























# Phyre2

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Description	RVBD0421c_(-)_507135_507764
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2hu7A_</a>	 Alignment		100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> acylamino-acid-releasing enzyme; <b>PDBTitle:</b> binding of inhibitors by acylaminoacyl peptidase
2	<a href="#">c2jwbB_</a>	 Alignment		100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 2,6-dihydroxy-pseudo-oxynicotine hydrolase; <b>PDBTitle:</b> crystal structure of the 2,6-dihydroxy-pseudo-oxynicotine hydrolase.
3	<a href="#">d2fuka1</a>	 Alignment		100.0	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Atu1826-like
4	<a href="#">c3azqA_</a>	 Alignment		100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> aminopeptidase; <b>PDBTitle:</b> crystal structure of puromycin hydrolase s511a mutant complexed with2 pgg
5	<a href="#">c2o2gA_</a>	 Alignment		100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dienelactone hydrolase; <b>PDBTitle:</b> crystal structure of dienelactone hydrolase (yp_324580.1) from2 anabaena variabilis atcc 29413 at 1.92 a resolution
6	<a href="#">d2jba1</a>	 Alignment		100.0	17	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> 2,6-dihydroseudooxynicotine hydrolase-like
7	<a href="#">c3llcA_</a>	 Alignment		100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative hydrolase; <b>PDBTitle:</b> crystal structure of putative hydrolase (yp_002548124.1) from2 agrobacterium vitis s4 at 1.80 a resolution
8	<a href="#">c3trdA_</a>	 Alignment		100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha/beta hydrolase; <b>PDBTitle:</b> structure of an alpha-beta serine hydrolase homologue from coxiella2 burnetii
9	<a href="#">c2ecfA_</a>	 Alignment		100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dipeptidyl peptidase iv; <b>PDBTitle:</b> crystal structure of dipeptidyl aminopeptidase iv from2 stenotrophomonas maltophilia
10	<a href="#">c3hkB_</a>	 Alignment		100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> acyl-coenzyme a thioesterase 2, mitochondrial; <b>PDBTitle:</b> crystal structure of human mitochondrial acyl-coa thioesterase (acot2)
11	<a href="#">c2wtmC_</a>	 Alignment		100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> est1e; <b>PDBTitle:</b> est1e from butyrvibrio proteoclasticus

12	<a href="#">c4hxgl_</a>	Alignment		100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> J: <b>PDB Molecule:</b> putative uncharacterized protein ph0594; <b>PDBTitle:</b> pyrococcus horikoshii acylaminoacyl peptidase (orthorhombic crystal2 form)
13	<a href="#">c5l8sD_</a>	Alignment		100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> amino acyl peptidase; <b>PDBTitle:</b> the crystal structure of a cold-adapted acylaminoacyl peptidase2 reveals a novel quaternary architecture based on the arm-exchange3 mechanism
14	<a href="#">c3mveB_</a>	Alignment		100.0	13	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> upf0255 protein vw1_0328; <b>PDBTitle:</b> crystal structure of a novel pyruvate decarboxylase
15	<a href="#">d1ufoa_</a>	Alignment		100.0	21	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Hypothetical protein TT1662
16	<a href="#">c5t88B_</a>	Alignment		100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> prolyl endopeptidase; <b>PDBTitle:</b> prolyl oligopeptidase from pyrococcus furiosus
17	<a href="#">c2qjwA_</a>	Alignment		99.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein xcc1541; <b>PDBTitle:</b> crystal structure of a putative hydrolase of the alpha/beta2 superfamily (xcc1541) from xanthomonas campestris pv. campestris at3 1.35 a resolution
18	<a href="#">c2i3dA_</a>	Alignment		99.9	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein atu1826; <b>PDBTitle:</b> crystal structure of protein of unknown function atu1826, a putative2 alpha/beta hydrolase from agrobacterium tumefaciens
19	<a href="#">d2i3da1</a>	Alignment		99.9	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Atu1826-like
20	<a href="#">c3fnbB_</a>	Alignment		99.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> acylaminoacyl peptidase smu_737; <b>PDBTitle:</b> crystal structure of acylaminoacyl peptidase smu_737 from streptococcus mutans ua159
21	<a href="#">c3k2iA_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-coenzyme a thioesterase 4; <b>PDBTitle:</b> human acyl-coenzyme a thioesterase 4
22	<a href="#">c3jw8A_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mgll protein; <b>PDBTitle:</b> crystal structure of human mono-glyceride lipase
