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Description	P51025
Date	Thu Jan 5 12:04:51 GMT 2012
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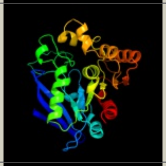
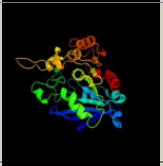
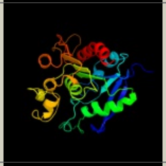
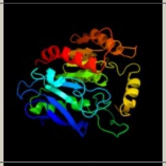
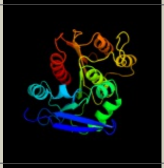
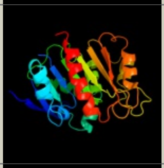
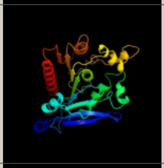
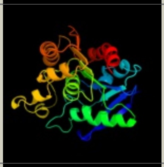
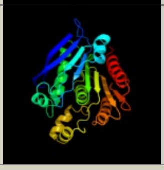
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3i6yA_	Alignment		100.0	55	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase apc40077; **PDBTitle:** structure of an esterase from the oil-degrading bacterium oleispira2 antarctica
2	c3e4dD_	Alignment		100.0	44	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**esterase d; **PDBTitle:** structural and kinetic study of an s-formylglutathione2 hydrolase from agrobacterium tumefaciens
3	c3ls2D_	Alignment		100.0	50	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**s-formylglutathione hydrolase; **PDBTitle:** crystal structure of an s-formylglutathione hydrolase from2 pseudoalteromonas haloplanktis tac125
4	d1pv1a_	Alignment		100.0	43	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Hypothetical esterase YJL068C
5	c3fcxA_	Alignment		100.0	48	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**s-formylglutathione hydrolase; **PDBTitle:** crystal structure of human esterase d
6	d1dqza_	Alignment		100.0	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Mycobacterial antigens
7	d1sfra_	Alignment		100.0	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Mycobacterial antigens
8	d1f0na_	Alignment		100.0	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Mycobacterial antigens
9	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
10	d1jjfa_	Alignment		100.0	19	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase
11	c1z68A_	Alignment		100.0	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**fibroblast activation protein, alpha subunit; **PDBTitle:** crystal structure of human fibroblast activation protein alpha

12	c2eepA_	Alignment		100.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dipeptidyl aminopeptidase iv, putative; **PDBTitle:** prolyl tripeptidyl aminopeptidase complexed with an inhibitor
13	c3azqA_	Alignment		100.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aminopeptidase; **PDBTitle:** crystal structure of puromycin hydrolase s511a mutant complexed with2 pgg
14	c2qtbB_	Alignment		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
15	d3c8da2	Alignment		100.0	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase
16	c2uz0B_	Alignment		100.0	23	**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	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
18	c2g5tA_	Alignment		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
19	d1r88a_	Alignment		100.0	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Mycobacterial antigens
20	c1qfmA_	Alignment		100.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein (prolyl oligopeptidase); **PDBTitle:** prolyl oligopeptidase from porcine muscle
21	c2hu7A_	Alignment	not modelled	100.0	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acylamino-acid-releasing enzyme; **PDBTitle:** binding of inhibitors by acylaminoacyl peptidase
22	c2bklB_	Alignment	not modelled	100.0	14	**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
23	c1wb4A_	Alignment	not modelled	100.0	20	**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
24	d1wb4a1	Alignment	not modelled	100.0	20	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase
25	c3doiA_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase; **PDBTitle:** crystal structure of a thermostable esterase complex with2 paraoxon
26	c1xfdD_	Alignment	not modelled	100.0	11	**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
27	c3iumA_	Alignment	not modelled	100.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**prolyl endopeptidase; **PDBTitle:** appep_wtx opened state
28	c2xe4A_	Alignment	not modelled	100.0	13	**PDB header:**hydrolase/inhibitor **Chain:** A: **PDB Molecule:**oligopeptidase b;

