	Alignment	not modelled	88.5	50	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lcc; **PDBTitle:** crystal structure of leaf-branch compost bacterial cutinase homolog
103	c4wfiA_	Alignment	not modelled	88.5	40	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cutinase; **PDBTitle:** crystal structure of pet-degrading cutinase cut190 s226p mutant in2 ca(2+)-free state
104	c5d6oB_	Alignment	not modelled	88.3	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**homoserine o-acetyltransferase; **PDBTitle:** orthorhombic crystal structure of an acetylester hydrolase from2 corynebacterium glutamicum
105	d1jmkc_	Alignment	not modelled	88.2	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Thioesterase domain of polypeptide, polyketide and fatty acid synthases
106	c5cxxC_	Alignment	not modelled	88.0	13	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**ferulic acid esterase, amce1/fae1a; **PDBTitle:** structure of a ce1 ferulic acid esterase, amce1/fae1a, from2 anaeromyces mucronatus in complex with ferulic acid

107	c3visB_	Alignment	not modelled	87.9	50	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**esterase; **PDBTitle:** crystal structure of cutinase est119 from thermobifida alba ahk119
108	c4oylC_	Alignment	not modelled	87.9	18	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**cutinase; **PDBTitle:** humicola insolens cutinase in complex with mono-ethylphosphate
109	d1jfra_	Alignment	not modelled	87.6	45	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Lipase
110	d1hpla2	Alignment	not modelled	87.2	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Pancreatic lipase, N-terminal domain
111	c2uz0B_	Alignment	not modelled	87.1	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**tributyrin esterase; **PDBTitle:** the crystal crystal structure of the esta protein, a2 virulence factor esta protein from streptococcus pneumonia
112	d1pv1a_	Alignment	not modelled	87.0	18	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Hypothetical esterase YJL068C
113	c4qloA_	Alignment	not modelled	87.0	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**homoserine o-acetyltransferase; **PDBTitle:** crystal structure of homoserine o-acetyltransferase from2 staphylococcus aureus
114	c3i6yA_	Alignment	not modelled	86.9	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase apc40077; **PDBTitle:** structure of an esterase from the oil-degrading bacterium oleispira2 antarctica
115	c2hu7A_	Alignment	not modelled	86.9	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acylamino-acid-releasing enzyme; **PDBTitle:** binding of inhibitors by acylaminoacyl peptidase
116	c3jyhD_	Alignment	not modelled	86.8	29	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**dipeptidyl-peptidase 2; **PDBTitle:** human dipeptidyl peptidase dpp7
117	c3doiA_	Alignment	not modelled	86.8	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase; **PDBTitle:** crystal structure of a thermostable esterase complex with2 paraoxon
118	c3e4dD_	Alignment	not modelled	86.7	22	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**esterase d; **PDBTitle:** structural and kinetic study of an s-formylglutathione2 hydrolase from agrobacterium tumefaciens
119	c4fhzA_	Alignment	not modelled	86.5	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phospholipase/carboxylesterase; **PDBTitle:** crystal structure of a carboxyl esterase at 2.0 angstrom resolution
120	c4b6gA_	Alignment	not modelled	86.5	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative esterase; **PDBTitle:** the crystal structure of the neisserial esterase d.