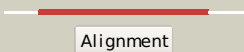

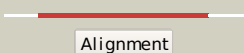

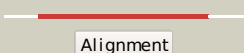

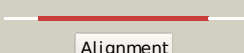



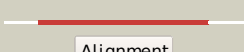

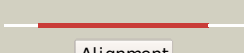

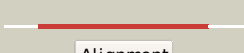









#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3e4dD_	 Alignment		100.0	46	PDB header: hydrolase Chain: D: PDB Molecule: esterase d; PDBTitle: structural and kinetic study of an s-formylglutathione2 hydrolase from agrobacterium tumefaciens
2	d1pv1a_	 Alignment		100.0	46	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hypothetical esterase YJL068C
3	c3ls2D_	 Alignment		100.0	56	PDB header: hydrolase Chain: D: PDB Molecule: s-formylglutathione hydrolase; PDBTitle: crystal structure of an s-formylglutathione hydrolase from2 pseudoalteromonas haloplanktis tac125
4	c3i6yA_	 Alignment		100.0	61	PDB header: hydrolase Chain: A: PDB Molecule: esterase apc40077; PDBTitle: structure of an esterase from the oil-degrading bacterium oleispira2 antarctica
5	c3fcxA_	 Alignment		100.0	52	PDB header: hydrolase Chain: A: PDB Molecule: s-formylglutathione hydrolase; PDBTitle: crystal structure of human esterase d
6	d1dqza_	 Alignment		100.0	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Mycobacterial antigens
7	c1z68A_	 Alignment		100.0	15	PDB header: lyase Chain: A: PDB Molecule: fibroblast activation protein, alpha subunit; PDBTitle: crystal structure of human fibroblast activation protein alpha
8	c2ecfA_	 Alignment		100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl peptidase iv; PDBTitle: crystal structure of dipeptidyl aminopeptidase iv from2 stenotrophomonas maltophilia
9	c2qtbB_	 Alignment		100.0	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
10	d1jjfa_	 Alignment		100.0	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
11	d1f0na_	 Alignment		100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Mycobacterial antigens

12	d1sfra_	Alignment		100.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Mycobacterial antigens
13	c2g5tA_	Alignment		100.0	15	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
14	c2eepA_	Alignment		100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl aminopeptidase iv, putative; PDBTitle: prolyl tripeptidyl aminopeptidase complexed with an inhibitor
15	d3c8da2	Alignment		100.0	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
16	c2uz0B_	Alignment		100.0	18	PDB header: hydrolase Chain: B: PDB Molecule: tributyrin esterase; PDBTitle: the crystal crystal structure of the esta protein, a2 virulence factor esta protein from streptococcus pneumonia
17	c3azqA_	Alignment		100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase; PDBTitle: crystal structure of puromycin hydrolase s511a mutant complexed with2 pgg
18	d1r88a_	Alignment		100.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Mycobacterial antigens
19	c1qfmA_	Alignment		100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: protein (prolyl oligopeptidase); PDBTitle: prolyl oligopeptidase from porcine muscle
20	c1wb4A_	Alignment		100.0	15	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
21	c3c8dA_	Alignment	not modelled	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
22	c2xe4A_	Alignment	not modelled	100.0	14	PDB header: hydrolase/inhibitor Chain: A: PDB Molecule: oligopeptidase b; PDBTitle: structure of oligopeptidase b from leishmania major
23	c2bklB_	Alignment	not modelled	100.0	15	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
24	c2hu7A_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: acylamino-acid-releasing enzyme; PDBTitle: binding of inhibitors by acylaminoacyl peptidase
25	c1xfdB_	Alignment	not modelled	100.0	16	PDB header: membrane protein Chain: D: PDB Molecule: dipeptidyl aminopeptidase-like protein 6; PDBTitle: structure of a human a-type potassium channel accelerating factor2 dpdx, a member of the dipeptidyl aminopeptidase family
26	c3iumA_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: prolyl endopeptidase; PDBTitle: appep_wtx opened state
27	d1wb4a1	Alignment	not modelled	100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
						PDB header: hydrolase Chain: A: PDB Molecule: esterase

