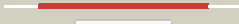



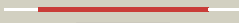
















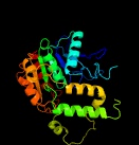



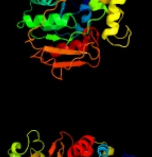

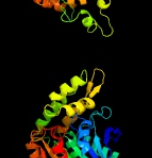


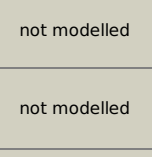


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0045c (-) _49043_49939
Date	Tue Jul 23 14:50:07 BST 2019
Unique Job ID	0c072f60a31eba29

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3p2mA_	 Alignment		100.0	96	PDB header: hydrolase Chain: A: PDB Molecule: possible hydrolase; PDBTitle: crystal structure of a novel esterase rv0045c from mycobacterium2 tuberculosis
2	c3i28A_	 Alignment		100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase 2; PDBTitle: crystal structure of soluble epoxide hydrolase
3	c1cr6A_	 Alignment		100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
4	c4d9jI_	 Alignment		100.0	15	PDB header: de novo protein Chain: I: PDB Molecule: designed 16nm tetrahedral protein cage containing non-haem PDBTitle: structure of a 16 nm protein cage designed by fusing symmetric2 oligomeric domains
5	c2r11D_	 Alignment		100.0	15	PDB header: hydrolase Chain: D: PDB Molecule: carboxylesterase np; PDBTitle: crystal structure of putative hydrolase (2632844) from bacillus2 subtilis at 1.96 a resolution
6	c4qloA_	 Alignment		100.0	14	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: crystal structure of homoserine o-acetyltransferase from2 staphylococcus aureus
7	c3oosA_	 Alignment		100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase family protein; PDBTitle: the structure of an alpha/beta fold family hydrolase from bacillus2 anthracis str. Sterne
8	c4f0jA_	 Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: probable hydrolytic enzyme; PDBTitle: crystal structure of a probable hydrolytic enzyme (pa3053) from2 pseudomonas aeruginosa pao1 at 1.50 a resolution
9	c3kdaB_	 Alignment		100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: cftr inhibitory factor (cif); PDBTitle: crystal structure of the cftr inhibitory factor cif with the h269a2 mutation
10	c2qmqa_	 Alignment		100.0	18	PDB header: signaling protein Chain: A: PDB Molecule: protein ndrg2; PDBTitle: crystal structure of a n-myc downstream regulated 2 protein (ndrg2,2 syld, ndr2, ai182517, au040374) from mus musculus at 1.70 a3 resolution
11	c5w8pA_	 Alignment		100.0	16	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: homoserine transacetylase meta from mycobacterium abscessus

12	c5xmdA	Alignment		100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase a; PDBTitle: crystal structure of epoxide hydrolase vreh1 from vigna radiata
13	c4oseA	Alignment		100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: putative hydrolase; PDBTitle: x-ray crystal structure of a putative hydrolase from rickettsia typhi
14	c2vavL	Alignment		100.0	17	PDB header: transferase Chain: L: PDB Molecule: acetyl-coa--deacetylcephalosporin c acetyltransferase; PDBTitle: crystal structure of deacetylcephalosporin c acetyltransferase (dac-2 soak)
15	c4qlaB	Alignment		100.0	15	PDB header: hydrolase Chain: B: PDB Molecule: juvenile hormone epoxide hydrolase; PDBTitle: crystal structure of juvenile hormone epoxide hydrolase from the2 silkworm bombyx mori
16	c4qlaA	Alignment		100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: juvenile hormone epoxide hydrolase; PDBTitle: crystal structure of juvenile hormone epoxide hydrolase from the2 silkworm bombyx mori
17	c2e3jA	Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase ephb; PDBTitle: the crystal structure of epoxide hydrolase b (rv1938) from2 mycobacterium tuberculosis at 2.1 angstrom
18	c3kxpD	Alignment		100.0	23	PDB header: hydrolase Chain: D: PDB Molecule: alpha-(n-acetylamino)methylene)succinic acid hydrolase; PDBTitle: crystal structure of e-2-(acetamidomethylene)succinate hydrolase
19	c4l0cA	Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: deformylase; PDBTitle: crystal structure of the n-fopmylmalemic acid deformylase nfo(s94a)2 from pseudomonas putida s16
20	c4opmB	Alignment		100.0	13	PDB header: hydrolase Chain: B: PDB Molecule: lipase; PDBTitle: crystal structure of a putative lipase (lip1) from acinetobacter2 baumannii aye at 1.70 a resolution
21	d1ehya	Alignment	not modelled	100.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
22	c4y7dA	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase fold protein; PDBTitle: alpha/beta hydrolase fold protein from nakamurella multipartita
23	c5f4zB	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: epoxide hydrolase; PDBTitle: the crystal structure of an epoxide hydrolase from streptomyces2 carzinostaticus subsp. neocarzinostaticus
24	c5esrA	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of haloalkane dehalogenase (dcca) from caulobacter2 crescentus
25	c2cjpA	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: structure of potato (solanum tuberosum) epoxide hydrolase i (steh1)
26	d1b6ga	Alignment	not modelled	100.0	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloalkane dehalogenase
27	c5w15D	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: D: PDB Molecule: alpha/beta hydrolase fold protein; PDBTitle: crystal structure of an alpha/beta hydrolase fold protein from2 burkholderia ambifaria.
28	d2b61a1	Alignment	not modelled	100.0	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
						Fold: alpha/beta-Hydrolases

