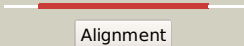

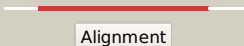

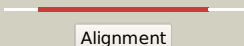







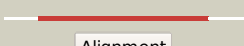











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2045c_(lipT)_2289693_2291228
Date	Mon Aug 5 13:25:15 BST 2019
Unique Job ID	fbe175949d1884ef

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4bdtA_	 Alignment		100.0	32	PDB header: hydrolase/inhibitor Chain: A: PDB Molecule: acetylcholinesterase; PDBTitle: human acetylcholinesterase in complex with huprine w and fasciculins 2
2	c6i2tC_	 Alignment		100.0	29	PDB header: hydrolase Chain: C: PDB Molecule: cholinesterase; PDBTitle: cryoem reconstruction of full-length, fully-glycosylated human2 butyrylcholinesterase tetramer
3	d2ha2a1	 Alignment		100.0	30	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like
4	c4fg5B_	 Alignment		100.0	31	PDB header: hydrolase Chain: B: PDB Molecule: e3 alpha-esterase-7 carboxylesterase; PDBTitle: crystal structure of the alpha-esterase-7 carboxylesterase, e3, from2 lucilia cuprina
5	c1f8uA_	 Alignment		100.0	31	PDB header: hydrolase/toxin Chain: A: PDB Molecule: acetylcholinesterase; PDBTitle: crystal structure of mutant e202q of human acetylcholinesterase2 complexed with green mamba venom peptide fasciculins-ii
6	d1f8ua_	 Alignment		100.0	31	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like
7	c5w1uA_	 Alignment		100.0	30	PDB header: hydrolase Chain: A: PDB Molecule: carboxylic ester hydrolase; PDBTitle: culex quinquefasciatus carboxylesterase b2
8	c4qwwA_	 Alignment		100.0	27	PDB header: hydrolase/immune system Chain: A: PDB Molecule: acetylcholinesterase; PDBTitle: crystal structure of the fab410-bfachs complex
9	d1p0ia_	 Alignment		100.0	29	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like
10	c5x61A_	 Alignment		100.0	33	PDB header: hydrolase Chain: A: PDB Molecule: acetylcholinesterase; PDBTitle: crystal structure of acetylcholinesterase catalytic subunit of the2 malaria vector anopheles gambiae, 3.4 a
11	d1ea5a_	 Alignment		100.0	27	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like

12	c2pm8A_	Alignment		100.0	29	PDB header: hydrolase Chain: A: PDB Molecule: cholinesterase; PDBTitle: crystal structure of recombinant full length human2 butyrylcholinesterase
13	d1dx4a_	Alignment		100.0	27	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like
14	c2w6cX_	Alignment		100.0	27	PDB header: hydrolase Chain: X: PDB Molecule: acetylcholinesterase; PDBTitle: ache in complex with a bis-(-)-nor-meptazinol derivative
15	c3biwD_	Alignment		100.0	30	PDB header: cell adhesion/cell adhesion Chain: D: PDB Molecule: neuroligin-1; PDBTitle: crystal structure of the neuroligin-1/neurexin-1beta synaptic adhesion2 complex
16	d1ukca_	Alignment		100.0	26	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
17	d2h7ca1	Alignment		100.0	33	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like
18	c2fj0A_	Alignment		100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: carboxylic ester hydrolase; PDBTitle: crystal structure of the juvenile hormone esterase from manduca sexta,2 with otfp covalently attached
19	c2ogsA_	Alignment		100.0	34	PDB header: hydrolase Chain: A: PDB Molecule: thermostable carboxylesterase est50; PDBTitle: crystal structure of the geobacillus stearotherophilus2 carboxylesterase est55 at ph 6.2
20	d1f6wa_	Alignment		100.0	29	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like
21	c5a2gB_	Alignment	not modelled	100.0	29	PDB header: hydrolase Chain: B: PDB Molecule: carboxylic ester hydrolase; PDBTitle: an esterase from anaerobic clostridium hathewayi can2 hydrolyze aliphatic aromatic polyesters
22	d1k4ya_	Alignment	not modelled	100.0	33	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like
23	d2bcea_	Alignment	not modelled	100.0	28	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like
24	d1qe3a_	Alignment	not modelled	100.0	36	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like
25	c4be4A_	Alignment	not modelled	100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: sterol esterase; PDBTitle: closed conformation of o. piceae sterol esterase
26	d1thga_	Alignment	not modelled	100.0	29	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
27	d1llfa_	Alignment	not modelled	100.0	27	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
28	d1gz7a_	Alignment	not modelled	100.0	26	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
29	d1crla_	Alignment	not modelled	100.0	26	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases

					Family:Fungal lipases
30	c5thmA	Alignment	not modelled	100.0	25 PDB header: hydrolase Chain: A: PDB Molecule: esterase-6; PDBTitle: esterase-6 from drosophila melanogaster
31	c4j0dB	Alignment	not modelled	100.0	30 PDB header: hydrolase Chain: B: PDB Molecule: tannase; PDBTitle: tannin acyl hydrolase from lactobacillus plantarum (cadmium)
32	c4c87A	Alignment	not modelled	99.9	18 PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: esterase lpest1 from lactobacillus plantarum wcf51
33	c2zshA	Alignment	not modelled	99.8	26 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
34	c4zrsA	Alignment	not modelled	99.8	29 PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of a cloned feruloyl esterase from a soil2 metagenomic library
35	c4n5iX	Alignment	not modelled	99.8	19 PDB header: hydrolase Chain: X: PDB Molecule: esterase/lipase; PDBTitle: crystal structure of a c8-c4 sn3 inhibited esterase b from2 lactobacillus rhamnosis
36	c4q3oB	Alignment	not modelled	99.7	16 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
37	c5hc4A	Alignment	not modelled	99.7	23 PDB header: hydrolase Chain: A: PDB Molecule: lipolytic enzyme; PDBTitle: structure of esterase est22
38	c3ed1E	Alignment	not modelled	99.7	24 PDB header: hydrolase receptor Chain: E: PDB Molecule: gibberellin receptor gid1; PDBTitle: crystal structure of rice gid1 complexed with ga3
39	c2o7vA	Alignment	not modelled	99.7	32 PDB header: hydrolase Chain: A: PDB Molecule: cxe carboxylesterase; PDBTitle: carboxylesterase aecxe1 from actinidia eriantha covalently inhibited2 by paraoxon
40	c3bxpA	Alignment	not modelled	99.7	20 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
41	c3ga7A	Alignment	not modelled	99.7	15 PDB header: hydrolase Chain: A: PDB Molecule: acetyl esterase; PDBTitle: 1.55 angstrom crystal structure of an acetyl esterase from salmonella2 typhimurium
42	c5miiD	Alignment	not modelled	99.6	23 PDB header: hydrolase Chain: D: PDB Molecule: carboxyl esterase 2; PDBTitle: crystal structure of carboxyl esterase 2 (tmelest2) from mycorrhizal2 fungus tuber melanosporum
43	d1jkma	Alignment	not modelled	99.6	21 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
44	c4j7aB	Alignment	not modelled	99.6	27 PDB header: hydrolase Chain: B: PDB Molecule: esterase; PDBTitle: crystal structure of est25 - a bacterial homolog of hormone-sensitive2 lipase from a metagenomic library
45	c3bjrA	Alignment	not modelled	99.6	27 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
46	c5jd5A	Alignment	not modelled	99.6	26 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
47	c4q05A	Alignment	not modelled	99.6	14 PDB header: hydrolase Chain: A: PDB Molecule: esterase e25; PDBTitle: crystal structure of an esterase e25
48	c4q3kB	Alignment	not modelled	99.6	20 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
49	d2pbla1	Alignment	not modelled	99.5	23 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
50	c5x6sB	Alignment	not modelled	99.5	17 PDB header: hydrolase Chain: B: PDB Molecule: acetylxytan esterase a; PDBTitle: acetyl xylan esterase from aspergillus awamori
51	d1jia	Alignment	not modelled	99.5	26 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
52	c3dnmA	Alignment	not modelled	99.5	17 PDB header: hydrolase Chain: A: PDB Molecule: esterase/lipase; PDBTitle: crystal structure hormone-sensitive lipase from a2 metagenome library
53	c5jd4D	Alignment	not modelled	99.5	27 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
54	c3doiA	Alignment	not modelled	99.5	18 PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of a thermostable esterase complex with2 paraoxon
55	c4wy5A	Alignment	not modelled	99.5	19 PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: structural analysis of two fungal esterases from

