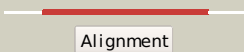

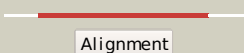

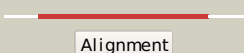

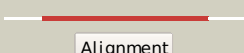



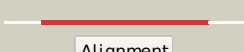

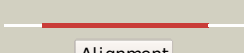

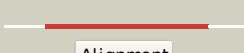




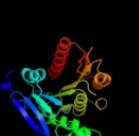













#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2ecfA_	 Alignment		100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl peptidase iv; PDBTitle: crystal structure of dipeptidyl aminopeptidase iv from2 stenotrophomonas maltophilia
2	c3azqA_	 Alignment		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase; PDBTitle: crystal structure of puromycin hydrolase s511a mutant complexed with2 pgg
3	c2eepA_	 Alignment		100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl aminopeptidase iv, putative; PDBTitle: prolyl tripeptidyl aminopeptidase complexed with an inhibitor
4	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
5	c2hu7A_	 Alignment		100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: acylamino-acid-releasing enzyme; PDBTitle: binding of inhibitors by acylaminoacyl peptidase
6	c1z68A_	 Alignment		100.0	16	PDB header: lyase Chain: A: PDB Molecule: fibroblast activation protein, alpha subunit; PDBTitle: crystal structure of human fibroblast activation protein alpha
7	c3f67A_	 Alignment		100.0	31	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
8	d1dina_	 Alignment		100.0	26	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Dienelactone hydrolase
9	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
10	c1qfmA_	 Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: protein (prolyl oligopeptidase); PDBTitle: prolyl oligopeptidase from porcine muscle
11	c2bklB_	 Alignment		100.0	21	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

12	c3h1kB	Alignment		100.0	27	PDB header: hydrolase Chain: B: PDB Molecule: acyl-coenzyme a thioesterase 2, mitochondrial; PDBTitle: crystal structure of human mitochondrial acyl-coa2 thioesterase (acot2)
13	c1xfdD	Alignment		100.0	20	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
14	c2xe4A	Alignment		100.0	17	PDB header: hydrolase/inhibitor Chain: A: PDB Molecule: oligopeptidase b; PDBTitle: structure of oligopeptidase b from leishmania major
15	c3k2iA	Alignment		100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: acyl-coenzyme a thioesterase 4; PDBTitle: human acyl-coenzyme a thioesterase 4
16	c3iumA	Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: prolyl endopeptidase; PDBTitle: appep_wtx opened state
17	d1qfma2	Alignment		100.0	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Prolyl oligopeptidase, C-terminal domain
18	c1yr2A	Alignment		100.0	20	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
19	d2hu7a2	Alignment		100.0	23	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acylamino-acid-releasing enzyme, C-terminal donain
20	c2o2gA	Alignment		100.0	26	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
21	d1l7aa	Alignment	not modelled	100.0	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetyl xylan esterase-like
22	d1vlqa	Alignment	not modelled	100.0	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetyl xylan esterase-like
23	d2i3da1	Alignment	not modelled	100.0	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Atu1826-like
24	c2i3dA	Alignment	not modelled	100.0	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
25	c3ksrA	Alignment	not modelled	100.0	24	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
26	d1lzlA	Alignment	not modelled	100.0	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
27	d2fuka1	Alignment	not modelled	100.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Atu1826-like
28	d1orva2	Alignment	not modelled	100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like
29	c3bxpA	Alignment	not modelled	100.0	14	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

30	c2hdwB_	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: B: PDB Molecule: hypothetical protein pa2218; PDBTitle: crystal structure of hypothetical protein pa2218 from <i>pseudomonas2 aeruginosa</i>
31	d2bgra2	Alignment	not modelled	100.0	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like
32	d1xfda2	Alignment	not modelled	100.0	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like
33	c3doiA_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of a thermostable esterase complex with2 paraoxon
34	c3ga7A_	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: acetyl esterase; PDBTitle: 1.55 angstrom crystal structure of an acetyl esterase from <i>salmonella2 typhimurium</i>
35	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
36	d1ju3a2	Alignment	not modelled	100.0	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PepX catalytic domain-like
37	c3trdA_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase; PDBTitle: structure of an alpha-beta serine hydrolase homologue from <i>coxiella2 burnetii</i>
38	c3hxB_	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: B: PDB Molecule: sugar hydrolase; PDBTitle: crystal structure of a sugar hydrolase (yeeb) from2 <i>lactococcus lactis</i> , northeast structural genomics3 consortium target kr108
39	c2jbwB_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: B: PDB Molecule: 2,6-dihydroxy-pseudo-oxynicotine hydrolase; PDBTitle: crystal structure of the 2,6-dihydroxy-pseudo-oxynicotine2 hydrolase.
40	c2b9vB_	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: B: PDB Molecule: alpha-amino acid ester hydrolase; PDBTitle: <i>acetobacter turbidans</i> alpha-amino acid ester hydrolase
41	d2jbwa1	Alignment	not modelled	100.0	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: 2,6-dihydropseudooxynicotine hydrolase-like
42	c1l7qA_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: cocaine esterase; PDBTitle: ser117ala mutant of bacterial cocaine esterase coce
43	c3bjrA_	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: putative carboxylesterase; PDBTitle: crystal structure of a putative carboxylesterase (lp_1002) from2 <i>lactobacillus plantarum</i> wcf51 at 2.09 a resolution
44	d1jfra_	Alignment	not modelled	99.9	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Lipase
45	c2wirB_	Alignment	not modelled	99.9	23	PDB header: hydrolase Chain: B: PDB Molecule: alpha/beta hydrolase fold-3 domain protein; PDBTitle: hyperthermophilic esterase from the archeon <i>pyrobaculum2 calidifontis</i>
46	d1jkma_	Alignment	not modelled	99.9	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
47	d2b9va2	Alignment	not modelled	99.9	24	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PepX catalytic domain-like
48	d1u4na_	Alignment	not modelled	99.9	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
49	c3fnbB_	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: B: PDB Molecule: acylaminoacyl peptidase smu_737; PDBTitle: crystal structure of acylaminoacyl peptidase smu_737 from2 <i>streptococcus mutans</i> ua159
50	c3fcyB_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: B: PDB Molecule: xylan esterase 1; PDBTitle: crystal structure of acetyl xylan esterase 1 from2 <i>thermoanaerobacterium</i> sp. jw/sl ys485
51	c2wtmC_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: C: PDB Molecule: est1e; PDBTitle: est1e from <i>butyrivibrio proteoclasticus</i>
52	c3fakA_	Alignment	not modelled	99.9	19	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
53	c3aikB_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: B: PDB Molecule: 303aa long hypothetical esterase; PDBTitle: crystal structure of a hsl-like carboxylesterase from <i>sulfolobus2 tokodaii</i>
54	c3dnmA_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: esterase/lipase; PDBTitle: crystal structure hormone-sensitive lipase from a2 metagenome library
55	c2zshA_	Alignment	not modelled	99.9	13	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
56	c2c7bA_	Alignment	not modelled	99.9	19 PDB header: hydrolase Chain: A: PDB Molecule: carboxylesterase; PDBTitle: the crystal structure of este1, a new thermophilic and2 thermostable carboxylesterase cloned from a metagenomic3 library
57	c3ib3A_	Alignment	not modelled	99.9	20 PDB header: hydrolase Chain: A: PDB Molecule: coce/nond family hydrolase; PDBTitle: crystal structure of sacol2612 - coce/nond family hydrolase from2 staphylococcus aureus
58	c3mveB_	Alignment	not modelled	99.9	19 PDB header: lyase Chain: B: PDB Molecule: upf0255 protein vv1_0328; PDBTitle: crystal structure of a novel pyruvate decarboxylase
59	c3ls2D_	Alignment	not modelled	99.9	17 PDB header: hydrolase Chain: D: PDB Molecule: s-formylglutathione hydrolase; PDBTitle: crystal structure of an s-formylglutathione hydrolase from2 pseudoalteromonas haloplanktis tac125
60	c2o7vA_	Alignment	not modelled	99.9	18 PDB header: hydrolase Chain: A: PDB Molecule: cxe carboxylesterase; PDBTitle: carboxylesterase aecxe1 from actinidia eriantha covalently inhibited2 by paraoxon
61	c3i6yA_	Alignment	not modelled	99.9	19 PDB header: hydrolase Chain: A: PDB Molecule: esterase apc40077; PDBTitle: structure of an esterase from the oil-degrading bacterium oleispira2 antarctica
62	c3fcxA_	Alignment	not modelled	99.9	15 PDB header: hydrolase Chain: A: PDB Molecule: s-formylglutathione hydrolase; PDBTitle: crystal structure of human esterase d
63	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
64	d1mpxA2	Alignment	not modelled	99.9	17 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PepX catalytic domain-like
65	c3d7rB_	Alignment	not modelled	99.9	14 PDB header: hydrolase Chain: B: PDB Molecule: esterase; PDBTitle: crystal structure of a putative esterase from staphylococcus aureus
66	c3jw8A_	Alignment	not modelled	99.9	15 PDB header: hydrolase Chain: A: PDB Molecule: mgll protein; PDBTitle: crystal structure of human mono-glyceride lipase
67	d1ufoa_	Alignment	not modelled	99.9	16 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hypothetical protein TT1662
68	c2qruA_	Alignment	not modelled	99.9	17 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
69	c3h2iA_	Alignment	not modelled	99.9	20 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
70	d1fj2a_	Alignment	not modelled	99.9	15 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
71	c3hjuB_	Alignment	not modelled	99.9	16 PDB header: hydrolase Chain: B: PDB Molecule: monoglyceride lipase; PDBTitle: crystal structure of human monoglyceride lipase
72	d2h1ia1	Alignment	not modelled	99.9	10 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
73	c3llcA_	Alignment	not modelled	99.9	13 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
74	d1jjia_	Alignment	not modelled	99.9	18 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
75	c3h04A_	Alignment	not modelled	99.9	13 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
76	c3qm1A_	Alignment	not modelled	99.9	19 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
77	c1mpxB_	Alignment	not modelled	99.9	20 PDB header: hydrolase Chain: B: PDB Molecule: alpha-amino acid ester hydrolase; PDBTitle: alpha-amino acid ester hydrolase labeled with selenomethionine
78	c3d0kA_	Alignment	not modelled	99.9	15 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
79	c3e4dD_	Alignment	not modelled	99.9	16 PDB header: hydrolase Chain: D: PDB Molecule: esterase d; PDBTitle: structural and kinetic study of an s-formylglutathione2 hydrolase from agrobacterium tumefaciens
80	d1lnsa3	Alignment	not modelled	99.9	24 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PepX catalytic domain-like
81	c2veoA_	Alignment	not modelled	99.9	21 PDB header: hydrolase Chain: A: PDB Molecule: lipase a; PDBTitle: x-ray structure of candida antarctica lipase a in its2

					closed state.
82	c2fx5A	Alignment	not modelled	99.9	18 PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: pseudomonas mendocina lipase
83	c3u0vA	Alignment	not modelled	99.9	13 PDB header: hydrolase Chain: A: PDB Molecule: lysophospholipase-like protein 1; PDBTitle: crystal structure analysis of human lyplal1
84	d1hlga	Alignment	not modelled	99.9	19 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Gastric lipase
85	c2h1iA	Alignment	not modelled	99.9	11 PDB header: hydrolase Chain: A: PDB Molecule: carboxylesterase; PDBTitle: crystal structure of the bacillus cereus carboxylesterase
86	c3cn9B	Alignment	not modelled	99.9	17 PDB header: hydrolase Chain: B: PDB Molecule: carboxylesterase; PDBTitle: crystal structure analysis of the carboxylesterase pa3859 from2 pseudomonas aeruginosa pao1- orthorhombic crystal form
87	c3g8yA	Alignment	not modelled	99.9	14 PDB header: hydrolase Chain: A: PDB Molecule: susd/ragb-associated esterase-like protein; PDBTitle: crystal structure of a putative hydrolase (bv4_4111) from bacteroides2 vulgatus atcc 8482 at 1.90 a resolution
88	c3d59B	Alignment	not modelled	99.9	15 PDB header: hydrolase Chain: B: PDB Molecule: platelet-activating factor acetylhydrolase; PDBTitle: crystal structure of human plasma platelet activating2 factor acetylhydrolase
89	c3og9A	Alignment	not modelled	99.9	12 PDB header: hydrolase Chain: A: PDB Molecule: protein yahd a copper inducible hydrolase; PDBTitle: structure of yahd with malic acid
90	d2gzsa1	Alignment	not modelled	99.9	8 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: IroE-like
91	d1jjfa	Alignment	not modelled	99.9	16 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
92	c1lnsA	Alignment	not modelled	99.9	24 PDB header: hydrolase Chain: A: PDB Molecule: x-prolyl dipeptidyl aminopetidase; PDBTitle: crystal structure analysis of the x-prolyl dipeptidyl2 aminopeptidase from lactococcus lactis
93	d1k8qa	Alignment	not modelled	99.9	18 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Gastric lipase
94	d1auoa	Alignment	not modelled	99.9	15 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
95	d2r8ba1	Alignment	not modelled	99.9	21 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
96	d1pv1a	Alignment	not modelled	99.9	15 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hypothetical esterase YJL068C
97	d3b5ea1	Alignment	not modelled	99.9	14 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
98	c2r8bA	Alignment	not modelled	99.9	21 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
99	d1sfra	Alignment	not modelled	99.9	12 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Mycobacterial antigens
100	c3dyvA	Alignment	not modelled	99.8	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
101	c3nuzF	Alignment	not modelled	99.8	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
102	c2uz0B	Alignment	not modelled	99.8	17 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
103	c2qm0B	Alignment	not modelled	99.8	15 PDB header: structural genomics, unknown function Chain: B: PDB Molecule: bes; PDBTitle: crystal structure of bes protein from bacillus cereus
104	d1f0na	Alignment	not modelled	99.8	11 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Mycobacterial antigens
105	d1vkha	Alignment	not modelled	99.8	13 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Putative serine hydrolase Ydr428c
106	d2pbla1	Alignment	not modelled	99.8	14 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
107	c2qjwA	Alignment	not modelled	99.8	14 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

108	dluxoa_	Alignment	not modelled	99.8	10	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: YdeN-like
109	d1mtza_	Alignment	not modelled	99.8	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Proline iminopeptidase-like
110	c2q0xA_	Alignment	not modelled	99.8	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: alpha/beta hydrolase fold protein of unknown function
111	clycdA_	Alignment	not modelled	99.8	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
112	c3i1iA_	Alignment	not modelled	99.8	18	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: x-ray crystal structure of homoserine o-acetyltransferase from2 bacillus anthracis
113	d1wb4a1	Alignment	not modelled	99.8	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
114	c2cjpA_	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: structure of potato (solanum tuberosum) epoxide hydrolase i2 (steh1)
115	d2b61a1	Alignment	not modelled	99.7	22	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
116	d1dqza_	Alignment	not modelled	99.7	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Mycobacterial antigens
117	d1tqha_	Alignment	not modelled	99.7	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/lipase
118	c3nwoA_	Alignment	not modelled	99.7	17	PDB header: hydrolase Chain: A: PDB Molecule: proline iminopeptidase; PDBTitle: crystal structure of proline iminopeptidase mycobacterium smegmatis
119	c3v48B_	Alignment	not modelled	99.7	17	PDB header: hydrolase Chain: B: PDB Molecule: putative aminoacrylate hydrolase rutd; PDBTitle: crystal structure of the putative alpha/beta hydrolase rutd from2 e.coli
120	c3picB_	Alignment	not modelled	99.7	17	PDB header: hydrolase Chain: B: PDB Molecule: cip2; PDBTitle: glucuronoyl esterase catalytic domain (cip2_ge) from hypocrea jecorina