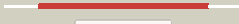



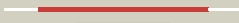



















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2854 (-) _3164162_3165202
Date	Wed Aug 7 12:50:52 BST 2019
Unique Job ID	9974f320459627a4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3i28A_</a>	 Alignment		100.0	15	<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
2	<a href="#">c1cr6A_</a>	 Alignment		100.0	15	<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
3	<a href="#">c4d9jl_</a>	 Alignment		100.0	15	<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
4	<a href="#">d1k8qa_</a>	 Alignment		100.0	13	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Gastric lipase
5	<a href="#">d1hlga_</a>	 Alignment		100.0	11	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Gastric lipase
6	<a href="#">c2y6vB_</a>	 Alignment		100.0	10	<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)
7	<a href="#">c3jw8A_</a>	 Alignment		100.0	16	<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
8	<a href="#">c5hdfB_</a>	 Alignment		100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hydrolase; <b>PDBTitle:</b> hydrolase semet-stna
9	<a href="#">c3i1iA_</a>	 Alignment		100.0	11	<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
10	<a href="#">c5d6oB_</a>	 Alignment		100.0	10	<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
11	<a href="#">c2cjpA_</a>	 Alignment		100.0	16	<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)

12	<a href="#">c3hjuB_</a>	Alignment		100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> monoglyceride lipase; <b>PDBTitle:</b> crystal structure of human monoglyceride lipase
13	<a href="#">c2vavL_</a>	Alignment		100.0	10	<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)
14	<a href="#">d2b61a1</a>	Alignment		100.0	11	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> O-acetyltransferase
15	<a href="#">c5oluA_</a>	Alignment		100.0	13	<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
16	<a href="#">c4qlaB_</a>	Alignment		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
17	<a href="#">c4qloA_</a>	Alignment		100.0	13	<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
18	<a href="#">c5esrA_</a>	Alignment		100.0	17	<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
19	<a href="#">c3vvIA_</a>	Alignment		100.0	11	<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
20	<a href="#">c4f0jA_</a>	Alignment		100.0	14	<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
21	<a href="#">c5f4zB_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> epoxide hydrolase; <b>PDBTitle:</b> the crystal structure of an epoxide hydrolase from streptomyces2 carzinostaticus subsp. neocarzinostaticus
22	<a href="#">c3qvmA_</a>	Alignment	not modelled	100.0	15	<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
23	<a href="#">c3v48B_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative aminoacrylate hydrolase rtdt; <b>PDBTitle:</b> crystal structure of the putative alpha/beta hydrolase rtdt from2 e.coli
24	<a href="#">c4i19A_</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> epoxide hydrolase; <b>PDBTitle:</b> the crystal structure of an epoxide hydrolase from streptomyces2 carzinostaticus subsp. neocarzinostaticus.
25	<a href="#">c2r11D_</a>	Alignment	not modelled	100.0	11	<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
26	<a href="#">d2vata1</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> O-acetyltransferase
27	<a href="#">c4qlaA_</a>	Alignment	not modelled	100.0	13	<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
28	<a href="#">c5uroA_</a>	Alignment	not modelled	100.0	14	<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
						<b>PDB header:</b> transferase

