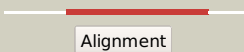

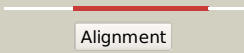



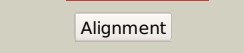



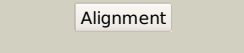

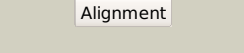



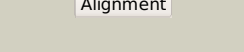

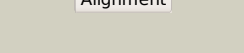

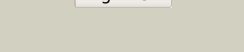



Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0220_(lipC)_262812_264023
 Date Tue Jul 23 14:50:27 BST 2019
 Unique Job ID 1c9951f508a21aca

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2zshA_	 Alignment		100.0	21	PDB header: hormone receptor Chain: A: PDB Molecule: probable gibberellin receptor gid11; PDBTitle: structural basis of gibberellin(ga3)-induced della2 recognition by the gibberellin receptor
2	c4zrsA_	 Alignment		100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of a cloned feruloyl esterase from a soil2 metagenomic library
3	c2o7vA_	 Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: cxe carboxylesterase; PDBTitle: carboxylesterase aecxe1 from actinidia eriantha covalently inhibited2 by paraoxon
4	c4c87A_	 Alignment		100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: esterase lpest1 from lactobacillus plantarum wcfs1
5	c3ed1E_	 Alignment		100.0	19	PDB header: hydrolase receptor Chain: E: PDB Molecule: gibberellin receptor gid1; PDBTitle: crystal structure of rice gid1 complexed with ga3
6	d1qe3a_	 Alignment		100.0	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like
7	c5jd5A_	 Alignment		100.0	25	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
8	c4fg5B_	 Alignment		100.0	19	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
9	c3d7rB_	 Alignment		100.0	12	PDB header: hydrolase Chain: B: PDB Molecule: esterase; PDBTitle: crystal structure of a putative esterase from staphylococcus aureus
10	c4bdtA_	 Alignment		100.0	22	PDB header: hydrolase/inhibitor Chain: A: PDB Molecule: acetylcholinesterase; PDBTitle: human acetylcholinesterase in complex with huprine w and fasciculin 2
11	c3ga7A_	 Alignment		100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: acetyl esterase; PDBTitle: 1.55 angstrom crystal structure of an acetyl esterase from salmonella2 typhimurium

12	c5x61A_	Alignment		100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: acetylcholinesterase; PDBTitle: crystal structure of acetylcholinesterase catalytic subunit of the2 malaria vector anopheles gambiae, 3.4 a
13	c3bxpA_	Alignment		100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: putative lipase/esterase; PDBTitle: crystal structure of a putative carboxylesterase (lp_2923) from2 lactobacillus plantarum wcfs1 at 1.70 a resolution
14	c2fj0A_	Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: carboxylic ester hydrolase; PDBTitle: crystal structure of juvenile hormone esterase from manduca sexta,2 with oftp covalently attached
15	c1f8uA_	Alignment		100.0	20	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
16	d1f8ua_	Alignment		100.0	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like
17	c5w1uA_	Alignment		100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: carboxylic ester hydrolase; PDBTitle: culex quinquefasciatus carboxylesterase b2
18	c4n5iX_	Alignment		100.0	20	PDB header: hydrolase Chain: X: PDB Molecule: esterase/lipase; PDBTitle: crystal structure of a c8-c4 sn3 inhibited esterase b from2 lactobacillus rhamosis
19	c2w6cX_	Alignment		100.0	18	PDB header: hydrolase Chain: X: PDB Molecule: acetylcholinesterase; PDBTitle: ache in complex with a bis-(-)-nor-meptazinol derivative
20	d2ha2a1	Alignment		100.0	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like
21	c3biwD_	Alignment	not modelled	100.0	17	PDB header: cell adhesion/cell adhesion Chain: D: PDB Molecule: neuroligin-1; PDBTitle: crystal structure of the neuroligin-1/neurexin-1beta synaptic adhesion2 complex
22	c4qwwA_	Alignment	not modelled	100.0	17	PDB header: hydrolase/immune system Chain: A: PDB Molecule: acetylcholinesterase; PDBTitle: crystal structure of the fab410-bfache complex
23	c4e14A_	Alignment	not modelled	100.0	19	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: kynurenine formamidase; PDBTitle: crystal structure of kynurenine formamidase conjugated with2 phenylmethylsulfonyl fluoride
24	d2h7ca1	Alignment	not modelled	100.0	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like
25	c6i2tC_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: C: PDB Molecule: cholinesterase; PDBTitle: cryoem reconstruction of full-length, fully-glycosylated human2 butyrylcholinesterase tetramer
26	d1ea5a_	Alignment	not modelled	100.0	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like
27	d1ukca_	Alignment	not modelled	100.0	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
28	c4v2iB_	Alignment	not modelled	100.0	18	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

