



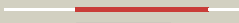




























Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	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
2	c1wb4A_	 Alignment		100.0	17	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
3	d1jjfa_	 Alignment		100.0	31	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
4	d3c8da2	 Alignment		100.0	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
5	d1pvia_	 Alignment		100.0	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hypothetical esterase YJL068C
6	d1wb4a1	 Alignment		100.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
7	c3i6yA_	 Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: esterase apc40077; PDBTitle: structure of an esterase from the oil-degrading bacterium oleispira2 antarctica
8	c3fcxA_	 Alignment		100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: s-formylglutathione hydrolase; PDBTitle: crystal structure of human esterase d
9	c3e4dD_	 Alignment		100.0	19	PDB header: hydrolase Chain: D: PDB Molecule: esterase d; PDBTitle: structural and kinetic study of an s-formylglutathione2 hydrolase from agrobacterium tumefaciens
10	c3ls2D_	 Alignment		100.0	19	PDB header: hydrolase Chain: D: PDB Molecule: s-formylglutathione hydrolase; PDBTitle: crystal structure of an s-formylglutathione hydrolase from2 pseudoalteromonas haloplanktis tac125
11	d1dqza_	 Alignment		100.0	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Mycobacterial antigens

12	c2ecfA_	Alignment		100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl peptidase iv; PDBTitle: crystal structure of dipeptidyl aminopeptidase iv from2 stenotrophomonas maltophilia
13	c3gffA_	Alignment		100.0	16	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
14	d1sfra_	Alignment		100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Mycobacterial antigens
15	d1f0na_	Alignment		100.0	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Mycobacterial antigens
16	d1r88a_	Alignment		100.0	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Mycobacterial antigens
17	c2uz0B_	Alignment		100.0	22	PDB header: hydrolase Chain: B: PDB Molecule: tributylin esterase; PDBTitle: the crystal crystal structure of the esta protein, a2 virulence factor esta protein from streptococcus pneumonia
18	c3doiA_	Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of a thermostable esterase complex with2 paraoxon
19	c2eepA_	Alignment		100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl aminopeptidase iv, putative; PDBTitle: prolyl tripeptidyl aminopeptidase complexed with an inhibitor
20	c3azqA_	Alignment		100.0	12	PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase; PDBTitle: crystal structure of puromycin hydrolase s511a mutant complexed with2 pgg
21	c1z68A_	Alignment	not modelled	100.0	16	PDB header: lyase Chain: A: PDB Molecule: fibroblast activation protein, alpha subunit; PDBTitle: crystal structure of human fibroblast activation protein alpha
22	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
23	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)2 complexed with cyanopyrrolidine (c5-pro-pro) inhibitor 21ag
24	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
25	c1qfma_	Alignment	not modelled	100.0	9	PDB header: hydrolase Chain: A: PDB Molecule: protein (prolyl oligopeptidase); PDBTitle: prolyl oligopeptidase from porcine muscle
26	c2qm0B_	Alignment	not modelled	100.0	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: bes; PDBTitle: crystal structure of bes protein from bacillus cereus
27	d2gzsa1	Alignment	not modelled	100.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: IroE-like
28	c1xfdD_	Alignment	not modelled	100.0	14	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
29	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
30	c3iumA_	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: A: PDB Molecule: prolyl endopeptidase; PDBTitle: appep_wtx opened state
31	c2xe4A_	Alignment	not modelled	100.0	15	PDB header: hydrolase/inhibitor Chain: A: PDB Molecule: oligopeptidase b; PDBTitle: structure of oligopeptidase b from leishmania major
32	c1yr2A_	Alignment	not modelled	100.0	12	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
33	d1qfma2	Alignment	not modelled	99.9	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Prolyl oligopeptidase, C-terminal domain
34	d1orva2	Alignment	not modelled	99.9	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like
