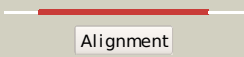
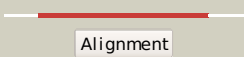
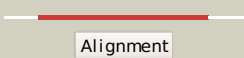
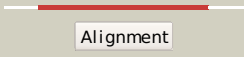
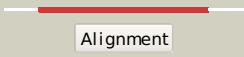
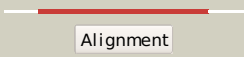
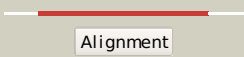
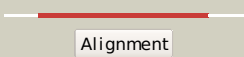
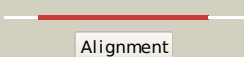
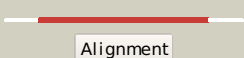
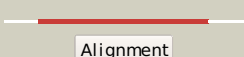


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3azqA_	 Alignment		100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase; PDBTitle: crystal structure of puromycin hydrolase s511a mutant complexed with2 pgg
2	c2ecfA_	 Alignment		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl peptidase iv; PDBTitle: crystal structure of dipeptidyl aminopeptidase iv from2 stenotrophomonas maltophilia
3	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
4	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
5	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
6	c2eepA_	 Alignment		100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl aminopeptidase iv, putative; PDBTitle: prolyl tripeptidyl aminopeptidase complexed with an inhibitor
7	c2hu7A_	 Alignment		100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: acylamino-acid-releasing enzyme; PDBTitle: binding of inhibitors by acylaminoacyl peptidase
8	c2xe4A_	 Alignment		100.0	14	PDB header: hydrolase/inhibitor Chain: A: PDB Molecule: oligopeptidase b; PDBTitle: structure of oligopeptidase b from leishmania major
9	c2bklB_	 Alignment		100.0	12	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
10	c3iumA_	 Alignment		100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: prolyl endopeptidase; PDBTitle: appep_wtx opened state
11	c1qfmA_	 Alignment		100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: protein (prolyl oligopeptidase); PDBTitle: prolyl oligopeptidase from porcine muscle

12	c1xfD_	Alignment		100.0	15	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
13	d1l7aa_	Alignment		100.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetyl xylan esterase-like
14	c1yr2A_	Alignment		100.0	13	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
15	c3k2iA_	Alignment		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: acyl-coenzyme a thioesterase 4; PDBTitle: human acyl-coenzyme a thioesterase 4
16	c3h1kB_	Alignment		100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: acyl-coenzyme a thioesterase 2, mitochondrial; PDBTitle: crystal structure of human mitochondrial acyl-coa2 thioesterase (acot2)
17	c2jwbB_	Alignment		100.0	18	PDB header: hydrolase Chain: B: PDB Molecule: 2,6-dihydroxy-pseudo-oxynicotine hydrolase; PDBTitle: crystal structure of the 2,6-dihydroxy-pseudo-oxynicotine2 hydrolase.
18	d2jbwa1	Alignment		100.0	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: 2,6-dihydropseudooxynicotine hydrolase-like
19	d1qfma2	Alignment		100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Prolyl oligopeptidase, C-terminal domain
20	d1ufoa_	Alignment		100.0	23	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hypothetical protein TT1662
21	c3fnbB_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: B: PDB Molecule: acylaminoacyl peptidase smu_737; PDBTitle: crystal structure of acylaminoacyl peptidase smu_737 from2 streptococcus mutans ua159
22	d1orva2	Alignment	not modelled	100.0	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like
23	c2hdwbB_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: hypothetical protein pa2218; PDBTitle: crystal structure of hypothetical protein pa2218 from pseudomonas2 aeruginosa
24	d2hu7a2	Alignment	not modelled	100.0	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acylamino-acid-releasing enzyme, C-terminal donain
25	d1vlqa_	Alignment	not modelled	100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetyl xylan esterase-like
26	c3ksrA_	Alignment	not modelled	100.0	18	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
27	d1fj2a_	Alignment	not modelled	100.0	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
28	c3doiA_	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of a thermostable esterase complex with2 paraoxon
						Fold: alpha/beta-Hydrolases

29	d2bgra2	Alignment	not modelled	100.0	14	Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like
30	c3fcyB	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: xylan esterase 1; PDBTitle: crystal structure of acetyl xylan esterase 1 from2 thermoanaerobacterium sp. jw/sl ys485
31	c3mveB	Alignment	not modelled	100.0	14	PDB header: lyase Chain: B: PDB Molecule: upf0255 protein vv1_0328; PDBTitle: crystal structure of a novel pyruvate decarboxylase
32	c3f67A	Alignment	not modelled	100.0	20	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
33	c2o2gA	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: diene lactone hydrolase; PDBTitle: crystal structure of diene lactone hydrolase (yp_324580.1) from2 anabaena variabilis atcc 29413 at 1.92 a resolution
34	d1xfda2	Alignment	not modelled	100.0	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like
35	c3bxaA	Alignment	not modelled	99.9	13	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
36	c2wtmC	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: C: PDB Molecule: est1e; PDBTitle: est1e from butyrivibrio proteoclasticus
37	c3ed1E	Alignment	not modelled	99.9	18	PDB header: hydrolase receptor Chain: E: PDB Molecule: gibberellin receptor gid1; PDBTitle: crystal structure of rice gid1 complexed with ga3
38	d1dina	Alignment	not modelled	99.9	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Diene lactone hydrolase
39	c3jw8A	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: mgll protein; PDBTitle: crystal structure of human mono-glyceride lipase
40	d2fuka1	Alignment	not modelled	99.9	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Atu1826-like
41	c2i3dA	Alignment	not modelled	99.9	16	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
42	d2i3da1	Alignment	not modelled	99.9	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Atu1826-like
43	d1hlga	Alignment	not modelled	99.9	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Gastric lipase
44	c3hjuB	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: B: PDB Molecule: monoglyceride lipase; PDBTitle: crystal structure of human monoglyceride lipase
45	c2b9vB	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: B: PDB Molecule: alpha-amino acid ester hydrolase; PDBTitle: acetobacter turbidans alpha-amino acid ester hydrolase
46	c3fcxA	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: s-formyl glutathione hydrolase; PDBTitle: crystal structure of human esterase d
47	c3ls2D	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: D: PDB Molecule: s-formyl glutathione hydrolase; PDBTitle: crystal structure of an s-formyl glutathione hydrolase from2 pseudoalteromonas haloplanktis tac125
48	c3d0kA	Alignment	not modelled	99.9	14	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	d1ju3a2	Alignment	not modelled	99.9	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PepX catalytic domain-like
50	d2h1ia1	Alignment	not modelled	99.9	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
51	c3i6yA	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: esterase apc40077; PDBTitle: structure of an esterase from the oil-degrading bacterium oleispira2 antarctica
52	c3g8yA	Alignment	not modelled	99.9	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
53	c1l7qA	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: cocaine esterase; PDBTitle: ser117ala mutant of bacterial cocaine esterase coce
54	c3u0vA	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: lysophospholipase-like protein 1; PDBTitle: crystal structure analysis of human lyp1a1
						PDB header: hydrolase Chain: B: PDB Molecule: sugar hydrolase;

55	c3hxB	Alignment	not modelled	99.9	16	PDBTitle: crystal structure of a sugar hydrolase (yeeb) from2 lactococcus lactis, northeast structural genomics3 consortium target kr108
56	c3e4dD	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: D: PDB Molecule: esterase d; PDBTitle: structural and kinetic study of an s-formylglutathione2 hydrolase from agrobacterium tumefaciens
57	c3h2iA	Alignment	not modelled	99.9	16	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
58	d2b9va2	Alignment	not modelled	99.9	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PepX catalytic domain-like
59	c3bjrA	Alignment	not modelled	99.9	16	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
60	c3ga7A	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: acetyl esterase; PDBTitle: 1.55 angstrom crystal structure of an acetyl esterase from salmonella2 typhimurium
61	c2h1iA	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: carboxylesterase; PDBTitle: crystal structure of the bacillus cereus carboxylesterase
62	d1k8qa	Alignment	not modelled	99.9	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Gastric lipase
63	c3h04A	Alignment	not modelled	99.9	15	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
64	c3ib3A	Alignment	not modelled	99.9	13	PDB header: hydrolase Chain: A: PDB Molecule: coce/nond family hydrolase; PDBTitle: crystal structure of sacol2612 - coce/nond family hydrolase from2 staphylococcus aureus
65	c3cn9B	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: B: PDB Molecule: carboxylesterase; PDBTitle: crystal structure analysis of the carboxylesterase pa3859 from2 pseudomonas aeruginosa pao1- orthorhombic crystal form
66	c3llcA	Alignment	not modelled	99.9	18	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
67	d1lzlA	Alignment	not modelled	99.9	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
68	c3og9A	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: protein yahd a copper inducible hydrolase; PDBTitle: structure of yahd with malic acid
69	c3dnmA	Alignment	not modelled	99.9	13	PDB header: hydrolase Chain: A: PDB Molecule: esterase/lipase; PDBTitle: crystal structure hormone-sensitive lipase from a2 metagenome library
70	c3trdA	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase; PDBTitle: structure of an alpha-beta serine hydrolase homologue from coxiella2 burnetii
71	c3qm1A	Alignment	not modelled	99.9	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
72	c2zshA	Alignment	not modelled	99.9	14	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
73	d1jkma	Alignment	not modelled	99.9	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
74	d1auoa	Alignment	not modelled	99.9	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
75	d1jfra	Alignment	not modelled	99.9	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Lipase
76	d1mpxa2	Alignment	not modelled	99.9	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PepX catalytic domain-like
77	c1cr6A	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
78	c2r8bA	Alignment	not modelled	99.9	17	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
79	d1pv1a	Alignment	not modelled	99.9	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hypothetical esterase YJL068C
80	c3dyvA	Alignment	not modelled	99.9	18	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
						PDB header: transferase

81	c3liiA_	Alignment	not modelled	99.9	14	Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: x-ray crystal structure of homoserine o-acetyltransferase from2 bacillus anthracis
82	c3fakA_	Alignment	not modelled	99.9	15	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
83	c2wirB_	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: B: PDB Molecule: alpha/beta hydrolase fold-3 domain protein; PDBTitle: hyperthermophilic esterase from the archeon pyrobaculum2 calidifontis
84	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
85	d2r8ba1	Alignment	not modelled	99.9	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
86	c1mpxB_	Alignment	not modelled	99.9	13	PDB header: hydrolase Chain: B: PDB Molecule: alpha-amino acid ester hydrolase; PDBTitle: alpha-amino acid ester hydrolase labeled with selenomethionine
87	c2c7bA_	Alignment	not modelled	99.9	20	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
88	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
89	c3nuzF_	Alignment	not modelled	99.9	15	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
90	c1ycdA_	Alignment	not modelled	99.9	14	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
91	c2veoA_	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: lipase a; PDBTitle: x-ray structure of candida antarctica lipase a in its2 closed state.
92	c2uz0B_	Alignment	not modelled	99.9	16	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
93	c2qrUA_	Alignment	not modelled	99.9	16	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
94	d3b5ea1	Alignment	not modelled	99.9	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
95	c2cjpA_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: structure of potato (solanum tuberosum) epoxide hydrolase i2 (steh1)
96	c2fx5A_	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: pseudomonas mendocina lipase
97	c2vavL_	Alignment	not modelled	99.9	15	PDB header: transferase Chain: L: PDB Molecule: acetyl-coa--deacetylcephalosporin c PDBTitle: crystal structure of deacetylcephalosporin c2 acetyltransferase (dac-soak)
98	d2b61a1	Alignment	not modelled	99.9	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
99	d1mtza_	Alignment	not modelled	99.9	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Proline iminopeptidase-like
100	c2y6vB_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: B: PDB Molecule: peroxisomal membrane protein lpx1; PDBTitle: peroxisomal alpha-beta-hydrolase lpx1 (yor084w) from2 saccharomyces cerevisiae (crystal form i)
101	d1f0na_	Alignment	not modelled	99.9	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Mycobacterial antigens
102	d2vata1	Alignment	not modelled	99.9	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
103	d1sfra_	Alignment	not modelled	99.9	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Mycobacterial antigens
104	d1u4na_	Alignment	not modelled	99.9	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
105	c3fleB_	Alignment	not modelled	99.9	11	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: se_1780 protein; PDBTitle: se_1780 protein of unknown function from staphylococcus epidermidis.
106	c3aikB_	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: B: PDB Molecule: 303aa long hypothetical esterase; PDBTitle: crystal structure of a hsl-like carboxylesterase from sulfolobus2 tokodaii
						Fold: alpha/beta-Hydrolases

107	dluxoa_	Alignment	not modelled	99.9	17	Superfamily: alpha/beta-Hydrolases Family: YdeN-like
108	c3qh4A_	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: A: PDB Molecule: esterase lipw; PDBTitle: crystal structure of esterase lipw from mycobacterium marinum
109	d2pl5a1	Alignment	not modelled	99.8	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
110	d1jjfa_	Alignment	not modelled	99.8	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
111	d1b6ga_	Alignment	not modelled	99.8	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloalkane dehalogenase
112	c2q0xA_	Alignment	not modelled	99.8	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: alpha/beta hydrolase fold protein of unknown function
113	c3qvmA_	Alignment	not modelled	99.8	12	PDB header: hydrolase Chain: A: PDB Molecule: olei00960; PDBTitle: the structure of olei00960, a hydrolase from oleispira antarctica
114	c3om8A_	Alignment	not modelled	99.8	14	PDB header: hydrolase Chain: A: PDB Molecule: probable hydrolase; PDBTitle: the crystal structure of a hydrolase from pseudomonas aeruginosa pa01
115	d1q0ra_	Alignment	not modelled	99.8	22	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Aclacinomycin methylesterase RdmC
116	d1zd3a2	Alignment	not modelled	99.8	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
117	d1cr6a2	Alignment	not modelled	99.8	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
118	c2qjwA_	Alignment	not modelled	99.8	21	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
119	d2pbla1	Alignment	not modelled	99.8	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
120	c2xt0A_	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase; PDBTitle: dehalogenase dppa from plasiocystis pacifica sir-i