

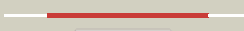





















Phyre2

Email	eduardo@epamig.br
Description	AcetylCholinesterase
Date	Thu Dec 31 01:04:51 GMT 2020
Unique Job ID	9a8664f55b7717b5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1dx4a_	 Alignment		100.0	91	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like
2	c6i2tC_	 Alignment		100.0	40	PDB header: hydrolase Chain: C: PDB Molecule: cholinesterase; PDBTitle: cryoem reconstruction of full-length, fully-glycosylated human2 butyrylcholinesterase tetramer
3	c4bdtA_	 Alignment		100.0	38	PDB header: hydrolase/inhibitor Chain: A: PDB Molecule: acetylcholinesterase; PDBTitle: human acetylcholinesterase in complex with huprine w and fasciculin 2
4	c5x61A_	 Alignment		100.0	40	PDB header: hydrolase Chain: A: PDB Molecule: acetylcholinesterase; PDBTitle: crystal structure of acetylcholinesterase catalytic subunit of the2 malaria vector anopheles gambiae, 3.4 a
5	d1ea5a_	 Alignment		100.0	40	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like
6	c2pm8A_	 Alignment		100.0	41	PDB header: hydrolase Chain: A: PDB Molecule: cholinesterase; PDBTitle: crystal structure of recombinant full length human2 butyrylcholinesterase
7	d2ha2a1	 Alignment		100.0	41	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like
8	c4qwwA_	 Alignment		100.0	42	PDB header: hydrolase/immune system Chain: A: PDB Molecule: acetylcholinesterase; PDBTitle: crystal structure of the fab410-bfache complex
9	d1p0ia_	 Alignment		100.0	41	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like
10	c2w6cX_	 Alignment		100.0	40	PDB header: hydrolase Chain: X: PDB Molecule: acetylcholinesterase; PDBTitle: ache in complex with a bis-(-)-nor-meptazinol derivative
11	c1f8uA_	 Alignment		100.0	40	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