35	d2bgra2	Alignment	not modelled	99.9	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like
36	d3b5ea1	Alignment	not modelled	99.9	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
37	d2h1ia1	Alignment	not modelled	99.9	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
38	c3bxaA_	Alignment	not modelled	99.9	14	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
39	c2o7vA_	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: cxe carboxylesterase; PDBTitle: carboxylesterase aecxe1 from actinidia eriantha covalently inhibited2 by paraoxon
40	c3d0kA_	Alignment	not modelled	99.9	19	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
41	d2hu7a2	Alignment	not modelled	99.9	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acylamino-acid-releasing enzyme, C-terminal donain
42	d1xfda2	Alignment	not modelled	99.9	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like
43	c3og9A_	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: protein yahd a copper inducible hydrolase; PDBTitle: structure of yahd with malic acid
44	c3u0vA_	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: lysophospholipase-like protein 1; PDBTitle: crystal structure analysis of human lyplal1
45	c2h1ia_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: carboxylesterase; PDBTitle: crystal structure of the bacillus cereus carboxylesterase
46	c3ed1E_	Alignment	not modelled	99.9	12	PDB header: hydrolase receptor Chain: E: PDB Molecule: gibberellin receptor gid1; PDBTitle: crystal structure of rice gid1 complexed with ga3
47	c2zsha_	Alignment	not modelled	99.8	16	PDB header: hormone receptor Chain: A: PDB Molecule: probable gibberellin receptor gid111; PDBTitle: structural basis of gibberellin(ga3)-induced della2 recognition by the gibberellin receptor
48	c3cn9B_	Alignment	not modelled	99.8	14	PDB header: hydrolase Chain: B: PDB Molecule: carboxylesterase; PDBTitle: crystal structure analysis of the carboxylesterase pa3859 from2 pseudomonas aeruginosa pao1- orthorhombic crystal form
49	c3ga7A_	Alignment	not modelled	99.8	12	PDB header: hydrolase Chain: A: PDB Molecule: acetyl esterase; PDBTitle: 1.55 angstrom crystal structure of an acetyl esterase from salmonella2 typhimurium
50	c3k2ia_	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: A: PDB Molecule: acyl-coenzyme a thioesterase 4; PDBTitle: human acyl-coenzyme a thioesterase 4
51	c2r8ba_	Alignment	not modelled	99.8	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atu2452; PDBTitle: the crystal structure of the protein atu2452 of unknown function from2 agrobacterium tumefaciens str. c58
52	c3f67A_	Alignment	not modelled	99.8	13	PDB header: hydrolase Chain: A: PDB Molecule: putative diene lactone hydrolase; PDBTitle: crystal structure of putative diene lactone hydrolase from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
53	d1fj2a_	Alignment	not modelled	99.8	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
54	d2r8ba1	Alignment	not modelled	99.8	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases

					Family: Carboxylesterase/thioesterase 1
55	d1jkma_	Alignment	not modelled	99.8	16 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
56	d1dina_	Alignment	not modelled	99.8	15 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Dienelactone hydrolase
57	c3hlkB_	Alignment	not modelled	99.8	19 PDB header: hydrolase Chain: B: PDB Molecule: acyl-coenzyme a thioesterase 2, mitochondrial; PDBTitle: crystal structure of human mitochondrial acyl-coa2 thioesterase (acot2)
58	c2o2gA_	Alignment	not modelled	99.8	21 PDB header: hydrolase Chain: A: PDB Molecule: dienelactone hydrolase; PDBTitle: crystal structure of dienelactone hydrolase (yp_324580.1) from2 anabaena variabilis atcc 29413 at 1.92 a resolution
59	d1lza_	Alignment	not modelled	99.8	16 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
60	d1vlqa_	Alignment	not modelled	99.8	16 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetyl xylan esterase-like
61	d1auoa_	Alignment	not modelled	99.8	16 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
62	d1u4na_	Alignment	not modelled	99.8	17 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
63	d2jbwa1	Alignment	not modelled	99.8	17 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: 2,6-dihydropseudooxynicotine hydrolase-like
64	c2jbwB_	Alignment	not modelled	99.8	16 PDB header: hydrolase Chain: B: PDB Molecule: 2,6-dihydroxy-pseudo-oxynicotine hydrolase; PDBTitle: crystal structure of the 2,6-dihydroxy-pseudo-oxynicotine2 hydrolase.
