







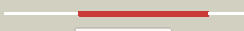





















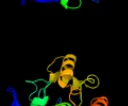


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0293c (-)_356862_358064
Date	Tue Jul 23 14:50:36 BST 2019
Unique Job ID	5f65cba3c2c655e7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4z8zA_</a>	 Alignment		100.0	18	<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
2	<a href="#">c3azqA_</a>	 Alignment		100.0	18	<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
3	<a href="#">c5yznA_</a>	 Alignment		100.0	18	<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
4	<a href="#">c2ecfA_</a>	 Alignment		100.0	16	<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 stentrophomonas maltophilia
5	<a href="#">c4hxxgI_</a>	 Alignment		100.0	14	<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)
6	<a href="#">c5oljA_</a>	 Alignment		100.0	16	<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
7	<a href="#">c5l8sD_</a>	 Alignment		100.0	14	<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
8	<a href="#">c5txeA_</a>	 Alignment		100.0	13	<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
9	<a href="#">c2hu7A_</a>	 Alignment		100.0	16	<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
10	<a href="#">c5t88B_</a>	 Alignment		100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> prolyl endopeptidase; <b>PDBTitle:</b> prolyl oligopeptidase from pyrococcus furiosus
11	<a href="#">c2eepA_</a>	 Alignment		100.0	15	<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

12	<a href="#">c1z68A_</a>	Alignment		100.0	17	<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
13	<a href="#">c2g5tA_</a>	Alignment		100.0	13	<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
14	<a href="#">c6eosB_</a>	Alignment		100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> dipeptidyl peptidase 8; <b>PDBTitle:</b> dpp8 - apo, space group 19
15	<a href="#">c1qfmA_</a>	Alignment		100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> protein (prolyl oligopeptidase); <b>PDBTitle:</b> prolyl oligopeptidase from porcine muscle
16	<a href="#">c4q1vA_</a>	Alignment		100.0	16	<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
17	<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.
18	<a href="#">c3fnbB_</a>	Alignment		100.0	17	<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 from2 streptococcus mutans ua159
19	<a href="#">c2qtbB_</a>	Alignment		100.0	13	<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
20	<a href="#">d2jbwa1</a>	Alignment		100.0	18	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> 2,6-dihydropseudooxynicotine hydrolase-like
21	<a href="#">c5jrlC_</a>	Alignment	not modelled	100.0	13	<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)
22	<a href="#">c6eotG_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> G; <b>PDB Molecule:</b> dipeptidyl peptidase 8; <b>PDBTitle:</b> dpp8 - slrflyeg, space group 19
23	<a href="#">c6eorD_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> D; <b>PDB Molecule:</b> dipeptidyl peptidase 9; <b>PDBTitle:</b> dpp9 - 1g244
24	<a href="#">c6eoqC_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> dipeptidyl peptidase 9; <b>PDBTitle:</b> dpp9 - apo
25	<a href="#">c2bklB_</a>	Alignment	not modelled	100.0	14	<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
26	<a href="#">c4wjlb_</a>	Alignment	not modelled	100.0	13	<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
27	<a href="#">c2xe4A_</a>	Alignment	not modelled	100.0	12	<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
28	<a href="#">c5g59A_</a>	Alignment	not modelled	100.0	17	<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

29	<a href="#">c3iumA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> prolyl endopeptidase; <b>PDBTitle:</b> appep_wtx opened state
30	<a href="#">c3i28A_</a>	Alignment	not modelled	100.0	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
31	<a href="#">c4bp9A_</a>	Alignment	not modelled	100.0	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
32	<a href="#">c1cr6A_</a>	Alignment	not modelled	100.0	16	<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
33	<a href="#">c5n4dA_</a>	Alignment	not modelled	100.0	13	<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
34	<a href="#">c4hvtA_</a>	Alignment	not modelled	100.0	12	<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
35	<a href="#">c1yr2A_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> prolyl oligopeptidase; <b>PDBTitle:</b> structural and mechanistic analysis of two prolyl endopeptidases: role2 of inter-domain dynamics in catalysis and specificity
36	<a href="#">c5uzwD_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> peptide cyclase 1; <b>PDBTitle:</b> pcy1 g696insertion variant in complex with follower peptide and the2 covalent inhibitor zpp
37	<a href="#">c1xfdD_</a>	Alignment	not modelled	100.0	17	<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
38	<a href="#">c5uroA_</a>	Alignment	not modelled	100.0	12	<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
39	<a href="#">d1l7aa_</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Acetyl xylan esterase-like
40	<a href="#">d2vata1</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> O-acetyltransferase
41	<a href="#">c4d9jl_</a>	Alignment	not modelled	100.0	20	<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
42	<a href="#">c5uw7B_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> peptide cyclase 1; <b>PDBTitle:</b> pcy1 y481f variant in complex with follower peptide
43	<a href="#">c6fkxD_</a>	Alignment	not modelled	100.0	22	<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
44	<a href="#">c6agqE_</a>	Alignment	not modelled	100.0	17	<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
45	<a href="#">c2vavL_</a>	Alignment	not modelled	100.0	15	<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)
46	<a href="#">c3fcyB_</a>	Alignment	not modelled	100.0	19	<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
47	<a href="#">c2wtmC_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> est1e; <b>PDBTitle:</b> est1e from butyrivibrio proteoclasticus
48	<a href="#">c5d6oB_</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> homoserine o-acetyltransferase; <b>PDBTitle:</b> orthorhombic crystal structure of an acetylerster hydrolase from2 corynebacterium glutamicum
49	<a href="#">d1hlga_</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Gastric lipase
50	<a href="#">c3mveB_</a>	Alignment	not modelled	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
51	<a href="#">d1k8qa_</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Gastric lipase
52	<a href="#">d1vlqa_</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Acetyl xylan esterase-like
53	<a href="#">c2y6vB_</a>	Alignment	not modelled	100.0	23	<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)
54	<a href="#">c1ao6A_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase;