29	d1p0ia_	Alignment	not modelled	100.0	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like
30	d1k4ya_	Alignment	not modelled	100.0	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like
31	c2pm8A_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: cholinesterase; PDBTitle: crystal structure of recombinant full length human2 butyrylcholinesterase
32	c4j7aB_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: esterase; PDBTitle: crystal structure of the est25 - a bacterial homolog of hormone-sensitive2 lipase from a metagenomic library
33	d1jkma_	Alignment	not modelled	100.0	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
34	c2ogsA_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: thermostable carboxylesterase est50; PDBTitle: crystal structure of the geobacillus stearothermophilus2 carboxylesterase est55 at ph 6.2
35	c5hc4A_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: lipolytic enzyme; PDBTitle: structure of esterase est22
36	d1dx4a_	Alignment	not modelled	100.0	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like
37	c3azqA_	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase; PDBTitle: crystal structure of puromycin hydrolase s511a mutant complexed with2 pgg
38	d1lfa_	Alignment	not modelled	100.0	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
39	c2ecfA_	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl peptidase iv; PDBTitle: crystal structure of dipeptidyl aminopeptidase iv from2 stenotrophomonas maltophilii
40	d2pbla1	Alignment	not modelled	100.0	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
41	c4q3kB_	Alignment	not modelled	100.0	19	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
42	c3bjrA_	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: putative carboxylesterase; PDBTitle: crystal structure of a putative carboxylesterase (lp_1002) from2 lactobacillus plantarum wcf51 at 2.09 a resolution
43	d1gz7a_	Alignment	not modelled	100.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
44	c5oljA_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl peptidase iv; PDBTitle: crystal structure of porphyromonas gingivalis dipeptidyl peptidase 4
45	c4q3oB_	Alignment	not modelled	100.0	20	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
46	d1crla_	Alignment	not modelled	100.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
47	c4be4A_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: sterol esterase; PDBTitle: closed conformation of o. piceae sterol esterase
48	c4krxB_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: acetyl esterase; PDBTitle: structure of aes from e. coli
49	c5jd4D_	Alignment	not modelled	100.0	20	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
50	c4q05A_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: esterase e25; PDBTitle: crystal structure of an esterase e25
51	c2hu7A_	Alignment	not modelled	100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: acylamino-acid-releasing enzyme; PDBTitle: binding of inhibitors by acylaminoacyl peptidase
52	c5a2gB_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: B: PDB Molecule: carboxylic ester hydrolase; PDBTitle: an esterase from anaerobic clostridium hathewayi can2 hydrolyze aliphatic aromatic polyesters
53	c5l8sD_	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: D: PDB Molecule: amino acyl peptidase; PDBTitle: the crystal structure of a cold-adapted acylaminoacyl peptidase2 reveals a novel quaternary architecture based on the arm-exchange3 mechanism
54	d1thga_	Alignment	not modelled	100.0	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
55	c5miiD_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: D: PDB Molecule: carboxyl esterase 2; PDBTitle: crystal structure of carboxyl esterase 2 (tmelest2) from

