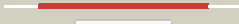



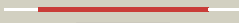



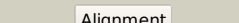

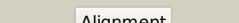

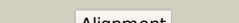




















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2296 (-)_2567514_2568416
Date	Mon Aug 5 13:25:43 BST 2019
Unique Job ID	df078bc456725b77

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5esrA_	 Alignment		100.0	49	PDB header: hydrolase Chain: A; PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of haloalkane dehalogenase (dcca) from caulobacter2 crescentus
2	c4mj3B_	 Alignment		100.0	55	PDB header: hydrolase Chain: B; PDB Molecule: haloalkane dehalogenase; PDBTitle: haloalkane dehalogenase dmra from mycobacterium rhodesiae js60
3	c6f9oA_	 Alignment		100.0	49	PDB header: hydrolase Chain: A; PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of cold-adapted haloalkane dehalogenase dpca from2 psychrobacter cryohalolentis k5
4	d1b6ga_	 Alignment		100.0	30	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloalkane dehalogenase
5	c2xt0A_	 Alignment		100.0	35	PDB header: hydrolase Chain: A; PDB Molecule: haloalkane dehalogenase; PDBTitle: dehalogenase dpqa from plesiocystis pacifica sir-i
6	c3i28A_	 Alignment		100.0	21	PDB header: hydrolase Chain: A; PDB Molecule: epoxide hydrolase 2; PDBTitle: crystal structure of soluble epoxide hydrolase
7	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
8	c4d9jl_	 Alignment		100.0	19	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
9	c4f0jA_	 Alignment		100.0	21	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
10	c4qloA_	 Alignment		100.0	10	PDB header: transferase Chain: A; PDB Molecule: homoserine o-acetyltransferase; PDBTitle: crystal structure of homoserine o-acetyltransferase from2 staphylococcus aureus
11	c5xmdA_	 Alignment		100.0	19	PDB header: hydrolase Chain: A; PDB Molecule: epoxide hydrolase a; PDBTitle: crystal structure of epoxide hydrolase vreh1 from vigna radiata