23	<a href="#">c4d9jl_</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> de novo protein <b>Chain:</b> I: <b>PDB Molecule:</b> designed 16nm tetrahedral protein cage containing non-haem <b>PDBTitle:</b> structure of a 16 nm protein cage designed by fusing symmetric2 oligomeric domains
24	<a href="#">c5oljA_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dipeptidyl peptidase iv; <b>PDBTitle:</b> crystal structure of porphyromonas gingivalis dipeptidyl peptidase 4
25	<a href="#">c3qm1A_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cinnamoyl esterase; <b>PDBTitle:</b> crystal structure of the lactobacillus johnsonii cinnamoyl esterase2 lj0536 s106a mutant in complex with ethylferulate, form ii
26	<a href="#">c4z8zA_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of the hypothetical protein from ruminiclostridium2 thermocellum atcc 27405
27	<a href="#">c5yznA_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-peptide hydrolase, putative; <b>PDBTitle:</b> crystal structure of s9 peptidase (active form) from deinococcus2 radiodurans r1
28	<a href="#">c6eosB_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dipeptidyl peptidase 8; <b>PDBTitle:</b> dpp8 - apo, space group 19

29	<a href="#">c4ao6A</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> native structure of a novel cold-adapted esterase from an2 arctic intertidal metagenomic library
30	<a href="#">c2eepA</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dipeptidyl aminopeptidase iv, putative; <b>PDBTitle:</b> prolyl tripeptidyl aminopeptidase complexed with an inhibitor
31	<a href="#">c3ksrA</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative serine hydrolase; <b>PDBTitle:</b> crystal structure of a putative serine hydrolase (xcc3885) from2 xanthomonas campestris pv. campestris at 2.69 a resolution
32	<a href="#">c4q1vA</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative dipeptidyl aminopeptidase iv; <b>PDBTitle:</b> crystal structure of a putative dipeptidyl aminopeptidase iv2 (bacova_01349) from bacteroides ovatus atcc 8483 at 2.48 a resolution
33	<a href="#">c6eotG</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> dipeptidyl peptidase 8; <b>PDBTitle:</b> dpp8 - slrflyeg, space group 19
34	<a href="#">c4zi5A</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> p91; <b>PDBTitle:</b> crystal structure of dieneactone hydrolase-like promiscuous2 phosphotriesterase p91 from metagenomic libraries
35	<a href="#">c2g5tA</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dipeptidyl peptidase 4; <b>PDBTitle:</b> crystal structure of human dipeptidyl peptidase iv (dppiv) complexed2 with cyanopyrrolidine (c5-pro-pro) inhibitor 21ag
36	<a href="#">c1z68A</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> fibroblast activation protein, alpha subunit; <b>PDBTitle:</b> crystal structure of human fibroblast activation protein alpha
37	<a href="#">c3hjuB</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> monoglyceride lipase; <b>PDBTitle:</b> crystal structure of human monoglyceride lipase
38	<a href="#">d1l7aa</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Acetyl xylan esterase-like
39	<a href="#">c6eoaC</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> dipeptidyl peptidase 9; <b>PDBTitle:</b> dpp9 - apo
40	<a href="#">c2qtbB</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dipeptidyl peptidase 4; <b>PDBTitle:</b> human dipeptidyl peptidase iv/cd26 in complex with a 4-aryl2 cyclohexylalanine inhibitor
41	<a href="#">d1k8qa</a>	Alignment	not modelled	99.9	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Gastric lipase
42	<a href="#">c3h04A</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> the crystal structure of the protein with unknown function from2 staphylococcus aureus subsp. aureus mu50
43	<a href="#">d1uxoa</a>	Alignment	not modelled	99.9	11	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> YdeN-like
44	<a href="#">c3i28A</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> epoxide hydrolase 2; <b>PDBTitle:</b> crystal structure of soluble epoxide hydrolase
45	<a href="#">c5xg0A</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> poly(ethylene terephthalate) hydrolase; <b>PDBTitle:</b> crystal structure of a novel pet hydrolase from ideonella sakaiensis2 201-f6
46	<a href="#">c5cmlA</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> osmc family protein; <b>PDBTitle:</b> crystal structure of the esterase domain from rhodothermus marinus2 rmar_1206 protein