54	<a href="#">c4800A</a>	Alignment	not modelled	100.0	13	<b>PDBTitle:</b> native structure of a novel cold-adapted esterase from an2 arctic intertidal metagenomic library
55	<a href="#">d2b61a1</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> O-acetyltransferase
56	<a href="#">c2xuaH</a>	Alignment	not modelled	100.0	18	<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
57	<a href="#">c5xb6D</a>	Alignment	not modelled	100.0	13	<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
58	<a href="#">c3v48B</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative aminoacrylate hydrolase rutt; <b>PDBTitle:</b> crystal structure of the putative alpha/beta hydrolase rutt from2 e.coli
59	<a href="#">c3om8A</a>	Alignment	not modelled	100.0	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
60	<a href="#">c5w8pA</a>	Alignment	not modelled	100.0	15	<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
61	<a href="#">c3vviA</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> homoserine o-acetyltransferase; <b>PDBTitle:</b> crystal structure of l-serine-o-acetyltransferase found in d-2 cycloserine biosynthetic pathway
62	<a href="#">c4zwnD</a>	Alignment	not modelled	100.0	14	<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
63	<a href="#">c3jw8A</a>	Alignment	not modelled	100.0	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
64	<a href="#">c3i1iA</a>	Alignment	not modelled	100.0	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
65	<a href="#">c3llcA</a>	Alignment	not modelled	100.0	16	<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
66	<a href="#">c4qloA</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> homoserine o-acetyltransferase; <b>PDBTitle:</b> crystal structure of homoserine o-acetyltransferase from2 staphylococcus aureus
67	<a href="#">c5ijkA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase e22; <b>PDBTitle:</b> crystal structure of esterase e22 l374d mutant
68	<a href="#">d1ufoa</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Hypothetical protein TT1662
69	<a href="#">c5efzC</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> homoserine o-acetyltransferase; <b>PDBTitle:</b> monoclinic structure of the acetyl esterase mekb
70	<a href="#">d2pl5a1</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> O-acetyltransferase
71	<a href="#">c4pw0A</a>	Alignment	not modelled	100.0	13	<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
72	<a href="#">c5hdfB</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hydrolase; <b>PDBTitle:</b> hydrolase semet-stna
73	<a href="#">c2e3jA</a>	Alignment	not modelled	100.0	17	<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
74	<a href="#">c3rm3A</a>	Alignment	not modelled	100.0	17	<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
75	<a href="#">c4qlaA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> juvenile hormone epoxide hydrolase; <b>PDBTitle:</b> crystal structure of juvenile hormone epoxide hydrolase from the2 silkworm bombyx mori
76	<a href="#">c6eicA</a>	Alignment	not modelled	100.0	14	<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
77	<a href="#">c3qvmA</a>	Alignment	not modelled	100.0	14	<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
78	<a href="#">c2cjpA</a>	Alignment	not modelled	100.0	13	<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)
79	<a href="#">d1b6ga</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloalkane dehalogenase
80	<a href="#">c3qm1A</a>	Alignment	not modelled	100.0	15	<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
81	<a href="#">c3dyvA</a>	Alignment	not modelled	100.0	16	<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
82	<a href="#">c2qmqa</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein ndr2; <b>PDBTitle:</b> crystal structure of a n-myc downstream regulated 2 protein (ndr2,2 syld, ndr2, ai182517, au040374) from mus musculus at 1.70 a3 resolution
83	<a href="#">c4f0ja</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable hydrolytic enzyme; <b>PDBTitle:</b> crystal structure of a probable hydrolytic enzyme (pa3053) from2 pseudomonas aeruginosa pao1 at 1.50 a resolution
84	<a href="#">c3k2ia</a>	Alignment	not modelled	100.0	16	<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
85	<a href="#">c4qlaB</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> juvenile hormone epoxide hydrolase; <b>PDBTitle:</b> crystal structure of juvenile hormone epoxide hydrolase from the2 silkworm bombyx mori
86	<a href="#">c2hdwb</a>	Alignment	not modelled	100.0	17	<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
87	<a href="#">d1cr6a2</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Epoxide hydrolase
88	<a href="#">c3hlkB</a>	Alignment	not modelled	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)
89	<a href="#">d1mtza</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Proline iminopeptidase-like
90	<a href="#">c3hjuB</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> monoglyceride lipase; <b>PDBTitle:</b> crystal structure of human monoglyceride lipase
91	<a href="#">c5xksB</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> thermostable monoacylglycerol lipase; <b>PDBTitle:</b> crystal structure of monoacylglycerol lipase from thermophilic2 geobacillus sp. 12amor
92	<a href="#">c2r11D</a>	Alignment	not modelled	100.0	16	<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
93	<a href="#">c5esrA</a>	Alignment	not modelled	100.0	12	<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
94	<a href="#">c3bwxA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha/beta hydrolase; <b>PDBTitle:</b> crystal structure of an alpha/beta hydrolase (yp_496220.1) from2 novosphingobium aromaticivorans dsm 12444 at 1.50 a resolution
95	<a href="#">c4oseA</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative hydrolase; <b>PDBTitle:</b> x-ray crystal structure of a putative hydrolase from rickettsia typhi
96	<a href="#">c1u2eA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-hydroxy-6-ketonona-2,4-dienedioic acid <b>PDBTitle:</b> crystal structure of the c-c bond hydrolase mhpc
97	<a href="#">c3ksrA</a>	Alignment	not modelled	100.0	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
98	<a href="#">c5oluA</a>	Alignment	not modelled	100.0	18	<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
99	<a href="#">d1zd3a2</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Epoxide hydrolase
100	<a href="#">d1c4xa</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carbon-carbon bond hydrolase
101	<a href="#">c6gupB</a>	Alignment	not modelled	100.0	22	<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
102	<a href="#">c5yhpB</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cold active proline iminopeptidase; <b>PDBTitle:</b> proline iminopeptidase from psychrophilic yeast glaciozyma antarctica
103	<a href="#">c4y7dA</a>	Alignment	not modelled	100.0	17	<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 nakamurella multipartita
104	<a href="#">c2q0xA</a>	Alignment	not modelled	100.0	14	<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
105	<a href="#">d2rhwa1</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carbon-carbon bond hydrolase
106	<a href="#">c5vmdA</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> epoxide hydrolase a;



