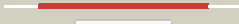


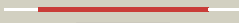












Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3338 (-) _3724075_3724719
Date	Thu Aug 8 16:20:55 BST 2019
Unique Job ID	a7ddf8a43ef7c156

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1cr6A_	 Alignment		99.9	12	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
2	c3i28A_	 Alignment		99.9	13	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase 2; PDBTitle: crystal structure of soluble epoxide hydrolase
3	c2vavL_	 Alignment		99.9	12	PDB header: transferase Chain: L: PDB Molecule: acetyl-coa--deacetylcephalosporin c acetyltransferase; PDBTitle: crystal structure of deacetylcephalosporin c acetyltransferase (dac-2 soak)
4	c3i1iA_	 Alignment		99.9	13	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: x-ray crystal structure of homoserine o-acetyltransferase from2 bacillus anthracis
5	d2b61a1	 Alignment		99.9	11	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
6	c4qloA_	 Alignment		99.9	16	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: crystal structure of homoserine o-acetyltransferase from2 staphylococcus aureus
7	c4d9jl_	 Alignment		99.9	14	PDB header: de novo protein Chain: I: PDB Molecule: designed 16nm tetrahedral protein cage containing non-haem PDBTitle: structure of a 16 nm protein cage designed by fusing symmetric2 oligomeric domains
8	c2y6vB_	 Alignment		99.9	13	PDB header: hydrolase Chain: B: PDB Molecule: peroxisomal membrane protein lpx1; PDBTitle: peroxisomal alpha-beta-hydrolase lpx1 (yor084w) from saccharomyces2 cerevisiae (crystal form i)
9	c3vv1A_	 Alignment		99.9	20	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: crystal structure of l-serine-o-acetyltransferase found in d-2 cycloserine biosynthetic pathway
10	c2qmqa_	 Alignment		99.9	13	PDB header: signaling protein Chain: A: PDB Molecule: protein ndr2; PDBTitle: crystal structure of a n-myc downstream regulated 2 protein (ndr2,2 syld, ndr2, ai182517, au040374) from mus musculus at 1.70 a3 resolution
11	c5w8pA_	 Alignment		99.9	16	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: homoserine transacetylase meta from mycobacterium abscessus

12	c5jkjA_	Alignment		99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: esterase e22; PDBTitle: crystal structure of esterase e22 I374d mutant
13	c4qlaB_	Alignment		99.9	12	PDB header: hydrolase Chain: B: PDB Molecule: juvenile hormone epoxide hydrolase; PDBTitle: crystal structure of juvenile hormone epoxide hydrolase from the2 silkworm bombyx mori
14	d2vata1	Alignment		99.9	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
15	c5d6oB_	Alignment		99.9	14	PDB header: transferase Chain: B: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: orthorhombic crystal structure of an acylester hydrolase from2 corynebacterium glutamicum
16	c4qlaA_	Alignment		99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: juvenile hormone epoxide hydrolase; PDBTitle: crystal structure of juvenile hormone epoxide hydrolase from the2 silkworm bombyx mori
17	c4i19A_	Alignment		99.9	12	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: the crystal structure of an epoxide hydrolase from streptomyces2 carzinostaticus subsp. neocarzinostaticus.
18	d2pl5a1	Alignment		99.9	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
19	c3v48B_	Alignment		99.9	17	PDB header: hydrolase Chain: B: PDB Molecule: putative aminoacrylate hydrolase rutd; PDBTitle: crystal structure of the putative alpha/beta hydrolase rutd from2 e.coli
20	c5f4zB_	Alignment		99.9	14	PDB header: hydrolase Chain: B: PDB Molecule: epoxide hydrolase; PDBTitle: the crystal structure of an epoxide hydrolase from streptomyces2 carzinostaticus subsp. neocarzinostaticus
21	c3qvmA_	Alignment	not modelled	99.9	13	PDB header: hydrolase Chain: A: PDB Molecule: olei00960; PDBTitle: the structure of olei00960, a hydrolase from oleispira antarctica
22	c2r11D_	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: D: PDB Molecule: carboxylesterase np; PDBTitle: crystal structure of putative hydrolase (2632844) from bacillus2 subtilis at 1.96 a resolution
23	c4f0jA_	Alignment	not modelled	99.8	14	PDB header: hydrolase Chain: A: PDB Molecule: probable hydrolytic enzyme; PDBTitle: crystal structure of a probable hydrolytic enzyme (pa3053) from2 pseudomonas aeruginosa pao1 at 1.50 a resolution
24	c3oosA_	Alignment	not modelled	99.8	13	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase family protein; PDBTitle: the structure of an alpha/beta fold family hydrolase from bacillus2 anthracis str. Sterne
25	c3fsgC_	Alignment	not modelled	99.8	12	PDB header: hydrolase Chain: C: PDB Molecule: alpha/beta superfamily hydrolase; PDBTitle: crystal structure of alpha/beta superfamily hydrolase from oenococcus2 oeni psu-1
26	c5esrA_	Alignment	not modelled	99.8	10	PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of haloalkane dehalogenase (dcca) from caulobacter2 crescentus
27	c5efzC_	Alignment	not modelled	99.8	12	PDB header: hydrolase Chain: C: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: monoclinic structure of the acetyl esterase mekb
28	c3om8A_	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: A: PDB Molecule: probable hydrolase; PDBTitle: the crystal structure of a hydrolase from pseudomonas aeruginosa pa01
						PDB header: hydrolase

29	c2e3jA_	Alignment	not modelled	99.8	16	Chain: A: PDB Molecule: epoxide hydrolase ephb; PDBTitle: the crystal structure of epoxide hydrolase b (rv1938) from2 mycobacterium tuberculosis at 2.1 angstrom
30	c2yysA_	Alignment	not modelled	99.8	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: proline iminopeptidase-related protein; PDBTitle: crystal structure of the proline iminopeptidase-related protein2 ttha1809 from thermus thermophilus hb8
31	c4pw0A_	Alignment	not modelled	99.8	11	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase fold protein; PDBTitle: alpha/beta hydrolase fold protein from chitinophaga pinensis
32	c3l80A_	Alignment	not modelled	99.8	11	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein smu.1393c; PDBTitle: crystal structure of smu.1393c from streptococcus mutans ua159
33	c2xuaH_	Alignment	not modelled	99.8	18	PDB header: hydrolase Chain: H: PDB Molecule: 3-oxoadipate enol-lactonase; PDBTitle: crystal structure of the enol-lactonase from burkholderia2 xenovorans lb400
34	c6brtB_	Alignment	not modelled	99.8	14	PDB header: ligase Chain: B: PDB Molecule: d3-cth-d14-d-ring; PDBTitle: f-box protein cth with hydrolase
35	c4rpcA_	Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: A: PDB Molecule: putative alpha/beta hydrolase; PDBTitle: crystal structure of the putative alpha/beta hydrolase family protein2 from desulfitobacterium hafniense
36	c5xmdA_	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase a; PDBTitle: crystal structure of epoxide hydrolase vreh1 from vigna radiata
37	d1b6ga_	Alignment	not modelled	99.8	10	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloalkane dehalogenase
38	c6f9oA_	Alignment	not modelled	99.8	13	PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of cold-adapted haloalkane dehalogenase dpca from2 psychrobacter cryohalolentis k5
39	c4psuA_	Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase; PDBTitle: crystal structure of alpha/beta hydrolase from rhodopseudomonas2 palustris cga009
40	c4l0cA_	Alignment	not modelled	99.8	12	PDB header: hydrolase Chain: A: PDB Molecule: deformylase; PDBTitle: crystal structure of the n-fopmylmaleamic acid deformylase nfo(s94a)2 from pseudomonas putida s16
41	d1ehya_	Alignment	not modelled	99.8	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