						PDBTitle: structure of oligopeptidase b from leishmania major
29	c2qm0B_	Alignment	not modelled	100.0	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**bes; **PDBTitle:** crystal structure of bes protein from bacillus cereus
30	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
31	c3gffA_	Alignment	not modelled	100.0	14	**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
32	d1qfma2	Alignment	not modelled	100.0	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Prolyl oligopeptidase, C-terminal domain
33	c3bxpA_	Alignment	not modelled	100.0	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
34	d2gzsa1	Alignment	not modelled	100.0	10	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**IroE-like
35	d1orva2	Alignment	not modelled	100.0	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**DPP6 catalytic domain-like
36	d2bgra2	Alignment	not modelled	100.0	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**DPP6 catalytic domain-like
37	d1xfda2	Alignment	not modelled	100.0	11	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**DPP6 catalytic domain-like
38	c2o7vA_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cxe carboxylesterase; **PDBTitle:** carboxylesterase aecxe1 from actinidia eriantha covalently inhibited2 by paraoxon
39	c3bjrA_	Alignment	not modelled	100.0	10	**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
40	c3ga7A_	Alignment	not modelled	99.9	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acetyl esterase; **PDBTitle:** 1.55 angstrom crystal structure of an acetyl esterase from salmonella2 typhimurium
41	c2zshA_	Alignment	not modelled	99.9	13	**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
42	d2hu7a2	Alignment	not modelled	99.9	10	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acylamino-acid-releasing enzyme, C-terminal donain
43	c3ed1E_	Alignment	not modelled	99.9	16	**PDB header:**hydrolase receptor **Chain:** E: **PDB Molecule:**gibberellin receptor gid1; **PDBTitle:** crystal structure of rice gid1 complexed with ga3
44	c3k2iA_	Alignment	not modelled	99.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acyl-coenzyme a thioesterase 4; **PDBTitle:** human acyl-coenzyme a thioesterase 4
45	d1jkma_	Alignment	not modelled	99.9	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase
46	c3hlkB_	Alignment	not modelled	99.9	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**acyl-coenzyme a thioesterase 2, mitochondrial; **PDBTitle:** crystal structure of human mitochondrial acyl-coa2 thioesterase (acot2)
47	c3hxkB_	Alignment	not modelled	99.9	9	**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
48	d1lzla_	Alignment	not modelled	99.9	12	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase
49	d2h1ia1	Alignment	not modelled	99.9	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase/thioesterase 1
50	c3d0kA_	Alignment	not modelled	99.9	12	**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	c3u0vA_	Alignment	not modelled	99.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lysophospholipase-like protein 1; **PDBTitle:** crystal structure analysis of human lyplal1
52	c2h1iA_	Alignment	not modelled	99.9	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**carboxylesterase; **PDBTitle:** crystal structure of the bacillus cereus carboxylesterase
53	c2o2gA_	Alignment	not modelled	99.9	13	**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
						PDB header:hydrolase

54	c2c7bA_	Alignment	not modelled	99.9	15	**Chain:** A: **PDB Molecule:**carboxylesterase; **PDBTitle:** the crystal structure of este1, a new thermophilic and2 thermostable carboxylesterase cloned from a metagenomic3 library
55	c3d7rB_	Alignment	not modelled	99.9	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**esterase; **PDBTitle:** crystal structure of a putative esterase from staphylococcus aureus
56	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
57	d3b5ea1	Alignment	not modelled	99.9	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase/thioesterase 1
58	c3fakA_	Alignment	not modelled	99.9	14	**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
59	c3fnbB_	Alignment	not modelled	99.9	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**acylaminoacyl peptidase smu_737; **PDBTitle:** crystal structure of acylaminoacyl peptidase smu_737 from2 streptococcus mutans ua159
60	d1fj2a_	Alignment	not modelled	99.9	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase/thioesterase 1
61	c2wirB_	Alignment	not modelled	99.9	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha/beta hydrolase fold-3 domain protein; **PDBTitle:** hyperthermophilic esterase from the archeon pyrobaculum2 calidifontis
62	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
63	d2jbwa1	Alignment	not modelled	99.9	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**2,6-dihydropseudooxynicotine hydrolase-like
64	c3dnmA_	Alignment	not modelled	99.9	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase/lipase; **PDBTitle:** crystal structure hormone-sensitive lipase from a2 metagenome library
65	c3ksrA_	Alignment	not modelled	99.9	15	**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
66	d1u4na_	Alignment	not modelled	99.9	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase
67	c2jbwB_	Alignment	not modelled	99.9	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**2,6-dihydroxy-pseudo-oxynicotine hydrolase; **PDBTitle:** crystal structure of the 2,6-dihydroxy-pseudo-oxynicotine2 hydrolase.
68	d1jjia_	Alignment	not modelled	99.9	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase
69	d1l7aa_	Alignment	not modelled	99.9	11	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetyl xylan esterase-like
70	c2wtmC_	Alignment	not modelled	99.9	16	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**est1e; **PDBTitle:** est1e from butyrivibrio proteoclasticus
71	c3f67A_	Alignment	not modelled	99.9	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
72	d1auoa_	Alignment	not modelled	99.9	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase/thioesterase 1
73	c3qh4A_	Alignment	not modelled	99.9	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase lipw; **PDBTitle:** crystal structure of esterase lipw from mycobacterium marinum
74	d1ju3a2	Alignment	not modelled	99.9	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**PepX catalytic domain-like
75	c3cn9B_	Alignment	not modelled	99.9	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**carboxylesterase; **PDBTitle:** crystal structure analysis of the carboxylesterase pa3859 from2 pseudomonas aeruginosa pao1- orthorhombic crystal form
76	c3aikB_	Alignment	not modelled	99.9	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**303aa long hypothetical esterase; **PDBTitle:** crystal structure of a hsl-like carboxylesterase from sulfolobus2 tokodaii
77	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
78	c3h2iA_	Alignment	not modelled	99.9	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
79	d1vlqa_	Alignment	not modelled	99.9	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetyl xylan esterase-like
						PDB header:lyase