47	<a href="#">c5f2hA</a>	Alignment	not modelled	99.9	10	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> 2.75 angstrom resolution crystal structure of uncharacterized protein2 from bacillus cereus atcc 10987
48	<a href="#">c1qfmA</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (prolyl oligopeptidase); <b>PDBTitle:</b> prolyl oligopeptidase from porcine muscle
49	<a href="#">c1cr6A</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> epoxide hydrolase; <b>PDBTitle:</b> crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
50	<a href="#">c6eicA</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mycobacterium tuberculosis monoglyceride lipase; <b>PDBTitle:</b> crystal structure of rv0183, a monoglyceride lipase from mycobacterium2 tuberculosis
51	<a href="#">c6eorD</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> dipeptidyl peptidase 9; <b>PDBTitle:</b> dpp9 - 1g244
52	<a href="#">c2bklB</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> prolyl endopeptidase; <b>PDBTitle:</b> structural and mechanistic analysis of two prolyl2 endopeptidases: role of inter-domain dynamics in3 catalysis and specificity
53	<a href="#">c5hdfB</a>	Alignment	not modelled	99.9	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hydrolase; <b>PDBTitle:</b> hydrolase semet-stna
54	<a href="#">c4wj1B</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> inactive dipeptidyl peptidase 10; <b>PDBTitle:</b> structure of human dipeptidyl peptidase 10 (dppy): a

						modulator of2 neuronal kv4 channels
55	<a href="#">d1hlga_</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Gastric lipase
56	<a href="#">c5txeA_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atxe2; <b>PDBTitle:</b> atxe2 isopeptidase - s527a variant with astexin3-dc4 bound
57	<a href="#">c5oluA_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha/beta hydrolase family protein; <b>PDBTitle:</b> the crystal structure of a highly thermostable carboxyl esterase from2 bacillus coagulans in complex with glycerol
58	<a href="#">c5g59A_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> structure of the pyrococcus furiosus esterase pf2001 with space group2 p3121
59	<a href="#">d1b6ga_</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloalkane dehalogenase
60	<a href="#">c5xb6D_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized protein ycyj; <b>PDBTitle:</b> crystal structure of ycyj from e. coli
61	<a href="#">c2hdwB_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein pa2218; <b>PDBTitle:</b> crystal structure of hypothetical protein pa2218 from pseudomonas2 aeruginosa
62	<a href="#">d1jfra_</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Lipase
63	<a href="#">c5esrA_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> haloalkane dehalogenase; <b>PDBTitle:</b> crystal structure of haloalkane dehalogenase (dcca) from caulobacter2 crescentus
64	<a href="#">c3bxpA_</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative lipase/esterase; <b>PDBTitle:</b> crystal structure of a putative carboxylesterase (lp_2923) from2 lactobacillus plantarum wcf51 at 1.70 a resolution
65	<a href="#">c3v48B_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative aminoacrylate hydrolase rutd; <b>PDBTitle:</b> crystal structure of the putative alpha/beta hydrolase rutd from2 e.coli
66	<a href="#">c2e3jA_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> epoxide hydrolase ephb; <b>PDBTitle:</b> the crystal structure of epoxide hydrolase b (rv1938) from2 mycobacterium tuberculosis at 2.1 angstrom
67	<a href="#">c2y6vB_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> peroxisomal membrane protein lpx1; <b>PDBTitle:</b> peroxisomal alpha-beta-hydrolase lpx1 (yor084w) from saccharomyces2 cerevisiae (crystal form i)
68	<a href="#">d1dina_</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Dienelactone hydrolase
69	<a href="#">c6avyA_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-protein thioesterase 2; <b>PDBTitle:</b> crystal structure of zea mays acyl-protein thioesterase 2
70	<a href="#">c4zwnD_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> monoglyceride lipase; <b>PDBTitle:</b> crystal structure of a soluble variant of the monoglyceride lipase2 from saccharomyces cerevisiae
71	<a href="#">c4l0cA_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> deformylase; <b>PDBTitle:</b> crystal structure of the n-fopmylmaaleamic acid deformylase nfo(s94a)2 from pseudomonas putida s16
