Phyre2

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Description	RVBD0782_(ptrBb)_874735_876393
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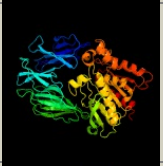
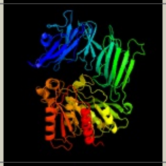
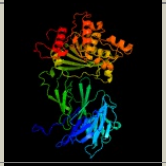
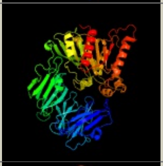
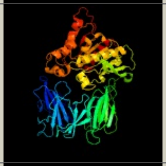
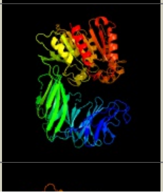
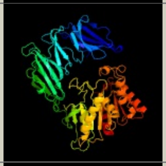
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4bp9A_	Alignment		100.0	41	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**oligopeptidasse b; **PDBTitle:** oligopeptidase b from trypanosoma brucei with covalently bound2 antipain - closed form
2	c2xe4A_	Alignment		100.0	40	**PDB header:**hydrolase/inhibitor **Chain:** A: **PDB Molecule:**oligopeptidase b; **PDBTitle:** structure of oligopeptidase b from leishmania major
3	c1yr2A_	Alignment		100.0	25	**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
4	c2bklB_	Alignment		100.0	28	**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
5	c1qfmA_	Alignment		100.0	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein (prolyl oligopeptidase); **PDBTitle:** prolyl oligopeptidase from porcine muscle
6	c5n4dA_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**prolyl oligopeptidase; **PDBTitle:** prolyl oligopeptidase b from galerina marginata bound to 25mer2 macrocyclization substrate - d661a mutant
7	c3iumA_	Alignment		100.0	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**prolyl endopeptidase; **PDBTitle:** appep_wtx opened state
8	c5uzwD_	Alignment		100.0	23	**PDB header:**lyase **Chain:** D: **PDB Molecule:**peptide cyclase 1; **PDBTitle:** pcy1 g696insertion variant in complex with follower peptide and the2 covalent inhibitor zpp
9	c5uw7B_	Alignment		100.0	21	**PDB header:**lyase **Chain:** B: **PDB Molecule:**peptide cyclase 1; **PDBTitle:** pcy1 y481f variant in complex with follower peptide
10	c4hvtA_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**post-proline cleaving enzyme; **PDBTitle:** structure of a post-proline cleaving enzyme from rickettsia typhi
11	c5t88B_	Alignment		100.0	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**prolyl endopeptidase; **PDBTitle:** prolyl oligopeptidase from pyrococcus furiosus

12	c5l8sD_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**amino acyl peptidase; **PDBTitle:** the crystal structure of a cold-adapted acylaminoacyl peptidase2 reveals a novel quaternary architecture based on the arm-exchange3 mechanism
13	c5oljA_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dipeptidyl peptidase iv; **PDBTitle:** crystal structure of porphyromonas gingivalis dipeptidyl peptidase 4
14	c3azqA_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aminopeptidase; **PDBTitle:** crystal structure of puromycin hydrolase s511a mutant complexed with2 pgg
15	c2g5tA_	Alignment		100.0	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dipeptidyl peptidase 4; **PDBTitle:** crystal structure of human dipeptidyl peptidase iv (dppiv) complexed2 with cyanopyrrolidine (c5-pro-pro) inhibitor 21ag
16	c2eepA_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dipeptidyl aminopeptidase iv, putative; **PDBTitle:** prolyl tripeptidyl aminopeptidase complexed with an inhibitor
17	c4hxgJ_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** J: **PDB Molecule:**putative uncharacterized protein ph0594; **PDBTitle:** pyrococcus horikoshii acylaminoacyl peptidase (orthorhombic crystal2 form)