28	c3doiA_	Alignment	not modelled	100.0	13	Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of a thermostable esterase complex with2 paraoxon
29	c1yr2A_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: prolyl oligopeptidase; PDBTitle: structural and mechanistic analysis of two prolyl endopeptidases: role2 of inter-domain dynamics in catalysis and specificity
30	c3gffA_	Alignment	not modelled	100.0	18	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
31	c2qm0B_	Alignment	not modelled	100.0	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: bes; PDBTitle: crystal structure of bes protein from bacillus cereus
32	d1orva2	Alignment	not modelled	100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like
33	d1qfma2	Alignment	not modelled	100.0	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Prolyl oligopeptidase, C-terminal domain
34	d2bgra2	Alignment	not modelled	100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like
35	d2gzsa1	Alignment	not modelled	100.0	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: IroE-like
36	c3bxaA_	Alignment	not modelled	100.0	11	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
37	c3ed1E_	Alignment	not modelled	100.0	15	PDB header: hydrolase receptor Chain: E: PDB Molecule: gibberellin receptor gid1; PDBTitle: crystal structure of rice gid1 complexed with ga3
38	d2hu7a2	Alignment	not modelled	100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acylamino-acid-releasing enzyme, C-terminal donain
39	d1xfda2	Alignment	not modelled	99.9	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like
40	c3k2iA_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: acyl-coenzyme a thioesterase 4; PDBTitle: human acyl-coenzyme a thioesterase 4
41	c2o7vA_	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: A: PDB Molecule: cxe carboxylesterase; PDBTitle: carboxylesterase aecxe1 from actinidia eriantha covalently inhibited2 by paraoxon
42	c2zshA_	Alignment	not modelled	99.9	16	PDB header: hormone receptor Chain: A: PDB Molecule: probable gibberellin receptor gid1l1; PDBTitle: structural basis of gibberellin(ga3)-induced della2 recognition by the gibberellin receptor
43	d2h1ia1	Alignment	not modelled	99.9	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
44	c3hlkB_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: B: PDB Molecule: acyl-coenzyme a thioesterase 2, mitochondrial; PDBTitle: crystal structure of human mitochondrial acyl-coa2 thioesterase (acot2)
45	c3ga7A_	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: A: PDB Molecule: acetyl esterase; PDBTitle: 1.55 angstrom crystal structure of an acetyl esterase from salmonella2 typhimurium
46	c3bjrA_	Alignment	not modelled	99.9	15	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
47	c2h1iA_	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: A: PDB Molecule: carboxylesterase; PDBTitle: crystal structure of the bacillus cereus carboxylesterase
48	c3d0kA_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: putative poly(3-hydroxybutyrate) depolymerase lpqc; PDBTitle: crystal structure of the lpqc, poly(3-hydroxybutyrate) depolymerase2 from bordetella parapertussis
49	c3og9A_	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: protein yahd a copper inducible hydrolase; PDBTitle: structure of yahd with malic acid
50	c2o2gA_	Alignment	not modelled	99.9	17	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
51	c3ksrA_	Alignment	not modelled	99.9	17	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
52	d1l7aa_	Alignment	not modelled	99.9	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetyl xylan esterase-like
53	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

54	c3fnbB_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: B: PDB Molecule: acylaminoacyl peptidase smu_737; PDBTitle: crystal structure of acylaminoacyl peptidase smu_737 from2 streptococcus mutans ua159
55	d3b5ea1	Alignment	not modelled	99.9	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
56	d1lzl_a_	Alignment	not modelled	99.9	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
57	d1jkma_	Alignment	not modelled	99.9	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
58	d1fj2a_	Alignment	not modelled	99.9	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
59	d2jbwa1	Alignment	not modelled	99.9	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: 2,6-dihydropseudooxynicotine hydrolase-like
60	c2jwbB_	Alignment	not modelled	99.9	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.
61	c3f67A_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: putative dienelactone hydrolase; PDBTitle: crystal structure of putative dienelactone hydrolase from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
62	c2hdwB_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: B: PDB Molecule: hypothetical protein pa2218; PDBTitle: crystal structure of hypothetical protein pa2218 from pseudomonas2 aeruginosa
63	c3hxbB_	Alignment	not modelled	99.9	10	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
64	d1vlqa_	Alignment	not modelled	99.9	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetyl xylan esterase-like
65	c3mveB_	Alignment	not modelled	99.9	13	PDB header: lyase Chain: B: PDB Molecule: upf0255 protein vv1_0328; PDBTitle: crystal structure of a novel pyruvate decarboxylase
66	c2r8bA_	Alignment	not modelled	99.9	15	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
67	c2wtmC_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: C: PDB Molecule: est1e; PDBTitle: est1e from butyrivibrio proteoclasticus
68	c3cn9B_	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: B: PDB Molecule: carboxylesterase; PDBTitle: crystal structure analysis of the carboxylesterase pa3859 from2 pseudomonas aeruginosa pao1- orthorhombic crystal form
69	c3d7rB_	Alignment	not modelled	99.9	11	PDB header: hydrolase Chain: B: PDB Molecule: esterase; PDBTitle: crystal structure of a putative esterase from staphylococcus aureus
70	d1ufoa_	Alignment	not modelled	99.9	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hypothetical protein TT1662
71	d1ju3a2	Alignment	not modelled	99.9	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PepX catalytic domain-like
72	d2r8ba1	Alignment	not modelled	99.9	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
73	d1u4na_	Alignment	not modelled	99.9	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
74	c2wirB_	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: B: PDB Molecule: alpha/beta hydrolase fold-3 domain protein; PDBTitle: hyperthermophilic esterase from the archeon pyrobaculum2 calidifontis
75	c2c7bA_	Alignment	not modelled	99.9	17	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
76	c1l7qA_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: cocaine esterase; PDBTitle: ser117ala mutant of bacterial cocaine esterase coce
77	c3h2iA_	Alignment	not modelled	99.9	18	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
78	c2qruA_	Alignment	not modelled	99.9	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
79	d1auoa_	Alignment	not modelled	99.9	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1