72	<a href="#">c4pw0A_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha/beta hydrolase fold protein; <b>PDBTitle:</b> alpha/beta hydrolase fold protein from chitinophaga pinensis
73	<a href="#">d1vlqa_</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Acetyl xylan esterase-like
74	<a href="#">c3fcyB_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> xylan esterase 1; <b>PDBTitle:</b> crystal structure of acetyl xylan esterase 1 from2 thermoanaerobacterium sp. jw/sl ys485
75	<a href="#">c6gupB_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> siderophore biosynthesis lipase/esterase, putative; <b>PDBTitle:</b> siderophore hydrolase estb from aspergillus fumigatus
76	<a href="#">c1xfdD_</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> dipeptidyl aminopeptidase-like protein 6; <b>PDBTitle:</b> structure of a human a-type potassium channel accelerating factor2 dppx, a member of the dipeptidyl aminopeptidase family
77	<a href="#">c2q0xA_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> alpha/beta hydrolase fold protein of unknown function
78	<a href="#">c2xe4A_</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> hydrolase/inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> oligopeptidase b; <b>PDBTitle:</b> structure of oligopeptidase b from leishmania major
79	<a href="#">c6aggE_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> acetyl xylan esterase; <b>PDBTitle:</b> acetyl xylan esterase from paenibacillus sp. r4
80	<a href="#">c4q3kB_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> mgs-m1; <b>PDBTitle:</b> crystal structure of mgs-m1, an alpha/beta hydrolase enzyme from a2 medee basin deep-sea metagenome library

81	<a href="#">c3bjrA</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative carboxylesterase; <b>PDBTitle:</b> crystal structure of a putative carboxylesterase (lp_1002) from2 lactobacillus plantarum wcf51 at 2.09 a resolution
82	<a href="#">c4bp9A</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> oligopeptidase b; <b>PDBTitle:</b> oligopeptidase b from trypanosoma brucei with covalently bound2 antipain - closed form
83	<a href="#">c2qruA</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of an alpha/beta hydrolase superfamily protein from2 enterococcus faecalis
84	<a href="#">c3visB</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> crystal structure of cutinase est119 from thermobifida alba ahk119
85	<a href="#">d1qfma2</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Prolyl oligopeptidase, C-terminal domain
86	<a href="#">c2vavL</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> transferase <b>Chain:</b> L: <b>PDB Molecule:</b> acetyl-coa--deacetylcephalosporin c acetyltransferase; <b>PDBTitle:</b> crystal structure of deacetylcephalosporin c acetyltransferase (dac-2 soak)
87	<a href="#">c5d6oB</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> homoserine o-acetyltransferase; <b>PDBTitle:</b> orthorhombic crystal structure of an acetyler hydrolase from2 corynebacterium glutamicum
88	<a href="#">c3rm3A</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> thermostable monoacylglycerol lipase; <b>PDBTitle:</b> crystal structure of monoacylglycerol lipase from bacillus sp. h257
89	<a href="#">c4wfiA</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cutinase; <b>PDBTitle:</b> crystal structure of pet-degrading cutinase cut190 s226p mutant in2 ca(2+)-free state
90	<a href="#">c3qvmA</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> olei00960; <b>PDBTitle:</b> the structure of olei00960, a hydrolase from oleispira antarctica
91	<a href="#">c6brtB</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> d3-cth-d14-d-ring; <b>PDBTitle:</b> f-box protein cth with hydrolase
92	<a href="#">c4h0cA</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phospholipase/carboxylesterase; <b>PDBTitle:</b> crystal structure of phospholipase/carboxylesterase from dyadobacter2 fermentans dsm 18053
93	<a href="#">d2b61a1</a>	Alignment	not modelled	99.9	18	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> O-acetyltransferase
94	<a href="#">c5jrlC</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> dipeptidyl aminopeptidases/acylaminoacyl-peptidases-like <b>PDBTitle:</b> crystal structure of the sphingopyxin i lasso peptide isopeptidase2 spi-isop (native)
95	<a href="#">c3dyvA</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase d; <b>PDBTitle:</b> snapshots of esterase d from lactobacillus rhamnosus:2 insights into a rotation driven catalytic mechanism
96	<a href="#">c3flaB</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> rifr; <b>PDBTitle:</b> rifr - type ii thioesterase from rifamycin nrps/pks biosynthetic2 pathway - form 1
97	<a href="#">c3iumA</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> prolyl endopeptidase; <b>PDBTitle:</b> appep_wtx opened state
98	<a href="#">c6fkxD</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> acetyl xylan esterase; <b>PDBTitle:</b> crystal structure of an acetyl xylan esterase from a desert metagenome
99	<a href="#">d1q0ra</a>	Alignment	not modelled	99.9	21	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Acilacinomycin methylesterase RdmC
100	<a href="#">c5x6sB</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> acetylxytan esterase a; <b>PDBTitle:</b> acetyl xylan esterase from aspergillus awamori
101	<a href="#">c2cjpA</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> epoxide hydrolase; <b>PDBTitle:</b> structure of potato (solanum tuberosum) epoxide hydrolase i (steh1)
102	<a href="#">c5w8pA</a>	Alignment	not modelled	99.9	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> homoserine o-acetyltransferase; <b>PDBTitle:</b> homoserine transacetylase meta from mycobacterium abscessus
103	<a href="#">d2hu7a2</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Acylamino-acid-releasing enzyme, C-terminal donain
104	<a href="#">c3i1iA</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> homoserine o-acetyltransferase; <b>PDBTitle:</b> x-ray crystal structure of homoserine o-acetyltransferase from2 bacillus anthracis
105	<a href="#">c2xuaH</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> 3-oxoadipate enol-lactonase; <b>PDBTitle:</b> crystal structure of the enol-lactonase from burkholderia2 xenovorans lb400
106	<a href="#">c3f67A</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative dienelactone hydrolase; <b>PDBTitle:</b> crystal structure of putative dienelactone hydrolase from

						klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
107	<a href="#">c2xt0A_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> haloalkane dehalogenase; <b>PDBTitle:</b> dehalogenase dppa from plesiocystis pacifica sir-i
108	<a href="#">c3om8A_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable hydrolase; <b>PDBTitle:</b> the crystal structure of a hydrolase from pseudomonas aeruginosa pa01
109	<a href="#">c2qmqa_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein ndrg2; <b>PDBTitle:</b> crystal structure of a n-myc downstream regulated 2 protein (ndrg2,2 syld, ndr2, ai182517, au040374) from mus musculus at 1.70 a3 resolution
110	<a href="#">c4eb0A_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lcc; <b>PDBTitle:</b> crystal structure of leaf-branch compost bacterial cutinase homolog
111	<a href="#">c5uroA_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> predicted protein; <b>PDBTitle:</b> structure of a soluble epoxide hydrolase identified in trichoderma2 reesei
112	<a href="#">c5xmdA_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> epoxide hydrolase a; <b>PDBTitle:</b> crystal structure of epoxide hydrolase vreh1 from vigna radiata
113	<a href="#">d2vata1</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> O-acetyltransferase
114	<a href="#">c2r11D_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> carboxylesterase np; <b>PDBTitle:</b> crystal structure of putative hydrolase (2632844) from bacillus2 subtilis at 1.96 a resolution
115	<a href="#">c3doiA_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> crystal structure of a thermostable esterase complex with2 paraoxon
116	<a href="#">c4hvtA_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> post-proline cleaving enzyme; <b>PDBTitle:</b> structure of a post-proline cleaving enzyme from rickettsia typhi
117	<a href="#">c3e0xB_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> lipase-esterase related protein; <b>PDBTitle:</b> the crystal structure of a lipase-esterase related protein2 from clostridium acetobutylicum atcc 824
118	<a href="#">c5n4dA_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> prolyl oligopeptidase; <b>PDBTitle:</b> prolyl oligopeptidase b from galerina marginata bound to 25mer2 macrocyclization substrate - d661a mutant
119	<a href="#">c2fx5A_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lipase; <b>PDBTitle:</b> pseudomonas mendocina lipase
120	<a href="#">c4f21G_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> G: <b>PDB Molecule:</b> carboxylesterase/phospholipase family protein; <b>PDBTitle:</b> crystal structure of carboxylesterase/phospholipase family protein2 from francisella tularensis