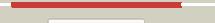
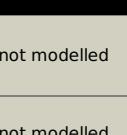


# Phyre<sup>2</sup>

Email	mdejesus@rockefeller.edu
Description	RVBD2579_(dhaA)_2903649_2904551
Date	Wed Aug 7 12:50:21 BST 2019
Unique Job ID	98e775ab45cd2859

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2qvbA</a>			100.0	100	<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
2	<a href="#">d1mj5a</a>			100.0	69	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloalkane dehalogenase
3	<a href="#">c4c6hA</a>			100.0	60	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> haloalkane dehalogenase; <b>PDBTitle:</b> haloalkane dehalogenase with 1-hexanol
4	<a href="#">c3i28A</a>			100.0	21	<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
5	<a href="#">c1cr6A</a>			100.0	20	<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
6	<a href="#">c3wibB</a>			100.0	32	<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
7	<a href="#">c4d9jl</a>			100.0	18	<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
8	<a href="#">c2pseA</a>			100.0	36	<b>PDB header:</b> oxidoreductase <b>Chain:</b> I; <b>PDB Molecule:</b> renilla-luciferin 2-monooxygenase; <b>PDBTitle:</b> crystal structures of the luciferase and green fluorescent2 protein from renilla reniformis
9	<a href="#">c1y37A</a>			100.0	16	<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
10	<a href="#">c3u1tA</a>			100.0	32	<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
11	<a href="#">c4b9aA</a>			100.0	15	<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.

12	<a href="#">c3kdaB</a>	Alignment		100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cfr inhibitory factor (cif); <b>PDBTitle:</b> crystal structure of the cfr inhibitory factor cif with the h269a2 mutation
13	<a href="#">d1bn7a</a>	Alignment		100.0	40	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloalkane dehalogenase
14	<a href="#">c5mxpB</a>	Alignment		100.0	36	<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
15	<a href="#">c6g75B</a>	Alignment		100.0	45	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> common ancestor of haloalkane dehalogenase and renilla <b>PDBTitle:</b> crystal structure of the common ancestor of haloalkane dehalogenases2 and renilla luciferase (anchld-rluc)
16	<a href="#">d1ehya</a>	Alignment		100.0	18	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Epoxide hydrolase
17	<a href="#">c4nvrc</a>	Alignment		100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> putative acyltransferase; <b>PDBTitle:</b> 2.22 angstrom resolution crystal structure of a putative2 acyltransferase from salmonella enterica
18	<a href="#">c2cpA</a>	Alignment		100.0	18	<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)
19	<a href="#">c5euroA</a>	Alignment		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
20	<a href="#">c3a2nF</a>	Alignment		100.0	31	<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)
21	<a href="#">c3qyjB</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> alr0039 protein; <b>PDBTitle:</b> crystal structure of alr0039, a putative alpha/beta hydrolase from2 nostoc sp pcc 7120.
22	<a href="#">d1brta</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloperoxidase
23	<a href="#">c4opmB</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> lipase; <b>PDBTitle:</b> crystal structure of a putative lipase (lip1) from acinetobacter2 baumannii aye at 1.70 a resolution
24	<a href="#">c5xmdA</a>	Alignment	not modelled	100.0	20	<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
25	<a href="#">c3r3xA</a>	Alignment	not modelled	100.0	16	<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
26	<a href="#">c4y7dA</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha/beta hydrolase fold protein; <b>PDBTitle:</b> alpha/beta hydrolase fold protein from nakamurella multipartita
27	<a href="#">c4psuA</a>	Alignment	not modelled	100.0	17	<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
28	<a href="#">c4inzB</a>	Alignment	not modelled	100.0	17	<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
						<b>PDB header:</b> hydrolase