80	c3mveB_	Alignment	not modelled	99.9	10	**Chain:** B: **PDB Molecule:**upf0255 protein vv1_0328; **PDBTitle:** crystal structure of a novel pyruvate decarboxylase
81	c2hdwB_	Alignment	not modelled	99.9	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hypothetical protein pa2218; **PDBTitle:** crystal structure of hypothetical protein pa2218 from pseudomonas2 aeruginosa
82	d1ufoa_	Alignment	not modelled	99.9	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Hypothetical protein TT1662
83	c1l7qA_	Alignment	not modelled	99.9	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cocaine esterase; **PDBTitle:** ser117ala mutant of bacterial cocaine esterase coce
84	d2r8ba1	Alignment	not modelled	99.9	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase/thioesterase 1
85	c2b9vB_	Alignment	not modelled	99.9	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-amino acid ester hydrolase; **PDBTitle:** acetobacter turbidans alpha-amino acid ester hydrolase
86	c3h04A_	Alignment	not modelled	99.9	7	**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
87	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
88	d2i3da1	Alignment	not modelled	99.9	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Atu1826-like
89	d1vkha_	Alignment	not modelled	99.9	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Putative serine hydrolase Ydr428c
90	d2b9va2	Alignment	not modelled	99.9	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**PepX catalytic domain-like
91	d2pbla1	Alignment	not modelled	99.8	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase
92	d1jfra_	Alignment	not modelled	99.8	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Lipase
93	c2fx5A_	Alignment	not modelled	99.8	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipase; **PDBTitle:** pseudomonas mendocina lipase
94	d1dina_	Alignment	not modelled	99.8	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Dienelactone hydrolase
95	c2veoA_	Alignment	not modelled	99.8	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipase a; **PDBTitle:** x-ray structure of candida antarctica lipase a in its2 closed state.
96	d2fuka1	Alignment	not modelled	99.8	18	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Atu1826-like
97	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
98	d1mpxa2	Alignment	not modelled	99.8	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**PepX catalytic domain-like
99	c3llcA_	Alignment	not modelled	99.8	19	**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
100	d1hlga_	Alignment	not modelled	99.8	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Gastric lipase
101	c1mpxB_	Alignment	not modelled	99.8	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-amino acid ester hydrolase; **PDBTitle:** alpha-amino acid ester hydrolase labeled with selenomethionine
102	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
103	c3qm1A_	Alignment	not modelled	99.8	16	**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	c3ib3A_	Alignment	not modelled	99.8	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**coce/nond family hydrolase; **PDBTitle:** crystal structure of sacol2612 - coce/nond family hydrolase from2 staphylococcus aureus
105	d1k8qa_	Alignment	not modelled	99.7	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Gastric lipase
106	c1ycdA_	Alignment	not modelled	99.7	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/yhr049w, a member of

						the2 serine hydrolase family
107	d2b61a1	Alignment	not modelled	99.7	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**O-acetyltransferase
108	c3jw8A_	Alignment	not modelled	99.7	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mgll protein; **PDBTitle:** crystal structure of human mono-glyceride lipase
109	c3hjuB_	Alignment	not modelled	99.7	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**monoglyceride lipase; **PDBTitle:** crystal structure of human monoglyceride lipase
110	c3dyvA_	Alignment	not modelled	99.7	16	**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
111	d1uxoa_	Alignment	not modelled	99.7	11	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**YdeN-like
112	c3i1iA_	Alignment	not modelled	99.7	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**homoserine o-acetyltransferase; **PDBTitle:** x-ray crystal structure of homoserine o-acetyltransferase from2 bacillus anthracis
113	c3g8yA_	Alignment	not modelled	99.7	11	**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	d1lnsa3	Alignment	not modelled	99.7	22	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**PepX catalytic domain-like
115	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)
116	c2q0xA_	Alignment	not modelled	99.7	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** alpha/beta hydrolase fold protein of unknown function
117	d2vata1	Alignment	not modelled	99.7	10	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**O-acetyltransferase
118	d1qe3a_	Alignment	not modelled	99.7	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetylcholinesterase-like
119	c2qjwA_	Alignment	not modelled	99.7	13	**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
120	d2pl5a1	Alignment	not modelled	99.7	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**O-acetyltransferase