29	d2rhwa1	Alignment	not modelled	100.0	20	Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase
30	c3i1aA	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: x-ray crystal structure of homoserine o-acetyltransferase from2 bacillus anthracis
31	d2vata1	Alignment	not modelled	100.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
32	c4pw0A	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase fold protein; PDBTitle: alpha/beta hydrolase fold protein from chitinophaga pinensis
33	c1y37A	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: fluoroacetate dehalogenase; PDBTitle: structure of fluoroacetate dehalogenase from burkholderia sp. fa1
34	d1zd3a2	Alignment	not modelled	100.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
35	c1u2eA	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: 2-hydroxy-6-ketonona-2,4-dienedioic acid PDBTitle: crystal structure of the c-c bond hydrolase mhpc
36	c3wibB	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of y109w mutant haloalkane dehalogenase data from2 agrobacterium tumefaciens c58
37	c4i19A	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: the crystal structure of an epoxide hydrolase from streptomyces2 carzinostaticus subsp. neocarzinostaticus.
38	d1cr6a2	Alignment	not modelled	100.0	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
39	c2y6vB	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: peroxisomal membrane protein lpx1; PDBTitle: peroxisomal alpha-beta-hydrolase lpx1 (yor084w) from saccharomyces2 cerevisiae (crystal form i)
40	c3u1tA	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: dmma haloalkane dehalogenase; PDBTitle: haloalkane dehalogenase, dmma, of marine microbial origin
41	c5ng7B	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: B: PDB Molecule: epoxide hydrolase; PDBTitle: novel epoxide hydrolases belonging to the alpha/beta hydrolases2 superfamily in metagenomes from hot environments
42	c4uhhA	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: structural studies of a thermophilic esterase from2 thermogutta terrifontis (cacodylate complex)
43	c3om8A	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: probable hydrolase; PDBTitle: the crystal structure of a hydrolase from pseudomonas aeruginosa pa01
44	c4psuA	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase; PDBTitle: crystal structure of alpha/beta hydrolase from rhodopseudomonas2 palustris cga009
45	c2xt0A	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase; PDBTitle: dehalogenase dppa from plesiocystis pacifica sir-i
46	c5jkjA	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: esterase e22; PDBTitle: crystal structure of esterase e22 l374d mutant
47	d1uk8a	Alignment	not modelled	100.0	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase
48	c3ibtA	Alignment	not modelled	100.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: 1h-3-hydroxy-4-oxoquinoline 2,4-dioxygenase; PDBTitle: structure of 1h-3-hydroxy-4-oxoquinoline 2,4-dioxygenase (qdo)
49	c2xuaH	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: H: PDB Molecule: 3-oxoadipate enol-lactonase; PDBTitle: crystal structure of the enol-lactonase from burkholderia2 xenovorans lb400
50	c5egnB	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: esterase; PDBTitle: est816 as an n-acyl homoserine lactone degrading enzyme
51	d1q0ra	Alignment	not modelled	100.0	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acilacinomycin methylesterase RdmC
52	c5mxbB	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: B: PDB Molecule: alpha/beta hydrolase; PDBTitle: haloalkane dehalogenase dmxa from marinobacter sp. elb17 possessing a2 unique catalytic residue
53	c5d6oB	Alignment	not modelled	100.0	14	PDB header: transferase Chain: B: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: orthorhombic crystal structure of an acetylerster hydrolase from2 corynebacterium glutamicum
54	c4rncB	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: B: PDB Molecule: esterase; PDBTitle: crystal structure of an esterase rhest1 from rhodococcus sp. ecu1013
55	c4nvc	Alignment	not modelled	100.0	20	PDB header: transferase Chain: C: PDB Molecule: putative acyltransferase;

