























# Phyre2

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 Description RVBD1900c\_(lip)\_2146252\_2147640  
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1cr6A_</a>	 Alignment		100.0	14	<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	14	<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	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
4	<a href="#">c6fhtB_</a>	 Alignment		100.0	24	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> bacteriophytochrome,adenylate cyclase; <b>PDBTitle:</b> crystal structure of an artificial phytochrome regulated2 adenylate/guanylate cyclase in its dark adapted pr form
5	<a href="#">c4qloA_</a>	 Alignment		100.0	13	<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
6	<a href="#">d2b61a1</a>	 Alignment		100.0	15	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> O-acetyltransferase
7	<a href="#">c3i1iA_</a>	 Alignment		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
8	<a href="#">c2vavL_</a>	 Alignment		100.0	16	<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)
9	<a href="#">c5d6oB_</a>	 Alignment		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 acetylester hydrolase from2 corynebacterium glutamicum
10	<a href="#">c5w8pA_</a>	 Alignment		100.0	13	<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
11	<a href="#">c2qmqa_</a>	 Alignment		100.0	10	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein ndr2; <b>PDBTitle:</b> crystal structure of a n-myc downstream regulated 2 protein (ndr2,2 syl2, ndr2, ai182517, au040374) from mus musculus at 1.70 a3 resolution

12	<a href="#">c3oosA_</a>	Alignment		100.0	14	<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
13	<a href="#">d2vata1</a>	Alignment		100.0	19	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> O-acetyltransferase
14	<a href="#">c1y10C_</a>	Alignment		100.0	23	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> hypothetical protein rv1264/mt1302; <b>PDBTitle:</b> mycobacterial adenyl cyclase rv1264, holoenzyme, inhibited state
15	<a href="#">c5jkjA_</a>	Alignment		100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase e22; <b>PDBTitle:</b> crystal structure of esterase e22 I374d mutant
16	<a href="#">c3vv1A_</a>	Alignment		100.0	18	<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
17	<a href="#">c2y6vB_</a>	Alignment		100.0	13	<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)
18	<a href="#">c3om8A_</a>	Alignment		100.0	23	<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
19	<a href="#">c4qlaA_</a>	Alignment		100.0	14	<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
20	<a href="#">c410cA_</a>	Alignment		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-fopmylmaaleamic acid deformylase nfo(s94a)2 from pseudomonas putida s16
21	<a href="#">c2e3jA_</a>	Alignment	not modelled	100.0	18	<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
22	<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
23	<a href="#">c3qvmA_</a>	Alignment	not modelled	100.0	18	<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
24	<a href="#">c2r11D_</a>	Alignment	not modelled	100.0	11	<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
25	<a href="#">c4qlaB_</a>	Alignment	not modelled	100.0	12	<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
26	<a href="#">c2xuaH_</a>	Alignment	not modelled	100.0	18	<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
27	<a href="#">c4yusA_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> family 3 adenylate cyclase; <b>PDBTitle:</b> crystal structure of photoactivated adenyl cyclase of a2 cyanobacteriaoscillatoria acuminata in hexagonal form
28	<a href="#">c5efzC_</a>	Alignment	not modelled	100.0	18	<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
						<b>PDB header:</b> hydrolase

29	<a href="#">c4pw0A_</a>	Alignment	not modelled	100.0	15	<b>Chain:</b> A: <b>PDB Molecule:</b> alpha/beta hydrolase fold protein; <b>PDBTitle:</b> alpha/beta hydrolase fold protein from chitinophaga pinensis
30	<a href="#">d1b6ga_</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloalkane dehalogenase
31	<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
32	<a href="#">d1ehya_</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Epoxide hydrolase
33	<a href="#">d1fx2a_</a>	Alignment	not modelled	100.0	29	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nucleotide cyclase <b>Family:</b> Adenylyl and guanylyl cyclase catalytic domain
34	<a href="#">c5xmdA_</a>	Alignment	not modelled	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
35	<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
36	<a href="#">c5esrA_</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> crystal structure of haloalkane dehalogenase (dcca) from caulobacter2 crescentus
37	<a href="#">c3u1tA_</a>	Alignment	not modelled	100.0	13	<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
38	<a href="#">c4oseA_</a>	Alignment	not modelled	100.0	16	<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
39	<a href="#">c3wibB_</a>	Alignment	not modelled	100.0	16	<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
40	<a href="#">d1zd3a2</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Epoxide hydrolase
41	<a href="#">c3kdaB_</a>	Alignment	not modelled	100.0	12	<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
42	<a href="#">c5f4zB_</a>	Alignment	not modelled	100.0	11	<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
43	<a href="#">d1m33a_</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Biotin biosynthesis protein BioH
44	<a href="#">c4y7dA_</a>	Alignment	not modelled	100.0	21	<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
45	<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
46	<a href="#">c6brtB_</a>	Alignment	not modelled	100.0	18	<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
47	<a href="#">d1azwa_</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Proline iminopeptidase-like
48	<a href="#">c3kxpD_</a>	Alignment	not modelled	100.0	19	<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
49	<a href="#">c5egnB_</a>	Alignment	not modelled	100.0	20	<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
50	<a href="#">c4inzB_</a>	Alignment	not modelled	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
51	<a href="#">c3v48B_</a>	Alignment	not modelled	100.0	18	<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
52	<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)
53	<a href="#">d1uk8a_</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carbon-carbon bond hydrolase
54	<a href="#">c4opmB_</a>	Alignment	not modelled	100.0	17	<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
						<b>Fold:</b> alpha/beta-Hydrolases

55	<a href="#">d1cr6a2</a>	Alignment	not modelled	100.0	15	<b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Epoxide hydrolase
56	<a href="#">d1fx4a</a>	Alignment	not modelled	100.0	30	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nucleotide cyclase <b>Family:</b> Adenylyl and guanylyl cyclase catalytic domain
57	<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
58	<a href="#">c5w15D</a>	Alignment	not modelled	100.0	16	<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.
59	<a href="#">c5nfqA</a>	Alignment	not modelled	100.0	14	<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
60	<a href="#">c4i19A</a>	Alignment	not modelled	100.0	13	<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.
61	<a href="#">c1y37A</a>	Alignment	not modelled	100.0	19	<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
62	<a href="#">d1c4xa</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
63	<a href="#">c2cjpA</a>	Alignment	not modelled	100.0	14	<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)
64	<a href="#">c5ng7B</a>	Alignment	not modelled	100.0	18	<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
65	<a href="#">c4i3fA</a>	Alignment	not modelled	100.0	18	<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 cycloclasticus zankles
66	<a href="#">c5h3hB</a>	Alignment	not modelled	100.0	17	<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
67	<a href="#">c5mxbB</a>	Alignment	not modelled	100.0	14	<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
68	<a href="#">d1q0ra</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Aclacinomycin methylesterase RdmC
69	<a href="#">d1mj5a</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloalkane dehalogenase
70	<a href="#">d2rhwa1</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carbon-carbon bond hydrolase
71	<a href="#">c5nbyA</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> beta subunit of photoactivated adenylyl cyclase; <b>PDBTitle:</b> structure of a bacterial light-regulated adenylyl cyclase
72	<a href="#">d1a8sa</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloperoxidase
73	<a href="#">c4lxgA</a>	Alignment	not modelled	100.0	13	<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
74	<a href="#">c3e3aA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> possible peroxidase bpoc; <b>PDBTitle:</b> the structure of rv0554 from mycobacterium tuberculosis
75	<a href="#">c1ybuA</a>	Alignment	not modelled	100.0	100	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lipj; <b>PDBTitle:</b> mycobacterium tuberculosis adenylyl cyclase rv1900c chd, in complex2 with a substrate analog.
76	<a href="#">c4nvrC</a>	Alignment	not modelled	100.0	16	<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
77	<a href="#">c1u2eA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-hydroxy-6-ketonona-2,4-dienedioic acid <b>PDBTitle:</b> crystal structure of the c-c bond hydrolase mhpc
78	<a href="#">c3a2nF</a>	Alignment	not modelled	100.0	16	<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)
79	<a href="#">c4b9aA</a>	Alignment	not modelled	100.0	16	<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.
80	<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
						<b>Fold:</b> alpha/beta-Hydrolases

81	<a href="#">d1a8qa_</a>	Alignment	not modelled	100.0	16	<b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloperoxidase
82	<a href="#">c4rncB_</a>	Alignment	not modelled	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
83	<a href="#">c5uroA_</a>	Alignment	not modelled	100.0	13	<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
84	<a href="#">c3fsgC_</a>	Alignment	not modelled	100.0	12	<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
85	<a href="#">d1wm1a_</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
86	<a href="#">c3ibtA_</a>	Alignment	not modelled	100.0	14	<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)
87	<a href="#">c4rpcA_</a>	Alignment	not modelled	100.0	10	<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
88	<a href="#">c3l80A_</a>	Alignment	not modelled	100.0	10	<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
89	<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-oxoquinaldine 2,4-dioxygenase; <b>PDBTitle:</b> 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
90	<a href="#">d1bn7a_</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloalkane dehalogenase
91	<a href="#">c5dnvA_</a>	Alignment	not modelled	100.0	18	<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)
92	<a href="#">c4q3lC_</a>	Alignment	not modelled	100.0	18	<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
93	<a href="#">c4c6hA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> haloalkane dehalogenase; <b>PDBTitle:</b> haloalkane dehalogenase with 1-hexanol
94	<a href="#">d1j1ia_</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
95	<a href="#">c1j1iA_</a>	Alignment	not modelled	100.0	15	<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)
96	<a href="#">d1va4a_</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloperoxidase
97	<a href="#">c3bwxA_</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 an alpha/beta hydrolase (yp_496220.1) from2 novosphingobium aromaticivorans dsm 12444 at 1.50 a resolution
98	<a href="#">c5cw2C_</a>	Alignment	not modelled	100.0	16	<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
99	<a href="#">c2xt0A_</a>	Alignment	not modelled	100.0	14	<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
100	<a href="#">c2qvbA_</a>	Alignment	not modelled	100.0	14	<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
101	<a href="#">c2vf2A_</a>	Alignment	not modelled	100.0	15	<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
102	<a href="#">d1mtza_</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Proline iminopeptidase-like
103	<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
104	<a href="#">c4dnqA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dad2; <b>PDBTitle:</b> crystal structure of dad2 s96a mutant
105	<a href="#">c5bovd_</a>	Alignment	not modelled	100.0	20	<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
106	<a href="#">c3r0vA_</a>	Alignment	not modelled	100.0	19 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha/beta hydrolase fold protein; <b>PDBTitle:</b> the crystal structure of an alpha/beta hydrolase from sphaerobacter2 thermophilus dsm 20745.
107	<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
108	<a href="#">d1hkha_</a>	Alignment	not modelled	100.0	19 <b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloperoxidase
109	<a href="#">c3qyjB_</a>	Alignment	not modelled	100.0	19 <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.
110	<a href="#">c6g75B_</a>	Alignment	not modelled	100.0	12 <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)
111	<a href="#">c4ccyA_</a>	Alignment	not modelled	100.0	13 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> carboxylesterase ybfk; <b>PDBTitle:</b> crystal structure of carboxylesterase cesb (ybfk) from bacillus2 subtilis
112	<a href="#">c3p2mA_</a>	Alignment	not modelled	100.0	14 <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
113	<a href="#">d1qo7a_</a>	Alignment	not modelled	100.0	10 <b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Epoxide hydrolase
114	<a href="#">c3fobA_</a>	Alignment	not modelled	100.0	14 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> bromoperoxidase; <b>PDBTitle:</b> crystal structure of bromoperoxidase from bacillus anthracis
115	<a href="#">c3mr7B_</a>	Alignment	not modelled	100.0	31 <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> adenylate/guanylate cyclase/hydrolase, alpha/beta fold <b>PDBTitle:</b> crystal structure of adenylate/guanylate cyclase/hydrolase from2 silicibacter pomeroyi
116	<a href="#">c1zoiC_</a>	Alignment	not modelled	100.0	16 <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
117	<a href="#">c5cbkA_</a>	Alignment	not modelled	100.0	19 <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
118	<a href="#">c3wzIB_</a>	Alignment	not modelled	100.0	15 <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> zearalenone hydrolase; <b>PDBTitle:</b> zen lactonase
119	<a href="#">c6f9oA_</a>	Alignment	not modelled	100.0	15 <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
120	<a href="#">c3e0xB_</a>	Alignment	not modelled	100.0	17 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> lipase-esterase related protein; <b>PDBTitle:</b> the crystal structure of a lipase-esterase related protein2 from clostridium acetobutylicum atcc 824