29	<a href="#">c5w8pA_</a>	Alignment	not modelled	100.0	13	<b>Chain:</b> A: <b>PDB Molecule:</b> homoserine o-acetyltransferase; <b>PDBTitle:</b> homoserine transacetylase meta from mycobacterium abscessus
30	<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
31	<a href="#">c5xmdA_</a>	Alignment	not modelled	100.0	13	<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
32	<a href="#">c6gupB_</a>	Alignment	not modelled	100.0	13	<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
33	<a href="#">c5jkjA_</a>	Alignment	not modelled	100.0	12	<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
34	<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
35	<a href="#">c4pw0A_</a>	Alignment	not modelled	100.0	14	<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
36	<a href="#">c2qmqA_</a>	Alignment	not modelled	100.0	10	<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
37	<a href="#">c6brtB_</a>	Alignment	not modelled	100.0	16	<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
38	<a href="#">c2rauA_</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative esterase; <b>PDBTitle:</b> crystal structure of a putative lipase (np_343859.1) from sulfobolbus2 solfataricus at 1.85 a resolution
39	<a href="#">c4zwnD_</a>	Alignment	not modelled	100.0	15	<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
40	<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
41	<a href="#">d1e89a_</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Hydroxynitrile lyase-like
42	<a href="#">c2q0xA_</a>	Alignment	not modelled	100.0	17	<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
43	<a href="#">d1zd3a2</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Epoxide hydrolase
44	<a href="#">d2pl5a1</a>	Alignment	not modelled	100.0	9	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> O-acetyltransferase
45	<a href="#">d3c70a1</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Hydroxynitrile lyase-like
46	<a href="#">c5yhpB_</a>	Alignment	not modelled	100.0	11	<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
47	<a href="#">c6f9oA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> haloalkane dehalogenase; <b>PDBTitle:</b> crystal structure of cold-adapted haloalkane dehalogenase dpca from2 psychrobacter cryohalolentis k5
48	<a href="#">c3oosA_</a>	Alignment	not modelled	100.0	13	<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
49	<a href="#">c3u1tA_</a>	Alignment	not modelled	100.0	13	<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
50	<a href="#">c3fsgC_</a>	Alignment	not modelled	100.0	14	<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
51	<a href="#">c3flaB_</a>	Alignment	not modelled	100.0	11	<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
52	<a href="#">c3stxB_</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> methylketone synthase 1; <b>PDBTitle:</b> crystal structure of tomato methylketone synthase i h243a variant2 complexed with beta-ketoheptanoate
53	<a href="#">c4mj3B_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> haloalkane dehalogenase; <b>PDBTitle:</b> haloalkane dehalogenase dmra from mycobacterium rhodesiae js60
54	<a href="#">c6eicA_</a>	Alignment	not modelled	100.0	22	<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

55	<a href="#">d1pjaa_</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Thioesterases
56	<a href="#">c1pjaA_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> palmitoyl-protein thioesterase 2 precursor; <b>PDBTitle:</b> the crystal structure of palmitoyl protein thioesterase-2 reveals the 2 basis for divergent substrate specificities of the two lysosomal 3 thioesterases (ppt1 and ppt2)
57	<a href="#">c3om8A_</a>	Alignment	not modelled	99.9	17	<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
58	<a href="#">c4y7dA_</a>	Alignment	not modelled	99.9	14	<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
59	<a href="#">c4i0cA_</a>	Alignment	not modelled	99.9	15	<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
60	<a href="#">c3wwoA_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> (s)-hydroxynitrile lyase; <b>PDBTitle:</b> s-selective hydroxynitrile lyase from baliospermum montanum (apo1)
61	<a href="#">d1cr6a2</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Epoxide hydrolase
62	<a href="#">c2xt0A_</a>	Alignment	not modelled	99.9	17	<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
63	<a href="#">c1zoiC_</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> crystal structure of a stereoselective esterase from 2 pseudomonas putida ifo12996
64	<a href="#">d1qo7a_</a>	Alignment	not modelled	99.9	10	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Epoxide hydrolase
65	<a href="#">c3h04A_</a>	Alignment	not modelled	99.9	13	<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 from 2 staphylococcus aureus subsp. aureus mu50
66	<a href="#">d1ehya_</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Epoxide hydrolase
67	<a href="#">c3dqzB_</a>	Alignment	not modelled	99.9	16	<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
68	<a href="#">c5xb6D_</a>	Alignment	not modelled	99.9	10	<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
69	<a href="#">d1a8qa_</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloperoxidase
70	<a href="#">c5dnvA_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> shkai2ib; <b>PDBTitle:</b> crystal structure of kai2-like protein from striga (apo state 2)
71	<a href="#">d1mtza_</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Proline iminopeptidase-like
72	<a href="#">d1hkha_</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloperoxidase
73	<a href="#">c2yysA_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> proline iminopeptidase-related protein; <b>PDBTitle:</b> crystal structure of the proline iminopeptidase-related protein 2 ttha1809 from thermus thermophilus hb8
74	<a href="#">c3wzlb_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> zearealenone hydrolase; <b>PDBTitle:</b> zen lactonase
75	<a href="#">c4rpcA_</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative alpha/beta hydrolase; <b>PDBTitle:</b> crystal structure of the putative alpha/beta hydrolase family protein 2 from desulfitobacterium hafniense
76	<a href="#">d1azwa_</a>	Alignment	not modelled	99.9	12	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Proline iminopeptidase-like
77	<a href="#">c6azdA_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ppkai2-like h; <b>PDBTitle:</b> crystal structure of physcomitrella patens kai2-like h
78	<a href="#">d1m33a_</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Biotin biosynthesis protein BioH
79	<a href="#">c1y37A_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> fluoroacetate dehalogenase; <b>PDBTitle:</b> structure of fluoroacetate dehalogenase from burkholderia sp. fa1
80	<a href="#">d1wm1a_</a>	Alignment	not modelled	99.9	12	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Proline iminopeptidase-like
						<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> epoxide hydrolase belonging to alpha/beta