						rhizomucor miehei2 explaining their substrate specificity
56	c4krxB	Alignment	not modelled	99.5	21	PDB header: hydrolase Chain: B: PDB Molecule: acetyl esterase; PDBTitle: structure of aes from e. coli
57	c3d7rB	Alignment	not modelled	99.5	13	PDB header: hydrolase Chain: B: PDB Molecule: esterase; PDBTitle: crystal structure of a putative esterase from staphylococcus aureus
58	c2c7bA	Alignment	not modelled	99.5	18	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
59	c6a6oA	Alignment	not modelled	99.5	21	PDB header: hydrolase Chain: A: PDB Molecule: esterase/lipase-like protein; PDBTitle: crystal structure of acetyl ester-xyloside bifunctional hydrolase from2 caldicellulosiruptor lactoaceticus
60	c3hxB	Alignment	not modelled	99.4	24	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
61	c4e14A	Alignment	not modelled	99.4	22	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: kynurenine formamidase; PDBTitle: crystal structure of kynurenine formamidase conjugated with2 phenylmethylsulfonyl fluoride
62	c6eoqC	Alignment	not modelled	99.4	22	PDB header: hydrolase Chain: C: PDB Molecule: dipeptidyl peptidase 9; PDBTitle: dpp9 - apo
63	d1lzlA	Alignment	not modelled	99.4	25	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
64	c3azqA	Alignment	not modelled	99.4	17	PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase; PDBTitle: crystal structure of puromycin hydrolase s511a mutant complexed with2 pgg
65	c4wy8A	Alignment	not modelled	99.4	20	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: structural analysis of two fungal esterases from rhizomucor miehei2 explaining their substrate specificity
66	c4v2iB	Alignment	not modelled	99.4	19	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
67	c4ob7A	Alignment	not modelled	99.4	26	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase fold-3 domain protein; PDBTitle: crystal structure of esterase rppe mutant w187h
68	c6aaeA	Alignment	not modelled	99.4	19	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of chloramphenicol-metabolizing enzyme estdl136
69	c5l8sD	Alignment	not modelled	99.4	11	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
70	c4wjlB	Alignment	not modelled	99.4	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
71	c2qruA	Alignment	not modelled	99.4	20	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
72	c2bkIB	Alignment	not modelled	99.4	17	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
73	c5oljA	Alignment	not modelled	99.4	15	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl peptidase iv; PDBTitle: crystal structure of porphyromonas gingivalis dipeptidyl peptidase 4
74	c6eotG	Alignment	not modelled	99.4	23	PDB header: hydrolase Chain: G: PDB Molecule: dipeptidyl peptidase 8; PDBTitle: dpp8 - slrflyeg, space group 19
75	c2eepA	Alignment	not modelled	99.4	16	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl aminopeptidase iv, putative; PDBTitle: prolyl tripeptidyl aminopeptidase complexed with an inhibitor
76	c6eosB	Alignment	not modelled	99.4	22	PDB header: hydrolase Chain: B: PDB Molecule: dipeptidyl peptidase 8; PDBTitle: dpp8 - apo, space group 19
77	c6eorD	Alignment	not modelled	99.4	23	PDB header: hydrolase Chain: D: PDB Molecule: dipeptidyl peptidase 9; PDBTitle: dpp9 - 1g244
78	c3iumA	Alignment	not modelled	99.4	16	PDB header: hydrolase Chain: A: PDB Molecule: prolyl endopeptidase; PDBTitle: appep_wtx opened state
79	c2g5tA	Alignment	not modelled	99.4	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
80	c1z68A	Alignment	not modelled	99.4	21	PDB header: lyase Chain: A: PDB Molecule: fibroblast activation protein, alpha subunit; PDBTitle: crystal structure of human fibroblast activation protein alpha

81	c4ypvA	Alignment	not modelled	99.4	18	PDB header: hydrolase Chain: A: PDB Molecule: est8; PDBTitle: high-resolution structure of a metagenome-derived esterase est8
82	c5l2pD	Alignment	not modelled	99.4	23	PDB header: hydrolase Chain: D: PDB Molecule: arylesterase; PDBTitle: structure of arylesterase
83	c4xvcG	Alignment	not modelled	99.4	20	PDB header: hydrolase Chain: G: PDB Molecule: esterase e40; PDBTitle: crystal structure of an esterase from the bacterial hormone-sensitive2 lipase (hsl) family
84	c1xfdD	Alignment	not modelled	99.4	18	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
85	c2ecfA	Alignment	not modelled	99.4	19	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl peptidase iv; PDBTitle: crystal structure of dipeptidyl aminopeptidase iv from2 stenotrophomonas maltophilia
86	c2hu7A	Alignment	not modelled	99.3	20	PDB header: hydrolase Chain: A: PDB Molecule: acylamino-acid-releasing enzyme; PDBTitle: binding of inhibitors by acylaminoacyl peptidase
87	c4q1vA	Alignment	not modelled	99.3	17	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
88	c3fakA	Alignment	not modelled	99.3	20	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
89	d1vkha	Alignment	not modelled	99.3	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Putative serine hydrolase Ydr428c
90	d1qfma2	Alignment	not modelled	99.3	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Prolyl oligopeptidase, C-terminal domain
91	c4bp9A	Alignment	not modelled	99.3	20	PDB header: hydrolase Chain: A: PDB Molecule: oligopeptidase b; PDBTitle: oligopeptidase b from trypanosoma brucei with covalently bound2 antipain - closed form
92	c5t88B	Alignment	not modelled	99.3	15	PDB header: hydrolase Chain: B: PDB Molecule: prolyl endopeptidase; PDBTitle: prolyl oligopeptidase from pyrococcus furiosus
93	c1yr2A	Alignment	not modelled	99.3	18	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
94	c3qh4A	Alignment	not modelled	99.3	29	PDB header: hydrolase Chain: A: PDB Molecule: esterase lipw; PDBTitle: crystal structure of esterase lipw from mycobacterium marinum
95	c2qtbB	Alignment	not modelled	99.3	15	PDB header: hydrolase Chain: B: PDB Molecule: dipeptidyl peptidase 4; PDBTitle: human dipeptidyl peptidase iv/cd26 in complex with a 4-aryl2 cyclohexylalanine inhibitor
96	c5yznA	Alignment	not modelled	99.3	17	PDB header: hydrolase Chain: A: PDB Molecule: acyl-peptide hydrolase, putative; PDBTitle: crystal structure of s9 peptidase (active form) from deinococcus2 radiodurans r1
97	c4hxgJ	Alignment	not modelled	99.3	17	PDB header: hydrolase Chain: J: PDB Molecule: putative uncharacterized protein ph0594; PDBTitle: pyrococcus horikoshii acylaminoacyl peptidase (orthorhombic crystal2 form)
98	c5txeA	Alignment	not modelled	99.3	17	PDB header: hydrolase Chain: A: PDB Molecule: atxe2; PDBTitle: atxe2 isopeptidase - s527a variant with astexin3-dc4 bound
99	c4h18D	Alignment	not modelled	99.3	18	PDB header: transferase Chain: D: PDB Molecule: cmt1; PDBTitle: three dimensional structure of corynomycoloyl tranferase c
100	c5uw7B	Alignment	not modelled	99.3	20	PDB header: lyase Chain: B: PDB Molecule: peptide cyclase 1; PDBTitle: pcy1 y481f variant in complex with follower peptide
101	c5aooA	Alignment	not modelled	99.3	32	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
102	c3fcxA	Alignment	not modelled	99.3	15	PDB header: hydrolase Chain: A: PDB Molecule: s-formylglutathione hydrolase; PDBTitle: crystal structure of human esterase d
103	c3d0kA	Alignment	not modelled	99.3	17	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
104	c3h04A	Alignment	not modelled	99.3	20	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
105	c3aikB	Alignment	not modelled	99.3	16	PDB header: hydrolase Chain: B: PDB Molecule: 303aa long hypothetical esterase; PDBTitle: crystal structure of a hsl-like carboxylesterase from sulfolobus2 tokodaii

106	c2wirB_	Alignment	not modelled	99.2	20	PDB header: hydrolase Chain: B: PDB Molecule: alpha/beta hydrolase fold-3 domain protein; PDBTitle: hyperthermophilic esterase from the archeon pyrobaculum2 caldifontis
107	d1u4na_	Alignment	not modelled	99.2	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
108	c1qfmA_	Alignment	not modelled	99.2	18	PDB header: hydrolase Chain: A: PDB Molecule: protein (prolyl oligopeptidase); PDBTitle: prolyl oligopeptidase from porcine muscle
109	c2xe4A_	Alignment	not modelled	99.2	23	PDB header: hydrolase/inhibitor Chain: A: PDB Molecule: oligopeptidase b; PDBTitle: structure of oligopeptidase b from leishmania major
110	c5cxcC_	Alignment	not modelled	99.2	17	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
111	c5uzwD_	Alignment	not modelled	99.2	19	PDB header: lyase Chain: D: PDB Molecule: peptide cyclase 1; PDBTitle: pcy1 g696insertion variant in complex with follower peptide and the2 covalent inhibitor zpp
112	c5yalA_	Alignment	not modelled	99.2	21	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: ferulic acid esterase from streptomyces cinnamoneus at 1.5 a2 resolution
113	c3i6yA_	Alignment	not modelled	99.2	15	PDB header: hydrolase Chain: A: PDB Molecule: esterase apc40077; PDBTitle: structure of an esterase from the oil-degrading bacterium oleispira2 antarctica
114	c4hvtA_	Alignment	not modelled	99.2	16	PDB header: hydrolase Chain: A: PDB Molecule: post-proline cleaving enzyme; PDBTitle: structure of a post-proline cleaving enzyme from rickettsia typhi
115	d2bgra2	Alignment	not modelled	99.2	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like
116	c5n4dA_	Alignment	not modelled	99.2	20	PDB header: hydrolase Chain: A: PDB Molecule: prolyl oligopeptidase; PDBTitle: prolyl oligopeptidase b from galerina marginata bound to 25mer2 macrocyclization substrate - d661a mutant
117	d1sfra_	Alignment	not modelled	99.2	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Mycobacterial antigens
118	c3k2iA_	Alignment	not modelled	99.2	20	PDB header: hydrolase Chain: A: PDB Molecule: acyl-coenzyme a thioesterase 4; PDBTitle: human acyl-coenzyme a thioesterase 4
119	d1f0na_	Alignment	not modelled	99.2	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Mycobacterial antigens
120	d1wb4a1	Alignment	not modelled	99.1	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase