

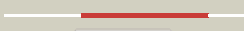























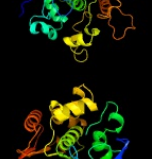
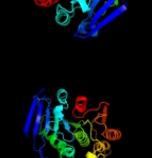


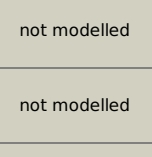


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1288 (-) _1441354_1442724
Date	Wed Jul 31 22:05:38 BST 2019
Unique Job ID	634c110b1a7d4b9b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1dqza_	 Alignment		100.0	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Mycobacterial antigens
2	c4h18D_	 Alignment		100.0	21	PDB header: transferase Chain: D; PDB Molecule: cmt1; PDBTitle: three dimensional structure of corynomycoloyl tranferase c
3	d1pv1a_	 Alignment		100.0	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hypothetical esterase YJL068C
4	c2ecfA_	 Alignment		100.0	16	PDB header: hydrolase Chain: A; PDB Molecule: dipeptidyl peptidase iv; PDBTitle: crystal structure of dipeptidyl aminopeptidase iv from2 stenotrophomonas maltophilia
5	c3c8dA_	 Alignment		100.0	18	PDB header: hydrolase Chain: A; PDB Molecule: enterochelin esterase; PDBTitle: crystal structure of the enterobactin esterase fes from2 shigella flexneri in the presence of 2,3-di-hydroxy-n-3 benzoyl-glycine
6	d1sfra_	 Alignment		100.0	22	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Mycobacterial antigens
7	c4q1vA_	 Alignment		100.0	13	PDB header: hydrolase Chain: A; PDB Molecule: putative dipeptidyl aminopeptidase iv; PDBTitle: crystal structure of a putative dipeptidyl aminopeptidase iv2 (bacova_01349) from bacteroides ovatus atcc 8483 at 2.48 a resolution
8	c3e4dD_	 Alignment		100.0	18	PDB header: hydrolase Chain: D; PDB Molecule: esterase d; PDBTitle: structural and kinetic study of an s-formylglutathione hydrolase from2 agrobacterium tumefaciens
9	c5cxcC_	 Alignment		100.0	21	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
10	c5oljA_	 Alignment		100.0	17	PDB header: hydrolase Chain: A; PDB Molecule: dipeptidyl peptidase iv; PDBTitle: crystal structure of porphyromonas gingivalis dipeptidyl peptidase 4
11	c1z68A_	 Alignment		100.0	16	PDB header: lyase Chain: A; PDB Molecule: fibroblast activation protein, alpha subunit; PDBTitle: crystal structure of human fibroblast activation protein alpha

12	c3fcxA	Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: s-formylglutathione hydrolase; PDBTitle: crystal structure of human esterase d
13	d1f0nA	Alignment		100.0	22	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Mycobacterial antigens
14	d3c8da2	Alignment		100.0	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
15	c2eepA	Alignment		100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl aminopeptidase iv, putative; PDBTitle: prolyl tripeptidyl aminopeptidase complexed with an inhibitor
16	c4wj1B	Alignment		100.0	15	PDB header: membrane protein Chain: B: PDB Molecule: inactive dipeptidyl peptidase 10; PDBTitle: structure of human dipeptidyl peptidase 10 (dppy): a modulator of2 neuronal kv4 channels
17	c4b6gA	Alignment		100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: putative esterase; PDBTitle: the crystal structure of the neisserial esterase d.