18	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
19	c4q1vA_	Alignment		100.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative dipeptidyl aminopeptidase iv; **PDBTitle:** crystal structure of a putative dipeptidyl aminopeptidase iv2 (bacova_01349) from bacteroides ovatus atcc 8483 at 2.48 a resolution
20	c2qtbB_	Alignment		100.0	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dipeptidyl peptidase 4; **PDBTitle:** human dipeptidyl peptidase iv/cd26 in complex with a 4-aryl2 cyclohexylalanine inhibitor
21	c4wjlB_	Alignment	not modelled	100.0	13	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**inactive dipeptidyl peptidase 10; **PDBTitle:** structure of human dipeptidyl peptidase 10 (dppy): a modulator of2 neuronal kv4 channels
22	c1z68A_	Alignment	not modelled	100.0	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**fibroblast activation protein, alpha subunit; **PDBTitle:** crystal structure of human fibroblast activation protein alpha
23	c5yznA_	Alignment	not modelled	100.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acyl-peptide hydrolase, putative; **PDBTitle:** crystal structure of s9 peptidase (active form) from deinococcus2 radiodurans r1
24	c6eoqC_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**dipeptidyl peptidase 9; **PDBTitle:** dpp9 - apo
25	c5jrlC_	Alignment	not modelled	100.0	13	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**dipeptidyl aminopeptidases/acylaminoacyl-peptidases-like **PDBTitle:** crystal structure of the sphingopyxin i lasso peptide isopeptidase2 spi-isop (native)
26	c5txeA_	Alignment	not modelled	100.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atxe2; **PDBTitle:** atxe2 isopeptidase - s527a variant with astexin3-dc4 bound
27	c6eorD_	Alignment	not modelled	100.0	16	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**dipeptidyl peptidase 9; **PDBTitle:** dpp9 - 1g244
28	c2hu7A_	Alignment	not modelled	100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acylamino-acid-releasing enzyme; **PDBTitle:** binding of inhibitors by acylaminoacyl peptidase
						PDB header:hydrolase

29	c6eotG_	Alignment	not modelled	100.0	13	**Chain:** G: **PDB Molecule:**dipeptidyl peptidase 8; **PDBTitle:** dpp8 - slrflyeg, space group 19
30	c6eosB_	Alignment	not modelled	100.0	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dipeptidyl peptidase 8; **PDBTitle:** dpp8 - apo, space group 19
31	c1xfdD_	Alignment	not modelled	100.0	14	**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
32	d1qfma2	Alignment	not modelled	100.0	30	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Prolyl oligopeptidase, C-terminal domain
33	c3doiA_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase; **PDBTitle:** crystal structure of a thermostable esterase complex with2 paraoxon
34	d2hu7a2	Alignment	not modelled	100.0	21	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acylamino-acid-releasing enzyme, C-terminal donain
35	c3k2iA_	Alignment	not modelled	100.0	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acyl-coenzyme a thioesterase 4; **PDBTitle:** human acyl-coenzyme a thioesterase 4
36	d2jbwa1	Alignment	not modelled	100.0	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**2,6-dihydropseudooxynicotine hydrolase-like
37	c2jbwB_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**2,6-dihydroxy-pseudo-oxynicotine hydrolase; **PDBTitle:** crystal structure of the 2,6-dihydroxy-pseudo-oxynicotine hydrolase.