42	c2cjpA_	Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: structure of potato (solanum tuberosum) epoxide hydrolase i (steh1)
43	d1m33a_	Alignment	not modelled	99.8	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Biotin biosynthesis protein BioH
44	c3e3aA_	Alignment	not modelled	99.8	17	PDB header: oxidoreductase Chain: A: PDB Molecule: possible peroxidase bpoC; PDBTitle: the structure of rv0554 from mycobacterium tuberculosis
45	c5hdfB_	Alignment	not modelled	99.8	11	PDB header: hydrolase Chain: B: PDB Molecule: hydrolase;hydrolase; PDBTitle: hydrolase semet-stna
46	c3flaB_	Alignment	not modelled	99.8	14	PDB header: hydrolase Chain: B: PDB Molecule: rifr; PDBTitle: rifr - type ii thioesterase from rifamycin nrps/pks biosynthetic2 pathway - form 1
47	d1qo7a_	Alignment	not modelled	99.8	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
48	c4mj3B_	Alignment	not modelled	99.8	11	PDB header: hydrolase Chain: B: PDB Molecule: haloalkane dehalogenase; PDBTitle: haloalkane dehalogenase dmra from mycobacterium rhodesiae js60
49	c3e0xB_	Alignment	not modelled	99.8	10	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: lipase-esterase related protein; PDBTitle: the crystal structure of a lipase-esterase related protein2 from clostridium acetobutylicum atcc 824
50	c2q0xA_	Alignment	not modelled	99.8	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: alpha/beta hydrolase fold protein of unknown function
51	d1k8qa_	Alignment	not modelled	99.8	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Gastric lipase
52	c4y7dA_	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase fold protein; PDBTitle: alpha/beta hydrolase fold protein from nakamurella multipartita
53	d1hlga_	Alignment	not modelled	99.8	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Gastric lipase
54	c3u1tA_	Alignment	not modelled	99.8	12	PDB header: hydrolase Chain: A: PDB Molecule: dmma haloalkane dehalogenase; PDBTitle: haloalkane dehalogenase, dmma, of marine microbial origin
55	c5vhpB_	Alignment	not modelled	99.8	14	PDB header: hydrolase Chain: B: PDB Molecule: cold active proline iminopeptidase;

55	c3ynpb	Alignment	not modelled	99.8	14	PDBTitle: proline iminopeptidase from psychrophilic yeast glaciozyma antarctica PDB header: structural genomics, unknown function
56	c3h04A	Alignment	not modelled	99.8	10	Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of the protein with unknown function from2 staphylococcus aureus subsp. aureus mu50
57	c4i3fA	Alignment	not modelled	99.8	18	PDB header: hydrolase Chain: A; PDB Molecule: serine hydrolase ccsp0084; PDBTitle: crystal structure of serine hydrolase ccsp0084 from the polyaromatic2 hydrocarbon (pah)-degrading bacterium cycloclasticus zankles
58	c3wzIB	Alignment	not modelled	99.7	13	PDB header: hydrolase Chain: B; PDB Molecule: zearealenone hydrolase; PDBTitle: zen lactonase
59	c5ugzA	Alignment	not modelled	99.7	13	PDB header: hydrolase Chain: A; PDB Molecule: putative thioesterase; PDBTitle: crystal structure of clbq from the colibactin nrps/pks pathway
60	c1y37A	Alignment	not modelled	99.7	14	PDB header: hydrolase Chain: A; PDB Molecule: fluoroacetate dehalogenase; PDBTitle: structure of fluoroacetate dehalogenase from burkholderia sp. fa1
61	d1c4xa	Alignment	not modelled	99.7	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase
62	c3ibtA	Alignment	not modelled	99.7	13	PDB header: oxidoreductase Chain: A; PDB Molecule: 1h-3-hydroxy-4-oxoquinoline 2,4-dioxygenase; PDBTitle: structure of 1h-3-hydroxy-4-oxoquinoline 2,4-dioxygenase (qdo)
63	d1a8qa	Alignment	not modelled	99.7	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
64	d1xkta	Alignment	not modelled	99.7	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
65	d1zd3a2	Alignment	not modelled	99.7	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
66	d1cr6a2	Alignment	not modelled	99.7	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
67	c1zoiC	Alignment	not modelled	99.7	14	PDB header: hydrolase Chain: C; PDB Molecule: esterase; PDBTitle: crystal structure of a stereoselective esterase from2 pseudomonas putida ifo12996
68	c5dnvA	Alignment	not modelled	99.7	12	PDB header: hydrolase Chain: A; PDB Molecule: shkai2ib; PDBTitle: crystal structure of kai2-like protein from striga (apo state 2)
69	c3kxpD	Alignment	not modelled	99.7	15	PDB header: hydrolase Chain: D; PDB Molecule: alpha-(n-acetylaminomethylene)succinic acid hydrolase; PDBTitle: crystal structure of e-2-(acetamidomethylene)succinate hydrolase
70	d1e89a	Alignment	not modelled	99.7	9	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hydroxynitrile lyase-like
71	d1pjaa	Alignment	not modelled	99.7	11	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterases
72	c1pjaA	Alignment	not modelled	99.7	11	PDB header: hydrolase Chain: A; PDB Molecule: palmitoyl-protein thioesterase 2 precursor; PDBTitle: the crystal structure of palmitoyl protein thioesterase-2 reveals the2 basis for divergent substrate specificities of the two lysosomal3 thioesterases (ppt1 and ppt2)
73	d1azwa	Alignment	not modelled	99.7	11	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Proline iminopeptidase-like
74	c2wj4B	Alignment	not modelled	99.7	17	PDB header: oxidoreductase Chain: B; PDB Molecule: 1h-3-hydroxy-4-oxoquinaldine 2,4-dioxygenase; PDBTitle: 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
75	c3bwxA	Alignment	not modelled	99.7	14	PDB header: hydrolase Chain: A; PDB Molecule: alpha/beta hydrolase; PDBTitle: crystal structure of an alpha/beta hydrolase (yp_496220.1) from2 novosphingobium aromaticivorans dsm 12444 at 1.50 a resolution
76	c3wibB	Alignment	not modelled	99.7	8	PDB header: hydrolase Chain: B; PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of y109w mutant haloalkane dehalogenase data from2 agrobacterium tumefaciens c58
77	c5egnB	Alignment	not modelled	99.7	21	PDB header: hydrolase Chain: B; PDB Molecule: esterase; PDBTitle: est816 as an n-acyl homoserine lactone degrading enzyme
78	c5mxpB	Alignment	not modelled	99.7	10	PDB header: hydrolase Chain: B; PDB Molecule: alpha/beta hydrolase; PDBTitle: haloalkane dehalogenase dmxa from marinobacter sp. elb17 possessing a2 unique catalytic residue
79	d1mtza	Alignment	not modelled	99.7	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Proline iminopeptidase-like

80	d1hkha_	Alignment	not modelled	99.7	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
81	c4gdmA_	Alignment	not modelled	99.7	15	PDB header: lyase Chain: A: PDB Molecule: 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate PDBTitle: crystal structure of e.coli menh
82	c2xt0A_	Alignment	not modelled	99.7	10	PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase; PDBTitle: dehalogenase dppa from plesiocystis pacifica sir-i
83	c4oseA_	Alignment	not modelled	99.7	10	PDB header: hydrolase Chain: A: PDB Molecule: putative hydrolase; PDBTitle: x-ray crystal structure of a putative hydrolase from rickettsia typhi
84	c3kdaB_	Alignment	not modelled	99.7	10	PDB header: hydrolase Chain: B: PDB Molecule: cftr inhibitory factor (cif); PDBTitle: crystal structure of the cftr inhibitory factor cif with the h269a2 mutation
85	c4nvrC_	Alignment	not modelled	99.7	16	PDB header: transferase Chain: C: PDB Molecule: putative acyltransferase; PDBTitle: 2.22 angstrom resolution crystal structure of a putative2 acyltransferase from salmonella enterica
86	c4uhhA_	Alignment	not modelled	99.7	20	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: structural studies of a thermophilic esterase from2 thermogutta terrifontis (cacodylate complex)
87	c3wwoA_	Alignment	not modelled	99.7	7	PDB header: lyase Chain: A: PDB Molecule: (s)-hydroxynitrile lyase; PDBTitle: s-selective hydroxynitrile lyase from baliospermum montanum (apo1)
88	c3fobA_	Alignment	not modelled	99.7	14	PDB header: oxidoreductase Chain: A: PDB Molecule: bromoperoxidase; PDBTitle: crystal structure of bromoperoxidase from bacillus anthracis
89	d1q0ra_	Alignment	not modelled	99.7	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Aclacinomycin methylesterase RdmC
90	c6gupB_	Alignment	not modelled	99.7	10	PDB header: hydrolase Chain: B: PDB Molecule: siderophore biosynthesis lipase/esterase, putative; PDBTitle: siderophore hydrolase estb from aspergillus fumigatus
91	c3stxB_	Alignment	not modelled	99.7	13	PDB header: hydrolase Chain: B: PDB Molecule: methylketone synthase 1; PDBTitle: crystal structure of tomato methylketone synthase i h243a variant2 complexed with beta-ketoheptanoate
92	d3c70a1	Alignment	not modelled	99.7	11	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hydroxynitrile lyase-like
93	d1imja_	Alignment	not modelled	99.7	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Ccg1/TafII250-interacting factor B (Cib)
94	c6ra2E_	Alignment	not modelled	99.7	14	PDB header: hydrolase Chain: E: PDB Molecule: putative dioxygenase (1h-3-hydroxy-4-oxoquinoline 2,4- PDBTitle: structural basis for recognition and ring-cleavage of the pseudomonas2 quinolone signal (pqs) by aqdc