18	c3i6yA	Alignment		100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: esterase apc40077; PDBTitle: structure of an esterase from the oil-degrading bacterium oleispira2 antarctica
19	d1r88a	Alignment		100.0	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Mycobacterial antigens
20	c3azqA	Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase; PDBTitle: crystal structure of puromycin hydrolase s511a mutant complexed with2 pgg
21	c6eotG	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: G: PDB Molecule: dipeptidyl peptidase 8; PDBTitle: dpp8 - slrflyeg, space group 19
22	d1jfa	Alignment	not modelled	100.0	26	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
23	c5jceA	Alignment	not modelled	100.0	27	PDB header: sugar binding protein Chain: A: PDB Molecule: chitin elicitor-binding protein; PDBTitle: crystal structure of oscebp complex
24	c6eosB	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: B: PDB Molecule: dipeptidyl peptidase 8; PDBTitle: dpp8 - apo, space group 19
25	c2qtbB	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: B: PDB Molecule: dipeptidyl peptidase 4; PDBTitle: human dipeptidyl peptidase iv/cd26 in complex with a 4-aryl2 cyclohexylalanine inhibitor
26	c6eoqC	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: C: PDB Molecule: dipeptidyl peptidase 9; PDBTitle: dpp9 - apo
27	c6eorD	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: D: PDB Molecule: dipeptidyl peptidase 9; PDBTitle: dpp9 - 1g244
28	c2uz0B	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: B: PDB Molecule: tributyryn esterase; PDBTitle: the crystal crystal structure of the esta protein, a2 virulence factor esta protein from streptococcus pneumonia
						PDB header: hydrolase Chain: D: PDB Molecule: amino acyl peptidase;

29	c5l8sD_	Alignment	not modelled	100.0	16	PDBTitle: the crystal structure of a cold-adapted acylaminoacyl peptidase2 reveals a novel quaternary architecture based on the arm-exchange3 mechanism
30	c2g5tA_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A; PDB Molecule: dipeptidyl peptidase 4; PDBTitle: crystal structure of human dipeptidyl peptidase iv (dppiv) complexed2 with cyanopyrrolidine (c5-pro-pro) inhibitor 21ag
31	c1xfdB_	Alignment	not modelled	100.0	15	PDB header: membrane protein Chain: D; PDB Molecule: dipeptidyl aminopeptidase-like protein 6; PDBTitle: structure of a human a-type potassium channel accelerating factor2 dppx, a member of the dipeptidyl aminopeptidase family
32	c3ls2D_	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: D; PDB Molecule: s-formylglutathione hydrolase; PDBTitle: crystal structure of an s-formylglutathione hydrolase from2 pseudoalteromonas haloplanktis tac125
33	c4hxgJ_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: J; PDB Molecule: putative uncharacterized protein ph0594; PDBTitle: pyrococcus horikoshii acylaminoacyl peptidase (orthorhombic crystal2 form)
34	c5JrIC_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: C; PDB Molecule: dipeptidyl aminopeptidases/acylaminoacyl-peptidases-like PDBTitle: crystal structure of the sphingopyxin i lasso peptide isopeptidase2 spi-isop (native)
35	c5volA_	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: A; PDB Molecule: putative esterase; PDBTitle: bacint_04212 ferulic acid esterase
36	c5yznA_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A; PDB Molecule: acyl-peptide hydrolase, putative; PDBTitle: crystal structure of s9 peptidase (active form) from deinococcus2 radiodurans r1
37	c1wb4A_	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: A; PDB Molecule: endo-1,4-beta-xylanase y; PDBTitle: s954a mutant of the feruloyl esterase module from2 clostridium thermocellum complexed with sinapinate