80	c3fakA	Alignment	not modelled	99.9	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
81	d1dina	Alignment	not modelled	99.9	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Dienelactone hydrolase
82	d2fuka1	Alignment	not modelled	99.9	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Atu1826-like
83	c2veoA	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: lipase a; PDBTitle: x-ray structure of candida antarctica lipase a in its2 closed state.
84	c3dnmA	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: esterase/lipase; PDBTitle: crystal structure hormone-sensitive lipase from a2 metagenome library
85	d1jfra	Alignment	not modelled	99.9	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Lipase
86	d1jjia	Alignment	not modelled	99.9	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
87	d2i3da1	Alignment	not modelled	99.9	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Atu1826-like
88	c2i3dA	Alignment	not modelled	99.9	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein atu1826; PDBTitle: crystal structure of protein of unknown function atu1826, a putative2 alpha/beta hydrolase from agrobacterium tumefaciens
89	c3qh4A	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: esterase lipw; PDBTitle: crystal structure of esterase lipw from mycobacterium marinum
90	c2fx5A	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: pseudomonas mendocina lipase
91	c3fcyB	Alignment	not modelled	99.8	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
92	d1hlga	Alignment	not modelled	99.8	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Gastric lipase
93	d2b9va2	Alignment	not modelled	99.8	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PepX catalytic domain-like
94	c3aikB	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: B: PDB Molecule: 303aa long hypothetical esterase; PDBTitle: crystal structure of a hsl-like carboxylesterase from sulfolobus2 tokodaii
95	c3h04A	Alignment	not modelled	99.8	12	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
96	c2b9vB	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: B: PDB Molecule: alpha-amino acid ester hydrolase; PDBTitle: acetobacter turbidans alpha-amino acid ester hydrolase
97	c1ycdA	Alignment	not modelled	99.8	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical 27.3 kda protein in aap1-smf2 PDBTitle: crystal structure of yeast fsh1/yrh049w, a member of the2 serine hydrolase family
98	c3ilcA	Alignment	not modelled	99.8	20	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	c3ib3A	Alignment	not modelled	99.8	12	PDB header: hydrolase Chain: A: PDB Molecule: coce/nond family hydrolase; PDBTitle: crystal structure of sacol2612 - coce/nond family hydrolase from2 staphylococcus aureus
100	c3trdA	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase; PDBTitle: structure of an alpha-beta serine hydrolase homologue from coxiella2 burnetii
101	d1vkha	Alignment	not modelled	99.8	9	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Putative serine hydrolase Ydr428c
102	d2pbla1	Alignment	not modelled	99.8	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
103	d1mpxa2	Alignment	not modelled	99.8	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PepX catalytic domain-like
104	c3qm1A	Alignment	not modelled	99.8	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
105	c3g8yA	Alignment	not modelled	99.8	13	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

106	d1k8qa_	Alignment	not modelled	99.8	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Gastric lipase
107	c3jw8A_	Alignment	not modelled	99.8	18	PDB header: hydrolase Chain: A: PDB Molecule: mgll protein; PDBTitle: crystal structure of human mono-glyceride lipase
108	d2d81a1	Alignment	not modelled	99.8	10	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PHB depolymerase-like
109	c1mpxB_	Alignment	not modelled	99.7	15	PDB header: hydrolase Chain: B: PDB Molecule: alpha-amino acid ester hydrolase; PDBTitle: alpha-amino acid ester hydrolase labeled with selenomethionine
110	c3hjuB_	Alignment	not modelled	99.7	19	PDB header: hydrolase Chain: B: PDB Molecule: monoglyceride lipase; PDBTitle: crystal structure of human monoglyceride lipase
111	c2qjwA_	Alignment	not modelled	99.7	18	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein xcc1541; PDBTitle: crystal structure of a putative hydrolase of the alpha/beta2 superfamily (xcc1541) from xanthomonas campestris pv. campestris at3 1.35 a resolution
112	c3dyvA_	Alignment	not modelled	99.7	20	PDB header: hydrolase Chain: A: PDB Molecule: esterase d; PDBTitle: snapshots of esterase d from lactobacillus rhamnosus:2 insights into a rotation driven catalytic mechanism
113	d1lnsa3	Alignment	not modelled	99.7	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PepX catalytic domain-like
114	d2b61a1	Alignment	not modelled	99.7	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
115	c3nuzF_	Alignment	not modelled	99.7	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
116	c2q0xA_	Alignment	not modelled	99.7	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: alpha/beta hydrolase fold protein of unknown function
117	c2vavL_	Alignment	not modelled	99.7	12	PDB header: transferase Chain: L: PDB Molecule: acetyl-coa--deacetylcephalosporin c PDBTitle: crystal structure of deacetylcephalosporin c2 acetyltransferase (dac-soak)
118	c1cr6A_	Alignment	not modelled	99.7	14	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
119	c2y6vB_	Alignment	not modelled	99.7	15	PDB header: hydrolase Chain: B: PDB Molecule: peroxisomal membrane protein lpx1; PDBTitle: peroxisomal alpha-beta-hydrolase lpx1 (yor084w) from2 saccharomyces cerevisiae (crystal form i)
120	d1uxoa_	Alignment	not modelled	99.7	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: YdeN-like