Phyre2

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Description	P13039
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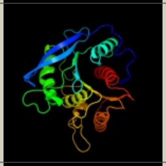
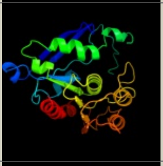
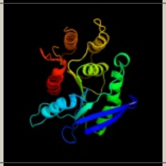
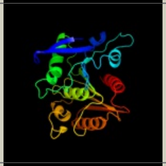
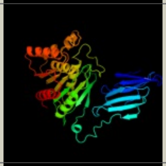
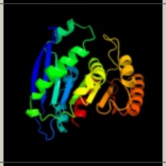
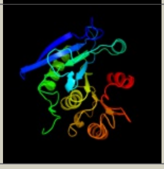
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3c8dA_	Alignment		100.0	98	**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	d3c8da2	Alignment		100.0	100	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase
3	d1jjfa_	Alignment		100.0	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase
4	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
5	d1wb4a1	Alignment		100.0	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase
6	c3e4dD_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**esterase d; **PDBTitle:** structural and kinetic study of an s-formylglutathione2 hydrolase from agrobacterium tumefaciens
7	d1dqza_	Alignment		100.0	18	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Mycobacterial antigens
8	d1pv1a_	Alignment		100.0	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Hypothetical esterase YJL068C
9	c3i6yA_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase apc40077; **PDBTitle:** structure of an esterase from the oil-degrading bacterium oleispira2 antarctica
10	d1sfra_	Alignment		100.0	20	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Mycobacterial antigens
11	c3fcxA_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**s-formylglutathione hydrolase; **PDBTitle:** crystal structure of human esterase d

12	d1f0na_	Alignment		100.0	18	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Mycobacterial antigens
13	c3gffA_	Alignment		100.0	20	**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	d1r88a_	Alignment		100.0	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Mycobacterial antigens
15	c3ls2D_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**s-formylglutathione hydrolase; **PDBTitle:** crystal structure of an s-formylglutathione hydrolase from2 pseudoalteromonas haloplanktis tac125
16	c2uz0B_	Alignment		100.0	19	**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	c2ecfA_	Alignment		100.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dipeptidyl peptidase iv; **PDBTitle:** crystal structure of dipeptidyl aminopeptidase iv from2 stenotrophomonas maltophilia
18	d2gzsa1	Alignment		100.0	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**IroE-like
19	c2qm0B_	Alignment		100.0	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**bes; **PDBTitle:** crystal structure of bes protein from bacillus cereus
20	c3doiA_	Alignment		100.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase; **PDBTitle:** crystal structure of a thermostable esterase complex with2 paraoxon
21	c1z68A_	Alignment	not modelled	100.0	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**fibroblast activation protein, alpha subunit; **PDBTitle:** crystal structure of human fibroblast activation protein alpha
22	c2eepA_	Alignment	not modelled	100.0	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dipeptidyl aminopeptidase iv, putative; **PDBTitle:** prolyl tripeptidyl aminopeptidase complexed with an inhibitor
23	c2qtbB_	Alignment	not modelled	100.0	9	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dipeptidyl peptidase 4; **PDBTitle:** human dipeptidyl peptidase iv/cd26 in complex with a 4-aryl2 cyclohexylalanine inhibitor
24	d3c8da1	Alignment	not modelled	100.0	96	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Enterochelin esterase N-terminal domain-like
25	c2g5tA_	Alignment	not modelled	100.0	8	**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
26	c2hu7A_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acylamino-acid-releasing enzyme; **PDBTitle:** binding of inhibitors by acylaminoacyl peptidase
27	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
						PDB header:hydrolase