38	d2bgra2	Alignment	not modelled	100.0	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**DPP6 catalytic domain-like
39	d1orva2	Alignment	not modelled	100.0	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**DPP6 catalytic domain-like
40	d1vlqa_	Alignment	not modelled	100.0	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetyl xylan esterase-like
41	c3hlkB_	Alignment	not modelled	100.0	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**acyl-coenzyme a thioesterase 2, mitochondrial; **PDBTitle:** crystal structure of human mitochondrial acyl-coa thioesterase (acot2)
42	c3fnbB_	Alignment	not modelled	100.0	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**acylaminoacyl peptidase smu_737; **PDBTitle:** crystal structure of acylaminoacyl peptidase smu_737 from2 streptococcus mutans ua159
43	d2b9va2	Alignment	not modelled	100.0	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**PepX catalytic domain-like
44	c4eziA_	Alignment	not modelled	100.0	13	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a putative hydrolase (lpg1103) from legionella2 pneumophila subsp. pneumophila str. philadelphia 1 at 1.15 a3 resolution
45	c6gocA_	Alignment	not modelled	100.0	14	**PDB header:**carbohydrate **Chain:** A: **PDB Molecule:**duf3826 domain-containing protein; **PDBTitle:** methylesterase bt1017
46	d1mpxa2	Alignment	not modelled	100.0	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**PepX catalytic domain-like
47	c4pf1D_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**peptidase s15/coce/nond; **PDBTitle:** crystal structure of aminopeptidase from marine sediment archaeon2 thaumarchaeota archaeon
48	c4h18D_	Alignment	not modelled	100.0	11	**PDB header:**transferase **Chain:** D: **PDB Molecule:**cmt1; **PDBTitle:** three dimensional structure of corynomycoloyl tranferase c
49	c3bxpA_	Alignment	not modelled	100.0	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
50	c2b9vB_	Alignment	not modelled	100.0	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-amino acid ester hydrolase; **PDBTitle:** acetobacter turbidans alpha-amino acid ester hydrolase
51	d1ju3a2	Alignment	not modelled	100.0	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**PepX catalytic domain-like
52	d1xfda2	Alignment	not modelled	100.0	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**DPP6 catalytic domain-like
53	c1l7qA_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cocaine esterase; **PDBTitle:** ser117ala mutant of bacterial cocaine esterase coce
54	c4zi5A_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**p91; **PDBTitle:** crystal structure of dienelactone hydrolase-like promiscuous2 phospotriesterase p91 from metagenomic libraries
						PDB header:hydrolase

55	c6fkxD_	Alignment	not modelled	100.0	15	**Chain:** D: **PDB Molecule:**acetyl xylan esterase; **PDBTitle:** crystal structure of an acetyl xylan esterase from a desert metagenome
56	c3ls2D_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**s-formylglutathione hydrolase; **PDBTitle:** crystal structure of an s-formylglutathione hydrolase from2 pseudoalteromonas haloplanktis tac125
57	c3ib3A_	Alignment	not modelled	100.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**coce/nond family hydrolase; **PDBTitle:** crystal structure of sacol2612 - coce/nond family hydrolase from2 staphylococcus aureus
58	d1l7aa_	Alignment	not modelled	100.0	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetyl xylan esterase-like
59	d1jkma_	Alignment	not modelled	100.0	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase
60	c6agqE_	Alignment	not modelled	100.0	19	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**acetyl xylan esterase; **PDBTitle:** acetyl xylan esterase from paenibacillus sp. r4
61	c5f2hA_	Alignment	not modelled	100.0	12	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** 2.75 angstrom resolution crystal structure of uncharacterized protein2 from bacillus cereus atcc 10987
62	c5hc4A_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipolytic enzyme; **PDBTitle:** structure of esterase est22
63	c5x6sB_	Alignment	not modelled	100.0	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**acetylxylan esterase a; **PDBTitle:** acetyl xylan esterase from aspergillus awamori
64	c5g59A_	Alignment	not modelled	100.0	13	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**esterase; **PDBTitle:** structure of the pyrococcus furiosus esterase pf2001 with space group2 p3121
65	c4b6gA_	Alignment	not modelled	100.0	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative esterase; **PDBTitle:** the crystal structure of the neisserial esterase d.