38	c5ls2B_	Alignment	not modelled	100.0	20	PDB header: plant protein Chain: B; PDB Molecule: lysm type receptor kinase; PDBTitle: receptor mediated chitin perception in legumes is functionally2 seperable from nod factor perception
39	c4rgyA_	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: A; PDB Molecule: esterase; PDBTitle: structural and functional analysis of a low-temperature-active2 alkaline esterase from south china sea marine sediment microbial3 metagenomic library
40	c4rotA_	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: A; PDB Molecule: esterase a; PDBTitle: crystal structure of esterase a from streptococcus pyogenes
41	c5t88B_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: B; PDB Molecule: prolyl endopeptidase; PDBTitle: prolyl oligopeptidase from pyrococcus furiosus
42	c1qfmA_	Alignment	not modelled	100.0	11	PDB header: hydrolase Chain: A; PDB Molecule: protein (prolyl oligopeptidase); PDBTitle: prolyl oligopeptidase from porcine muscle
43	c4bp9A_	Alignment	not modelled	100.0	11	PDB header: hydrolase Chain: A; PDB Molecule: oligopeptidase b; PDBTitle: oligopeptidase b from trypanosoma brucei with covalently bound2 antipain - closed form
44	c2xe4A_	Alignment	not modelled	100.0	11	PDB header: hydrolase/inhibitor Chain: A; PDB Molecule: oligopeptidase b; PDBTitle: structure of oligopeptidase b from leishmania major
45	d1wb4a1	Alignment	not modelled	100.0	22	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
46	c2hu7A_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A; PDB Molecule: acylamino-acid-releasing enzyme; PDBTitle: binding of inhibitors by acylaminoacyl peptidase
47	c3doiA_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A; PDB Molecule: esterase; PDBTitle: crystal structure of a thermostable esterase complex with2 paraoxon
48	c4b9hA_	Alignment	not modelled	100.0	35	PDB header: sugar binding protein Chain: A; PDB Molecule: extracellular protein 6; PDBTitle: cladosporium fulvum lysm effector ecp6 in complex with a2 beta-1,4-linked n-acetyl-d-glucosamine tetramer: i3c heavy3 atom derivative
49	c2bklB_	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: B; PDB Molecule: prolyl endopeptidase; PDBTitle: structural and mechanistic analysis of two prolyl2 endopeptidases: role of inter-domain dynamics in3 catalysis and specificity
50	c3iumA_	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: A; PDB Molecule: prolyl endopeptidase; PDBTitle: appep_wtx opened state
51	c5txeA_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A; PDB Molecule: atxe2; PDBTitle: atxe2 isopeptidase - s527a variant with astexin3-dc4 bound
52	c6guiA_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A; PDB Molecule: siderophore esterase iroe-like, putative; PDBTitle: siderophore hydrolase estb mutant h267n from aspergillus fumigatus
53	c4ebzA_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A; PDB Molecule: chitin elicitor receptor kinase 1; PDBTitle: crystal structure of the ectodomain of a receptor like kinase
						PDB header: hydrolase

54	c6gunB_	Alignment	not modelled	100.0	19	Chain: B: PDB Molecule: estb from aspergillus nidulans; PDBTitle: siderophore hydrolase estb from aspergillus nidulans
55	c6gi5A_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: ferric enterobactin esterase; PDBTitle: crystal structure of the ferric enterobactin esterase (pfee) from2 pseudomonas aeruginosa in complex with the tris-catechol vector
56	c6guoC_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: C: PDB Molecule: putative siderophore-degrading esterase (eurofung); PDBTitle: siderophore hydrolase esta from aspergillus nidulans
57	c3gffA_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: iroe-like serine hydrolase; PDBTitle: crystal structure of iroe-like serine hydrolase (np_718593.1) from2 shewanella oneidensis at 2.12 a resolution