65	c3fnbB_	Alignment	not modelled	99.8	13 PDB header: hydrolase Chain: B: PDB Molecule: acylaminoacyl peptidase smu_737; PDBTitle: crystal structure of acylaminoacyl peptidase smu_737 from2 streptococcus mutans ua159
66	c2c7bA_	Alignment	not modelled	99.7	19 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
67	c3bjrA_	Alignment	not modelled	99.7	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
68	c2wirB_	Alignment	not modelled	99.7	20 PDB header: hydrolase Chain: B: PDB Molecule: alpha/beta hydrolase fold-3 domain protein; PDBTitle: hyperthermophilic esterase from the archeon pyrobaculum2 calidifontis
69	d1ufoa_	Alignment	not modelled	99.7	15 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hypothetical protein TT1662
70	d1l7aa_	Alignment	not modelled	99.7	14 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetyl xylan esterase-like
71	c3aikB_	Alignment	not modelled	99.7	18 PDB header: hydrolase Chain: B: PDB Molecule: 303aa long hypothetical esterase; PDBTitle: crystal structure of a hsl-like carboxylesterase from sulfobus2 tokodaii
72	c2fx5A_	Alignment	not modelled	99.7	16 PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: pseudomonas mendocina lipase
73	d1jjia_	Alignment	not modelled	99.7	17 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
74	c3ksrA_	Alignment	not modelled	99.7	20 PDB header: hydrolase Chain: A: PDB Molecule: putative serine hydrolase; PDBTitle: crystal structure of a putative serine hydrolase (xcc3885) from2 xanthomonas campestris pv. campestris at 2.69 a resolution
75	c3mveB_	Alignment	not modelled	99.7	9 PDB header: lyase Chain: B: PDB Molecule: upf0255 protein vv1_0328; PDBTitle: crystal structure of a novel pyruvate decarboxylase
76	c3hxB_	Alignment	not modelled	99.7	11 PDB header: hydrolase Chain: B: PDB Molecule: sugar hydrolase; PDBTitle: crystal structure of a sugar hydrolase (yeeb) from2 lactococcus lactis, northeast structural genomics3 consortium target kr108
77	c2wtmC_	Alignment	not modelled	99.7	17 PDB header: hydrolase Chain: C: PDB Molecule: est1e; PDBTitle: est1e from butyrivibrio proteoclasticus
78	c3qh4A_	Alignment	not modelled	99.7	16 PDB header: hydrolase Chain: A: PDB Molecule: esterase lipw; PDBTitle: crystal structure of esterase lipw from mycobacterium marinum
79	c3fakA_	Alignment	not modelled	99.7	16 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
					PDB header: structural genomics, unknown function

80	c2i3dA_	Alignment	not modelled	99.7	15	Chain: A: PDB Molecule: hypothetical protein atu1826; PDBTitle: crystal structure of protein of unknown function atu1826, a putative2 alpha/beta hydrolase from agrobacterium tumefaciens
81	d2i3da1	Alignment	not modelled	99.7	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Atu1826-like
82	c3fcyB_	Alignment	not modelled	99.7	14	PDB header: hydrolase Chain: B: PDB Molecule: xylan esterase 1; PDBTitle: crystal structure of acetyl xylan esterase 1 from2 thermoanaerobacterium sp. jw/sl ys485
83	d1jfra_	Alignment	not modelled	99.7	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Lipase
84	c3h04A_	Alignment	not modelled	99.7	14	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
85	c3h2iA_	Alignment	not modelled	99.7	19	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of n228w mutant of the rice cell wall2 degrading esterase lipa from xanthomonas oryzae
86	c2hdwB_	Alignment	not modelled	99.7	14	PDB header: hydrolase Chain: B: PDB Molecule: hypothetical protein pa2218; PDBTitle: crystal structure of hypothetical protein pa2218 from pseudomonas2 aeruginosa
87	c2qruA_	Alignment	not modelled	99.7	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an alpha/beta hydrolase superfamily protein from2 enterococcus faecalis
88	d1ju3a2	Alignment	not modelled	99.7	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PepX catalytic domain-like
89	d2fuka1	Alignment	not modelled	99.7	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Atu1826-like
90	d1vkha_	Alignment	not modelled	99.7	11	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Putative serine hydrolase Ydr428c
91	c3d7rB_	Alignment	not modelled	99.7	15	PDB header: hydrolase Chain: B: PDB Molecule: esterase; PDBTitle: crystal structure of a putative esterase from staphylococcus aureus
92	c2b9vB_	Alignment	not modelled	99.6	12	PDB header: hydrolase Chain: B: PDB Molecule: alpha-amino acid ester hydrolase; PDBTitle: acetobacter turbidans alpha-amino acid ester hydrolase
93	d1hlga_	Alignment	not modelled	99.6	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Gastric lipase
94	c3trdA_	Alignment	not modelled	99.6	15	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase; PDBTitle: structure of an alpha-beta serine hydrolase homologue from coxiella2 burnetii
95	c3dnmA_	Alignment	not modelled	99.6	17	PDB header: hydrolase Chain: A: PDB Molecule: esterase/lipase; PDBTitle: crystal structure hormone-sensitive lipase from a2 metagenome library
96	d2b9va2	Alignment	not modelled	99.6	10	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PepX catalytic domain-like
97	c1l7qA_	Alignment	not modelled	99.6	13	PDB header: hydrolase Chain: A: PDB Molecule: cocaine esterase; PDBTitle: ser117ala mutant of bacterial cocaine esterase coce
98	c3llcA_	Alignment	not modelled	99.6	14	PDB header: hydrolase Chain: A: PDB Molecule: putative hydrolase; PDBTitle: crystal structure of putative hydrolase (yp_002548124.1) from2 agrobacterium vitis s4 at 1.80 a resolution
99	c2veoA_	Alignment	not modelled	99.6	18	PDB header: hydrolase Chain: A: PDB Molecule: lipase a; PDBTitle: x-ray structure of candida antarctica lipase a in its2 closed state.