12	d1f8ua_	Alignment		100.0	40	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like
13	c4fg5B_	Alignment		100.0	28	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
14	d2h7ca1	Alignment		100.0	29	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like
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	d1f6wa_	Alignment		100.0	31	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like
17	c2fj0A_	Alignment		100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: carboxylic ester hydrolase; PDBTitle: crystal structure of juvenile hormone esterase from manduca sexta,2 with otfp covalently attached
18	d2bcea_	Alignment		100.0	30	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like
19	c5w1uA_	Alignment		100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: carboxylic ester hydrolase; PDBTitle: culex quinquefasciatus carboxylesterase b2
20	d1k4ya_	Alignment		100.0	29	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like
21	d1ukca_	Alignment	not modelled	100.0	27	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
22	c2ogsA_	Alignment	not modelled	100.0	32	PDB header: hydrolase Chain: A: PDB Molecule: thermostable carboxylesterase est50; PDBTitle: crystal structure of the geobacillus stearothermophilus2 carboxylesterase est55 at ph 6.2
23	c5a2gB_	Alignment	not modelled	100.0	25	PDB header: hydrolase Chain: B: PDB Molecule: carboxylic ester hydrolase; PDBTitle: an esterase from anaerobic clostridium hathewayi can2 hydrolyze aliphatic aromatic polyesters
24	c4be4A_	Alignment	not modelled	100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: sterol esterase; PDBTitle: closed conformation of o. piceae sterol esterase
25	d1thga_	Alignment	not modelled	100.0	25	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
26	d1lifa_	Alignment	not modelled	100.0	26	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
27	d1qe3a_	Alignment	not modelled	100.0	34	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like
28	d1gz7a_	Alignment	not modelled	100.0	27	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	27 PDB header: hydrolase Chain: A: PDB Molecule: esterase-6; PDBTitle: esterase-6 from drosophila melanogaster
31	c6scjA	Alignment	not modelled	100.0	29 PDB header: hormone Chain: A: PDB Molecule: thyroglobulin; PDBTitle: the structure of human thyroglobulin
32	c4j0dB	Alignment	not modelled	100.0	23 PDB header: hydrolase Chain: B: PDB Molecule: tannase; PDBTitle: tannin acyl hydrolase from lactobacillus plantarum (cadmium)
33	c4c87A	Alignment	not modelled	99.9	18 PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: esterase lpest1 from lactobacillus plantarum wcfs1
34	c6rt8H	Alignment	not modelled	99.8	21 PDB header: hydrolase Chain: H: PDB Molecule: catharanthine synthase; PDBTitle: structure of catharanthine synthase - an alpha-beta hydrolase from2 catharanthus roseus with a cleaviminium intermediate bound
35	c2zshA	Alignment	not modelled	99.8	21 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
36	c6mlyA	Alignment	not modelled	99.8	19 PDB header: hydrolase Chain: A: PDB Molecule: bifunctional gh43-ce protein; PDBTitle: bifunctional gh43-ce bacteroides eggerthii, bacegg_01304
37	c4zrsA	Alignment	not modelled	99.8	27 PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of a cloned feruloyl esterase from a soil2 metagenomic library
38	c6mlyD	Alignment	not modelled	99.8	17 PDB header: hydrolase Chain: D: PDB Molecule: bifunctional gh43-ce protein; PDBTitle: bifunctional gh43-ce bacteroides eggerthii, bacegg_01304
39	c5hc4A	Alignment	not modelled	99.7	21 PDB header: hydrolase Chain: A: PDB Molecule: lipolytic enzyme; PDBTitle: structure of esterase est22
40	c4n5iX	Alignment	not modelled	99.7	25 PDB header: hydrolase Chain: X: PDB Molecule: esterase/lipase; PDBTitle: crystal structure of a c8-c4 sn3 inhibited esterase b from2 lactobacillus rhamnosis
41	c4q3oB	Alignment	not modelled	99.7	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
42	c2o7vA	Alignment	not modelled	99.7	30 PDB header: hydrolase Chain: A: PDB Molecule: cxe carboxylesterase; PDBTitle: carboxylesterase aecxe1 from actinidia eriantha covalently inhibited2 by paraoxon
43	c3ed1E	Alignment	not modelled	99.7	23 PDB header: hydrolase receptor Chain: E: PDB Molecule: gibberellin receptor gid1; PDBTitle: crystal structure of rice gid1 complexed with ga3
44	c3bxpA	Alignment	not modelled	99.6	22 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
45	c5miiD	Alignment	not modelled	99.6	19 PDB header: hydrolase Chain: D: PDB Molecule: carboxyl esterase 2; PDBTitle: crystal structure of carboxyl esterase 2 (tmelest2) from mycorrhizal2 fungus tuber melanosporum
46	c3ga7A	Alignment	not modelled	99.6	16 PDB header: hydrolase Chain: A: PDB Molecule: acetyl esterase; PDBTitle: 1.55 angstrom crystal structure of an acetyl esterase from salmonella2 typhimurium
47	d1jkma	Alignment	not modelled	99.6	17 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
48	c4j7aB	Alignment	not modelled	99.6	28 PDB header: hydrolase Chain: B: PDB Molecule: esterase; PDBTitle: crystal structure of est25 - a bacterial homolog of hormone-sensitive2 lipase from a metagenomic library
49	c5jd5A	Alignment	not modelled	99.6	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
50	c4q3kB	Alignment	not modelled	99.5	25 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
51	c6kd0A	Alignment	not modelled	99.5	24 PDB header: hydrolase Chain: A: PDB Molecule: vibrilactone cyclase; PDBTitle: crystal structure of vibrilactone cyclase
52	c3bjrA	Alignment	not modelled	99.5	24 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
53	d2pbla1	Alignment	not modelled	99.5	19 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
54	d1jja	Alignment	not modelled	99.5	23 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
55	c5x6sB	Alignment	not modelled	99.5	17 PDB header: hydrolase Chain: B: PDB Molecule: acetylxytan esterase a; PDBTitle: acetyl xylan esterase from aspergillus awamori

56	c4krxB_	Alignment	not modelled	99.5	19	PDB header: hydrolase Chain: B: PDB Molecule: acetyl esterase; PDBTitle: structure of aes from e. coli
57	c3doiA_	Alignment	not modelled	99.5	13	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of a thermostable esterase complex with2 paraoxon
58	c4q05A_	Alignment	not modelled	99.4	19	PDB header: hydrolase Chain: A: PDB Molecule: esterase e25; PDBTitle: crystal structure of an esterase e25
59	c6kf7D_	Alignment	not modelled	99.4	20	PDB header: hydrolase Chain: D: PDB Molecule: lipase; PDBTitle: microbial hormone-sensitive lipase e53 mutant s285g
60	c6kmoB_	Alignment	not modelled	99.4	24	PDB header: hydrolase Chain: B: PDB Molecule: alpha/beta hydrolase; PDBTitle: crystal structure of a novel esterase cinb from enterobacter asburiae
61	c3d7rB_	Alignment	not modelled	99.4	13	PDB header: hydrolase Chain: B: PDB Molecule: esterase; PDBTitle: crystal structure of a putative esterase from staphylococcus aureus
62	c4e14A_	Alignment	not modelled	99.4	15	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: kynurenine formamidase; PDBTitle: crystal structure of kynurenine formamidase conjugated with2 phenylmethylsulfonyl fluoride
63	c6ii2D_	Alignment	not modelled	99.4	14	PDB header: toxin Chain: D: PDB Molecule: putative rtx-toxin; PDBTitle: crystal structure of alpha-beta hydrolase (abh) and makes caterpillars2 floppy (mcf)-like effectors of vibrio vulnificus mo6-24/o
64	c6a6oA_	Alignment	not modelled	99.4	20	PDB header: hydrolase Chain: A: PDB Molecule: esterase/lipase-like protein; PDBTitle: crystal structure of acetyl ester-xyloside bifunctional hydrolase from2 caldicellulosiruptor lactoaceticus
65	c4v2iB_	Alignment	not modelled	99.4	17	PDB header: hydrolase Chain: B: PDB Molecule: esterase/lipase; PDBTitle: biochemical characterization and structural analysis of a new cold-2 active and salt tolerant esterase from the marine bacterium3 thalassospira sp
66	c2qruA_	Alignment	not modelled	99.4	19	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
67	c5jd4D_	Alignment	not modelled	99.4	25	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
68	d1lza_	Alignment	not modelled	99.4	27	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
69	c3dnmA_	Alignment	not modelled	99.4	27	PDB header: hydrolase Chain: A: PDB Molecule: esterase/lipase; PDBTitle: crystal structure hormone-sensitive lipase from a2 metagenome library
70	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
71	c6k34A_	Alignment	not modelled	99.4	21	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: crystal structure of dphmb1
72	c4ob7A_	Alignment	not modelled	99.4	18	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase fold-3 domain protein; PDBTitle: crystal structure of esterase rppe mutant w187h
73	c6qinA_	Alignment	not modelled	99.4	26	PDB header: hydrolase Chain: A: PDB Molecule: pmgl2; PDBTitle: crystal structure of the pmgl2 esterase from permafrost metagenomic2 library
74	c6k1tA_	Alignment	not modelled	99.4	23	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase fold family protein; PDBTitle: the structure of francisella virulence factor bioj
75	c6aaeA_	Alignment	not modelled	99.3	21	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of chloramphenicol-metabolizaing enzyme estdl136
76	c4wy5A_	Alignment	not modelled	99.3	24	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: structural analysis of two fungal esterases from rhizomucor miehei2 explaining their substrate specificity
77	c4wy8A_	Alignment	not modelled	99.3	24	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: structural analysis of two fungal esterases from rhizomucor miehei2 explaining their substrate specificity
78	c2c7bA_	Alignment	not modelled	99.3	28	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
79	d1vkha_	Alignment	not modelled	99.3	22	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Putative serine hydrolase Ydr428c
80	c6eorD_	Alignment	not modelled	99.3	24	PDB header: hydrolase Chain: D: PDB Molecule: dipeptidyl peptidase 9; PDBTitle: dpp9 - 1g244
81	c1z68A_	Alignment	not modelled	99.3	22	PDB header: lyase Chain: A: PDB Molecule: fibroblast activation protein, alpha subunit; PDBTitle: crystal structure of human fibroblast activation protein

