Phyre2

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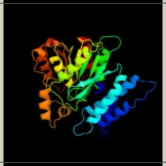
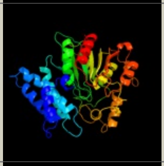
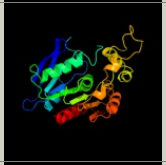
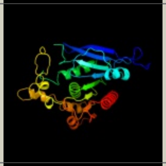
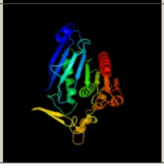
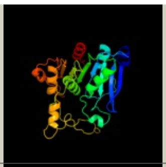
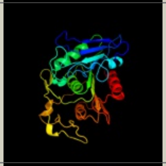
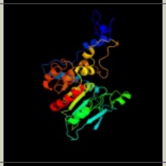
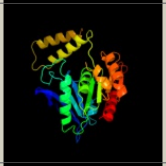
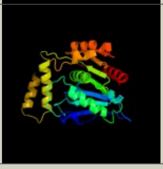
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3mveB_	Alignment		100.0	42	**PDB header:**lyase **Chain:** B: **PDB Molecule:**upf0255 protein vv1_0328; **PDBTitle:** crystal structure of a novel pyruvate decarboxylase
2	d2jbwa1	Alignment		100.0	21	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**2,6-dihydropseudooxynicotine hydrolase-like
3	c3fnbB_	Alignment		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
4	c2jbwB_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**2,6-dihydroxy-pseudo-oxynicotine hydrolase; **PDBTitle:** crystal structure of the 2,6-dihydroxy-pseudo-oxynicotine2 hydrolase.
5	c2ecfA_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dipeptidyl peptidase iv; **PDBTitle:** crystal structure of dipeptidyl aminopeptidase iv from2 stenotrophomonas maltophilia
6	d1l7aa_	Alignment		100.0	18	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetyl xylan esterase-like
7	c2eepA_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dipeptidyl aminopeptidase iv, putative; **PDBTitle:** prolyl tripeptidyl aminopeptidase complexed with an inhibitor
8	c3azqA_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aminopeptidase; **PDBTitle:** crystal structure of puromycin hydrolase s511a mutant complexed with2 pgg
9	c2hu7A_	Alignment		100.0	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acylamino-acid-releasing enzyme; **PDBTitle:** binding of inhibitors by acylaminoacyl peptidase
10	c2g5tA_	Alignment		100.0	13	**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
11	c1z68A_	Alignment		100.0	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**fibroblast activation protein, alpha subunit; **PDBTitle:** crystal structure of human fibroblast activation protein alpha

12	c2qtbB_	Alignment		100.0	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
13	d1vlqa_	Alignment		100.0	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetyl xylan esterase-like
14	c3hlkB_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**acyl-coenzyme a thioesterase 2, mitochondrial; **PDBTitle:** crystal structure of human mitochondrial acyl-coa2 thioesterase (acot2)
15	c3g8yA_	Alignment		100.0	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
16	c1l7qA_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cocaine esterase; **PDBTitle:** ser117ala mutant of bacterial cocaine esterase coce
17	c3ib3A_	Alignment		100.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**coce/nond family hydrolase; **PDBTitle:** crystal structure of sacol2612 - coce/nond family hydrolase from2 staphylococcus aureus
18	c3k2iA_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acyl-coenzyme a thioesterase 4; **PDBTitle:** human acyl-coenzyme a thioesterase 4
19	c2hdwB_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hypothetical protein pa2218; **PDBTitle:** crystal structure of hypothetical protein pa2218 from pseudomonas2 aeruginosa
20	d1ju3a2	Alignment		100.0	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**PepX catalytic domain-like
21	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
22	c2o2gA_	Alignment	not modelled	100.0	20	**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
23	d1hlga_	Alignment	not modelled	100.0	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Gastric lipase
24	c2b9vB_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-amino acid ester hydrolase; **PDBTitle:** acetobacter turbidans alpha-amino acid ester hydrolase
25	c2bklB_	Alignment	not modelled	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
26	c1xfdD_	Alignment	not modelled	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
27	d2b9va2	Alignment	not modelled	100.0	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**PepX catalytic domain-like
						PDB header:hydrolase

28	c3ksrA_	Alignment	not modelled	99.9	16	**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
29	d1k8qa_	Alignment	not modelled	99.9	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Gastric lipase
30	c1qfmA_	Alignment	not modelled	99.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein (prolyl oligopeptidase); **PDBTitle:** prolyl oligopeptidase from porcine muscle
31	d1mpxa2	Alignment	not modelled	99.9	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**PepX catalytic domain-like
32	c2xe4A_	Alignment	not modelled	99.9	14	**PDB header:**hydrolase/inhibitor **Chain:** A: **PDB Molecule:**oligopeptidase b; **PDBTitle:** structure of oligopeptidase b from leishmania major
33	c2wtmC_	Alignment	not modelled	99.9	14	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**est1e; **PDBTitle:** est1e from butyrivibrio proteoclasticus
34	c3iumA_	Alignment	not modelled	99.9	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**prolyl endopeptidase; **PDBTitle:** appep_wtx opened state
35	c1yr2A_	Alignment	not modelled	99.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**prolyl oligopeptidase; **PDBTitle:** structural and mechanistic analysis of two prolyl endopeptidases: role2 of inter-domain dynamics in catalysis and specificity
36	c1mpxB_	Alignment	not modelled	99.9	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-amino acid ester hydrolase; **PDBTitle:** alpha-amino acid ester hydrolase labeled with selenomethionine
37	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)
38	c2r11D_	Alignment	not modelled	99.9	10	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**carboxylesterase np; **PDBTitle:** crystal structure of putative hydrolase (2632844) from2 bacillus subtilis at 1.96 a resolution
39	c1cr6A_	Alignment	not modelled	99.9	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**epoxide hydrolase; **PDBTitle:** crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
40	d1qfma2	Alignment	not modelled	99.9	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Prolyl oligopeptidase, C-terminal domain
41	d2fuka1	Alignment	not modelled	99.9	19	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Atu1826-like
42	c3jw8A_	Alignment	not modelled	99.9	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mgll protein; **PDBTitle:** crystal structure of human mono-glyceride lipase
43	c3llcA_	Alignment	not modelled	99.9	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
44	c3qm1A_	Alignment	not modelled	99.9	15	**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
45	c3hjuB_	Alignment	not modelled	99.9	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**monoglyceride lipase; **PDBTitle:** crystal structure of human monoglyceride lipase
46	d2vata1	Alignment	not modelled	99.9	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**O-acetyltransferase
47	c3v48B_	Alignment	not modelled	99.9	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative aminoacrylate hydrolase rutd; **PDBTitle:** crystal structure of the putative alpha/beta hydrolase rutd from2 e.coli
48	c2y6vB_	Alignment	not modelled	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)
49	c3i1iA_	Alignment	not modelled	99.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**homoserine o-acetyltransferase; **PDBTitle:** x-ray crystal structure of homoserine o-acetyltransferase from2 bacillus anthracis
50	d1jfra_	Alignment	not modelled	99.9	22	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Lipase
51	c3doiA_	Alignment	not modelled	99.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase; **PDBTitle:** crystal structure of a thermostable esterase complex with2 paraoxon
52	d1lnsa3	Alignment	not modelled	99.9	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**PepX catalytic domain-like
53	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
54	c3om8A	Alignment	not modelled	99.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable hydrolase;

		Alignment	not modelled	99.9		**PDBTitle:** the crystal structure of a hydrolase from pseudomonas aeruginosa pa01
55	c3h04A_	Alignment	not modelled	99.9	11	**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
56	c2q0xA_	Alignment	not modelled	99.9	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** alpha/beta hydrolase fold protein of unknown function
57	d2i3da1	Alignment	not modelled	99.9	19	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Atu1826-like
58	c2i3dA_	Alignment	not modelled	99.9	19	**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
59	c2xuaH_	Alignment	not modelled	99.9	15	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**3-oxoadipate enol-lactonase; **PDBTitle:** crystal structure of the enol-lactonase from burkholderia2 xenovorans lb400
60	d1mtza_	Alignment	not modelled	99.9	20	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Proline iminopeptidase-like
61	d2hu7a2	Alignment	not modelled	99.9	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acylamino-acid-releasing enzyme, C-terminal donain
62	d1orva2	Alignment	not modelled	99.9	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**DPP6 catalytic domain-like
63	c2qruA_	Alignment	not modelled	99.9	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an alpha/beta hydrolase superfamily protein from2 enterococcus faecalis
64	d2bgra2	Alignment	not modelled	99.9	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**DPP6 catalytic domain-like
65	d1ufoa_	Alignment	not modelled	99.9	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Hypothetical protein TT1662
66	c3bxpA_	Alignment	not modelled	99.9	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
67	d2b61a1	Alignment	not modelled	99.9	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**O-acetyltransferase
68	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
69	c3h2iA_	Alignment	not modelled	99.9	17	**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	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)
71	c3fcxA_	Alignment	not modelled	99.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**s-formylglutathione hydrolase; **PDBTitle:** crystal structure of human esterase d
72	c3nuzF_	Alignment	not modelled	99.9	17	**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
73	c3u1tA_	Alignment	not modelled	99.9	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dmma haloalkane dehalogenase; **PDBTitle:** haloalkane dehalogenase, dmma, of marine microbial origin
74	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
75	c2qmqA_	Alignment	not modelled	99.9	8	**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
76	d1cr6a2	Alignment	not modelled	99.9	18	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Epoxide hydrolase
77	d2pl5a1	Alignment	not modelled	99.9	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**O-acetyltransferase
78	d1b6ga_	Alignment	not modelled	99.9	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Haloalkane dehalogenase
79	c2e3jA_	Alignment	not modelled	99.9	14	**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
80	c1lnsA_	Alignment	not modelled	99.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**x-prolyl dipeptidyl aminopetidase; **PDBTitle:** crystal structure analysis of the x-prolyl dipeptidyl2 aminopeptidase from lactococcus lactis