28	c1qfmA_	Alignment	not modelled	100.0	15	**Chain:** A: **PDB Molecule:**protein (prolyl oligopeptidase); **PDBTitle:** prolyl oligopeptidase from porcine muscle
29	c3azqA_	Alignment	not modelled	100.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aminopeptidase; **PDBTitle:** crystal structure of puromycin hydrolase s511a mutant complexed with2 pgg
30	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
31	c2xe4A_	Alignment	not modelled	100.0	12	**PDB header:**hydrolase/inhibitor **Chain:** A: **PDB Molecule:**oligopeptidase b; **PDBTitle:** structure of oligopeptidase b from leishmania major
32	c3iumA_	Alignment	not modelled	100.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**prolyl endopeptidase; **PDBTitle:** appep_wtx opened state
33	c1yr2A_	Alignment	not modelled	99.9	11	**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
34	d3b5ea1	Alignment	not modelled	99.9	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase/thioesterase 1
35	c2o7vA_	Alignment	not modelled	99.9	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cxe carboxylesterase; **PDBTitle:** carboxylesterase aecxe1 from actinidia eriantha covalently inhibited2 by paraoxon
36	d2h1ia1	Alignment	not modelled	99.9	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase/thioesterase 1
37	d1qfma2	Alignment	not modelled	99.9	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Prolyl oligopeptidase, C-terminal domain
38	c2h1iA_	Alignment	not modelled	99.9	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**carboxylesterase; **PDBTitle:** crystal structure of the bacillus cereus carboxylesterase
39	c3ed1E_	Alignment	not modelled	99.9	13	**PDB header:**hydrolase receptor **Chain:** E: **PDB Molecule:**gibberellin receptor gid1; **PDBTitle:** crystal structure of rice gid1 complexed with ga3
40	d1orva2	Alignment	not modelled	99.9	10	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**DPP6 catalytic domain-like
41	c3bxpA_	Alignment	not modelled	99.9	9	**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
42	c2zshA_	Alignment	not modelled	99.9	12	**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	d2bgra2	Alignment	not modelled	99.9	8	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**DPP6 catalytic domain-like
44	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
45	d1jkma_	Alignment	not modelled	99.9	10	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase
46	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
47	d2hu7a2	Alignment	not modelled	99.8	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acylamino-acid-releasing enzyme, C-terminal donain
48	d1xfda2	Alignment	not modelled	99.8	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**DPP6 catalytic domain-like
49	c3u0vA_	Alignment	not modelled	99.8	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lysophospholipase-like protein 1; **PDBTitle:** crystal structure analysis of human lyplal1
50	c3d0kA_	Alignment	not modelled	99.8	13	**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
51	d2jbwa1	Alignment	not modelled	99.8	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**2,6-dihydropseudooxynicotine hydrolase-like
52	c2r8bA_	Alignment	not modelled	99.8	18	**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
53	c3bjrA_	Alignment	not modelled	99.8	14	**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
54	c3cn9B_	Alignment	not modelled	99.8	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**carboxylesterase;