					alpha
82	c4h18D_	Alignment	not modelled	99.3	18 PDB header: transferase Chain: D: PDB Molecule: cmt1; PDBTitle: three dimensional structure of corynomycoloyl tranferase c
83	c6nkfA_	Alignment	not modelled	99.3	24 PDB header: hydrolase Chain: A: PDB Molecule: lip_vut4, c3l; PDBTitle: crystal structure of the lipase lip_vut4 from goat rumen metagenome.
84	c6eotG_	Alignment	not modelled	99.3	20 PDB header: hydrolase Chain: G: PDB Molecule: dipeptidyl peptidase 8; PDBTitle: dpp8 - slrflyeg, space group 19
85	c3azqA_	Alignment	not modelled	99.3	20 PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase; PDBTitle: crystal structure of puromycin hydrolase s511a mutant complexed with2 pgg
86	c4wj1B_	Alignment	not modelled	99.3	20 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
87	c1xfdD_	Alignment	not modelled	99.3	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
88	c6eosB_	Alignment	not modelled	99.3	20 PDB header: hydrolase Chain: B: PDB Molecule: dipeptidyl peptidase 8; PDBTitle: dpp8 - apo, space group 19
89	c5l2pD_	Alignment	not modelled	99.3	31 PDB header: hydrolase Chain: D: PDB Molecule: arylesterase; PDBTitle: structure of arylesterase
90	c3qh4A_	Alignment	not modelled	99.3	25 PDB header: hydrolase Chain: A: PDB Molecule: esterase lipw; PDBTitle: crystal structure of esterase lipw from mycobacterium marinum
91	d1qfma2	Alignment	not modelled	99.3	20 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Prolyl oligopeptidase, C-terminal domain
92	c4xvcG_	Alignment	not modelled	99.3	31 PDB header: hydrolase Chain: G: PDB Molecule: esterase e40; PDBTitle: crystal structure of an esterase from the bacterial hormone-sensitive2 lipase (hsl) family
93	c3fakA_	Alignment	not modelled	99.3	24 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
94	c6eoqC_	Alignment	not modelled	99.3	22 PDB header: hydrolase Chain: C: PDB Molecule: dipeptidyl peptidase 9; PDBTitle: dpp9 - apo
95	c2eepA_	Alignment	not modelled	99.3	16 PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl aminopeptidase iv, putative; PDBTitle: prolyl tripeptidyl aminopeptidase complexed with an inhibitor
96	c2hu7A_	Alignment	not modelled	99.2	27 PDB header: hydrolase Chain: A: PDB Molecule: acylamino-acid-releasing enzyme; PDBTitle: binding of inhibitors by acylaminoacyl peptidase
97	c4ypvA_	Alignment	not modelled	99.2	23 PDB header: hydrolase Chain: A: PDB Molecule: est8; PDBTitle: high-resolution structure of a metagenome-derived esterase est8
98	c2qtbB_	Alignment	not modelled	99.2	20 PDB header: hydrolase Chain: B: PDB Molecule: dipeptidyl peptidase 4; PDBTitle: human dipeptidyl peptidase iv/cd26 in complex with a 4-aryl2 cyclohexylalanine inhibitor
99	c1yr2A_	Alignment	not modelled	99.2	21 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
100	c3d0kA_	Alignment	not modelled	99.2	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
101	c5aoaA_	Alignment	not modelled	99.2	21 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	c4q1vA_	Alignment	not modelled	99.2	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
103	c3h04A_	Alignment	not modelled	99.2	22 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
104	c3aikB_	Alignment	not modelled	99.2	22 PDB header: hydrolase Chain: B: PDB Molecule: 303aa long hypothetical esterase; PDBTitle: crystal structure of a hsl-like carboxylesterase from sulfolobus2 tokodaii
105	c5oljA_	Alignment	not modelled	99.2	17 PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl peptidase iv; PDBTitle: crystal structure of porphyromonas gingivalis dipeptidyl peptidase 4
106	d1u4na_	Alignment	not modelled	99.2	26 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases

					Family: Carboxylesterase
107	c6ii2C_	Alignment	not modelled	99.2	16 PDB header: toxin Chain: C: PDB Molecule: putative rtx-toxin; PDBTitle: crystal structure of alpha-beta hydrolase (abh) and makes caterpillars2 floppy (mcf)-like effectors of vibrio vulnificus mo6-24/o
108	d1f0na_	Alignment	not modelled	99.2	15 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Mycobacterial antigens
109	c2ecfA_	Alignment	not modelled	99.2	22 PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl peptidase iv; PDBTitle: crystal structure of dipeptidyl aminopeptidase iv from2 stenotrophomonas maltophilia
110	c2g5tA_	Alignment	not modelled	99.2	22 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
111	c3fcxA_	Alignment	not modelled	99.2	17 PDB header: hydrolase Chain: A: PDB Molecule: s-formylglutathione hydrolase; PDBTitle: crystal structure of human esterase d
112	c4bp9A_	Alignment	not modelled	99.2	20 PDB header: hydrolase Chain: A: PDB Molecule: oligopeptidase b; PDBTitle: oligopeptidase b from trypanosoma brucei with covalently bound2 antipain - closed form
113	c2wirB_	Alignment	not modelled	99.2	23 PDB header: hydrolase Chain: B: PDB Molecule: alpha/beta hydrolase fold-3 domain protein; PDBTitle: hyperthermophilic esterase from the archeon pyrobaculum2 calidifontis
114	c5txeA_	Alignment	not modelled	99.2	19 PDB header: hydrolase Chain: A: PDB Molecule: atxe2; PDBTitle: atxe2 isopeptidase - s527a variant with astexin3-dc4 bound
115	c5l8sD_	Alignment	not modelled	99.1	14 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
116	c2bklB_	Alignment	not modelled	99.1	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
117	d1wb4a1	Alignment	not modelled	99.1	20 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
118	d2bgra2	Alignment	not modelled	99.1	18 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like
119	d1sfra_	Alignment	not modelled	99.1	15 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Mycobacterial antigens
120	c5yznA_	Alignment	not modelled	99.1	18 PDB header: hydrolase Chain: A: PDB Molecule: acyl-peptide hydrolase, putative; PDBTitle: crystal structure of s9 peptidase (active form) from deinococcus2 radiodurans r1