Phyre^2

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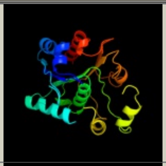
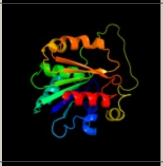
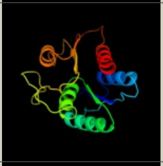
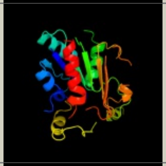
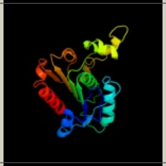
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1cr6A_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**epoxide hydrolase; **PDBTitle:** crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
2	d1uxoa_	Alignment		99.9	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**YdeN-like
3	c2hu7A_	Alignment		99.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acylamino-acid-releasing enzyme; **PDBTitle:** binding of inhibitors by acylaminoacyl peptidase
4	c2y6vB_	Alignment		99.9	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**peroxisomal membrane protein lpx1; **PDBTitle:** peroxisomal alpha-beta-hydrolase lpx1 (yor084w) from2 saccharomyces cerevisiae (crystal form i)
5	c2qjwA_	Alignment		99.9	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
6	c3llcA_	Alignment		99.9	17	**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
7	c3qvmA_	Alignment		99.9	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**olei00960; **PDBTitle:** the structure of olei00960, a hydrolase from oleispira antarctica
8	c2ecfA_	Alignment		99.9	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dipeptidyl peptidase iv; **PDBTitle:** crystal structure of dipeptidyl aminopeptidase iv from2 stenotrophomonas maltophilia
9	c2vavL_	Alignment		99.9	15	**PDB header:**transferase **Chain:** L: **PDB Molecule:**acetyl-coa--deacetylcephalosporin c **PDBTitle:** crystal structure of deacetylcephalosporin c2 acetyltransferase (dac-soak)
10	c3i1iA_	Alignment		99.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**homoserine o-acetyltransferase; **PDBTitle:** x-ray crystal structure of homoserine o-acetyltransferase from2 bacillus anthracis
11	d1k8qa_	Alignment		99.9	20	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Gastric lipase

12	c3v48B_	Alignment		99.9	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
13	d1hlga_	Alignment		99.9	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Gastric lipase
14	c3azqA_	Alignment		99.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aminopeptidase; **PDBTitle:** crystal structure of puromycin hydrolase s511a mutant complexed with2 pgg
15	c3h04A_	Alignment		99.9	14	**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
16	c1z68A_	Alignment		99.9	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**fibroblast activation protein, alpha subunit; **PDBTitle:** crystal structure of human fibroblast activation protein alpha
17	c2qs9A_	Alignment		99.9	13	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**retinoblastoma-binding protein 9; **PDBTitle:** crystal structure of the human retinoblastoma-binding2 protein 9 (rbbp-9). nesg target hr2978
18	c2r11D_	Alignment		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
19	d2b61a1	Alignment		99.9	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**O-acetyltransferase
20	c2g5tA_	Alignment		99.9	12	**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
21	c2wtmC_	Alignment	not modelled	99.9	13	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**est1e; **PDBTitle:** est1e from butyrivibrio proteoclasticus
22	c2qmqA_	Alignment	not modelled	99.9	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**protein ndrg2; **PDBTitle:** crystal structure of a n-myc downstream regulated 2 protein (ndrg2,2 syld, ndr2, ai182517, au040374) from mus musculus at 1.70 a3 resolution
23	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
24	d2vata1	Alignment	not modelled	99.9	18	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**O-acetyltransferase
25	c3oosA_	Alignment	not modelled	99.9	16	**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
26	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
27	c3fleB_	Alignment	not modelled	99.9	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**se_1780 protein; **PDBTitle:** se_1780 protein of unknown function from staphylococcus epidermidis.
28	c3fsgC_	Alignment	not modelled	99.9	17	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**alpha/beta superfamily hydrolase; **PDBTitle:** crystal structure of alpha/beta superfamily hydrolase from oenococcus2 oeni psu-1

29	c2qtbB_	Alignment	not modelled	99.9	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dipeptidyl peptidase 4; **PDBTitle:** human dipeptidyl peptidase iv/cd26 in complex with a 4-aryl2 cyclohexylalanine inhibitor
30	c2eepA_	Alignment	not modelled	99.9	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dipeptidyl aminopeptidase iv, putative; **PDBTitle:** prolyl tripeptidyl aminopeptidase complexed with an inhibitor
31	d1b6ga_	Alignment	not modelled	99.9	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Haloalkane dehalogenase
32	c3bdvB_	Alignment	not modelled	99.9	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**uncharacterized protein duf1234; **PDBTitle:** crystal structure of a putative yden-like hydrolase (eca3091) from2 pectobacterium atrosepticum scri1043 at 1.66 a resolution
33	c3jw8A_	Alignment	not modelled	99.9	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mgll protein; **PDBTitle:** crystal structure of human mono-glyceride lipase
34	c2cjpA_	Alignment	not modelled	99.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**epoxide hydrolase; **PDBTitle:** structure of potato (solanum tuberosum) epoxide hydrolase i2 (steh1)
35	c2q0xA_	Alignment	not modelled	99.9	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** alpha/beta hydrolase fold protein of unknown function
36	c3ksrA_	Alignment	not modelled	99.9	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
37	c3flaB_	Alignment	not modelled	99.9	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**rifr; **PDBTitle:** rifr - type ii thioesterase from rifamycin nrps/pks biosynthetic2 pathway - form 1
38	c3c5wP_	Alignment	not modelled	99.9	16	**PDB header:**hydrolase **Chain:** P: **PDB Molecule:**pp2a-specific methylesterase pme-1; **PDBTitle:** complex between pp2a-specific methylesterase pme-1 and pp2a core2 enzyme
39	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
40	d3c70a1	Alignment	not modelled	99.9	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Hydroxynitrile lyase-like
41	c2e3jA_	Alignment	not modelled	99.9	17	**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
42	c3e0xB_	Alignment	not modelled	99.9	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**lipase-esterase related protein; **PDBTitle:** the crystal structure of a lipase-esterase related protein2 from clostridium acetobutylicum atcc 824
43	d2pl5a1	Alignment	not modelled	99.9	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**O-acetyltransferase
44	c3l80A_	Alignment	not modelled	99.9	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein smu.1393c; **PDBTitle:** crystal structure of smu.1393c from streptococcus mutans ua159
45	d1zd3a2	Alignment	not modelled	99.9	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Epoxide hydrolase
46	c3hjuB_	Alignment	not modelled	99.9	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**monoglyceride lipase; **PDBTitle:** crystal structure of human monoglyceride lipase
47	d1imja_	Alignment	not modelled	99.9	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Ccg1/TafII250-interacting factor B (Cib)
48	c2o2gA_	Alignment	not modelled	99.9	18	**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
49	d1e89a_	Alignment	not modelled	99.9	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Hydroxynitrile lyase-like
50	d1m33a_	Alignment	not modelled	99.9	18	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Biotin biosynthesis protein BioH
51	d1cr6a2	Alignment	not modelled	99.9	18	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Epoxide hydrolase
52	c3u1tA_	Alignment	not modelled	99.9	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dmma haloalkane dehalogenase; **PDBTitle:** haloalkane dehalogenase, dmma, of marine microbial origin
53	c2qruA_	Alignment	not modelled	99.9	15	**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
54	d1ufoa_	Alignment	not modelled	99.9	20	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases

						Family: Hypothetical protein TT1662
55	c2xuaH_	Alignment	not modelled	99.9	13	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**3-oxoadipate enol-lactonase; **PDBTitle:** crystal structure of the enol-lactonase from burkholderia2 xenovorans lb400
56	d1mtza_	Alignment	not modelled	99.9	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Proline iminopeptidase-like
57	c3fnbB_	Alignment	not modelled	99.9	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**acylaminoacyl peptidase smu_737; **PDBTitle:** crystal structure of acylaminoacyl peptidase smu_737 from2 streptococcus mutans ua159
58	c3bxpA_	Alignment	not modelled	99.8	11	**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
59	c3k2iA_	Alignment	not modelled	99.8	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acyl-coenzyme a thioesterase 4; **PDBTitle:** human acyl-coenzyme a thioesterase 4
60	c2xt0A_	Alignment	not modelled	99.8	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**haloalkane dehalogenase; **PDBTitle:** dehalogenase dppa from plesiocystis pacifica sir-i
61	c3mveB_	Alignment	not modelled	99.8	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**upf0255 protein vv1_0328; **PDBTitle:** crystal structure of a novel pyruvate decarboxylase
62	c3dqzB_	Alignment	not modelled	99.8	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**alpha-hydroxynitrile lyase-like protein; **PDBTitle:** structure of the hydroxynitrile lyase from arabidopsis2 thaliana
63	d1tqha_	Alignment	not modelled	99.8	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase/lipase
64	c2yysA_	Alignment	not modelled	99.8	18	**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
65	c3hlkB_	Alignment	not modelled	99.8	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**acyl-coenzyme a thioesterase 2, mitochondrial; **PDBTitle:** crystal structure of human mitochondrial acyl-coa2 thioesterase (acot2)
66	d1c4xa_	Alignment	not modelled	99.8	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carbon-carbon bond hydrolase
67	d2fuka1	Alignment	not modelled	99.8	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Atu1826-like
68	d1xkla_	Alignment	not modelled	99.8	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Hydroxynitrile lyase-like
69	c2jbwB_	Alignment	not modelled	99.8	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**2,6-dihydroxy-pseudo-oxynicotine hydrolase; **PDBTitle:** crystal structure of the 2,6-dihydroxy-pseudo-oxynicotine2 hydrolase.
70	d2jbwa1	Alignment	not modelled	99.8	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**2,6-dihydropseudooxynicotine hydrolase-like
71	d1pjaa_	Alignment	not modelled	99.8	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Thioesterases
72	c1pjaA_	Alignment	not modelled	99.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**palmitoyl-protein thioesterase 2 precursor; **PDBTitle:** the crystal structure of palmitoyl protein thioesterase-2 reveals the2 basis for divergent substrate specificities of the two lysosomal3 thioesterases (ppt1 and ppt2)
73	c3bwxA_	Alignment	not modelled	99.8	20	**PDB header:**hydrolase **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
74	c3kxpD_	Alignment	not modelled	99.8	16	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**alpha-(n-acetylaminomethylene)succinic acid **PDBTitle:** crystal structure of e-2-(acetamidomethylene)succinate2 hydrolase
75	c1zoiC_	Alignment	not modelled	99.8	12	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**esterase; **PDBTitle:** crystal structure of a stereoselective esterase from2 pseudomonas putida ifo12996
76	c3e3aA_	Alignment	not modelled	99.8	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**possible peroxidase bpoc; **PDBTitle:** the structure of rv0554 from mycobacterium tuberculosis
77	d1ispa_	Alignment	not modelled	99.8	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Bacterial lipase
78	c3bjrA_	Alignment	not modelled	99.8	11	**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
79	d1wm1a_	Alignment	not modelled	99.8	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Proline iminopeptidase-like

80	c3lp5A_	Alignment	not modelled	99.8	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative cell surface hydrolase; **PDBTitle:** the crystal structure of the putative cell surface hydrolase from2 lactobacillus plantarum wcfs1
81	c1ycdA_	Alignment	not modelled	99.8	17	**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
82	c1xfdD_	Alignment	not modelled	99.8	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
83	d1ehya_	Alignment	not modelled	99.8	20	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Epoxide hydrolase
84	d1a8qa_	Alignment	not modelled	99.8	12	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Haloperoxidase
85	c3bdiA_	Alignment	not modelled	99.8	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized protein ta0194; **PDBTitle:** crystal structure of predicted cib-like hydrolase (np_393672.1) from2 thermoplasma acidophilum at 1.45 a resolution
86	d1hkha_	Alignment	not modelled	99.8	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Haloperoxidase
87	d2r8ba1	Alignment	not modelled	99.8	11	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase/thioesterase 1
88	d1q0ra_	Alignment	not modelled	99.8	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Aclacinomycin methylesterase RdmC
89	d2hu7a2	Alignment	not modelled	99.8	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acylamino-acid-releasing enzyme, C-terminal donain
90	c2ronA_	Alignment	not modelled	99.8	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**surfactin synthetase thioesterase subunit; **PDBTitle:** the external thioesterase of the surfactin-synthetase
91	c1y37A_	Alignment	not modelled	99.8	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**fluoroacetate dehalogenase; **PDBTitle:** structure of fluoroacetate dehalogenase from burkholderia sp. fa1
92	d2i3da1	Alignment	not modelled	99.8	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Atu1826-like
93	c2i3dA_	Alignment	not modelled	99.8	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
94	c3gzjB_	Alignment	not modelled	99.8	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**polyneuridine-aldehyde esterase; **PDBTitle:** crystal structure of polyneuridine aldehyde esterase2 complexed with 16-epi-vellosimine
95	d1azwa_	Alignment	not modelled	99.8	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Proline iminopeptidase-like
96	c3r0vA_	Alignment	not modelled	99.8	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha/beta hydrolase fold protein; **PDBTitle:** the crystal structure of an alpha/beta hydrolase from sphaerobacter2 thermophilus dsm 20745.