66	c3fcxA_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**s-formylglutathione hydrolase; **PDBTitle:** crystal structure of human esterase d
67	d1lns a3	Alignment	not modelled	100.0	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**PepX catalytic domain-like
68	c5cxxC_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**ferulic acid esterase, amce1/fae1a; **PDBTitle:** structure of a ce1 ferulic acid esterase, amce1/fae1a, from2 anaeromyces mucronatus in complex with ferulic acid
69	c4q3kB_	Alignment	not modelled	100.0	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mgs-m1; **PDBTitle:** crystal structure of mgs-m1, an alpha/beta hydrolase enzyme from a2 medee basin deep-sea metagenome library
70	c3h2iA_	Alignment	not modelled	100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase; **PDBTitle:** crystal structure of n228w mutant of the rice cell wall2 degrading esterase lipa from xanthomonas oryzae
71	c3e4dD_	Alignment	not modelled	100.0	14	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**esterase d; **PDBTitle:** structural and kinetic study of an s-formylglutathione hydrolase from2 agrobacterium tumefaciens
72	c2o2gA_	Alignment	not modelled	100.0	17	**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
73	c5aoaA_	Alignment	not modelled	100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase; **PDBTitle:** the structure of a novel thermophilic esterase from the planctomycetes2 species, thermogutta terrifontis, est2-propionate bound
74	c4ao6A_	Alignment	not modelled	99.9	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase; **PDBTitle:** native structure of a novel cold-adapted esterase from an2 arctic intertidal metagenomic library
75	c1mpxB_	Alignment	not modelled	99.9	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-amino acid ester hydrolase; **PDBTitle:** alpha-amino acid ester hydrolase labeled with selenomethionine
76	d1qfma1	Alignment	not modelled	99.9	16	**Fold:**7-bladed beta-propeller **Superfamily:**Peptidase/esterase 'gauge' domain **Family:**Prolyl oligopeptidase, N-terminal domain
77	c3i6yA_	Alignment	not modelled	99.9	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase apc40077; **PDBTitle:** structure of an esterase from the oil-degrading bacterium oleispira2 antarctica
78	c3mveB_	Alignment	not modelled	99.9	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**upf0255 protein vv1_0328; **PDBTitle:** crystal structure of a novel pyruvate decarboxylase
79	c3wlaA_	Alignment	not modelled	99.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**oxidized polyvinyl alcohol hydrolase; **PDBTitle:** crystal structure of soph native
80	c4j7aB_	Alignment	not modelled	99.9	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**esterase; **PDBTitle:** crystal structure of est25 - a bacterial homolog of hormone-sensitive2 lipase from a metagenomic library
						PDB header:hydrolase **Chain:** A: **PDB Molecule:**ferric enterobactin esterase;

81	c6gi5A_	Alignment	not modelled	99.9	14	**PDBTitle:** crystal structure of the ferric enterobactin esterase (pfee) from2 pseudomonas aeruginosa in complex with the tris-catechol vector
82	c3d0kA_	Alignment	not modelled	99.9	12	**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
83	c3fcyB_	Alignment	not modelled	99.9	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
84	c2veoA_	Alignment	not modelled	99.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipase a; **PDBTitle:** x-ray structure of candida antarctica lipase a in its closed state.
85	c3ed1E_	Alignment	not modelled	99.9	15	**PDB header:**hydrolase receptor **Chain:** E: **PDB Molecule:**gibberellin receptor gid1; **PDBTitle:** crystal structure of rice gid1 complexed with ga3
86	c6guiA_	Alignment	not modelled	99.9	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**siderophore esterase iroe-like, putative; **PDBTitle:** siderophore hydrolase estb mutant h267n from aspergillus fumigatus
87	c5jd5A_	Alignment	not modelled	99.9	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mgs-mile3; **PDBTitle:** crystal structure of mgs-mile3, an alpha/beta hydrolase enzyme from2 the metagenome of pyrene-phenanthrene enrichment culture with3 sediment sample of milazzo harbor, italy
88	d1sfra_	Alignment	not modelled	99.9	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Mycobacterial antigens
89	c4zv9E_	Alignment	not modelled	99.9	15	**PDB header:**structural genomics, unknown function **Chain:** E: **PDB Molecule:**uncharacterized protein; **PDBTitle:** 2.00 angstrom resolution crystal structure of an uncharacterized2 protein from escherichia coli o157:h7 str. sakai
90	c4v2iB_	Alignment	not modelled	99.9	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**esterase/lipase; **PDBTitle:** biochemical characterization and structural analysis of a2 new cold-active and salt tolerant esterase from the marine3 bacterium thalassospira sp
91	c4xvcG_	Alignment	not modelled	99.9	14	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**esterase e40; **PDBTitle:** crystal structure of an esterase from the bacterial hormone-sensitive2 lipase (hsl) family