55	c4nvlC	Alignment	not modelled	100.0	20	PDBTitle: 2.22 angstrom resolution crystal structure of a putative2 acyltransferase from salmonella enterica PDB header: oxidoreductase Chain: B: PDB Molecule: 1h-3-hydroxy-4-oxoquinaldine 2,4-dioxygenase;
56	c2wj4B	Alignment	not modelled	100.0	12	PDBTitle: crystal structure of the cofactor-devoid 1-h-3-hydroxy-4-2 oxoquinaldine 2,4-dioxygenase (hod) from arthrobacter3 nitroguajacolicus ru61a anaerobically complexed with its4 natural substrate 1-h-3-hydroxy-4-oxoquinaldine PDB header: hydrolase Chain: B: PDB Molecule: soluble epoxide hydrolase; PDBTitle: the crystal structure of m145a mutant of an epoxide hydrolase from2 bacillus megaterium
57	c4inzB	Alignment	not modelled	100.0	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
58	d1a8sa	Alignment	not modelled	100.0	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
59	d1mtza	Alignment	not modelled	100.0	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Proline iminopeptidase-like
60	c6brtB	Alignment	not modelled	100.0	16	PDB header: ligase Chain: B: PDB Molecule: d3-cth-d14-d-ring; PDBTitle: f-box protein cth with hydrolase
61	c3fsgC	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: C: PDB Molecule: alpha/beta superfamily hydrolase; PDBTitle: crystal structure of alpha/beta superfamily hydrolase from oenococcus2 oeni psu-1
62	c5efzC	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: C: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: monoclinic structure of the acetyl esterase mekb
63	c4ccyA	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: carboxylesterase ybfk; PDBTitle: crystal structure of carboxylesterase cesb (ybfk) from bacillus2 subtilis
64	c3qvmA	Alignment	not modelled	100.0	11	PDB header: hydrolase Chain: A: PDB Molecule: olei00960; PDBTitle: the structure of olei00960, a hydrolase from oleispira antarctica
65	c1jliA	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: meta cleavage compound hydrolase; PDBTitle: crystal structure of a his-tagged serine hydrolase involved2 in the carbazole degradation (carc enzyme)
66	d1jlia	Alignment	not modelled	100.0	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase
67	d2pl5a1	Alignment	not modelled	100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
68	c2yysA	Alignment	not modelled	100.0	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: proline iminopeptidase-related protein; PDBTitle: crystal structure of the proline iminopeptidase-related protein2 ttha1809 from thermus thermophilus hb8
69	c2vf2A	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate PDBTitle: x-ray crystal structure of hsd from mycobacterium2 tuberculosis
70	c3vvlA	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: crystal structure of l-serine-o-acetyltransferase found in d-2 cycloserine biosynthetic pathway
71	c3v48B	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: putative aminoacrylate hydrolase rutd; PDBTitle: crystal structure of the putative alpha/beta hydrolase rutd from2 e.coli
72	c3e3aA	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: possible peroxidase bpoq; PDBTitle: the structure of rv0554 from mycobacterium tuberculosis
73	c5cw2C	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: C: PDB Molecule: putative epoxide hydrolase epha; PDBTitle: crystal structure of epoxide hydrolase a from mycobacterium2 thermoresistibile
74	d1va4a	Alignment	not modelled	100.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
75	c3qyjb	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: alr0039 protein; PDBTitle: crystal structure of alr0039, a putative alpha/beta hydrolase from2 nostoc sp pcc 7120.
76	c4b9aA	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: probable epoxide hydrolase; PDBTitle: structure of a putative epoxide hydrolase from pseudomonas2 aeruginosa.
77	d1c4xa	Alignment	not modelled	100.0	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase
78	c5h3hB	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: abhydrolase domain-containing protein; PDBTitle: esterase (eaest) from exiguobacterium antarcticum
79	c5nfgA	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase belonging to alpha/beta hydrolase PDBTitle: novel epoxide hydrolases belonging to the alpha/beta hydrolases2 superfamily in metagenomes from hot environments
80	c4lxgA	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: mcp hydrolase; PDBTitle: crystal structure of dxnb2, a carbon - carbon bond

					hydrolase from2 sphingomonas wittichii rw1
81	c4i3fA_	Alignment	not modelled	100.0	17 PDB header: hydrolase Chain: A: PDB Molecule: serine hydrolase ccsp0084; PDBTitle: crystal structure of serine hydrolase ccsp0084 from the polyaromatic2 hydrocarbon (pah)-degrading bacterium cycloclasticus zankles
82	c3a2nF_	Alignment	not modelled	100.0	18 PDB header: hydrolase Chain: F: PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of dbja (wild type type ii p21)
83	d1a8qa_	Alignment	not modelled	100.0	16 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
84	c4q3lC_	Alignment	not modelled	100.0	14 PDB header: hydrolase Chain: C: PDB Molecule: mgs-m2; PDBTitle: crystal structure of mgs-m2, an alpha/beta hydrolase enzyme from a2 medee basin deep-sea metagenome library
85	d1bn7a_	Alignment	not modelled	100.0	15 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloalkane dehalogenase
86	c5bovD_	Alignment	not modelled	100.0	15 PDB header: hydrolase Chain: D: PDB Molecule: putative epoxide hydrolase protein; PDBTitle: crystal structure of a putative epoxide hydrolase (kpn_01808) from2 klebsiella pneumoniae subsp. pneumoniae mgh 78578 at 1.60 a3 resolution
87	d1m33a_	Alignment	not modelled	100.0	20 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Biotin biosynthesis protein BioH
88	c5dnvA_	Alignment	not modelled	100.0	17 PDB header: hydrolase Chain: A: PDB Molecule: shkai2ib; PDBTitle: crystal structure of kai2-like protein from striga (apo state 2)
89	d1brta_	Alignment	not modelled	100.0	13 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
90	c5cbkA_	Alignment	not modelled	100.0	16 PDB header: signaling protein Chain: A: PDB Molecule: shhtl5; PDBTitle: crystal structure of the strigolactone receptor shhtl5 from striga2 hermonthica
91	c5yhpB_	Alignment	not modelled	100.0	18 PDB header: hydrolase Chain: B: PDB Molecule: cold active proline iminopeptidase; PDBTitle: proline iminopeptidase from psychrophilic yeast glaciozyma antarctica
92	c5a62A_	Alignment	not modelled	100.0	19 PDB header: hydrolase Chain: A: PDB Molecule: putative alpha/beta hydrolase fold protein; PDBTitle: hydrolytic potential of the ammonia-oxidizing thaumarchaeon2 nitrososphaera gargasensis - crystal structure and activity profiles of3 carboxylesterases linked to their metabolic function
93	d1mj5a_	Alignment	not modelled	100.0	10 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloalkane dehalogenase
94	c3r3xA_	Alignment	not modelled	100.0	20 PDB header: hydrolase Chain: A: PDB Molecule: fluoroacetate dehalogenase; PDBTitle: crystal structure of the fluoroacetate dehalogenase rpa1163 -2 asp110asn/bromoacetate
95	d1azwa_	Alignment	not modelled	100.0	17 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Proline iminopeptidase-like
96	c1wprA_	Alignment	not modelled	100.0	16 PDB header: signaling protein Chain: A: PDB Molecule: sigma factor sigb regulation protein rsbq; PDBTitle: crystal structure of rsbq inhibited by pmsf
97	c5uroA_	Alignment	not modelled	100.0	15 PDB header: hydrolase Chain: A: PDB Molecule: predicted protein; PDBTitle: structure of a soluble epoxide hydrolase identified in trichoderma2 reesei
98	c1zoiC_	Alignment	not modelled	100.0	17 PDB header: hydrolase Chain: C: PDB Molecule: esterase; PDBTitle: crystal structure of a stereoselective esterase from2 pseudomonas putida ifo12996
99	c4x00D_	Alignment	not modelled	100.0	17 PDB header: hydrolase Chain: D: PDB Molecule: putative hydrolase; PDBTitle: x-ray crystal structure of a putative aryl esterase from burkholderia2 cenocepacia
100	c2pseA_	Alignment	not modelled	100.0	14 PDB header: oxidoreductase Chain: A: PDB Molecule: renilla-luciferin 2-monooxygenase; PDBTitle: crystal structures of the luciferase and green fluorescent2 protein from renilla reniformis
101	c3bwxA_	Alignment	not modelled	100.0	20 PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase; PDBTitle: crystal structure of an alpha/beta hydrolase (yp_496220.1) from2 novosphingobium aromaticivorans dsm 12444 at 1.50 a resolution
102	c4dnqA_	Alignment	not modelled	100.0	15 PDB header: hydrolase Chain: A: PDB Molecule: dad2; PDBTitle: crystal structure of dad2 s96a mutant
103	c6f9oA_	Alignment	not modelled	100.0	16 PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of cold-adapted haloalkane dehalogenase dpca from2 psychrobacter cryohalolentis k5
104	c4ns4A_	Alignment	not modelled	100.0	15 PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase fold protein; PDBTitle: crystal structure of cold-active esterase from psychrobacter2 cryohalolentis k5t
105	c4rpcA_	Alignment	not modelled	100.0	15 PDB header: hydrolase Chain: A: PDB Molecule: putative alpha/beta hydrolase; PDBTitle: crystal structure of the putative alpha/beta hydrolase family protein2 from desulfitobacterium hafniense

106	c4c6hA_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase; PDBTitle: haloalkane dehalogenase with 1-hexanol
107	d1hkha_	Alignment	not modelled	100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
108	c6g75B_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: common ancestor of haloalkane dehalogenase and renilla PDBTitle: crystal structure of the common ancestor of haloalkane dehalogenases2 and renilla luciferase (anchld-rluc)
109	d1a88a_	Alignment	not modelled	100.0	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
110	c4g9gA_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase fold protein; PDBTitle: crystal structures of n-acyl homoserine lactonase aidh e219g mutant
111	c5z89A_	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: A: PDB Molecule: hyposensitive to light 7; PDBTitle: structural basis for specific inhibition of highly sensitive shhl72 receptor
112	c2qvbA_	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase 3; PDBTitle: crystal structure of haloalkane dehalogenase rv2579 from mycobacterium2 tuberculosis
113	c4mj3B_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: B: PDB Molecule: haloalkane dehalogenase; PDBTitle: haloalkane dehalogenase dmra from mycobacterium rhodesiae js60
114	d1wm1a_	Alignment	not modelled	100.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Proline iminopeptidase-like
115	c3l80A_	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein smu.1393c; PDBTitle: crystal structure of smu.1393c from streptococcus mutans ua159
116	c3qitB_	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: B: PDB Molecule: polyketide synthase; PDBTitle: thioesterase domain from curacin biosynthetic pathway
117	c3jw8A_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: mgll protein; PDBTitle: crystal structure of human mono-glyceride lipase
118	c3r0vA_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase fold protein; PDBTitle: the crystal structure of an alpha/beta hydrolase from sphaerobacter2 thermophilus dsm 20745.
119	d1qo7a_	Alignment	not modelled	100.0	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
120	c2xmzA_	Alignment	not modelled	100.0	15	PDB header: lyase Chain: A: PDB Molecule: hydrolase, alpha/beta hydrolase fold family; PDBTitle: structure of menh from s. aureus