100	c3qm1A_	Alignment	not modelled	99.6	17	PDB header: hydrolase Chain: A: PDB Molecule: cinnamoyl esterase; PDBTitle: crystal structure of the lactobacillus johnsonii cinnamoyl esterase2 lj0536 s106a mutant in complex with ethylferulate, form ii
101	d1mpxa2	Alignment	not modelled	99.6	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PepX catalytic domain-like
102	c2y6vB_	Alignment	not modelled	99.6	19	PDB header: hydrolase Chain: B: PDB Molecule: peroxisomal membrane protein lpx1; PDBTitle: peroxisomal alpha-beta-hydrolase lpx1 (yor084w) from2 saccharomyces cerevisiae (crystal form i)
103	d2b61a1	Alignment	not modelled	99.5	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
104	d2pbla1	Alignment	not modelled	99.5	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
105	d1k8qa_	Alignment	not modelled	99.5	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Gastric lipase
106	c3iliA_	Alignment	not modelled	99.5	15	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: x-ray crystal structure of homoserine o-acetyltransferase

					from2 bacillus anthracis
107	d2d81a1	Alignment	not modelled	99.5	21 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PHB depolymerase-like
108	c2vavL	Alignment	not modelled	99.5	11 PDB header: transferase Chain: L: PDB Molecule: acetyl-coa--deacetylcephalosporin c PDBTitle: crystal structure of deacetylcephalosporin c2 acetyltransferase (dac-soak)
109	c2qmQA	Alignment	not modelled	99.5	15 PDB header: signaling protein Chain: A: PDB Molecule: protein ndrg2; PDBTitle: crystal structure of a n-myc downstream regulated 2 protein (ndrg2,2 syl d, ndr2, ai182517, au040374) from mus musculus at 1.70 a3 resolution
110	d2pl5a1	Alignment	not modelled	99.5	17 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
111	c3jw8A	Alignment	not modelled	99.5	20 PDB header: hydrolase Chain: A: PDB Molecule: mgII protein; PDBTitle: crystal structure of human mono-glyceride lipase
112	c3hjuB	Alignment	not modelled	99.5	20 PDB header: hydrolase Chain: B: PDB Molecule: monoglyceride lipase; PDBTitle: crystal structure of human monoglyceride lipase
113	c3g8yA	Alignment	not modelled	99.4	15 PDB header: hydrolase Chain: A: PDB Molecule: susd/ragb-associated esterase-like protein; PDBTitle: crystal structure of a putative hydrolase (bvU_4111) from bacteroides2 vulgatus atcc 8482 at 1.90 a resolution
114	dluxoa	Alignment	not modelled	99.4	11 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: YdeN-like
115	dlimja	Alignment	not modelled	99.4	13 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Ccg1/TafII250-interacting factor B (Cib)
116	c3nuZF	Alignment	not modelled	99.4	14 PDB header: hydrolase Chain: F: PDB Molecule: putative acetyl xylan esterase; PDBTitle: crystal structure of a putative acetyl xylan esterase (bf1801) from2 bacteroides fragilis nctc 9343 at 2.30 a resolution
117	d2vata1	Alignment	not modelled	99.4	12 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
118	c1mpxB	Alignment	not modelled	99.4	14 PDB header: hydrolase Chain: B: PDB Molecule: alpha-amino acid ester hydrolase; PDBTitle: alpha-amino acid ester hydrolase labeled with selenomethionine
119	c3ib3A	Alignment	not modelled	99.4	10 PDB header: hydrolase Chain: A: PDB Molecule: coce/nond family hydrolase; PDBTitle: crystal structure of sacol2612 - coce/nond family hydrolase from2 staphylococcus aureus
120	c1cr6A	Alignment	not modelled	99.4	21 PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor