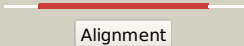

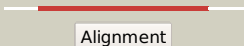

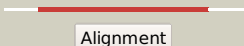







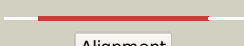












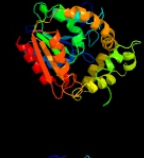




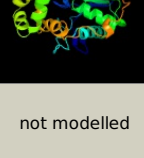


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0077c_(-)_85633_86463
Date	Tue Jul 23 14:50:11 BST 2019
Unique Job ID	9dd64fe65c4b37e0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1cr6A_</a>	 Alignment		100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> epoxide hydrolase; <b>PDBTitle:</b> crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
2	<a href="#">c3i28A_</a>	 Alignment		100.0	19	<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
3	<a href="#">c4d9jl_</a>	 Alignment		100.0	21	<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="#">c4y7dA_</a>	 Alignment		100.0	18	<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
5	<a href="#">c4oseA_</a>	 Alignment		100.0	11	<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
6	<a href="#">d1b6ga_</a>	 Alignment		100.0	15	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloalkane dehalogenase
7	<a href="#">c2e3jA_</a>	 Alignment		100.0	19	<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
8	<a href="#">c5xmdA_</a>	 Alignment		100.0	17	<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
9	<a href="#">c4pw0A_</a>	 Alignment		100.0	12	<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
10	<a href="#">c4rncB_</a>	 Alignment		100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> crystal structure of an esterase rhest1 from rhodococcus sp. ecu1013
11	<a href="#">c3oosA_</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 structure of an alpha/beta fold family hydrolase from bacillus2 anthracis str. Sterne

12	<a href="#">d1zd3a2</a>	Alignment		100.0	18	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Epoxide hydrolase
13	<a href="#">c4q3lC_</a>	Alignment		100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> mgs-m2; <b>PDBTitle:</b> crystal structure of mgs-m2, an alpha/beta hydrolase enzyme from a2 medee basin deep-sea metagenome library
14	<a href="#">c5nfgA_</a>	Alignment		100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> epoxide hydrolase belonging to alpha/beta hydrolase <b>PDBTitle:</b> novel epoxide hydrolases belonging to the alpha/beta hydrolases2 superfamily in metagenomes from hot environments
15	<a href="#">c3kdaB_</a>	Alignment		100.0	14	<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
16	<a href="#">d1q0ra_</a>	Alignment		100.0	17	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Aclacinomycin methylesterase RdmC
17	<a href="#">c4inzB_</a>	Alignment		100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> soluble epoxide hydrolase; <b>PDBTitle:</b> the crystal structure of m145a mutant of an epoxide hydrolase from2 bacillus megaterium
18	<a href="#">c4opmB_</a>	Alignment		100.0	16	<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
19	<a href="#">d1cr6a2</a>	Alignment		100.0	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Epoxide hydrolase
20	<a href="#">d1ehya_</a>	Alignment		100.0	15	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Epoxide hydrolase
21	<a href="#">c4qloA_</a>	Alignment	not modelled	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 homoserine o-acetyltransferase from2 staphylococcus aureus
22	<a href="#">c5ng7B_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> epoxide hydrolase; <b>PDBTitle:</b> novel epoxide hydrolases belonging to the alpha/beta hydrolases2 superfamily in metagenomes from hot environments
23	<a href="#">c4f0jA_</a>	Alignment	not modelled	100.0	17	<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
24	<a href="#">c4psuA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha/beta hydrolase; <b>PDBTitle:</b> crystal structure of alpha/beta hydrolase from rhodopseudomonas2 palustris cga009
25	<a href="#">c3a2nF_</a>	Alignment	not modelled	100.0	13	<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)
26	<a href="#">d1mtza_</a>	Alignment	not modelled	100.0	12	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Proline iminopeptidase-like
27	<a href="#">c2cjpA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> epoxide hydrolase; <b>PDBTitle:</b> structure of potato (solanum tuberosum) epoxide hydrolase i (steh1)
28	<a href="#">c3om8A_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable hydrolase; <b>PDBTitle:</b> the crystal structure of a hydrolase from pseudomonas aeruginosa pa01
						<b>Fold:</b> alpha/beta-Hydrolases

29	<a href="#">d1brta_</a>	Alignment	not modelled	100.0	17	<b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloperoxidase
30	<a href="#">c5egnB_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> est816 as an n-acyl homoserine lactone degrading enzyme
31	<a href="#">c3u1tA_</a>	Alignment	not modelled	100.0	19	<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
32	<a href="#">c2vavL_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> L: <b>PDB Molecule:</b> acetyl-coa--deacetylcephalosporin c acetyltransferase; <b>PDBTitle:</b> crystal structure of deacetylcephalosporin c acetyltransferase (dac-2 soak)
33	<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
34	<a href="#">c5cw2C_</a>	Alignment	not modelled	100.0	15	<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
35	<a href="#">c5h3hB_</a>	Alignment	not modelled	100.0	18	<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
36	<a href="#">c5uroA_</a>	Alignment	not modelled	100.0	19	<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
37	<a href="#">c2xuaH_</a>	Alignment	not modelled	100.0	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
38	<a href="#">c2r11D_</a>	Alignment	not modelled	100.0	17	<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
39	<a href="#">c2pseA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> renilla-luciferin 2-monooxygenase; <b>PDBTitle:</b> crystal structures of the luciferase and green fluorescent2 protein from renilla reniformis
40	<a href="#">c5w15D_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> alpha/beta hydrolase fold protein; <b>PDBTitle:</b> crystal structure of an alpha/beta hydrolase fold protein from2 burkholderia ambifaria.
41	<a href="#">c2xt0A_</a>	Alignment	not modelled	100.0	16	<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
42	<a href="#">c4uhhA_</a>	Alignment	not modelled	100.0	21	<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)
43	<a href="#">d1a88a_</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloperoxidase
44	<a href="#">c5bovD_</a>	Alignment	not modelled	100.0	18	<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
45	<a href="#">c2vf2A_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate <b>PDBTitle:</b> x-ray crystal structure of hsd from mycobacterium2 tuberculosis
46	<a href="#">d1c4xa_</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carbon-carbon bond hydrolase
47	<a href="#">c5yhpB_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cold active proline iminopeptidase; <b>PDBTitle:</b> proline iminopeptidase from psychrophilic yeast glaciozyma antarctica
48	<a href="#">c3wibB_</a>	Alignment	not modelled	100.0	14	<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
49	<a href="#">c3i1iA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> homoserine o-acetyltransferase; <b>PDBTitle:</b> x-ray crystal structure of homoserine o-acetyltransferase from2 bacillus anthracis
50	<a href="#">c3ibtA_</a>	Alignment	not modelled	100.0	11	<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)
51	<a href="#">c5d6oB_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> homoserine o-acetyltransferase; <b>PDBTitle:</b> orthorhombic crystal structure of an acylester hydrolase from2 corynebacterium glutamicum
52	<a href="#">c5esrA_</a>	Alignment	not modelled	100.0	21	<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
53	<a href="#">d1a8sa_</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloperoxidase <b>PDB header:</b> hydrolase

54	<a href="#">c4i3fA_</a>	Alignment	not modelled	100.0	16	<b>Chain:</b> A; <b>PDB Molecule:</b> serine hydrolase ccsp0084; <b>PDBTitle:</b> crystal structure of serine hydrolase ccsp0084 from the polyaromatic2 hydrocarbon (pah)-degrading bacterium cycloclasticus zankles
55	<a href="#">d2b61a1</a>	Alignment	not modelled	100.0	11	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> O-acetyltransferase
56	<a href="#">c3kxpD_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> D; <b>PDB Molecule:</b> alpha-(n-acetylaminoethylene)succinic acid hydrolase; <b>PDBTitle:</b> crystal structure of e-2-(acetamidomethylene)succinate hydrolase
57	<a href="#">c4l0cA_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> deformylase; <b>PDBTitle:</b> crystal structure of the n-fopmylmalemic acid deformylase nfo(s94a)2 from pseudomonas putida s16
58	<a href="#">c5efzC_</a>	Alignment	not modelled	100.0	11	<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
59	<a href="#">d1va4a_</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloperoxidase
60	<a href="#">c2y6vB_</a>	Alignment	not modelled	100.0	16	<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)
61	<a href="#">c5a62A_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> putative alpha/beta hydrolase fold protein; <b>PDBTitle:</b> hydrolytic potential of the ammonia-oxidizing thaumarchaeon2 nitrososphaera gargenis - crystal structure and activity profiles of3 carboxylesterases linked to their metabolic function
62	<a href="#">c1zoiC_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> crystal structure of a stereoselective esterase from2 pseudomonas putida ifo12996
63	<a href="#">c5mxbB_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> alpha/beta hydrolase; <b>PDBTitle:</b> haloalkane dehalogenase dmxa from marinobacter sp. elb17 possessing a2 unique catalytic residue
64	<a href="#">c5f4zB_</a>	Alignment	not modelled	100.0	15	<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
65	<a href="#">c4qlaB_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> juvenile hormone epoxide hydrolase; <b>PDBTitle:</b> crystal structure of juvenile hormone epoxide hydrolase from the2 silkworm bombyx mori
66	<a href="#">c3qitB_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> polyketide synthase; <b>PDBTitle:</b> thioesterase domain from curacin biosynthetic pathway
67	<a href="#">d1bn7a_</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloalkane dehalogenase
68	<a href="#">d1azwa_</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Proline iminopeptidase-like
69	<a href="#">c4qlaA_</a>	Alignment	not modelled	100.0	17	<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
70	<a href="#">d2vata1</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> O-acetyltransferase
71	<a href="#">d2rhwa1</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carbon-carbon bond hydrolase
72	<a href="#">c4lxgA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> mcp hydrolase; <b>PDBTitle:</b> crystal structure of dxnb2, a carbon - carbon bond hydrolase from2 sphingomonas wittichii rw1
73	<a href="#">c2yysA_</a>	Alignment	not modelled	100.0	16	<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 protein2 ttha1809 from thermus thermophilus hb8
74	<a href="#">d1a8qa_</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloperoxidase
75	<a href="#">d1uk8a_</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carbon-carbon bond hydrolase
76	<a href="#">c4i19A_</a>	Alignment	not modelled	100.0	17	<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.
77	<a href="#">c1y37A_</a>	Alignment	not modelled	100.0	17	<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
78	<a href="#">c4b9aA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> probable epoxide hydrolase; <b>PDBTitle:</b> structure of a putative epoxide hydrolase from pseudomonas2 aeruginosa.
79	<a href="#">c6f9oA_</a>	Alignment	not modelled	100.0	19	<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 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> homoserine o-acetyltransferase; <b>PDBTitle:</b> homoserine transacetylase meta from mycobacterium abscessus
80	<a href="#">c5w8pA_</a>	Alignment	not modelled	100.0	18
81	<a href="#">c3e3aA_</a>	Alignment	not modelled	100.0	18
82	<a href="#">c4nvrC_</a>	Alignment	not modelled	100.0	14
83	<a href="#">c3qyjB_</a>	Alignment	not modelled	100.0	12
84	<a href="#">c4ccyA_</a>	Alignment	not modelled	100.0	16
85	<a href="#">c3nwoA_</a>	Alignment	not modelled	100.0	16
86	<a href="#">c4mj3B_</a>	Alignment	not modelled	100.0	19
87	<a href="#">c3bwxA_</a>	Alignment	not modelled	100.0	14
88	<a href="#">c5ijkA_</a>	Alignment	not modelled	100.0	12
89	<a href="#">c2wj4B_</a>	Alignment	not modelled	100.0	11
90	<a href="#">c4x00D_</a>	Alignment	not modelled	100.0	18
91	<a href="#">d1xkla_</a>	Alignment	not modelled	100.0	14
92	<a href="#">c1u2eA_</a>	Alignment	not modelled	100.0	18
93	<a href="#">c3vvlA_</a>	Alignment	not modelled	100.0	13
94	<a href="#">d1wm1a_</a>	Alignment	not modelled	100.0	16
95	<a href="#">d1mj5a_</a>	Alignment	not modelled	100.0	21
96	<a href="#">c6ra2E_</a>	Alignment	not modelled	100.0	11
97	<a href="#">c3fsgC_</a>	Alignment	not modelled	100.0	12
98	<a href="#">d1j1ia_</a>	Alignment	not modelled	100.0	18
99	<a href="#">c1j1ia_</a>	Alignment	not modelled	100.0	18
100	<a href="#">c3fobA_</a>	Alignment	not modelled	100.0	15
101	<a href="#">c2ockA_</a>	Alignment	not modelled	100.0	15
102	<a href="#">c6g75B_</a>	Alignment	not modelled	100.0	14
103	<a href="#">d1qo7a_</a>	Alignment	not modelled	100.0	15
104	<a href="#">c3wz1B_</a>	Alignment	not modelled	100.0	18

					<b>PDBTitle:</b> zen lactonase
105	<a href="#">d1hkha_</a>	Alignment	not modelled	100.0	16 <b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloperoxidase
106	<a href="#">c3v48B_</a>	Alignment	not modelled	100.0	14 <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative aminoacrylate hydrolase rutd; <b>PDBTitle:</b> crystal structure of the putative alpha/beta hydrolase rutd from 2 e.coli
107	<a href="#">c4ns4A_</a>	Alignment	not modelled	100.0	16 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha/beta hydrolase fold protein; <b>PDBTitle:</b> crystal structure of cold-active esterase from psychrobacter2 cryohalolentis k5t
108	<a href="#">c2qvba_</a>	Alignment	not modelled	100.0	17 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> haloalkane dehalogenase 3; <b>PDBTitle:</b> crystal structure of haloalkane dehalogenase rv2579 from mycobacterium2 tuberculosis
109	<a href="#">c3qvmA_</a>	Alignment	not modelled	100.0	17 <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
110	<a href="#">c1wprA_</a>	Alignment	not modelled	100.0	19 <b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> sigma factor sigb regulation protein rsbq; <b>PDBTitle:</b> crystal structure of rsbq inhibited by pmsf
111	<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
112	<a href="#">d1m33a_</a>	Alignment	not modelled	100.0	15 <b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Biotin biosynthesis protein BioH
113	<a href="#">c3p2mA_</a>	Alignment	not modelled	100.0	17 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> possible hydrolase; <b>PDBTitle:</b> crystal structure of a novel esterase rv0045c from mycobacterium2 tuberculosis
114	<a href="#">c2xmzA_</a>	Alignment	not modelled	100.0	16 <b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrolase, alpha/beta hydrolase fold family; <b>PDBTitle:</b> structure of menh from s. aureus
115	<a href="#">c4rpcA_</a>	Alignment	not modelled	100.0	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 protein2 from desulfitobacterium hafniense
116	<a href="#">d2pl5a1</a>	Alignment	not modelled	100.0	14 <b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> O-acetyltransferase
117	<a href="#">c4c6hA_</a>	Alignment	not modelled	100.0	17 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> haloalkane dehalogenase; <b>PDBTitle:</b> haloalkane dehalogenase with 1-hexanol
118	<a href="#">c5xo6F_</a>	Alignment	not modelled	100.0	18 <b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> lactonase for protein; <b>PDBTitle:</b> crystal structure of a novel zen lactonase mutant
119	<a href="#">c3r3xA_</a>	Alignment	not modelled	100.0	18 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> fluoroacetate dehalogenase; <b>PDBTitle:</b> crystal structure of the fluoroacetate dehalogenase rpa1163 -2 asp110asn/bromoacetate
120	<a href="#">c5jd6A_</a>	Alignment	not modelled	100.0	25 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mgs-mche2; <b>PDBTitle:</b> crystal structure of mgs-mche2, an alpha/beta hydrolase enzyme from 2 the metagenome of sediments from the lagoon of mar chica, morocco