81	d1wm1a_	Alignment	not modelled	99.9	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Proline iminopeptidase-like
82	c3dyvA_	Alignment	not modelled	99.9	8	**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
83	d1a8qa_	Alignment	not modelled	99.9	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Haloperoxidase
84	d1q0ra_	Alignment	not modelled	99.9	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Aclacinomycin methylesterase RdmC
85	d1zd3a2	Alignment	not modelled	99.9	18	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Epoxide hydrolase
86	c3bwxA_	Alignment	not modelled	99.9	15	**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
87	c3f67A_	Alignment	not modelled	99.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative dienelactone hydrolase; **PDBTitle:** crystal structure of putative dienelactone hydrolase from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
88	c3e3aA_	Alignment	not modelled	99.9	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**possible peroxidase bpoc; **PDBTitle:** the structure of rv0554 from mycobacterium tuberculosis
89	d1dina_	Alignment	not modelled	99.9	19	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Dienelactone hydrolase
90	d1xfda2	Alignment	not modelled	99.9	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**DPP6 catalytic domain-like
91	c3e0xB_	Alignment	not modelled	99.9	13	**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
92	c3oosA_	Alignment	not modelled	99.9	14	**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
93	d1azwa_	Alignment	not modelled	99.9	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Proline iminopeptidase-like
94	c2qjwA_	Alignment	not modelled	99.9	12	**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
95	c2ockA_	Alignment	not modelled	99.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**valacyclovir hydrolase; **PDBTitle:** crystal structure of valacyclovir hydrolase d123n mutant
96	d1m33a_	Alignment	not modelled	99.9	12	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Biotin biosynthesis protein BioH
97	c3bjrA_	Alignment	not modelled	99.8	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
98	d1hkha_	Alignment	not modelled	99.8	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Haloperoxidase
99	c2veoA_	Alignment	not modelled	99.8	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipase a; **PDBTitle:** x-ray structure of candida antarctica lipase a in its2 closed state.
100	c3d0kA_	Alignment	not modelled	99.8	17	**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
101	c1u2eA_	Alignment	not modelled	99.8	16	**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
102	c2xt0A_	Alignment	not modelled	99.8	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**haloalkane dehalogenase; **PDBTitle:** dehalogenase dppa from plesiocystis pacifica sir-i
103	c2xmzA_	Alignment	not modelled	99.8	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hydrolase, alpha/beta hydrolase fold family; **PDBTitle:** structure of menh from s. aureus
104	c3nwoA_	Alignment	not modelled	99.8	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**proline iminopeptidase; **PDBTitle:** crystal structure of proline iminopeptidase mycobacterium smegmatis
105	c2fx5A_	Alignment	not modelled	99.8	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipase; **PDBTitle:** pseudomonas mendocina lipase
106	d1uxoa_	Alignment	not modelled	99.8	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**YdeN-like

107	c3d59B_	Alignment	not modelled	99.8	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**platelet-activating factor acetylhydrolase; **PDBTitle:** crystal structure of human plasma platelet activating2 factor acetylhydrolase
108	c3ls2D_	Alignment	not modelled	99.8	15	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**s-formylglutathione hydrolase; **PDBTitle:** crystal structure of an s-formylglutathione hydrolase from2 pseudoalteromonas haloplanktis tac125
109	c1zoiC_	Alignment	not modelled	99.8	16	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**esterase; **PDBTitle:** crystal structure of a stereoselective esterase from2 pseudomonas putida ifo12996
110	c2rauA_	Alignment	not modelled	99.8	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative esterase; **PDBTitle:** crystal structure of a putative lipase (np_343859.1) from sulfolobus2 solfataricus at 1.85 a resolution
111	c3fsgC_	Alignment	not modelled	99.8	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
112	c3ed1E_	Alignment	not modelled	99.8	15	**PDB header:**hydrolase receptor **Chain:** E: **PDB Molecule:**gibberellin receptor gid1; **PDBTitle:** crystal structure of rice gid1 complexed with ga3
113	c3kdaB_	Alignment	not modelled	99.8	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cftr inhibitory factor (cif); **PDBTitle:** crystal structure of the cftr inhibitory factor cif with the h269a2 mutation
114	d1a8sa_	Alignment	not modelled	99.8	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Haloperoxidase
115	c2vf2A_	Alignment	not modelled	99.8	18	**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
116	c3a2nF_	Alignment	not modelled	99.8	14	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**haloalkane dehalogenase; **PDBTitle:** crystal structure of dbja (wild type type ii p21)
117	d1a88a_	Alignment	not modelled	99.8	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Haloperoxidase
118	c3fobA_	Alignment	not modelled	99.8	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**bromoperoxidase; **PDBTitle:** crystal structure of bromoperoxidase from bacillus anthracis
119	d2rhwa1	Alignment	not modelled	99.8	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carbon-carbon bond hydrolase
120	d1c4xa_	Alignment	not modelled	99.8	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carbon-carbon bond hydrolase