95	d1wm1a_	Alignment	not modelled	99.7	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Proline iminopeptidase-like
96	c2xmzA_	Alignment	not modelled	99.7	12	PDB header: lyase Chain: A: PDB Molecule: hydrolase, alpha/beta hydrolase fold family; PDBTitle: structure of menh from s. aureus
97	d1a8sa_	Alignment	not modelled	99.7	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
98	d1a88a_	Alignment	not modelled	99.7	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
99	d1bn7a_	Alignment	not modelled	99.7	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloalkane dehalogenase
100	c3c5wP_	Alignment	not modelled	99.7	10	PDB header: hydrolase Chain: P: PDB Molecule: pp2a-specific methylesterase pme-1; PDBTitle: complex between pp2a-specific methylesterase pme-1 and pp2a core2 enzyme
101	c3nwoA_	Alignment	not modelled	99.7	18	PDB header: hydrolase Chain: A: PDB Molecule: proline iminopeptidase; PDBTitle: crystal structure of proline iminopeptidase mycobacterium smegmatis
102	c1u2eA_	Alignment	not modelled	99.7	17	PDB header: hydrolase Chain: A: PDB Molecule: 2-hydroxy-6-ketonona-2,4-dienedioic acid PDBTitle: crystal structure of the c-c bond hydrolase mhpc
103	c4x00D_	Alignment	not modelled	99.7	19	PDB header: hydrolase Chain: D: PDB Molecule: putative hydrolase; PDBTitle: x-ray crystal structure of a putative aryl esterase from burkholderia2 cenocepacia
104	c5nfgA_	Alignment	not modelled	99.7	15	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase belonging to alpha/beta hydrolase PDBTitle: novel epoxide hydrolases belonging to the alpha/beta hydrolases2 superfamily in metagenomes from hot environments
105	c5h3hB_	Alignment	not modelled	99.7	16	PDB header: hydrolase Chain: B: PDB Molecule: abhydrolase domain-containing protein; PDBTitle: esterase (eaest) from exiguobacterium antarcticum

106	c5uroA_	Alignment	not modelled	99.7	11	PDB header: hydrolase Chain: A: PDB Molecule: predicted protein; PDBTitle: structure of a soluble epoxide hydrolase identified in trichoderma2 reesei
107	d1uk8a_	Alignment	not modelled	99.7	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase
108	d2rhwa1	Alignment	not modelled	99.7	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase
109	c3w06A_	Alignment	not modelled	99.7	13	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase, alpha/beta fold family protein; PDBTitle: crystal structure of arabidopsis thaliana dwarf14 like (atd14l)
110	c4rncB_	Alignment	not modelled	99.7	19	PDB header: hydrolase Chain: B: PDB Molecule: esterase; PDBTitle: crystal structure of an esterase rhest1 from rhodococcus sp. ecu1013
111	d1va4a_	Alignment	not modelled	99.7	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
112	c3jw8A_	Alignment	not modelled	99.7	12	PDB header: hydrolase Chain: A: PDB Molecule: mgl1 protein; PDBTitle: crystal structure of human mono-glyceride lipase
113	c4dnqA_	Alignment	not modelled	99.7	14	PDB header: hydrolase Chain: A: PDB Molecule: dad2; PDBTitle: crystal structure of dad2 s96a mutant
114	c4inzB_	Alignment	not modelled	99.7	13	PDB header: hydrolase Chain: B: PDB Molecule: soluble epoxide hydrolase; PDBTitle: the crystal structure of m145a mutant of an epoxide hydrolase from2 bacillus megaterium
115	c4q3lC_	Alignment	not modelled	99.7	14	PDB header: hydrolase Chain: C: PDB Molecule: mgs-m2; PDBTitle: crystal structure of mgs-m2, an alpha/beta hydrolase enzyme from a2 medee basin deep-sea metagenome library
116	c6fvjB_	Alignment	not modelled	99.7	17	PDB header: hydrolase Chain: B: PDB Molecule: thioesterase; PDBTitle: tesa a major thioesterase from mycobacterium tuberculosis
117	c1wprA_	Alignment	not modelled	99.7	15	PDB header: signaling protein Chain: A: PDB Molecule: sigma factor sigb regulation protein rsbq; PDBTitle: crystal structure of rsbq inhibited by pmsf
118	c4b9aA_	Alignment	not modelled	99.7	12	PDB header: hydrolase Chain: A: PDB Molecule: probable epoxide hydrolase; PDBTitle: structure of a putative epoxide hydrolase from pseudomonas2 aeruginosa.
119	c6ba8A_	Alignment	not modelled	99.7	13	PDB header: hydrolase Chain: A: PDB Molecule: iron aquisition yersiniabactin synthesis enzyme, ybtt; PDBTitle: ybtt - type ii thioesterase from yersiniabactin nrps/pks biosynthetic2 pathway
120	c4lxgA_	Alignment	not modelled	99.7	16	PDB header: hydrolase Chain: A: PDB Molecule: mcp hydrolase; PDBTitle: crystal structure of dxnb2, a carbon - carbon bond hydrolase from2 sphingomonas wittichii rw1