



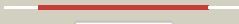









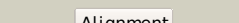

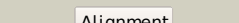



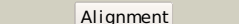



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2hdwB_	 Alignment		100.0	32	PDB header: hydrolase Chain: B: PDB Molecule: hypothetical protein pa2218; PDBTitle: crystal structure of hypothetical protein pa2218 from pseudomonas2 aeruginosa
2	c3azqA_	 Alignment		100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase; PDBTitle: crystal structure of puromycin hydrolase s511a mutant complexed with2 pgg
3	c3jw8A_	 Alignment		100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: mgII protein; PDBTitle: crystal structure of human mono-glyceride lipase
4	c3hjuB_	 Alignment		100.0	15	PDB header: hydrolase Chain: B: PDB Molecule: monoglyceride lipase; PDBTitle: crystal structure of human monoglyceride lipase
5	d1l7aa_	 Alignment		100.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetyl xylan esterase-like
6	d1k8qa_	 Alignment		100.0	11	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Gastric lipase
7	c2ecfA_	 Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl peptidase iv; PDBTitle: crystal structure of dipeptidyl aminopeptidase iv from2 stenotrophomonas maltophilia
8	c2q5tA_	 Alignment		100.0	16	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
9	c2qtbB_	 Alignment		100.0	16	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	d1hlga_	 Alignment		100.0	11	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Gastric lipase
11	c3mveB_	 Alignment		100.0	16	PDB header: lyase Chain: B: PDB Molecule: upf0255 protein vw1_0328; PDBTitle: crystal structure of a novel pyruvate decarboxylase

12	c2eepA_	Alignment		100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl aminopeptidase iv, putative; PDBTitle: prolyl tripeptidyl aminopeptidase complexed with an inhibitor
13	c2hu7A_	Alignment		100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: acylamino-acid-releasing enzyme; PDBTitle: binding of inhibitors by acylaminoacyl peptidase
14	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
15	c1cr6A_	Alignment		100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
16	c3k2iA_	Alignment		100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: acyl-coenzyme a thioesterase 4; PDBTitle: human acyl-coenzyme a thioesterase 4
17	c2y6vB_	Alignment		100.0	11	PDB header: hydrolase Chain: B: PDB Molecule: peroxisomal membrane protein lpx1; PDBTitle: peroxisomal alpha-beta-hydrolase lpx1 (yor084w) from2 saccharomyces cerevisiae (crystal form i)
18	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)
19	c2o2gA_	Alignment		100.0	21	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
20	c3fcyB_	Alignment		100.0	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
21	c1l7qA_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: cocaine esterase; PDBTitle: ser117ala mutant of bacterial cocaine esterase coce
22	c2wtmC_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: C: PDB Molecule: est1e; PDBTitle: est1e from butyrivibrio proteoclasticus
23	d1ju3a2	Alignment	not modelled	100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PepX catalytic domain-like
24	c3i1iA_	Alignment	not modelled	100.0	12	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: x-ray crystal structure of homoserine o-acetyltransferase from2 bacillus anthracis
25	d1vlqa_	Alignment	not modelled	100.0	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetyl xylan esterase-like
26	d2b61a1	Alignment	not modelled	100.0	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
27	c2vavL_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: L: PDB Molecule: acetyl-coa--deacetylcephalosporin c PDBTitle: crystal structure of deacetylcephalosporin c2 acetyltransferase (dac-soak)
28	c3llcA_	Alignment	not modelled	100.0	14	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
						PDB header: hydrolase Chain: B: PDB Molecule: 2,6-dihydroxy-pseudo-oxynicotine

29	c2jwbB_	Alignment	not modelled	100.0	19	hydrolase; PDBTitle: crystal structure of the 2,6-dihydroxy-pseudo-oxynicotine2 hydrolase.
30	d1qfma2	Alignment	not modelled	100.0	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Prolyl oligopeptidase, C-terminal domain
31	c3h04A_	Alignment	not modelled	100.0	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of the protein with unknown function from2 staphylococcus aureus subsp. aureus mu50
32	d2vata1	Alignment	not modelled	100.0	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
33	c3ksrA_	Alignment	not modelled	100.0	16	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
34	d2jbwa1	Alignment	not modelled	99.9	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: 2,6-dihydropseudooxynicotine hydrolase-like
35	d1mtza_	Alignment	not modelled	99.9	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Proline iminopeptidase-like
36	c3ib3A_	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: coce/nond family hydrolase; PDBTitle: crystal structure of sacol2612 - coce/nond family hydrolase from2 staphylococcus aureus
37	d1b6ga_	Alignment	not modelled	99.9	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloalkane dehalogenase
38	c3qm1A_	Alignment	not modelled	99.9	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
39	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
40	c1xfD_	Alignment	not modelled	99.9	13	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
41	c3fnbB_	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: B: PDB Molecule: acylaminoacyl peptidase smu_737; PDBTitle: crystal structure of acylaminoacyl peptidase smu_737 from2 streptococcus mutans ua159
42	d1e89a_	Alignment	not modelled	99.9	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hydroxynitrile lyase-like
43	c2e3jA_	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase ephb; PDBTitle: the crystal structure of epoxide hydrolase b (rv1938) from2 mycobacterium tuberculosis at 2.1 angstrom
44	d1xkla_	Alignment	not modelled	99.9	11	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hydroxynitrile lyase-like
45	d3c70a1	Alignment	not modelled	99.9	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hydroxynitrile lyase-like
46	c2cjpA_	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: structure of potato (solanum tuberosum) epoxide hydrolase i2 (steh1)
47	c3dqzB_	Alignment	not modelled	99.9	11	PDB header: lyase Chain: B: PDB Molecule: alpha-hydroxynitrile lyase-like protein; PDBTitle: structure of the hydroxynitrile lyase from arabidopsis2 thaliana
48	c3nwoA_	Alignment	not modelled	99.9	13	PDB header: hydrolase Chain: A: PDB Molecule: proline iminopeptidase; PDBTitle: crystal structure of proline iminopeptidase mycobacterium smegmatis
49	d2b9va2	Alignment	not modelled	99.9	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PepX catalytic domain-like
50	d1q0ra_	Alignment	not modelled	99.9	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Aclacinomycin methylesterase RdmC
51	d1zd3a2	Alignment	not modelled	99.9	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
52	d1orva2	Alignment	not modelled	99.9	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like
53	c3u1tA_	Alignment	not modelled	99.9	11	PDB header: hydrolase Chain: A: PDB Molecule: dmma haloalkane dehalogenase; PDBTitle: haloalkane dehalogenase, dmma, of marine microbial origin
54	d1hkha_	Alignment	not modelled	99.9	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
						PDB header: hydrolase

55	c3bwxA	Alignment	not modelled	99.9	11	Chain: A: PDB Molecule: alpha/beta hydrolase; PDBTitle: crystal structure of an alpha/beta hydrolase (yp_496220.1) from2 novosphingobium aromaticivorans dsm 12444 at 1.50 a resolution
56	d1mpxA	Alignment	not modelled	99.9	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PepX catalytic domain-like
57	d2bgra	Alignment	not modelled	99.9	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like
58	c1qfmA	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: protein (prolyl oligopeptidase); PDBTitle: prolyl oligopeptidase from porcine muscle
59	c3h2iA	Alignment	not modelled	99.9	9	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
60	c3fobA	Alignment	not modelled	99.9	14	PDB header: oxidoreductase Chain: A: PDB Molecule: bromoperoxidase; PDBTitle: crystal structure of bromoperoxidase from bacillus anthracis
61	c2qmQA	Alignment	not modelled	99.9	14	PDB header: signaling protein Chain: A: PDB Molecule: protein ndrg2; PDBTitle: crystal structure of a n-myc downstream regulated 2 protein (ndrg2,2 sylld, ndr2, ai182517, au040374) from mus musculus at 1.70 a3 resolution
62	d1cr6a	Alignment	not modelled	99.9	11	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
63	d1brta	Alignment	not modelled	99.9	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
64	c1u2eA	Alignment	not modelled	99.9	12	PDB header: hydrolase Chain: A: PDB Molecule: 2-hydroxy-6-ketona-2,4-dienedioic acid PDBTitle: crystal structure of the c-c bond hydrolase mhpc
65	c3qvmA	Alignment	not modelled	99.9	12	PDB header: hydrolase Chain: A: PDB Molecule: olei00960; PDBTitle: the structure of olei00960, a hydrolase from oleispira antarctica
66	d1c4xa	Alignment	not modelled	99.9	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase
67	c2yysA	Alignment	not modelled	99.9	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: proline iminopeptidase-related protein; PDBTitle: crystal structure of the proline iminopeptidase-related protein2 ttha1809 from thermus thermophilus hb8
68	c2r11D	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: D: PDB Molecule: carboxylesterase np; PDBTitle: crystal structure of putative hydrolase (2632844) from2 bacillus subtilis at 1.96 a resolution
69	d2pl5a1	Alignment	not modelled	99.9	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
70	d1a8qa	Alignment	not modelled	99.9	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
71	c2xt0A	Alignment	not modelled	99.9	11	PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase; PDBTitle: dehalogenase dppa from plesiocystis pacifica sir-i
72	c3v48B	Alignment	not modelled	99.9	11	PDB header: hydrolase Chain: B: PDB Molecule: putative aminoacrylate hydrolase rutd; PDBTitle: crystal structure of the putative alpha/beta hydrolase rutd from2 e.coli
73	d1va4a	Alignment	not modelled	99.9	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
74	d2rhw1	Alignment	not modelled	99.9	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase
75	c3gzjB	Alignment	not modelled	99.9	12	PDB header: hydrolase Chain: B: PDB Molecule: polynuridine-aldehyde esterase; PDBTitle: crystal structure of polynuridine aldehyde esterase2 complexed with 16-epi-vellimosimine
76	d1a8sa	Alignment	not modelled	99.9	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
77	c2bklB	Alignment	not modelled	99.9	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
78	c3kdaB	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: B: PDB Molecule: cftr inhibitory factor (cif); PDBTitle: crystal structure of the cftr inhibitory factor cif with the h269a2 mutation
79	d1wmla	Alignment	not modelled	99.9	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Proline iminopeptidase-like
80	c1zoiC	Alignment	not modelled	99.9	10	PDB header: hydrolase Chain: C: PDB Molecule: esterase; PDBTitle: crystal structure of a stereoselective esterase from2 pseudomonas putida ifo12996
						Fold: alpha/beta-Hydrolases

81	d2fuka1	Alignment	not modelled	99.9	13	Superfamily: alpha/beta-Hydrolases Family: Atu1826-like
82	d1dina	Alignment	not modelled	99.9	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Dienelactone hydrolase
83	c2qruA	Alignment	not modelled	99.9	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
84	c3qitB	Alignment	not modelled	99.9	13	PDB header: hydrolase Chain: B: PDB Molecule: polyketide synthase; PDBTitle: thioesterase domain from curacin biosynthetic pathway
85	d1azwa	Alignment	not modelled	99.9	11	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Proline iminopeptidase-like
86	d1xfda2	Alignment	not modelled	99.9	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: DPP6 catalytic domain-like
87	c1mpxB	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: B: PDB Molecule: alpha-amino acid ester hydrolase; PDBTitle: alpha-amino acid ester hydrolase labeled with selenomethionine
88	d1a88a	Alignment	not modelled	99.9	11	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
89	c2xe4A	Alignment	not modelled	99.9	10	PDB header: hydrolase/inhibitor Chain: A: PDB Molecule: oligopeptidase b; PDBTitle: structure of oligopeptidase b from leishmania major
90	c3oosA	Alignment	not modelled	99.9	11	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase family protein; PDBTitle: the structure of an alpha/beta fold family hydrolase from bacillus2 anthracis str. sterne
91	c2rauA	Alignment	not modelled	99.9	13	PDB header: hydrolase Chain: A: PDB Molecule: putative esterase; PDBTitle: crystal structure of a putative lipase (np_343859.1) from sulfobolus2 solfataricus at 1.85 a resolution
92	c1wprA	Alignment	not modelled	99.9	11	PDB header: signaling protein Chain: A: PDB Molecule: sigma factor sigb regulation protein rsbq; PDBTitle: crystal structure of rsbq inhibited by pmsf
93	c3f67A	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: A: PDB Molecule: putative dienelactone hydrolase; PDBTitle: crystal structure of putative dienelactone hydrolase from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
94	d1luk8a	Alignment	not modelled	99.9	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase
95	c2xmzA	Alignment	not modelled	99.9	13	PDB header: lyase Chain: A: PDB Molecule: hydrolase, alpha/beta hydrolase fold family; PDBTitle: structure of menh from s. aureus
96	c3e3aA	Alignment	not modelled	99.9	12	PDB header: oxidoreductase Chain: A: PDB Molecule: possible peroxidase bpoc; PDBTitle: the structure of rv0554 from mycobacterium tuberculosis
97	d2hu7a2	Alignment	not modelled	99.9	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acylamino-acid-releasing enzyme, C-terminal donain
98	c2xuaH	Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: H: PDB Molecule: 3-oxoadipate enol-lactonase; PDBTitle: crystal structure of the enol-lactonase from burkholderia2 xenovorans lb400
99	d1ehya	Alignment	not modelled	99.9	10	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
100	c3a2nF	Alignment	not modelled	99.9	10	PDB header: hydrolase Chain: F: PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of dbja (wild type type ii p21)
101	c2vf2A	Alignment	not modelled	99.9	13	PDB header: hydrolase Chain: A: PDB Molecule: 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate PDBTitle: x-ray crystal structure of hsd from mycobacterium2 tuberculosis
102	d1m33a	Alignment	not modelled	99.9	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Biotin biosynthesis protein BioH
103	c2q0xA	Alignment	not modelled	99.9	8	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: alpha/beta hydrolase fold protein of unknown function
104	d1jfra	Alignment	not modelled	99.9	23	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Lipase
105	c3om8A	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: probable hydrolase; PDBTitle: the crystal structure of a hydrolase from pseudomonas aeruginosa pa01
106	c3dyvA	Alignment	not modelled	99.9	14	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
107	c3fsgC	Alignment	not modelled	99.9	13	PDB header: hydrolase Chain: C: PDB Molecule: alpha/beta superfamily hydrolase; PDBTitle: crystal structure of alpha/beta superfamily hydrolase from oenococcus2 oeni psu-1

108	c3trdA_	 Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase; PDBTitle: structure of an alpha-beta serine hydrolase homologue from coxiella2 burnetii
109	d1mj5a_	 Alignment	not modelled	99.9	11	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloalkane dehalogenase
110	c3c5wP_	 Alignment	not modelled	99.9	14	PDB header: hydrolase Chain: P: PDB Molecule: pp2a-specific methylsterase pme-1; PDBTitle: complex between pp2a-specific methylsterase pme-1 and pp2a core2 enzyme
111	c3iumA_	 Alignment	not modelled	99.9	12	PDB header: hydrolase Chain: A: PDB Molecule: prolyl endopeptidase; PDBTitle: appep_wx opened state
112	c3bf7B_	 Alignment	not modelled	99.9	13	PDB header: hydrolase Chain: B: PDB Molecule: esterase ybff; PDBTitle: 1.1 resolution structure of ybff, a new esterase from2 escherichia coli: a unique substrate-binding crevice3 generated by domain arrangement
113	d1bn7a_	 Alignment	not modelled	99.9	10	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloalkane dehalogenase
114	c3bxaA_	 Alignment	not modelled	99.9	12	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
115	c2wj4B_	 Alignment	not modelled	99.9	10	PDB header: oxidoreductase Chain: B: PDB Molecule: 1h-3-hydroxy-4-oxoquinaldine 2,4-dioxygenase; PDBTitle: crystal structure of the cofactor-devoid 1-h-3-hydroxy-4-2 oxoquinaldine 2,4-dioxygenase (hod) from arthrobacter3 nitroguajacolicus ru61a anaerobically complexed with its4 natural substrate 1-h-3-hydroxy-4-oxoquinaldine
116	d1qo7a_	 Alignment	not modelled	99.9	10	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
117	d2i3da1	 Alignment	not modelled	99.9	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Atu1826-like
118	c2i3dA_	 Alignment	not modelled	99.9	20	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
119	c2qvbA_	 Alignment	not modelled	99.9	12	PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase 3; PDBTitle: crystal structure of haloalkane dehalogenase rv2579 from mycobacterium2 tuberculosis
120	c1y37A_	 Alignment	not modelled	99.9	13	PDB header: hydrolase Chain: A: PDB Molecule: fluoroacetate dehalogenase; PDBTitle: structure of fluoroacetate dehalogenase from burkholderia sp. fa1