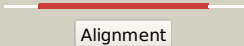

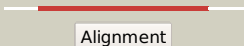

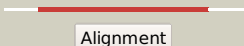







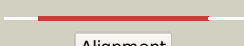











# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1190_(-)_1332986_1333864
Date	Wed Jul 31 22:05:27 BST 2019
Unique Job ID	6cd721a1f2ddd992

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1cr6A_</a>	 Alignment		100.0	17	<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	17	<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="#">c3u1tA_</a>	 Alignment		100.0	25	<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
5	<a href="#">c5mxbB_</a>	 Alignment		100.0	22	<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
6	<a href="#">c3kdaB_</a>	 Alignment		100.0	17	<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
7	<a href="#">c3wibB_</a>	 Alignment		100.0	19	<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
8	<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
9	<a href="#">c3kxpD_</a>	 Alignment		100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> alpha-(n-acetylamino)methylene)succinic acid hydrolase; <b>PDBTitle:</b> crystal structure of e-2-(acetamidomethylene)succinate hydrolase
10	<a href="#">d1zd3a2</a>	 Alignment		100.0	17	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Epoxide hydrolase
11	<a href="#">d1ehya_</a>	 Alignment		100.0	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Epoxide hydrolase

12	<a href="#">c5w15D_</a>	Alignment		100.0	23	<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.
13	<a href="#">c5ng7B_</a>	Alignment		100.0	17	<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
14	<a href="#">d1bn7a_</a>	Alignment		100.0	21	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloalkane dehalogenase
15	<a href="#">c4b9aA_</a>	Alignment		100.0	18	<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.
16	<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
17	<a href="#">c5egnB_</a>	Alignment		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
18	<a href="#">d1b6ga_</a>	Alignment		100.0	17	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloalkane dehalogenase
19	<a href="#">c2qmqA_</a>	Alignment		100.0	14	<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
20	<a href="#">c3ibtA_</a>	Alignment		100.0	16	<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)
21	<a href="#">c4y7dA_</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> alpha/beta hydrolase fold protein from nakamurella multipartita
22	<a href="#">c4qloA_</a>	Alignment	not modelled	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
23	<a href="#">c4f0jA_</a>	Alignment	not modelled	100.0	16	<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="#">c4qlaA_</a>	Alignment	not modelled	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
25	<a href="#">c1y37A_</a>	Alignment	not modelled	100.0	21	<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
26	<a href="#">d1cr6a2</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Epoxide hydrolase
27	<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
28	<a href="#">c2wj4B_</a>	Alignment	not modelled	100.0	18	<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
29	<a href="#">c4inzB_</a>	Alignment	not modelled	100.0	18	<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
30	<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)
31	<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
32	<a href="#">c4uhhA_</a>	Alignment	not modelled	100.0	18	<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)
33	<a href="#">c4pw0A_</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 chitinophaga pinensis
34	<a href="#">d1uk8a_</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
35	<a href="#">c2r11D_</a>	Alignment	not modelled	100.0	18	<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
36	<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
37	<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
38	<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
39	<a href="#">c4nvrC_</a>	Alignment	not modelled	100.0	21	<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
40	<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)
41	<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) from2 mycobacterium tuberculosis at 2.1 angstrom
42	<a href="#">d1mj5a_</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloalkane dehalogenase
43	<a href="#">c5esrA_</a>	Alignment	not modelled	100.0	20	<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
44	<a href="#">c5yhpB_</a>	Alignment	not modelled	100.0	17	<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
45	<a href="#">d1a8sa_</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloperoxidase
46	<a href="#">c3r3xA_</a>	Alignment	not modelled	100.0	23	<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
47	<a href="#">c4opmB_</a>	Alignment	not modelled	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 acetobacter2 baumannii aye at 1.70 a resolution
48	<a href="#">d1brta_</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloperoxidase
49	<a href="#">c4q3lC_</a>	Alignment	not modelled	100.0	11	<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
50	<a href="#">c2y6vB_</a>	Alignment	not modelled	100.0	15	<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)
51	<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
52	<a href="#">c3qyjB_</a>	Alignment	not modelled	100.0	18	<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.
53	<a href="#">c5f4zB_</a>	Alignment	not modelled	100.0	16	<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
54	<a href="#">c4i30A_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> epoxide hydrolase;

54	<a href="#">c413A_</a>	Alignment	not modelled	100.0	10	<b>PDBTitle:</b> the crystal structure of an epoxide hydrolase from streptomyces2 carzinostaticus subsp. neocarzinostaticus. <b>PDB header:</b> transferase
55	<a href="#">c311a_</a>	Alignment	not modelled	100.0	14	<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
56	<a href="#">c410cA_</a>	Alignment	not modelled	100.0	15	<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
57	<a href="#">c30m8A_</a>	Alignment	not modelled	100.0	24	<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
58	<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
59	<a href="#">c3a2nF_</a>	Alignment	not modelled	100.0	19	<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)
60	<a href="#">c40seA_</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
61	<a href="#">c5jkjA_</a>	Alignment	not modelled	100.0	14	<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
62	<a href="#">c41xgA_</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 rw1
63	<a href="#">d1q0ra_</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Aclacinomycin methylesterase RdmC
64	<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
65	<a href="#">c2pseA_</a>	Alignment	not modelled	100.0	19	<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
66	<a href="#">d1c4xa_</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
67	<a href="#">d1va4a_</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloperoxidase
68	<a href="#">c2qvba_</a>	Alignment	not modelled	100.0	23	<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
69	<a href="#">c6f9oA_</a>	Alignment	not modelled	100.0	23	<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
70	<a href="#">d1j1ia_</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
71	<a href="#">c1j1iA_</a>	Alignment	not modelled	100.0	18	<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)
72	<a href="#">c5w8pA_</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> homoserine transacetylase meta from mycobacterium abscessus
73	<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 cycloclasticus zankles
74	<a href="#">c3fsgC_</a>	Alignment	not modelled	100.0	13	<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
75	<a href="#">c2yysA_</a>	Alignment	not modelled	100.0	18	<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
76	<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 acetyler hydrolase from2 corynebacterium glutamicum
77	<a href="#">c2xt0A_</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> dehalogenase dpca from plesiocystis pacifica sir-i
78	<a href="#">c4mj3B_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> haloalkane dehalogenase; <b>PDBTitle:</b> haloalkane dehalogenase dmra from mycobacterium rhodesiae js60
79	<a href="#">d1a8qa_</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloperoxidase
						<b>Fold:</b> alpha/beta-Hydrolases

80	<a href="#">d1hkha_</a>	Alignment	not modelled	100.0	19	<b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloperoxidase
81	<a href="#">c3nwoA_</a>	Alignment	not modelled	100.0	19	<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
82	<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
83	<a href="#">c4c6hA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> haloalkane dehalogenase; <b>PDBTitle:</b> haloalkane dehalogenase with 1-hexanol
84	<a href="#">c3vvlA_</a>	Alignment	not modelled	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
85	<a href="#">c6g75B_</a>	Alignment	not modelled	100.0	18	<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)
86	<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
87	<a href="#">c5efzC_</a>	Alignment	not modelled	100.0	15	<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
88	<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
89	<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
90	<a href="#">c3bwxA_</a>	Alignment	not modelled	100.0	20	<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
91	<a href="#">d1mtza_</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Proline iminopeptidase-like
92	<a href="#">c4ccyA_</a>	Alignment	not modelled	100.0	20	<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
93	<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
94	<a href="#">c6brtB_</a>	Alignment	not modelled	100.0	19	<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
95	<a href="#">c3wz1B_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> zearealenone hydrolase; <b>PDBTitle:</b> zen lactonase
96	<a href="#">c1zoiC_</a>	Alignment	not modelled	100.0	19	<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
97	<a href="#">c3fobA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> bromoperoxidase; <b>PDBTitle:</b> crystal structure of bromoperoxidase from bacillus anthracis
98	<a href="#">c5uroA_</a>	Alignment	not modelled	100.0	15	<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
99	<a href="#">c6ra2E_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> putative dioxygenase (1h-3-hydroxy-4-oxoquinaldine 2,4- <b>PDBTitle:</b> structural basis for recognition and ring-cleavage of the pseudomonas2 quinolone signal (pqs) by aqdc
100	<a href="#">c4rpcA_</a>	Alignment	not modelled	100.0	9	<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
101	<a href="#">c5cw2C_</a>	Alignment	not modelled	100.0	17	<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
102	<a href="#">d1m33a_</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Biotin biosynthesis protein BioH
103	<a href="#">c3v48B_</a>	Alignment	not modelled	100.0	17	<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
104	<a href="#">c2vf2A_</a>	Alignment	not modelled	100.0	17	<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
105	<a href="#">d1a88a_</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Haloperoxidase

106	<a href="#">c5bovD_</a>	 Alignment	not modelled	100.0	19	<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>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i> mgh 78578 at 1.60 Å resolution
107	<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 <i>Streptococcus mutans</i> ua159
108	<a href="#">c4rncB_</a>	 Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> crystal structure of an esterase rhest1 from <i>Rhodococcus</i> sp. <i>ecul013</i>
109	<a href="#">c2xmzA_</a>	 Alignment	not modelled	100.0	12	<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 <i>S. aureus</i>
110	<a href="#">d1qo7a_</a>	 Alignment	not modelled	100.0	12	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Epoxide hydrolase
111	<a href="#">c5xo6F_</a>	 Alignment	not modelled	100.0	19	<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
112	<a href="#">c5cbkA_</a>	 Alignment	not modelled	100.0	15	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> shht15; <b>PDBTitle:</b> crystal structure of the strigolactone receptor shht15 from <i>Striga</i> <i>hermonthica</i>
113	<a href="#">c5a62A_</a>	 Alignment	not modelled	100.0	16	<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 <i>Thaumarchaeon</i> <i>Nitrososphaera gargensis</i> - crystal structure and activity profiles of 3 carboxylesterases linked to their metabolic function
114	<a href="#">c3p2mA_</a>	 Alignment	not modelled	100.0	18	<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 <i>Mycobacterium</i> <i>tuberculosis</i>
115	<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
116	<a href="#">c5dvnA_</a>	 Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> shkai2ib; <b>PDBTitle:</b> crystal structure of kai2-like protein from <i>Striga</i> (apo state 2)
117	<a href="#">d2pl5a1</a>	 Alignment	not modelled	100.0	11	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> O-acetyltransferase
118	<a href="#">c5frdA_</a>	 Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> carboxylesterase (est-2); <b>PDBTitle:</b> structure of a thermophilic esterase
119	<a href="#">c3r0vA_</a>	 Alignment	not modelled	100.0	18	<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 <i>Sphaerobacter</i> <i>thermophilus</i> DSM 20745.
120	<a href="#">c4x00D_</a>	 Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> putative hydrolase; <b>PDBTitle:</b> x-ray crystal structure of a putative aryl esterase from <i>Burkholderia</i> <i>cenocapacia</i>