58	c5n4dA_	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: prolyl oligopeptidase; PDBTitle: prolyl oligopeptidase b from galerina marginata bound to 25mer2 macrocyclization substrate - d661a mutant
59	c5uzwD_	Alignment	not modelled	100.0	12	PDB header: lyase Chain: D: PDB Molecule: peptide cyclase 1; PDBTitle: pcy1 g696insertion variant in complex with follower peptide and the2 covalent inhibitor zpp
60	c1yr2A_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: prolyl oligopeptidase; PDBTitle: structural and mechanistic analysis of two prolyl endopeptidases: role2 of inter-domain dynamics in catalysis and specificity
61	c4hvtA_	Alignment	not modelled	100.0	11	PDB header: hydrolase Chain: A: PDB Molecule: post-proline cleaving enzyme; PDBTitle: structure of a post-proline cleaving enzyme from rickettsia typhi
62	c5uw7B_	Alignment	not modelled	100.0	12	PDB header: lyase Chain: B: PDB Molecule: peptide cyclase 1; PDBTitle: pcy1 y481f variant in complex with follower peptide
63	d2gzsa1	Alignment	not modelled	99.9	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: IroE-like
64	c4w9rA_	Alignment	not modelled	99.9	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterised protein coch_1243 from2 capnocytophaga ochracea dsm 7271
65	d1orva2	Alignment	not modelled	99.9	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like
66	c2o7vA_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: cxe carboxylesterase; PDBTitle: carboxylesterase aece1 from actinidia eriantha covalently inhibited2 by paraoxon
67	c2qm0B_	Alignment	not modelled	99.9	20	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: bes; PDBTitle: crystal structure of bes protein from bacillus cereus
68	d2bgra2	Alignment	not modelled	99.9	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like
69	d1xfda2	Alignment	not modelled	99.9	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like
70	c2zshA_	Alignment	not modelled	99.9	17	PDB header: hormone receptor Chain: A: PDB Molecule: probable gibberellin receptor gid11; PDBTitle: structural basis of gibberellin(ga3)-induced dela2 recognition by the gibberellin receptor
71	c5x6sB_	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: B: PDB Molecule: acetyl xylan esterase a; PDBTitle: acetyl xylan esterase from aspergillus awamori
72	c3bxpA_	Alignment	not modelled	99.9	11	PDB header: hydrolase Chain: A: PDB Molecule: putative lipase/esterase; PDBTitle: crystal structure of a putative carboxylesterase (lp_2923) from2 lactobacillus plantarum wcf51 at 1.70 a resolution
73	c5hc4A_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: lipolytic enzyme; PDBTitle: structure of esterase est22
74	c3ed1E_	Alignment	not modelled	99.9	14	PDB header: hydrolase receptor Chain: E: PDB Molecule: gibberellin receptor gid1; PDBTitle: crystal structure of rice gid1 complexed with ga3
75	c3wlaA_	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: oxidized polyvinyl alcohol hydrolase; PDBTitle: crystal structure of soph native
76	c4s3jC_	Alignment	not modelled	99.9	23	PDB header: hydrolase Chain: C: PDB Molecule: cortical-lytic enzyme; PDBTitle: crystal structure of the bacillus cereus spore cortex-lytic enzyme2 sle1
77	d1qfma2	Alignment	not modelled	99.9	10	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Prolyl oligopeptidase, C-terminal domain
78	c3wydA_	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: A: PDB Molecule: lc-est1c; PDBTitle: c-terminal esterase domain of lc-est1
79	c3ga7A_	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: acetyl esterase; PDBTitle: 1.55 angstrom crystal structure of an acetyl esterase from salmonella2 typhimurium
80	c4c87A_	Alignment	not modelled	99.9	13	PDB header: hydrolase Chain: A: PDB Molecule: esterase;

					PDBTitle: esterase lpest1 from lactobacillus plantarum wcfs1
