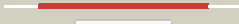



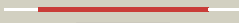



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0840c_(pip)_936460_937320
Date	Fri Jul 26 01:50:42 BST 2019
Unique Job ID	3814d45c3355ed2e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1cr6A_	 Alignment		100.0	20	PDB header: hydrolase Chain: A; PDB Molecule: epoxide hydrolase; PDBTitle: crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
2	c3i28A_	 Alignment		100.0	18	PDB header: hydrolase Chain: A; PDB Molecule: epoxide hydrolase 2; PDBTitle: crystal structure of soluble epoxide hydrolase
3	d1mtza_	 Alignment		100.0	28	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Proline iminopeptidase-like
4	c5nfgA_	 Alignment		100.0	19	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
5	c5ng7B_	 Alignment		100.0	17	PDB header: hydrolase Chain: B; PDB Molecule: epoxide hydrolase; PDBTitle: novel epoxide hydrolases belonging to the alpha/beta hydrolases2 superfamily in metagenomes from hot environments
6	c4d9jl_	 Alignment		100.0	18	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
7	c4oseA_	 Alignment		100.0	12	PDB header: hydrolase Chain: A; PDB Molecule: putative hydrolase; PDBTitle: x-ray crystal structure of a putative hydrolase from rickettsia typhi
8	d1q0ra_	 Alignment		100.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Aclacinomycin methylesterase RdmC
9	c3oosA_	 Alignment		100.0	22	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
10	c4inzB_	 Alignment		100.0	16	PDB header: hydrolase Chain: B; PDB Molecule: soluble epoxide hydrolase; PDBTitle: the crystal structure of m145a mutant of an epoxide hydrolase from2 bacillus megaterium
11	c3kdaB_	 Alignment		100.0	15	PDB header: hydrolase Chain: B; PDB Molecule: cftr inhibitory factor (cif); PDBTitle: crystal structure of the cftr inhibitory factor cif with the h269a2 mutation

12	c4pw0A_	Alignment		100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase fold protein; PDBTitle: alpha/beta hydrolase fold protein from chitinophaga pinensis
13	c4qloA_	Alignment		100.0	13	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: crystal structure of homoserine o-acetyltransferase from2 staphylococcus aureus
14	c3nwoA_	Alignment		100.0	38	PDB header: hydrolase Chain: A: PDB Molecule: proline iminopeptidase; PDBTitle: crystal structure of proline iminopeptidase mycobacterium smegmatis
15	d1zd3a2	Alignment		100.0	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
16	c2e3jA_	Alignment		100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase ephb; PDBTitle: the crystal structure of epoxide hydrolase b (rv1938) from2 mycobacterium tuberculosis at 2.1 angstrom
17	c4psuA_	Alignment		100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase; PDBTitle: crystal structure of alpha/beta hydrolase from rhodopseudomonas2 palustris cga009
18	c4opmB_	Alignment		100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: lipase; PDBTitle: crystal structure of a putative lipase (lip1) from acinetobacter2 baumannii aye at 1.70 a resolution
19	d1cr6a2	Alignment		100.0	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
20	d2b61a1	Alignment		100.0	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
21	c4q3lC_	Alignment	not modelled	100.0	16	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
22	c5cw2C_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: C: PDB Molecule: putative epoxide hydrolase epha; PDBTitle: crystal structure of epoxide hydrolase a from mycobacterium2 thermoresistibile
23	d1azwa_	Alignment	not modelled	100.0	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Proline iminopeptidase-like
24	c2qmqa_	Alignment	not modelled	100.0	12	PDB header: signaling protein Chain: A: PDB Molecule: protein ndr2; PDBTitle: crystal structure of a n-myc downstream regulated 2 protein (ndrg2,2 syld, ndr2, ai182517, au040374) from mus musculus at 1.70 a3 resolution
25	c4y7dA_	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase fold protein; PDBTitle: alpha/beta hydrolase fold protein from nakamurella multipartita
26	d1ehya_	Alignment	not modelled	100.0	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
27	c5xmdA_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase a; PDBTitle: crystal structure of epoxide hydrolase vreh1 from vigna radiata
28	c5yhpB_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: cold active proline iminopeptidase; PDBTitle: proline iminopeptidase from psychrophilic yeast glaciozyma antarctica

29	d1c4xa_	Alignment	not modelled	100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase
30	c2vavL_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: L: PDB Molecule: acetyl-coa--deacetylcephalosporin c acetyltransferase; PDBTitle: crystal structure of deacetylcephalosporin c acetyltransferase (dac-2 soak)
31	c3wibB_	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: B: PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of y109w mutant haloalkane dehalogenase data from2 agrobacterium tumefaciens c58
32	c5d6oB_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: B: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: orthorhombic crystal structure of an acylester hydrolase from2 corynebacterium glutamicum
33	c4b9aA_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: probable epoxide hydrolase; PDBTitle: structure of a putative epoxide hydrolase from pseudomonas2 aeruginosa.
34	c3a2nF_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: F: PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of dbja (wild type type ii p21)
35	c2cjpA_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: structure of potato (solanum tuberosum) epoxide hydrolase i (steh1)
36	d1b6ga_	Alignment	not modelled	100.0	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloalkane dehalogenase
37	c3u1tA_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: dmma haloalkane dehalogenase; PDBTitle: haloalkane dehalogenase, dmma, of marine microbial origin
38	c4nvrC_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: C: PDB Molecule: putative acyltransferase; PDBTitle: 2.22 angstrom resolution crystal structure of a putative2 acyltransferase from salmonella enterica
39	c2r11D_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: D: PDB Molecule: carboxylesterase np; PDBTitle: crystal structure of putative hydrolase (2632844) from bacillus2 subtilis at 1.96 a resolution
40	c4rncB_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: esterase; PDBTitle: crystal structure of an esterase rhest1 from rhodococcus sp. ecu1013
41	c1y37A_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: fluoroacetate dehalogenase; PDBTitle: structure of fluoroacetate dehalogenase from burkholderia sp. fa1
42	c3kxpD_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: D: PDB Molecule: alpha-(n-acetylamino)methylene)succinic acid hydrolase; PDBTitle: crystal structure of e-2-(acetamidomethylene)succinate hydrolase
43	c2yysA_	Alignment	not modelled	100.0	19	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
44	c5mxpB_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: alpha/beta hydrolase; PDBTitle: haloalkane dehalogenase dmxa from marinobacter sp. elb17 possessing a2 unique catalytic residue
45	c3qyjB_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: B: PDB Molecule: alr0039 protein; PDBTitle: crystal structure of alr0039, a putative alpha/beta hydrolase from2 nostoc sp pcc 7120.
46	c5egnB_	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: B: PDB Molecule: esterase; PDBTitle: est816 as an n-acyl homoserine lactone degrading enzyme
47	c4l0cA_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: deformylase; PDBTitle: crystal structure of the n-fopmylmaeamic acid deformylase nfo(s94a)2 from pseudomonas putida s16
48	c4i3fA_	Alignment	not modelled	100.0	15	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
49	c2xuaH_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: H: PDB Molecule: 3-oxoadipate enol-lactonase; PDBTitle: crystal structure of the enol-lactonase from burkholderia2 xenovorans lb400
50	c5esrA_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of haloalkane dehalogenase (dccca) from caulobacter2 crescentus
51	c5efzC_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: C: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: monoclinic structure of the acetyl esterase mekb
52	c4qlaB_	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: B: PDB Molecule: juvenile hormone epoxide hydrolase; PDBTitle: crystal structure of juvenile hormone epoxide hydrolase from the2 silkworm bombyx mori
53	d1bn7a_	Alignment	not modelled	100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloalkane dehalogenase
54	c2am9A_	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: probable hydrolase;

54	c50m6A	Alignment	not modelled	100.0	23	PDBTitle: the crystal structure of a hydrolase from pseudomonas aeruginosa pa01 PDB header: transferase
55	c5w8pA	Alignment	not modelled	100.0	14	Chain: A; PDB Molecule: homoserine o-acetyltransferase; PDBTitle: homoserine transacetylase meta from mycobacterium abscessus
56	c5f4zB	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B; PDB Molecule: epoxide hydrolase; PDBTitle: the crystal structure of an epoxide hydrolase from streptomyces2 carzinostaticus subsp. neocarzinostaticus
57	c2y6vB	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: B; PDB Molecule: peroxisomal membrane protein lpx1; PDBTitle: peroxisomal alpha-beta-hydrolase lpx1 (yor084w) from saccharomyces2 cerevisiae (crystal form i)
58	c5bovD	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: D; PDB Molecule: putative epoxide hydrolase protein; PDBTitle: crystal structure of a putative epoxide hydrolase (kpn_01808) from2 klebsiella pneumoniae subsp. pneumoniae mgh 78578 at 1.60 a3 resolution
59	c3bwxA	Alignment	not modelled	100.0	13	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
60	c4qlaA	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: A; PDB Molecule: juvenile hormone epoxide hydrolase; PDBTitle: crystal structure of juvenile hormone epoxide hydrolase from the2 silkworm bombyx mori
61	c5w15D	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: D; PDB Molecule: alpha/beta hydrolase fold protein; PDBTitle: crystal structure of an alpha/beta hydrolase fold protein from2 burkholderia ambifaria.
62	c4i19A	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: A; PDB Molecule: epoxide hydrolase; PDBTitle: the crystal structure of an epoxide hydrolase from streptomyces2 carzinostaticus subsp. neocarzinostaticus.
63	d2rhwa1	Alignment	not modelled	100.0	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase
64	c3ibtA	Alignment	not modelled	100.0	12	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)
65	c6f9oA	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A; PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of cold-adapted haloalkane dehalogenase dpca from2 psychrobacter cryohalolentis k5
66	c4mj3B	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: B; PDB Molecule: haloalkane dehalogenase; PDBTitle: haloalkane dehalogenase dmra from mycobacterium rhodesiae js60
67	c4f0jA	Alignment	not modelled	100.0	20	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
68	c5h3hB	Alignment	not modelled	100.0	26	PDB header: hydrolase Chain: B; PDB Molecule: abhydrolase domain-containing protein; PDBTitle: esterase (eaest) from exiguobacterium antarcticum
69	c3i1iA	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A; PDB Molecule: homoserine o-acetyltransferase; PDBTitle: x-ray crystal structure of homoserine o-acetyltransferase from2 bacillus anthracis
70	c5jkjA	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A; PDB Molecule: esterase e22; PDBTitle: crystal structure of esterase e22 l374d mutant
71	c5a62A	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A; PDB Molecule: putative alpha/beta hydrolase fold protein; PDBTitle: hydrolytic potential of the ammonia-oxidizing thaumarchaeon2 nitrososphaera gargasii - crystal structure and activity profiles of3 carboxylesterases linked to their metabolic function
72	d1wm1a	Alignment	not modelled	100.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Proline iminopeptidase-like
73	c2xt0A	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A; PDB Molecule: haloalkane dehalogenase; PDBTitle: dehalogenase dpca from plesiocystis pacifica sir-i
74	d2vata1	Alignment	not modelled	100.0	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
75	c5uroA	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: A; PDB Molecule: predicted protein; PDBTitle: structure of a soluble epoxide hydrolase identified in trichoderma2 reesei
76	d1mj5a	Alignment	not modelled	100.0	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloalkane dehalogenase
77	d1uk8a	Alignment	not modelled	100.0	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase
78	c4uhhA	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: A; PDB Molecule: esterase; PDBTitle: structural studies of a thermophilic esterase from2 thermogutta terrifontis (cacodylate complex)
79	d1j1ia	Alignment	not modelled	100.0	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases

				Family:Carbon-carbon bond hydrolase		
80	c1j1a	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: meta cleavage compound hydrolase; PDBTitle: crystal structure of a his-tagged serine hydrolase involved2 in the carbazole degradation (carc enzyme)
81	c2pseA	Alignment	not modelled	100.0	9	PDB header: oxidoreductase Chain: A: PDB Molecule: renilla-luciferin 2-monooxygenase; PDBTitle: crystal structures of the luciferase and green fluorescent2 protein from renilla reniformis
82	c4c6hA	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase; PDBTitle: haloalkane dehalogenase with 1-hexanol
83	c2vf2A	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate PDBTitle: x-ray crystal structure of hsd from mycobacterium2 tuberculosis
84	c1zoiC	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: C: PDB Molecule: esterase; PDBTitle: crystal structure of a stereoselective esterase from2 pseudomonas putida ifo12996
85	c1u2eA	Alignment	not modelled	100.0	19	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
86	c6g75B	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: B: PDB Molecule: common ancestor of haloalkane dehalogenase and renilla PDBTitle: crystal structure of the common ancestor of haloalkane dehalogenases2 and renilla luciferase (anchld-lruc)
87	c4lxgA	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: mcp hydrolase; PDBTitle: crystal structure of dxnb2, a carbon - carbon bond hydrolase from2 sphingomonas wittichii rw1
88	c4ccyA	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: carboxylesterase ybfk; PDBTitle: crystal structure of carboxylesterase cesb (ybfk) from bacillus2 subtilis
89	c2xmzA	Alignment	not modelled	100.0	18	PDB header: lyase Chain: A: PDB Molecule: hydrolase, alpha/beta hydrolase fold family; PDBTitle: structure of menh from s. aureus
90	d1a88a	Alignment	not modelled	100.0	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
91	d1brta	Alignment	not modelled	100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
92	c2qvba	Alignment	not modelled	100.0	10	PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase 3; PDBTitle: crystal structure of haloalkane dehalogenase rv2579 from mycobacterium2 tuberculosis
93	c1wprA	Alignment	not modelled	100.0	15	PDB header: signaling protein Chain: A: PDB Molecule: sigma factor sigb regulation protein rsbq; PDBTitle: crystal structure of rsbq inhibited by pmsf
94	c3vviA	Alignment	not modelled	100.0	18	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
95	c2wj4B	Alignment	not modelled	100.0	14	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
96	c3qitB	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: B: PDB Molecule: polyketide synthase; PDBTitle: thioesterase domain from curacin biosynthetic pathway
97	d1a8sa	Alignment	not modelled	100.0	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
98	c3r3xA	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: fluoroacetate dehalogenase; PDBTitle: crystal structure of the fluoroacetate dehalogenase rpa1163 -2 asp110asn/bromoacetate
99	c4x00D	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: D: PDB Molecule: putative hydrolase; PDBTitle: x-ray crystal structure of a putative aryl esterase from burkholderia2 cenocepacia
100	c3v48B	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: putative aminoacrylate hydrolase rutd; PDBTitle: crystal structure of the putative alpha/beta hydrolase rutd from2 e.coli
101	c3qvmA	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: olei00960; PDBTitle: the structure of olei00960, a hydrolase from oleispira antarctica
102	c3e3aA	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: possible peroxidase bpsc; PDBTitle: the structure of rv0554 from mycobacterium tuberculosis
103	d1va4a	Alignment	not modelled	100.0	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
104	c3wz1B	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: B: PDB Molecule: zearalenone hydrolase; PDBTitle: zen lactonase

105	d1a8qa_	Alignment	not modelled	100.0	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
106	c4ns4A_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase fold protein; PDBTitle: crystal structure of cold-active esterase from psychrobacter2 cryohalolentis k5t
107	d1hkha_	Alignment	not modelled	100.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
108	d1m33a_	Alignment	not modelled	100.0	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Biotin biosynthesis protein BioH
109	d1qo7a_	Alignment	not modelled	100.0	11	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
110	c4rpcA_	Alignment	not modelled	100.0	12	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
111	c3p2mA_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: possible hydrolase; PDBTitle: crystal structure of a novel esterase rv0045c from mycobacterium2 tuberculosis
112	d2pl5a1	Alignment	not modelled	100.0	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
113	c6brtB_	Alignment	not modelled	100.0	15	PDB header: ligase Chain: B: PDB Molecule: d3-cth-d14-d-ring; PDBTitle: f-box protein cth with hydrolase
114	c6ra2E_	Alignment	not modelled	100.0	13	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
115	c2ockA_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: valacyclovir hydrolase; PDBTitle: crystal structure of valacyclovir hydrolase d123n mutant
116	c3fsgC_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: C: PDB Molecule: alpha/beta superfamily hydrolase; PDBTitle: crystal structure of alpha/beta superfamily hydrolase from oenococcus2 oeni psu-1
117	c3l80A_	Alignment	not modelled	100.0	11	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein smu.1393c; PDBTitle: crystal structure of smu.1393c from streptococcus mutans ua159
118	c5cbkA_	Alignment	not modelled	100.0	13	PDB header: signaling protein Chain: A: PDB Molecule: shhtl5; PDBTitle: crystal structure of the strigolactone receptor shhtl5 from striga2 hermonthica
119	c3jw8A_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: mgll protein; PDBTitle: crystal structure of human mono-glyceride lipase
120	c5xo6F_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: F: PDB Molecule: lactonase for protein; PDBTitle: crystal structure of a novel zen lactonase mutant