54	c3cn9B_	Alignment	not modelled	99.8	14	**PDBTitle:** crystal structure analysis of the carboxylesterase pa3859 from2 pseudomonas aeruginosa pao1- orthorhombic crystal form
55	c2jbwB_	Alignment	not modelled	99.8	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**2,6-dihydroxy-pseudo-oxynicotine hydrolase; **PDBTitle:** crystal structure of the 2,6-dihydroxy-pseudo-oxynicotine2 hydrolase.
56	c3fnbB_	Alignment	not modelled	99.8	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**acylaminoacyl peptidase smu_737; **PDBTitle:** crystal structure of acylaminoacyl peptidase smu_737 from2 streptococcus mutans ua159
57	c2o2gA_	Alignment	not modelled	99.8	16	**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
58	d2r8ba1	Alignment	not modelled	99.8	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase/thioesterase 1
59	c3k2iA_	Alignment	not modelled	99.8	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acyl-coenzyme a thioesterase 4; **PDBTitle:** human acyl-coenzyme a thioesterase 4
60	c3hlkB_	Alignment	not modelled	99.8	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**acyl-coenzyme a thioesterase 2, mitochondrial; **PDBTitle:** crystal structure of human mitochondrial acyl-coa2 thioesterase (acot2)
61	c3f67A_	Alignment	not modelled	99.8	13	**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	c3hxkB_	Alignment	not modelled	99.7	12	**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
63	c2c7bA_	Alignment	not modelled	99.7	13	**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
64	c3aikB_	Alignment	not modelled	99.7	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**303aa long hypothetical esterase; **PDBTitle:** crystal structure of a hsl-like carboxylesterase from sulfolobus2 tokodaii
65	d2i3da1	Alignment	not modelled	99.7	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Atu1826-like
66	c2i3dA_	Alignment	not modelled	99.7	14	**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
67	d1auoa_	Alignment	not modelled	99.7	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase/thioesterase 1
68	d1lzla_	Alignment	not modelled	99.7	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase
69	d1u4na_	Alignment	not modelled	99.7	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase
70	c3fakA_	Alignment	not modelled	99.7	12	**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
71	d1dina_	Alignment	not modelled	99.7	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Dienelactone hydrolase
72	c3mveB_	Alignment	not modelled	99.7	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**upf0255 protein vv1_0328; **PDBTitle:** crystal structure of a novel pyruvate decarboxylase
73	c2wirB_	Alignment	not modelled	99.7	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha/beta hydrolase fold-3 domain protein; **PDBTitle:** hyperthermophilic esterase from the archeon pyrobaculum2 calidifontis
74	d1jjia_	Alignment	not modelled	99.7	10	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase
75	c2fx5A_	Alignment	not modelled	99.7	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipase; **PDBTitle:** pseudomonas mendocina lipase
76	c3ksrA_	Alignment	not modelled	99.7	13	**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
77	c3d7rB_	Alignment	not modelled	99.7	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**esterase; **PDBTitle:** crystal structure of a putative esterase from staphylococcus aureus
78	d1fj2a_	Alignment	not modelled	99.7	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase/thioesterase 1
79	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
80	c3h2iA_	Alignment	not modelled	99.7	15	**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
81	d1vkha_	Alignment	not modelled	99.7	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Putative serine hydrolase Ydr428c
82	d1jfra_	Alignment	not modelled	99.7	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Lipase
83	c2wtmC_	Alignment	not modelled	99.7	14	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**est1e; **PDBTitle:** est1e from butyrivibrio proteoclasticus
84	c3dnmA_	Alignment	not modelled	99.7	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase/lipase; **PDBTitle:** crystal structure hormone-sensitive lipase from a2 metagenome library
85	c3qh4A_	Alignment	not modelled	99.7	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase lipw; **PDBTitle:** crystal structure of esterase lipw from mycobacterium marinum
86	d1ju3a2	Alignment	not modelled	99.7	10	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**PepX catalytic domain-like
87	d2fuka1	Alignment	not modelled	99.7	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Atu1826-like
88	c2veoA_	Alignment	not modelled	99.6	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipase a; **PDBTitle:** x-ray structure of candida antarctica lipase a in its2 closed state.
89	d2pbla1	Alignment	not modelled	99.6	11	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase
90	c1l7qA_	Alignment	not modelled	99.6	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cocaine esterase; **PDBTitle:** ser117ala mutant of bacterial cocaine esterase coce
91	c2qruA_	Alignment	not modelled	99.6	14	**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
92	d1ufoa_	Alignment	not modelled	99.6	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Hypothetical protein TT1662
93	c3trdA_	Alignment	not modelled	99.6	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha/beta hydrolase; **PDBTitle:** structure of an alpha-beta serine hydrolase homologue from coxiella2 burnetii
94	d1l7aa_	Alignment	not modelled	99.6	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetyl xylan esterase-like
95	c3h04A_	Alignment	not modelled	99.6	9	**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	d1vlqa_	Alignment	not modelled	99.6	12	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetyl xylan esterase-like
97	c2qjwA_	Alignment	not modelled	99.5	19	**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
98	c2b9vB_	Alignment	not modelled	99.5	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-amino acid ester hydrolase; **PDBTitle:** acetobacter turbidans alpha-amino acid ester hydrolase
99	d2b9va2	Alignment	not modelled	99.5	12	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**PepX catalytic domain-like
100	d2d81a1	Alignment	not modelled	99.5	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**PHB depolymerase-like
101	d1lnsa3	Alignment	not modelled	99.5	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**PepX catalytic domain-like
102	d1mpxa2	Alignment	not modelled	99.5	12	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**PepX catalytic domain-like
103	c3qm1A_	Alignment	not modelled	99.4	12	**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
104	c3fcyB_	Alignment	not modelled	99.4	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**xylan esterase 1; **PDBTitle:** crystal structure of acetyl xylan esterase 1 from2 thermoanaerobacterium sp. jw/sl ys485
105	c3llcA_	Alignment	not modelled	99.4	15	**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

106	d1k4ya_	Alignment	not modelled	99.4	20	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetylcholinesterase-like
107	c3ib3A_	Alignment	not modelled	99.4	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**coce/nond family hydrolase; **PDBTitle:** crystal structure of sacol2612 - coce/nond family hydrolase from2 staphylococcus aureus
108	c3biwD_	Alignment	not modelled	99.4	14	**PDB header:**cell adhesion/cell adhesion **Chain:** D: **PDB Molecule:**neuroligin-1; **PDBTitle:** crystal structure of the neuroligin-1/neurexin-1beta synaptic adhesion2 complex
109	d1crla_	Alignment	not modelled	99.3	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
110	d1uxoa_	Alignment	not modelled	99.3	12	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**YdeN-like
111	d2h7ca1	Alignment	not modelled	99.3	19	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetylcholinesterase-like
112	d1k8qa_	Alignment	not modelled	99.3	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Gastric lipase
113	c3g8yA_	Alignment	not modelled	99.3	12	**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	d1ukca_	Alignment	not modelled	99.3	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
115	d1llfa_	Alignment	not modelled	99.3	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
116	d1dx4a_	Alignment	not modelled	99.3	11	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetylcholinesterase-like
117	d1qe3a_	Alignment	not modelled	99.3	19	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetylcholinesterase-like
118	d1f6wa_	Alignment	not modelled	99.3	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetylcholinesterase-like
119	c1mpxB_	Alignment	not modelled	99.3	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-amino acid ester hydrolase; **PDBTitle:** alpha-amino acid ester hydrolase labeled with selenomethionine
120	d1hlga_	Alignment	not modelled	99.3	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Gastric lipase