29	<a href="#">c2y6vB</a>	Alignment	not modelled	100.0	13	<b>Chain:</b> B; <b>PDB Molecule:</b> peroxisomal membrane protein lpx1; <b>PDBTitle:</b> peroxisomal alpha-beta-hydrolase lpx1 (yor084w) from <i>saccharomyces2 cerevisiae</i> (crystal form i) <b>PDB header:</b> hydrolase
30	<a href="#">c4uhhA</a>	Alignment	not modelled	100.0	19	<b>Chain:</b> A; <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> structural studies of a thermophilic esterase from <i>thermogutta terrifontis</i> (cacodylate complex)
31	<a href="#">c5ng7B</a>	Alignment	not modelled	100.0	21	<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
32	<a href="#">d1cr6a2</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Epoxyde hydrolase
33	<a href="#">c3oosA</a>	Alignment	not modelled	100.0	11	<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 <i>bacillus2 anthracis</i> str. sterne
34	<a href="#">c2e3jA</a>	Alignment	not modelled	100.0	20	<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) from <i>2 mycobacterium tuberculosis</i> at 2.1 angstrom
35	<a href="#">d1q0ra</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Aclacinomycin methylesterase RdmC
36	<a href="#">c3kxpD</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> D; <b>PDB Molecule:</b> alpha-(n-acetylaminomethylene)succinic acid hydrolase; <b>PDBTitle:</b> crystal structure of e-2-(acetamidomethylene)succinate hydrolase
37	<a href="#">c5d6oB</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> homoserine o-acetyltransferase; <b>PDBTitle:</b> orthorhombic crystal structure of an acetylest erolase from <i>2 corynebacterium glutamicum</i>
38	<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
39	<a href="#">d1zd3a2</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Epoxyde hydrolase
40	<a href="#">c4qlaB</a>	Alignment	not modelled	100.0	15	<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 <i>bombyx mori</i>
41	<a href="#">c4qlaA</a>	Alignment	not modelled	100.0	15	<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 <i>bombyx mori</i>
42	<a href="#">c5w15D</a>	Alignment	not modelled	100.0	19	<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 from <i>2 burkholderia ambifaria</i> .
43	<a href="#">c2xuaH</a>	Alignment	not modelled	100.0	14	<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 <i>burkholderia2 xenovorans</i> lb400
44	<a href="#">c5egnB</a>	Alignment	not modelled	100.0	18	<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
45	<a href="#">c4gloA</a>	Alignment	not modelled	100.0	12	<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 from <i>2 staphylococcus aureus</i>
46	<a href="#">c3vvIA</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> homoserine o-acetyltransferase; <b>PDBTitle:</b> crystal structure of l-serine-o-acetyltransferase found in d-2 cycloserine biosynthetic pathway
47	<a href="#">d2b61a1</a>	Alignment	not modelled	100.0	10	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> O-acetyltransferase
48	<a href="#">c5yhpB</a>	Alignment	not modelled	100.0	15	<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 <i>glaciozyma antarctica</i>
49	<a href="#">d2rhwa1</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carbon-carbon bond hydrolase
50	<a href="#">c5bovD</a>	Alignment	not modelled	100.0	14	<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) from <i>2 klebsiella pneumoniae</i> subsp. <i>pneumoniae</i> mgh 78578 at 1.60 a3 resolution
51	<a href="#">c5w8pA</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> homoserine o-acetyltransferase; <b>PDBTitle:</b> homoserine transacetylase meta from <i>mycobacterium abscessus</i>
52	<a href="#">d1b6ga</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloalkane dehalogenase
53	<a href="#">c4i3fA</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <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 <i>cycloclasticus zankles</i>
54	<a href="#">d1va4a</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloperoxidase

55	<a href="#">c4oseA</a>	Alignment	not modelled	100.0	15	<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
56	<a href="#">c3bwxA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha/beta hydrolase; <b>PDBTitle:</b> crystal structure of an alpha/beta hydrolase (yp_496220_1) from2 novosphingobium aromaticivorans dsm 12444 at 1.50 a resolution
57	<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. neocarinostaticus
58	<a href="#">c3om8A</a>	Alignment	not modelled	100.0	16	<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
59	<a href="#">c4rncB</a>	Alignment	not modelled	100.0	16	<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
60	<a href="#">c3nwoA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> proline iminopeptidase; <b>PDBTitle:</b> crystal structure of proline iminopeptidase mycobacterium smegmatis
61	<a href="#">d1j1ia</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
62	<a href="#">c1j1iA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> meta cleavage compound hydrolase; <b>PDBTitle:</b> crystal structure of a his-tagged serine hydrolase involved2 in the carbazole degradation (carc enzyme)
63	<a href="#">d1uk8a</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carbon-carbon bond hydrolase
64	<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
65	<a href="#">c4lxgA</a>	Alignment	not modelled	100.0	17	<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 rrw1
66	<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
67	<a href="#">c4l0cA</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> deformylase; <b>PDBTitle:</b> crystal structure of the n-formylmaleamic acid deformylase nfo(s94a)2 from pseudomonas putida s16
68	<a href="#">d1a8sa</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloperoxidase
69	<a href="#">d2vata1</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> O-acetyltransferase
70	<a href="#">c5nfqA</a>	Alignment	not modelled	100.0	18	<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
71	<a href="#">c4q3IC</a>	Alignment	not modelled	100.0	13	<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
72	<a href="#">c2vavL</a>	Alignment	not modelled	100.0	13	<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)
73	<a href="#">c2qmqa</a>	Alignment	not modelled	100.0	13	<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 syl, ndr2, a1182517, au040374) from mus musculus at 1.70 a3 resolution
74	<a href="#">c4i19A</a>	Alignment	not modelled	100.0	12	<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. neocarinostaticus.
75	<a href="#">d1go7a</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Epoxide hydrolase
76	<a href="#">c5h3hb</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> abhydrolase domain-containing protein; <b>PDBTitle:</b> esterase (eaest) from exigubacterium antarcticum
77	<a href="#">c2wj4B</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 1h-3-hydroxy-4-oxoquinoline 2,4-dioxygenase; <b>PDBTitle:</b> crystal structure of the cofactor-devoid 1-h-3-hydroxy-4-2 oxoquinoline 2,4-dioxygenase (hod) from arthrobacter3 nitroguajacolicus ru61a anaerobically complexed with its4 natural substrate 1-h-3-hydroxy-4-oxoquinoline
78	<a href="#">c3ibtA</a>	Alignment	not modelled	100.0	13	<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)
						<b>PDB header:</b> hydrolase

79	<a href="#">c3qitB</a>	Alignment	not modelled	100.0	13	<b>Chain: B: PDB Molecule:</b> polyketide synthase; <b>PDBTitle:</b> thioesterase domain from curacin biosynthetic pathway
80	<a href="#">c4pw0A</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> hydrolase <b>Chain: A: PDB Molecule:</b> alpha/beta hydrolase fold protein; <b>PDBTitle:</b> alpha/beta hydrolase fold protein from chitinophaga pinensis
81	<a href="#">c3i1iA</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> transferase <b>Chain: A: PDB Molecule:</b> homoserine o-acetyltransferase; <b>PDBTitle:</b> x-ray crystal structure of homoserine o-acetyltransferase from2 bacillus anthracis
82	<a href="#">c5jkjA</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain: A: PDB Molecule:</b> esterase e22; <b>PDBTitle:</b> crystal structure of esterase e22 l374d mutant
83	<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
84	<a href="#">c5esrA</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> hydrolase <b>Chain: A: PDB Molecule:</b> haloalkane dehalogenase; <b>PDBTitle:</b> crystal structure of haloalkane dehalogenase (dcca) from caulobacter2 crescentus
85	<a href="#">d1a8qa</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloperoxidase
86	<a href="#">c2xt0A</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> hydrolase <b>Chain: A: PDB Molecule:</b> haloalkane dehalogenase; <b>PDBTitle:</b> dehalogenase dppa from plesiocystis pacifica sir-i
87	<a href="#">c1u2eA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain: A: PDB Molecule:</b> 2-hydroxy-6-ketonona-2,4-dienedioic acid <b>PDBTitle:</b> crystal structure of the c-c bond hydrolase mhpc
88	<a href="#">c5frdA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain: A: PDB Molecule:</b> carboxylesterase (est-2); <b>PDBTitle:</b> structure of a thermophilic esterase
89	<a href="#">d1hkha</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloperoxidase
90	<a href="#">c5cw2C</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain: C: PDB Molecule:</b> putative epoxide hydrolase epha; <b>PDBTitle:</b> crystal structure of epoxide hydrolase a from mycobacterium2 thermostresistible
91	<a href="#">c2r11D</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> hydrolase <b>Chain: D: PDB Molecule:</b> carboxylesterase np; <b>PDBTitle:</b> crystal structure of putative hydrolase (2632844) from bacillus2 subtilis at 1.96 a resolution
92	<a href="#">c5xo6F</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain: F: PDB Molecule:</b> lactonase for protein; <b>PDBTitle:</b> crystal structure of a novel zen lactonase mutant
93	<a href="#">c2yysA</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain: A: PDB Molecule:</b> proline iminopeptidase-related protein; <b>PDBTitle:</b> crystal structure of the proline iminopeptidase-related protein2 ttha1809 from thermus thermophilus hb8
94	<a href="#">c3e3aA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain: A: PDB Molecule:</b> possible peroxidase bpoc; <b>PDBTitle:</b> the structure of rv0554 from mycobacterium tuberculosis
95	<a href="#">d2pl5a1</a>	Alignment	not modelled	100.0	12	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> O-acetyltransferase
96	<a href="#">c4x00D</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain: D: PDB Molecule:</b> putative hydrolase; <b>PDBTitle:</b> x-ray crystal structure of a putative aryl esterase from burkholderia2 cenocepacia
97	<a href="#">c3wzIB</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> hydrolase <b>Chain: B: PDB Molecule:</b> zearelenone hydrolase; <b>PDBTitle:</b> zen lactonase
98	<a href="#">c5a62A</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> hydrolase <b>Chain: A: 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
99	<a href="#">c4f0jA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain: A: 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
100	<a href="#">c4ns4A</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain: A: PDB Molecule:</b> alpha/beta hydrolase fold protein; <b>PDBTitle:</b> crystal structure of cold-active esterase from psychrobacter2 cryohalolentis k5t
101	<a href="#">c4mj3B</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> hydrolase <b>Chain: B: PDB Molecule:</b> haloalkane dehalogenase; <b>PDBTitle:</b> haloalkane dehalogenase dmra from mycobacterium rhodesiae js60
102	<a href="#">c2vf2A</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain: A: PDB Molecule:</b> 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate <b>PDBTitle:</b> x-ray crystal structure of hsad from mycobacterium2 tuberculosis
103	<a href="#">c4ccyA</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> hydrolase <b>Chain: A: PDB Molecule:</b> carboxylesterase ybfk; <b>PDBTitle:</b> crystal structure of carboxylesterase cesb (ybfk) from bacillus2 subtilis
104	<a href="#">d1m33a</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Biotin biosynthesis protein BioH
						<b>PDB header:</b> hydrolase

105	<a href="#">c6f9oA</a>	Alignment	not modelled	100.0	21	<b>Chain:</b> A: <b>PDB Molecule:</b> haloalkane dehalogenase; <b>PDBTitle:</b> crystal structure of cold-adapted haloalkane dehalogenase dpc from2 psychrobacter cryohalolentis k5
106	<a href="#">d1wm1a</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Proline iminopeptidase-like
107	<a href="#">c6brtB</a>	Alignment	not modelled	100.0	15	<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
108	<a href="#">c3fobA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> bromoperoxidase; <b>PDBTitle:</b> crystal structure of bromoperoxidase from bacillus anthracis
109	<a href="#">c5cbkA</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> shhtl5; <b>PDBTitle:</b> crystal structure of the strigolactone receptor shhtl5 from striga2 hermonthica
110	<a href="#">c2xrnzA</a>	Alignment	not modelled	100.0	13	<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
111	<a href="#">c5z89A</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hyposensitive to light 7; <b>PDBTitle:</b> structural basis for specific inhibition of highly sensitive shhtl72 receptor
112	<a href="#">c4rpcA</a>	Alignment	not modelled	100.0	13	<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
113	<a href="#">c3qvmA</a>	Alignment	not modelled	100.0	16	<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
114	<a href="#">d1a88a</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloperoxidase
115	<a href="#">c3fsgC</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> alpha/beta superfamily hydrolase; <b>PDBTitle:</b> crystal structure of alpha/beta superfamily hydrolase from oenococcus2 oeni psu-1
116	<a href="#">c3p2mA</a>	Alignment	not modelled	100.0	13	<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
117	<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 from2 e.coli
118	<a href="#">c1wprA</a>	Alignment	not modelled	100.0	15	<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
119	<a href="#">c5dnvA</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> shkai2ib; <b>PDBTitle:</b> crystal structure of kai2-like protein from striga (apo state 2)
120	<a href="#">c3l80A</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein smu.1393c; <b>PDBTitle:</b> crystal structure of smu.1393c from streptococcus mutans ua159