					mycorrhizal2 fungus tuber melanosporum
56	c1z68A_	Alignment	not modelled	100.0	21 PDB header: lyase Chain: A; PDB Molecule: fibroblast activation protein, alpha subunit; PDBTitle: crystal structure of human fibroblast activation protein alpha
57	d1f6wa_	Alignment	not modelled	100.0	20 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like
58	d2bcea_	Alignment	not modelled	100.0	18 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like
59	d1lzla_	Alignment	not modelled	100.0	18 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
60	c4hxgj_	Alignment	not modelled	100.0	19 PDB header: hydrolase Chain: J; PDB Molecule: putative uncharacterized protein ph0594; PDBTitle: pyrococcus horikoshii acylaminoacyl peptidase (orthorhombic crystal2 form)
61	c5yznA_	Alignment	not modelled	100.0	17 PDB header: hydrolase Chain: A; PDB Molecule: acyl-peptide hydrolase, putative; PDBTitle: crystal structure of s9 peptidase (active form) from deinococcus2 radiodurans r1
62	c4wy8A_	Alignment	not modelled	100.0	18 PDB header: hydrolase Chain: A; PDB Molecule: esterase; PDBTitle: structural analysis of two fungal esterases from rhizomucor miehei2 explaining their substrate specificity
63	c2xe4A_	Alignment	not modelled	100.0	13 PDB header: hydrolase/inhibitor Chain: A; PDB Molecule: oligopeptidase b; PDBTitle: structure of oligopeptidase b from leishmania major
64	d1jia_	Alignment	not modelled	100.0	23 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
65	c4wy5A_	Alignment	not modelled	100.0	21 PDB header: hydrolase Chain: A; PDB Molecule: esterase; PDBTitle: structural analysis of two fungal esterases from rhizomucor miehei2 explaining their substrate specificity
66	c2g5tA_	Alignment	not modelled	100.0	17 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
67	c5thmA_	Alignment	not modelled	100.0	21 PDB header: hydrolase Chain: A; PDB Molecule: esterase-6; PDBTitle: esterase-6 from drosophila melanogaster
68	c4hvtA_	Alignment	not modelled	100.0	15 PDB header: hydrolase Chain: A; PDB Molecule: post-proline cleaving enzyme; PDBTitle: structure of a post-proline cleaving enzyme from rickettsia typhi
69	c2qtbB_	Alignment	not modelled	100.0	17 PDB header: hydrolase Chain: B; PDB Molecule: dipeptidyl peptidase 4; PDBTitle: human dipeptidyl peptidase iv/cd26 in complex with a 4-aryl2 cyclohexylalanine inhibitor
70	c4bp9A_	Alignment	not modelled	100.0	16 PDB header: hydrolase Chain: A; PDB Molecule: oligopeptidase b; PDBTitle: oligopeptidase b from trypanosoma brucei with covalently bound2 antipain - closed form
71	c3hxB_	Alignment	not modelled	100.0	19 PDB header: hydrolase Chain: B; PDB Molecule: sugar hydrolase; PDBTitle: crystal structure of a sugar hydrolase (yeeb) from lactococcus lactis,2 northeast structural genomics consortium target kr108
72	c3dnmA_	Alignment	not modelled	100.0	17 PDB header: hydrolase Chain: A; PDB Molecule: esterase/lipase; PDBTitle: crystal structure hormone-sensitive lipase from a2 metagenome library
73	c4ob7A_	Alignment	not modelled	100.0	20 PDB header: hydrolase Chain: A; PDB Molecule: alpha/beta hydrolase fold-3 domain protein; PDBTitle: crystal structure of esterase rppe mutant w187h
74	c1qfmA_	Alignment	not modelled	100.0	16 PDB header: hydrolase Chain: A; PDB Molecule: protein (prolyl oligopeptidase); PDBTitle: prolyl oligopeptidase from porcine muscle
75	c6a6oA_	Alignment	not modelled	100.0	22 PDB header: hydrolase Chain: A; PDB Molecule: esterase/lipase-like protein; PDBTitle: crystal structure of acetyl ester-xyloside bifunctional hydrolase from2 caldicellulosiruptor lactoaceticus
76	c3qh4A_	Alignment	not modelled	100.0	20 PDB header: hydrolase Chain: A; PDB Molecule: esterase lipw; PDBTitle: crystal structure of esterase lipw from mycobacterium marinum
77	c4ypvA_	Alignment	not modelled	100.0	24 PDB header: hydrolase Chain: A; PDB Molecule: est8; PDBTitle: high-resolution structure of a metagenome-derived esterase est8
78	c5l2pD_	Alignment	not modelled	100.0	20 PDB header: hydrolase Chain: D; PDB Molecule: arylesterase; PDBTitle: structure of arylesterase
79	c3fakA_	Alignment	not modelled	100.0	17 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
80	c6eoqC_	Alignment	not modelled	100.0	22 PDB header: hydrolase Chain: C; PDB Molecule: dipeptidyl peptidase 9; PDBTitle: dpp9 - apo
81	c2eepA_	Alignment	not modelled	100.0	19 PDB header: hydrolase Chain: A; PDB Molecule: dipeptidyl aminopeptidase iv, putative; PDBTitle: prolyl tripeptidyl aminopeptidase complexed with an inhibitor

82	c2wirB	Alignment	not modelled	100.0	25	PDB header: hydrolase Chain: B: PDB Molecule: alpha/beta hydrolase fold-3 domain protein; PDBTitle: hyperthermophilic esterase from the archeon pyrobaculum2 calidifontis
83	c4xvcG	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: G: PDB Molecule: esterase e40; PDBTitle: crystal structure of an esterase from the bacterial hormone-sensitive2 lipase (hsl) family
84	c6eorD	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: D: PDB Molecule: dipeptidyl peptidase 9; PDBTitle: dpp9 - 1g244
85	c2bklB	Alignment	not modelled	100.0	19	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
86	c5t88B	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: B: PDB Molecule: prolyl endopeptidase; PDBTitle: prolyl oligopeptidase from pyrococcus furiosus
87	d1u4na	Alignment	not modelled	100.0	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
88	c4q1vA	Alignment	not modelled	100.0	21	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
89	c1xfdD	Alignment	not modelled	100.0	17	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
90	c6eosB	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: B: PDB Molecule: dipeptidyl peptidase 8; PDBTitle: dpp8 - apo, space group 19
91	c4wj1B	Alignment	not modelled	100.0	13	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
92	c6eotG	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: G: PDB Molecule: dipeptidyl peptidase 8; PDBTitle: dpp8 - slrflyeg, space group 19
93	d1vkha	Alignment	not modelled	100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Putative serine hydrolase Ydr428c
94	c5n4dA	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: prolyl oligopeptidase; PDBTitle: prolyl oligopeptidase b from galerina marginata bound to 25mer2 macrocyclization substrate - d661a mutant
95	c2c7bA	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: carboxylesterase; PDBTitle: the crystal structure of este1, a new thermophilic and2 thermostable carboxylesterase cloned from a metagenomic3 library
96	c3wj2A	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: carboxylesterase; PDBTitle: crystal structure of estfa (fe-lacking apo form)
97	c3iumA	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: prolyl endopeptidase; PDBTitle: appep_wtx opened state
98	c6aaeA	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of chloramphenicol-metabolizaing enzyme estdl136
99	c5txeA	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: atxe2; PDBTitle: atxe2 isopeptidase - s527a variant with astexin3-dc4 bound
100	c3aikB	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: 303aa long hypothetical esterase; PDBTitle: crystal structure of a hsl-like carboxylesterase from sulfolobus2 tokodaii
101	c1yr2A	Alignment	not modelled	100.0	19	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
102	c5jr1C	Alignment	not modelled	100.0	14	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)
103	c5uzwD	Alignment	not modelled	100.0	14	PDB header: lyase Chain: D: PDB Molecule: peptide cyclase 1; PDBTitle: pcy1 g696insertion variant in complex with follower peptide and the2 covalent inhibitor zpp
104	c2qruA	Alignment	not modelled	100.0	12	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
105	c4j0dB	Alignment	not modelled	100.0	26	PDB header: hydrolase Chain: B: PDB Molecule: tannase; PDBTitle: tannin acyl hydrolase from lactobacillus plantarum (cadmium)
106	c5aoaA	Alignment	not modelled	100.0	24	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
107	c5uw7B_	Alignment	not modelled	100.0	13	PDB header: lyase Chain: B: PDB Molecule: peptide cyclase 1; PDBTitle: pcy1 y481f variant in complex with follower peptide
108	d1qfma2	Alignment	not modelled	100.0	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Prolyl oligopeptidase, C-terminal domain
109	c3h04A_	Alignment	not modelled	100.0	17	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
110	c3h1kB_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: acyl-coenzyme a thioesterase 2, mitochondrial; PDBTitle: crystal structure of human mitochondrial acyl-coa thioesterase (acot2)
111	d1orva2	Alignment	not modelled	100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like
112	d2hu7a2	Alignment	not modelled	100.0	25	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acylamino-acid-releasing enzyme, C-terminal donain
113	d1xfda2	Alignment	not modelled	100.0	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like
114	c3doiA_	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of a thermostable esterase complex with2 paraoxon
115	c3k2iA_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: acyl-coenzyme a thioesterase 4; PDBTitle: human acyl-coenzyme a thioesterase 4
116	d2bgra2	Alignment	not modelled	100.0	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like
117	c5x6sB_	Alignment	not modelled	99.9	12	PDB header: hydrolase Chain: B: PDB Molecule: acetylxylyan esterase a; PDBTitle: acetyl xylan esterase from aspergillus awamori
118	c4eziA_	Alignment	not modelled	99.9	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
119	c3fnbB_	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: B: PDB Molecule: acylaminoacyl peptidase smu_737; PDBTitle: crystal structure of acylaminoacyl peptidase smu_737 from2 streptococcus mutans ua159
120	c3i6yA_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: esterase apc40077; PDBTitle: structure of an esterase from the oil-degrading bacterium oleispira2 antarctica