12	c2e3jA_	Alignment		100.0	24	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
13	c4qlaA_	Alignment		100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: juvenile hormone epoxide hydrolase; PDBTitle: crystal structure of juvenile hormone epoxide hydrolase from the2 silkworm bombyx mori
14	c4qlaB_	Alignment		100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: juvenile hormone epoxide hydrolase; PDBTitle: crystal structure of juvenile hormone epoxide hydrolase from the2 silkworm bombyx mori
15	c3u1tA_	Alignment		100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: dmma haloalkane dehalogenase; PDBTitle: haloalkane dehalogenase, dmma, of marine microbial origin
16	d1zd3a2	Alignment		100.0	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
17	c4i19A_	Alignment		100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: the crystal structure of an epoxide hydrolase from streptomycetes2 carzinostaticus subsp. neocarzinostaticus.
18	d2b61a1	Alignment		100.0	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
19	c5f4zB_	Alignment		100.0	15	PDB header: hydrolase Chain: B: PDB Molecule: epoxide hydrolase; PDBTitle: the crystal structure of an epoxide hydrolase from streptomycetes2 carzinostaticus subsp. neocarzinostaticus
20	d1cr6a2	Alignment		100.0	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
21	c3i1iA_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: x-ray crystal structure of homoserine o-acetyltransferase from2 bacillus anthracis
22	c2r11D_	Alignment	not modelled	100.0	18	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	c4pw0A_	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase fold protein; PDBTitle: alpha/beta hydrolase fold protein from chitinophaga pinensis
24	c2vavL_	Alignment	not modelled	100.0	9	PDB header: transferase Chain: L: PDB Molecule: acetyl-coa--deacetylcephalosporin c acetyltransferase; PDBTitle: crystal structure of deacetylcephalosporin c acetyltransferase (dac-2 soak)
25	c5yhpB_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: cold active proline iminopeptidase; PDBTitle: proline iminopeptidase from psychrophilic yeast glaciozyma antarctica
26	c5w8pA_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: homoserine transacetylase meta from mycobacterium abscessus
27	c2cjpA_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: structure of potato (solanum tuberosum) epoxide hydrolase i (steh1)
28	c2qmqa_	Alignment	not modelled	100.0	11	PDB header: signaling protein Chain: A: PDB Molecule: protein ndrg2; 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
29	c4opmB_	Alignment	not modelled	100.0	14 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
30	d1bn7a_	Alignment	not modelled	100.0	28 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloalkane dehalogenase
31	c5uroA_	Alignment	not modelled	100.0	17 PDB header: hydrolase Chain: A: PDB Molecule: predicted protein; PDBTitle: structure of a soluble epoxide hydrolase identified in trichoderma2 reesei
32	c3oosA_	Alignment	not modelled	100.0	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
33	c3om8A_	Alignment	not modelled	100.0	21 PDB header: hydrolase Chain: A: PDB Molecule: probable hydrolase; PDBTitle: the crystal structure of a hydrolase from pseudomonas aeruginosa pa01
34	c5mxbB_	Alignment	not modelled	100.0	27 PDB header: hydrolase Chain: B: PDB Molecule: alpha/beta hydrolase; PDBTitle: haloalkane dehalogenase dmxa from marinobacter sp. elb17 possessing a2 unique catalytic residue
35	c5nfgA_	Alignment	not modelled	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
36	c4psuA_	Alignment	not modelled	100.0	18 PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase; PDBTitle: crystal structure of alpha/beta hydrolase from rhodospseudomonas2 palustris cga009
37	d1qo7a_	Alignment	not modelled	100.0	14 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
38	c5cw2C_	Alignment	not modelled	100.0	21 PDB header: hydrolase Chain: C: PDB Molecule: putative epoxide hydrolase epha; PDBTitle: crystal structure of epoxide hydrolase a from mycobacterium2 thermoresistibile
39	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)
40	d1ehya_	Alignment	not modelled	100.0	17 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
41	c4oseA_	Alignment	not modelled	100.0	13 PDB header: hydrolase Chain: A: PDB Molecule: putative hydrolase; PDBTitle: x-ray crystal structure of a putative hydrolase from rickettsia typhi
42	d1azwa_	Alignment	not modelled	100.0	17 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Proline iminopeptidase-like
43	c5ijkA_	Alignment	not modelled	100.0	14 PDB header: hydrolase Chain: A: PDB Molecule: esterase e22; PDBTitle: crystal structure of esterase e22 l374d mutant
44	d2pl5a1	Alignment	not modelled	100.0	11 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
45	c3vvlA_	Alignment	not modelled	100.0	16 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
46	c5bovD_	Alignment	not modelled	100.0	18 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
47	d2rhwa1	Alignment	not modelled	100.0	17 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase
48	c5d6oB_	Alignment	not modelled	100.0	11 PDB header: transferase Chain: B: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: orthorhombic crystal structure of an acylester hydrolase from2 corynebacterium glutamicum
49	c3kdaB_	Alignment	not modelled	100.0	17 PDB header: hydrolase Chain: B: PDB Molecule: cfr inhibitory factor (cif); PDBTitle: crystal structure of the cfr inhibitory factor cif with the h269a2 mutation
50	c5ng7B_	Alignment	not modelled	100.0	20 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
51	d1c4xa_	Alignment	not modelled	100.0	18 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase
52	d1q0ra_	Alignment	not modelled	100.0	17 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Aclacinomycin methylesterase RdmC
53	c3wibB_	Alignment	not modelled	100.0	29 PDB header: hydrolase Chain: B: PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of y109w mutant haloalkane dehalogenase data from2 agrobacterium tumefaciens c58

54	c4inzB_	Alignment	not modelled	100.0	22	Chain: B; PDB Molecule: soluble epoxide hydrolase; PDBTitle: the crystal structure of m145a mutant of an epoxide hydrolase from2 bacillus megaterium
55	c4y7dA_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A; PDB Molecule: alpha/beta hydrolase fold protein; PDBTitle: alpha/beta hydrolase fold protein from nakamurella multipartita
56	d2vata1	Alignment	not modelled	100.0	10	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
57	c2vf2A_	Alignment	not modelled	100.0	20	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
58	c3ibtA_	Alignment	not modelled	100.0	11	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)
59	c3bwxA_	Alignment	not modelled	100.0	16	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	c4b9aA_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A; PDB Molecule: probable epoxide hydrolase; PDBTitle: structure of a putative epoxide hydrolase from pseudomonas2 aeruginosa.
61	d1mtza_	Alignment	not modelled	100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Proline iminopeptidase-like
62	c5efzC_	Alignment	not modelled	100.0	11	PDB header: hydrolase Chain: C; PDB Molecule: homoserine o-acetyltransferase; PDBTitle: monoclinic structure of the acetyl esterase mekb
63	c3kxpD_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: D; PDB Molecule: alpha-(n-acetylaminoethylene)succinic acid hydrolase; PDBTitle: crystal structure of e-2-(acetamidomethylene)succinate hydrolase
64	d1brta_	Alignment	not modelled	100.0	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
65	c4i3fA_	Alignment	not modelled	100.0	13	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
66	d1hkha_	Alignment	not modelled	100.0	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
67	c1u2eA_	Alignment	not modelled	100.0	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
68	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
69	c2yysA_	Alignment	not modelled	100.0	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
70	c3a2nF_	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: F; PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of dbja (wild type type ii p21)
71	c2xuaH_	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: H; PDB Molecule: 3-oxoadipate enol-lactonase; PDBTitle: crystal structure of the enol-lactonase from burkholderia2 xenovorans lb400
72	d1wm1a_	Alignment	not modelled	100.0	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Proline iminopeptidase-like
73	c4nvrC_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: C; PDB Molecule: putative acyltransferase; PDBTitle: 2.22 angstrom resolution crystal structure of a putative2 acyltransferase from salmonella enterica
74	c4x00D_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: D; PDB Molecule: putative hydrolase; PDBTitle: x-ray crystal structure of a putative aryl esterase from burkholderia2 cenocepacia
75	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
76	c4ccyA_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A; PDB Molecule: carboxylesterase ybfk; PDBTitle: crystal structure of carboxylesterase cesb (ybfk) from bacillus2 subtilis
77	c1zoiC_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: C; PDB Molecule: esterase; PDBTitle: crystal structure of a stereoselective esterase from2 pseudomonas putida ifo12996
78	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

79	d1va4a_	Alignment	not modelled	100.0	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
80	c4l0cA_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: deformylase; PDBTitle: crystal structure of the n-fopmylmaleamic acid deformylase nfo(s94a)2 from pseudomonas putida s16
81	d1mj5a_	Alignment	not modelled	100.0	24	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloalkane dehalogenase
82	c4uhhA_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: structural studies of a thermophilic esterase from2 thermogutta terrifontis (cacodylate complex)
83	c2wj4B_	Alignment	not modelled	100.0	16	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
84	c3v48B_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: B: PDB Molecule: putative aminoacrylate hydrolase rutd; PDBTitle: crystal structure of the putative alpha/beta hydrolase rutd from2 e.coli
85	c3e3aA_	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: possible peroxidase bpsc; PDBTitle: the structure of rv0554 from mycobacterium tuberculosis
86	c3r3xA_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: fluoroacetate dehalogenase; PDBTitle: crystal structure of the fluoroacetate dehalogenase rpa1163 -2 asp110asn/bromoacetate
87	c5egnB_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: esterase; PDBTitle: est816 as an n-acyl homoserine lactone degrading enzyme
88	c3fsgC_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: C: PDB Molecule: alpha/beta superfamily hydrolase; PDBTitle: crystal structure of alpha/beta superfamily hydrolase from oenococcus2 oeni psu-1
89	c2pseA_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: renilla-luciferin 2-monooxygenase; PDBTitle: crystal structures of the luciferase and green fluorescent2 protein from renilla reniformis
90	c5h3hB_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: abhydrolase domain-containing protein; PDBTitle: esterase (eaest) from exiguobacterium antarcticum
91	c3qitB_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: polyketide synthase; PDBTitle: thioesterase domain from curacin biosynthetic pathway
92	d1a8sa_	Alignment	not modelled	100.0	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
93	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
94	c4lxgA_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: mcp hydrolase; PDBTitle: crystal structure of dxnb2, a carbon - carbon bond hydrolase from2 sphingomonas wittichii rw1
95	c5w15D_	Alignment	not modelled	100.0	21	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.
96	c3fobA_	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: bromoperoxidase; PDBTitle: crystal structure of bromoperoxidase from bacillus anthracis
97	c4rpcA_	Alignment	not modelled	100.0	10	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
98	c4q3lC_	Alignment	not modelled	100.0	17	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
99	d1luk8a_	Alignment	not modelled	100.0	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase
100	d1a8qa_	Alignment	not modelled	100.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
101	c3qyjB_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: alr0039 protein; PDBTitle: crystal structure of alr0039, a putative alpha/beta hydrolase from2 nostoc sp pcc 7120.
102	c6g75B_	Alignment	not modelled	100.0	24	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)
103	c3wzlb_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: zearealenone hydrolase; PDBTitle: zen lactonase
104	d1hlga_	Alignment	not modelled	100.0	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases

						Family: Gastric lipase
105	c2xmzA_	Alignment	not modelled	100.0	15	PDB header: lyase Chain: A: PDB Molecule: hydrolase, alpha/beta hydrolase fold family; PDBTitle: structure of menh from s. aureus
106	d1a88a_	Alignment	not modelled	100.0	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
107	c3qvmA_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: olei00960; PDBTitle: the structure of olei00960, a hydrolase from oleispira antarctica
108	d3c70a1	Alignment	not modelled	100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hydroxynitrile lyase-like
109	c2qvba_	Alignment	not modelled	100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase 3; PDBTitle: crystal structure of haloalkane dehalogenase rv2579 from mycobacterium2 tuberculosis
110	c4c6hA_	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase; PDBTitle: haloalkane dehalogenase with 1-hexanol
111	c5xo6F_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: F: PDB Molecule: lactonase for protein; PDBTitle: crystal structure of a novel zen lactonase mutant
112	c3nwoA_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: proline iminopeptidase; PDBTitle: crystal structure of proline iminopeptidase mycobacterium smegmatis
113	d1xkla_	Alignment	not modelled	100.0	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hydroxynitrile lyase-like
114	d1k8qa_	Alignment	not modelled	100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Gastric lipase
115	c3p2mA_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: possible hydrolase; PDBTitle: crystal structure of a novel esterase rv0045c from mycobacterium2 tuberculosis
116	c3dqzB_	Alignment	not modelled	100.0	12	PDB header: lyase Chain: B: PDB Molecule: alpha-hydroxynitrile lyase-like protein; PDBTitle: structure of the hydroxynitrile lyase from arabidopsis thaliana
117	c3wwoA_	Alignment	not modelled	100.0	14	PDB header: lyase Chain: A: PDB Molecule: (s)-hydroxynitrile lyase; PDBTitle: s-selective hydroxynitrile lyase from baliospermum montanum (apo1)
118	d1e89a_	Alignment	not modelled	100.0	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hydroxynitrile lyase-like
119	c4ns4A_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase fold protein; PDBTitle: crystal structure of cold-active esterase from psychrobacter2 cryohalolentis k5t
120	c3e0xB_	Alignment	not modelled	100.0	15	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