97	d1l7aa_	Alignment	not modelled	99.8	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetyl xylan esterase-like
98	d1uk8a_	Alignment	not modelled	99.8	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carbon-carbon bond hydrolase
99	c1wprA_	Alignment	not modelled	99.8	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**sigma factor sigb regulation protein rsbq; **PDBTitle:** crystal structure of rsbq inhibited by pmsf
100	d1va4a_	Alignment	not modelled	99.8	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Haloperoxidase
101	c3kdaB_	Alignment	not modelled	99.8	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cftr inhibitory factor (cif); **PDBTitle:** crystal structure of the cftr inhibitory factor cif with the h269a2 mutation
102	c1qfmA_	Alignment	not modelled	99.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein (prolyl oligopeptidase); **PDBTitle:** prolyl oligopeptidase from porcine muscle
103	c2r8bA_	Alignment	not modelled	99.8	10	**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
104	c3ibtA_	Alignment	not modelled	99.8	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**1h-3-hydroxy-4-oxoquinoline 2,4-dioxygenase; **PDBTitle:** structure of 1h-3-hydroxy-4-oxoquinoline 2,4-dioxygenase (qdo)
						PDB header:hydrolase **Chain:** B: **PDB Molecule:**prolyl endopeptidase;

105	c2bklB_	Alignment	not modelled	99.8	15	**PDBTitle:** structural and mechanistic analysis of two prolyl2 endopeptidases: role of inter-domain dynamics in3 catalysis and specificity
106	d1a8sa_	Alignment	not modelled	99.8	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Haloperoxidase
107	c2vf2A_	Alignment	not modelled	99.8	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate **PDBTitle:** x-ray crystal structure of hsad from mycobacterium2 tuberculosis
108	d1ex9a_	Alignment	not modelled	99.8	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Bacterial lipase
109	c1u2eA_	Alignment	not modelled	99.8	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**2-hydroxy-6-ketonona-2,4-dienedioic acid **PDBTitle:** crystal structure of the c-c bond hydrolase mhpc
110	c3bf7B_	Alignment	not modelled	99.8	17	**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
111	d1brta_	Alignment	not modelled	99.8	18	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Haloperoxidase
112	c3nwoA_	Alignment	not modelled	99.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**proline iminopeptidase; **PDBTitle:** crystal structure of proline iminopeptidase mycobacterium smegmatis
113	c3p2mA_	Alignment	not modelled	99.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**possible hydrolase; **PDBTitle:** crystal structure of a novel esterase rv0045c from mycobacterium2 tuberculosis
114	c3fobA_	Alignment	not modelled	99.8	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**bromoperoxidase; **PDBTitle:** crystal structure of bromoperoxidase from bacillus anthracis
115	d1a88a_	Alignment	not modelled	99.8	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Haloperoxidase
116	d2rhwa1	Alignment	not modelled	99.8	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carbon-carbon bond hydrolase
117	d2h1ia1	Alignment	not modelled	99.8	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase/thioesterase 1
118	c2xmzA_	Alignment	not modelled	99.8	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hydrolase, alpha/beta hydrolase fold family; **PDBTitle:** structure of menh from s. aureus
119	c3a2nF_	Alignment	not modelled	99.8	16	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**haloalkane dehalogenase; **PDBTitle:** crystal structure of dbja (wild type type ii p21)
120	c2hdwB_	Alignment	not modelled	99.8	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hypothetical protein pa2218; **PDBTitle:** crystal structure of hypothetical protein pa2218 from pseudomonas2 aeruginosa