81	<a href="#">c5nfqA_</a>	Alignment	not modelled	99.9	12	hydrolase <b>PDBTitle:</b> novel epoxide hydrolases belonging to the alpha/beta hydrolases2 superfamily in metagenomes from hot environments
82	<a href="#">d1xkla_</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Hydroxynitrile lyase-like
83	<a href="#">c3fobA_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> bromoperoxidase; <b>PDBTitle:</b> crystal structure of bromoperoxidase from bacillus anthracis
84	<a href="#">c4fbmA_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lips lipolytic enzyme; <b>PDBTitle:</b> lips and lip, two metagenome-derived lipolytic enzymes increase the2 diversity of known lipase and esterase families
85	<a href="#">c5ugzA_</a>	Alignment	not modelled	99.9	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative thioesterase; <b>PDBTitle:</b> crystal structure of clbq from the colibactin nrps/pks pathway
86	<a href="#">c3rm3A_</a>	Alignment	not modelled	99.9	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
87	<a href="#">c2xuaH_</a>	Alignment	not modelled	99.9	16	<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
88	<a href="#">c4x00D_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> putative hydrolase; <b>PDBTitle:</b> x-ray crystal structure of a putative aryl esterase from burkholderia2 cenocepacia
89	<a href="#">c3qmwD_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> thioesterase; <b>PDBTitle:</b> redj with peg molecule bound in the active site
90	<a href="#">d1brta_</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloperoxidase
91	<a href="#">d1mj5a_</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloalkane dehalogenase
92	<a href="#">c3kdaB_</a>	Alignment	not modelled	99.9	10	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cftr inhibitory factor (cif); <b>PDBTitle:</b> crystal structure of the cftr inhibitory factor cif with the h269a2 mutation
93	<a href="#">d1c4xa_</a>	Alignment	not modelled	99.9	10	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carbon-carbon bond hydrolase
94	<a href="#">d1a8sa_</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloperoxidase
95	<a href="#">c4oseA_</a>	Alignment	not modelled	99.9	13	<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="#">c3fleB_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> se_1780 protein; <b>PDBTitle:</b> se_1780 protein of unknown function from staphylococcus epidermidis.
97	<a href="#">c3e0xB_</a>	Alignment	not modelled	99.9	12	<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
98	<a href="#">c4nvrC_</a>	Alignment	not modelled	99.9	12	<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
99	<a href="#">d1a88a_</a>	Alignment	not modelled	99.9	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloperoxidase
100	<a href="#">c5bovD_</a>	Alignment	not modelled	99.9	10	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> putative epoxide hydrolase protein; <b>PDBTitle:</b> crystal structure of a putative epoxide hydrolase (kpn_01808) from2 klebsiella pneumoniae subsp. pneumoniae mgh 78578 at 1.60 a3 resolution
101	<a href="#">c3w06A_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrolase, alpha/beta fold family protein; <b>PDBTitle:</b> crystal structure of arabidopsis thaliana dwarf14 like (atd14l)
102	<a href="#">c3gziB_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> polyneuridine-aldehyde esterase; <b>PDBTitle:</b> crystal structure of polyneuridine aldehyde esterase complexed with2 16-epi-vellosimine
103	<a href="#">c4uhhA_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> structural studies of a thermophilic esterase from2 thermogutta terrifontis (cacodylate complex)
104	<a href="#">c3dyvA_</a>	Alignment	not modelled	99.9	17	<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
105	<a href="#">c5h3hB_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> abhydrolase domain-containing protein; <b>PDBTitle:</b> esterase (eaest) from exiguobacterium antarcticum
106	<a href="#">c2wj4B_</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 1h-3-hydroxy-4-oxoquinaldine 2,4-dioxygenase; <b>PDBTitle:</b> crystal structure of the cofactor-devoid 1-h-3-hydroxy-4-2 oxoquinaldine 2,4-dioxygenase (hod) from arthrobacter3