81	c4q05A_	Alignment	not modelled	99.9	10 PDB header: hydrolase Chain: A: PDB Molecule: esterase e25; PDBTitle: crystal structure of an esterase e25
82	c4s3kA_	Alignment	not modelled	99.9	26 PDB header: hydrolase Chain: A: PDB Molecule: spore germination protein yaah; PDBTitle: crystal structure of the bacillus megaterium qm b1551 spore cortex-2 lytic enzyme slel
83	c5f2hA_	Alignment	not modelled	99.9	15 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
84	c4q3oB_	Alignment	not modelled	99.9	11 PDB header: hydrolase Chain: B: PDB Molecule: mgs-mt1; PDBTitle: crystal structure of mgs-mt1, an alpha/beta hydrolase enzyme from a2 lake matapan deep-sea metagenome library
85	d2h1ia1	Alignment	not modelled	99.9	19 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
86	c4wy5A_	Alignment	not modelled	99.9	17 PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: structural analysis of two fungal esterases from rhizomucor miehei2 explaining their substrate specificity
87	d2hu7a2	Alignment	not modelled	99.9	16 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acylamino-acid-releasing enzyme, C-terminal donain
88	c5jd5A_	Alignment	not modelled	99.9	18 PDB header: hydrolase Chain: A: PDB Molecule: mgs-mile3; PDBTitle: crystal structure of mgs-mile3, an alpha/beta hydrolase enzyme from2 the metagenome of pyrene-phenanthrene enrichment culture with3 sediment sample of milazzo harbor, italy
89	c2h1iA_	Alignment	not modelled	99.9	19 PDB header: hydrolase Chain: A: PDB Molecule: carboxylesterase; PDBTitle: crystal structure of the bacillus cereus carboxylesterase
90	d3b5ea1	Alignment	not modelled	99.9	14 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
91	c3d0kA_	Alignment	not modelled	99.9	16 PDB header: hydrolase Chain: A: PDB Molecule: putative poly(3-hydroxybutyrate) depolymerase lpqc; PDBTitle: crystal structure of the lpqc, poly(3-hydroxybutyrate) depolymerase2 from bordetella parapertussis
92	c3k2iA_	Alignment	not modelled	99.9	15 PDB header: hydrolase Chain: A: PDB Molecule: acyl-coenzyme a thioesterase 4; PDBTitle: human acyl-coenzyme a thioesterase 4
93	c4j7aB_	Alignment	not modelled	99.9	16 PDB header: hydrolase Chain: B: PDB Molecule: esterase; PDBTitle: crystal structure of est25 - a bacterial homolog of hormone-sensitive2 lipase from a metagenomic library
94	c6a6oA_	Alignment	not modelled	99.9	14 PDB header: hydrolase Chain: A: PDB Molecule: esterase/lipase-like protein; PDBTitle: crystal structure of acetyl ester-xyloside bifunctional hydrolase from2 caldicellulosiruptor lactoaceticus
95	c4krxB_	Alignment	not modelled	99.9	19 PDB header: hydrolase Chain: B: PDB Molecule: acetyl esterase; PDBTitle: structure of aes from e. coli
96	c4zrsA_	Alignment	not modelled	99.9	17 PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of a cloned feruloyl esterase from a soil2 metagenomic library
97	c4n5iX_	Alignment	not modelled	99.9	17 PDB header: hydrolase Chain: X: PDB Molecule: esterase/lipase; PDBTitle: crystal structure of a c8-c4 sn3 inhibited esterase b from2 lactobacillus rhamnosis
98	c4wy8A_	Alignment	not modelled	99.9	16 PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: structural analysis of two fungal esterases from rhizomucor miehei2 explaining their substrate specificity
99	c4ob7A_	Alignment	not modelled	99.8	15 PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase fold-3 domain protein; PDBTitle: crystal structure of esterase rppe mutant w187h
100	c4v2iB_	Alignment	not modelled	99.8	15 PDB header: hydrolase Chain: B: PDB Molecule: esterase/lipase; PDBTitle: biochemical characterization and structural analysis of a2 new cold-active and salt tolerant esterase from the marine3 bacterium thalassospira sp