92	c4c87A_	Alignment	not modelled	99.9	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase; **PDBTitle:** esterase lpest1 from lactobacillus plantarum wcfs1
93	c4krxB_	Alignment	not modelled	99.9	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**acetyl esterase; **PDBTitle:** structure of aes from e. coli
94	c3ksrA_	Alignment	not modelled	99.9	13	**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
95	c2wtmC_	Alignment	not modelled	99.9	16	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**est1e; **PDBTitle:** est1e from butyrivibrio proteoclasticus
96	c2o7vA_	Alignment	not modelled	99.9	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cxe carboxylesterase; **PDBTitle:** carboxylesterase aecxe1 from actinidia eriantha covalently inhibited2 by paraoxon
97	c4q3oB_	Alignment	not modelled	99.9	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mgs-mt1; **PDBTitle:** crystal structure of mgs-mt1, an alpha/beta hydrolase enzyme from a2 lake matapan deep-sea metagenome library
98	c4zrsA_	Alignment	not modelled	99.9	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase; **PDBTitle:** crystal structure of a cloned feruloyl esterase from a soil2 metagenomic library
99	c2zshA_	Alignment	not modelled	99.9	14	**PDB header:**hormone receptor **Chain:** A: **PDB Molecule:**probable gibberellin receptor gid1l1; **PDBTitle:** structural basis of gibberellin(ga3)-induced della2 recognition by the gibberellin receptor
100	c4wy8A_	Alignment	not modelled	99.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase; **PDBTitle:** structural analysis of two fungal esterases from rhizomucor miehei2 explaining their substrate specificity
101	c3f67A_	Alignment	not modelled	99.9	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative dienelactone hydrolase; **PDBTitle:** crystal structure of putative dienelactone hydrolase from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
102	c6gunB_	Alignment	not modelled	99.9	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**estb from aspergillus nidulans; **PDBTitle:** siderophore hydrolase estb from aspergillus nidulans
103	c3qh4A_	Alignment	not modelled	99.9	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase lipw; **PDBTitle:** crystal structure of esterase lipw from mycobacterium marinum
104	c4q05A_	Alignment	not modelled	99.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase e25; **PDBTitle:** crystal structure of an esterase e25
105	c3ga7A_	Alignment	not modelled	99.9	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acetyl esterase; **PDBTitle:** 1.55 angstrom crystal structure of an acetyl esterase from salmonella2 typhimurium
106	c4ob7A_	Alignment	not modelled	99.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha/beta hydrolase fold-3 domain protein;

						PDBTitle: crystal structure of esterase rppe mutant w187h
107	c5cmlA_	Alignment	not modelled	99.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**osmc family protein; **PDBTitle:** crystal structure of the esterase domain from rhodothermus marinus2 rmar_1206 protein
108	d1pv1a_	Alignment	not modelled	99.9	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Hypothetical esterase YJL068C
109	d1lzla_	Alignment	not modelled	99.9	18	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase
110	c4wfiA_	Alignment	not modelled	99.9	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cutinase; **PDBTitle:** crystal structure of pet-degrading cutinase cut190 s226p mutant in2 ca(2+)-free state
111	d1f0na_	Alignment	not modelled	99.9	11	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Mycobacterial antigens
112	c4q82A_	Alignment	not modelled	99.9	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phospholipase/carboxylesterase; **PDBTitle:** crystal structure of phospholipase/carboxylesterase from haliangium2 ochraceum
113	c5jd4D_	Alignment	not modelled	99.9	18	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**lae6; **PDBTitle:** crystal structure of lae6 ser161ala mutant, an alpha/beta hydrolase2 enzyme from the metagenome of lake arreo, spain
114	d2i3da1	Alignment	not modelled	99.9	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Atu1826-like
115	c2i3dA_	Alignment	not modelled	99.9	14	**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
116	c6aaeA_	Alignment	not modelled	99.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase; **PDBTitle:** crystal structure of chloramphenicol-metabolizaing enzyme estdl136
117	c4z8zA_	Alignment	not modelled	99.9	18	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the hypothetical protein from ruminiclostridium2 thermocellum atcc 27405
118	c5xg0A_	Alignment	not modelled	99.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**poly(ethylene terephthalate) hydrolase; **PDBTitle:** crystal structure of a novel pet hydrolase from ideonella sakaiensis2 201-f6
119	c3bjrA_	Alignment	not modelled	99.9	15	**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
120	c4n5iX_	Alignment	not modelled	99.9	14	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**esterase/lipase; **PDBTitle:** crystal structure of a c8-c4 sn3 inhibited esterase b from2 lactobacillus rhamnosis