106	<a href="#">c3x1t9A_</a>	Alignment	not modelled	99.9	16	<b>PDBTitle:</b> crystal structure of epoxide hydrolase vreh1 from vigna radiata <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
107	<a href="#">c3h04A_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dmma haloalkane dehalogenase; <b>PDBTitle:</b> haloalkane dehalogenase, dmma, of marine microbial origin
108	<a href="#">c3u1tA_</a>	Alignment	not modelled	99.9	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Hydroxynitrile lyase-like
109	<a href="#">d1e89a_</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Aclacinomycin methyltransferase RdmC
110	<a href="#">d1q0ra_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> alpha/beta superfamily hydrolase; <b>PDBTitle:</b> crystal structure of alpha/beta superfamily hydrolase from oenococcus2 oeni psu-1
111	<a href="#">c3fsgC_</a>	Alignment	not modelled	99.9	21	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carboxylesterase/lipase
112	<a href="#">d1tqha_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha/beta hydrolase family protein; <b>PDBTitle:</b> the structure of an alpha/beta fold family hydrolase from bacillus2 anthracis str. Sterne
113	<a href="#">c3oosA_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cocaine esterase; <b>PDBTitle:</b> ser117ala mutant of bacterial cocaine esterase coce
114	<a href="#">c1l7qA_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> putative acyltransferase; <b>PDBTitle:</b> 2.22 angstrom resolution crystal structure of a putative2 acyltransferase from salmonella enterica
115	<a href="#">c4nvrC_</a>	Alignment	not modelled	99.9	16	<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
116	<a href="#">c4l0cA_</a>	Alignment	not modelled	99.9	13	<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
117	<a href="#">c2xt0A_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-hydroxynitrile lyase-like protein; <b>PDBTitle:</b> structure of the hydroxynitrile lyase from arabidopsis thaliana
118	<a href="#">c3dqzB_</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> PepX catalytic domain-like
119	<a href="#">d1ju3a2</a>	Alignment	not modelled	99.9	18	<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
120	<a href="#">c3flaB_</a>	Alignment	not modelled	99.9	18	