						nitroguajacolicus ru61a anaerobically complexed with its4 natural substrate 1-h-3-hydroxy-4-oxoquinaldine
107	<a href="#">c5xksB_</a>	Alignment	not modelled	99.9	13	<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
108	<a href="#">c6ba8A_</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> iron acquisition yersiniabactin synthesis enzyme, ybtt; <b>PDBTitle:</b> ybtt - type ii thioesterase from yersiniabactin nrps/pks biosynthetic2 pathway
109	<a href="#">d1q0ra_</a>	Alignment	not modelled	99.9	12	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> AcIacinomycin methylesterase RdmC
110	<a href="#">c5cbkA_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> shhtl5; <b>PDBTitle:</b> crystal structure of the strigolactone receptor shhtl5 from striga2 hermonthica
111	<a href="#">c3a2nF_</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> haloalkane dehalogenase; <b>PDBTitle:</b> crystal structure of dbja (wild type type ii p21)
112	<a href="#">c3e3aA_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> possible peroxidase bpoC; <b>PDBTitle:</b> the structure of rv0554 from mycobacterium tuberculosis
113	<a href="#">c3l80A_</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein smu.1393c; <b>PDBTitle:</b> crystal structure of smu.1393c from streptococcus mutans ua159
114	<a href="#">c2hdwB_</a>	Alignment	not modelled	99.9	12	<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
115	<a href="#">c3wibB_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> haloalkane dehalogenase; <b>PDBTitle:</b> crystal structure of y109w mutant haloalkane dehalogenase data from2 agrobacterium tumefaciens c58
116	<a href="#">c2pseA_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> renilla-luciferin 2-monoxygenase; <b>PDBTitle:</b> crystal structures of the luciferase and green fluorescent2 protein from renilla reniformis
117	<a href="#">c5cw2C_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> putative epoxide hydrolase epha; <b>PDBTitle:</b> crystal structure of epoxide hydrolase a from mycobacterium2 thermoresistibile
118	<a href="#">c3bwxA_</a>	Alignment	not modelled	99.9	13	<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
119	<a href="#">c3ibtA_</a>	Alignment	not modelled	99.9	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 1h-3-hydroxy-4-oxoquinoline 2,4-dioxygenase; <b>PDBTitle:</b> structure of 1h-3-hydroxy-4-oxoquinoline 2,4-dioxygenase (qdo)
120	<a href="#">c4opmB_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> lipase; <b>PDBTitle:</b> crystal structure of a putative lipase (lip1) from acinetobacter2 baumannii aye at 1.70 a resolution