101	c4uz2D_	Alignment	not modelled	99.8	30 PDB header: hydrolase Chain: D: PDB Molecule: cell wall-binding endopeptidase-related protein; PDBTitle: crystal structure of the n-terminal lysm domains from the putative2 nlpc/p60 d,l endopeptidase from t. thermophilus
102	c5l2pD_	Alignment	not modelled	99.8	17 PDB header: hydrolase Chain: D: PDB Molecule: arylesterase; PDBTitle: structure of arylesterase
103	c3og9A_	Alignment	not modelled	99.8	16 PDB header: hydrolase Chain: A: PDB Molecule: protein yahd a copper inducible hydrolase; PDBTitle: structure of yahd with malic acid
104	c5aooA_	Alignment	not modelled	99.8	15 PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: the structure of a novel thermophilic esterase from the planctomycetes2 species, thermogutta terrifontis, est2-propionate bound
105	c5jd4D_	Alignment	not modelled	99.8	18 PDB header: hydrolase Chain: D: PDB Molecule: lae6; PDBTitle: crystal structure of lae6 ser161ala mutant, an alpha/beta

					hydrolase2 enzyme from the metagenome of lake arreo, spain PDB header: hydrolase
106	c4h0cA_	Alignment	not modelled	99.8	16 Chain: A: PDB Molecule: phospholipase/carboxylesterase; PDBTitle: crystal structure of phospholipase/carboxylesterase from dyadobacter2 fermentans dsm 18053
107	c4xvcG_	Alignment	not modelled	99.8	14 PDB header: hydrolase Chain: G: PDB Molecule: esterase e40; PDBTitle: crystal structure of an esterase from the bacterial hormone-sensitive2 lipase (hsl) family
108	c5miiD_	Alignment	not modelled	99.8	14 PDB header: hydrolase Chain: D: PDB Molecule: carboxyl esterase 2; PDBTitle: crystal structure of carboxyl esterase 2 (tmelest2) from mycorrhizal2 fungus tuber melanosporum
109	c3d7rB_	Alignment	not modelled	99.8	11 PDB header: hydrolase Chain: B: PDB Molecule: esterase; PDBTitle: crystal structure of a putative esterase from staphylococcus aureus
110	d1jkma_	Alignment	not modelled	99.8	14 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
111	c6aaeA_	Alignment	not modelled	99.8	18 PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of chloramphenicol-metabolizaing enzyme estdl136
112	c2wirB_	Alignment	not modelled	99.8	15 PDB header: hydrolase Chain: B: PDB Molecule: alpha/beta hydrolase fold-3 domain protein; PDBTitle: hyperthermophilic esterase from the archeon pyrobaculum2 caldifontis
113	d1u4na_	Alignment	not modelled	99.8	17 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
114	c4ypvA_	Alignment	not modelled	99.8	16 PDB header: hydrolase Chain: A: PDB Molecule: est8; PDBTitle: high-resolution structure of a metagenome-derived esterase est8
115	c4fhzA_	Alignment	not modelled	99.8	21 PDB header: hydrolase Chain: A: PDB Molecule: phospholipase/carboxylesterase; PDBTitle: crystal structure of a carboxyl esterase at 2.0 angstrom resolution
116	c3hkB_	Alignment	not modelled	99.8	18 PDB header: hydrolase Chain: B: PDB Molecule: acyl-coenzyme a thioesterase 2, mitochondrial; PDBTitle: crystal structure of human mitochondrial acyl-coa thioesterase (acot2)
117	c3bjrA_	Alignment	not modelled	99.8	13 PDB header: hydrolase Chain: A: PDB Molecule: putative carboxylesterase; PDBTitle: crystal structure of a putative carboxylesterase (lp_1002) from2 lactobacillus plantarum wcfs1 at 2.09 a resolution
118	c3fakA_	Alignment	not modelled	99.8	12 PDB header: hydrolase Chain: A: PDB Molecule: esterase/lipase; PDBTitle: structural and functional analysis of a hormone-sensitive2 lipase like este5 from a metagenome library
119	c3wj2A_	Alignment	not modelled	99.8	14 PDB header: hydrolase Chain: A: PDB Molecule: carboxylesterase; PDBTitle: crystal structure of estfa (fe-lacking apo form)
120	c4q3kB_	Alignment	not modelled	99.8	21 PDB header: hydrolase Chain: B: PDB Molecule: mgs-m1; PDBTitle: crystal structure of mgs-m1, an alpha/beta hydrolase enzyme from a2 medee basin deep-sea metagenome library