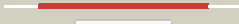



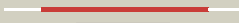






















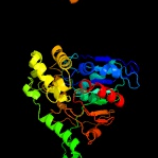





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2223c (-)_2493845_2495407
Date	Mon Aug 5 13:25:35 BST 2019
Unique Job ID	5aac9c464cae4e67

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5uohA_	 Alignment		100.0	53	PDB header: hydrolase Chain: A: PDB Molecule: carboxylesterase a; PDBTitle: crystal structure of hip1 (rv2224c) t466a mutant
2	c3vvlA_	 Alignment		99.9	14	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
3	c2vavL_	 Alignment		99.9	11	PDB header: transferase Chain: L: PDB Molecule: acetyl-coa--deacetylcephalosporin c acetyltransferase; PDBTitle: crystal structure of deacetylcephalosporin c acetyltransferase (dac-2 soak)
4	d2vata1	 Alignment		99.9	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
5	c1cr6A_	 Alignment		99.8	12	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
6	c5w8pA_	 Alignment		99.8	16	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: homoserine transacetylase meta from mycobacterium abscessus
7	c3i28A_	 Alignment		99.8	16	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase 2; PDBTitle: crystal structure of soluble epoxide hydrolase
8	c3i1iA_	 Alignment		99.8	12	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: x-ray crystal structure of homoserine o-acetyltransferase from2 bacillus anthracis
9	c5d6oB_	 Alignment		99.8	16	PDB header: transferase Chain: B: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: orthorhombic crystal structure of an acetylester hydrolase from2 corynebacterium glutamicum
10	d2b61a1	 Alignment		99.8	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
11	d2pl5a1	 Alignment		99.8	11	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase

12	c5jkjA_	Alignment		99.8	12	PDB header: hydrolase Chain: A: PDB Molecule: esterase e22; PDBTitle: crystal structure of esterase e22 I374d mutant
13	c4qloA_	Alignment		99.8	15	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: crystal structure of homoserine o-acetyltransferase from2 staphylococcus aureus
14	c5efzC_	Alignment		99.8	14	PDB header: hydrolase Chain: C: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: monoclinic structure of the acetyl esterase mekb
15	c5yhpB_	Alignment		99.8	19	PDB header: hydrolase Chain: B: PDB Molecule: cold active proline iminopeptidase; PDBTitle: proline iminopeptidase from psychrophilic yeast glaciozyma antarctica
16	c2e3jA_	Alignment		99.8	11	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
17	c5f4zB_	Alignment		99.8	19	PDB header: hydrolase Chain: B: PDB Molecule: epoxide hydrolase; PDBTitle: the crystal structure of an epoxide hydrolase from streptomycetes2 carzinostaticus subsp. neocarzinostaticus
18	c4i19A_	Alignment		99.7	15	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: the crystal structure of an epoxide hydrolase from streptomycetes2 carzinostaticus subsp. neocarzinostaticus.
19	c4d9jl_	Alignment		99.7	18	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
20	d1k8qa_	Alignment		99.7	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Gastric lipase
21	d1azwa_	Alignment	not modelled	99.7	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Proline iminopeptidase-like
22	c2qmqa_	Alignment	not modelled	99.7	11	PDB header: signaling protein Chain: A: PDB Molecule: protein ndr2; PDBTitle: crystal structure of a n-myc downstream regulated 2 protein (ndr2,2 syld, ndr2, ai182517, au040374) from mus musculus at 1.70 a3 resolution
23	c4qlaA_	Alignment	not modelled	99.7	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
24	d1hlga_	Alignment	not modelled	99.7	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Gastric lipase
25	c3v48B_	Alignment	not modelled	99.7	15	PDB header: hydrolase Chain: B: PDB Molecule: putative aminoacrylate hydrolase rutd; PDBTitle: crystal structure of the putative alpha/beta hydrolase rutd from2 e.coli
26	d1wm1a_	Alignment	not modelled	99.7	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Proline iminopeptidase-like
27	d1cr6a2	Alignment	not modelled	99.7	11	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
28	c4qlaB_	Alignment	not modelled	99.7	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

29	c2xuaH	Alignment	not modelled	99.7	17	PDB header: hydrolase Chain: H: PDB Molecule: 3-oxoadipate enol-lactonase; PDBTitle: crystal structure of the eno-lactonase from burkholderia2 xenovorans lb400
30	c3oosA	Alignment	not modelled	99.7	18	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
31	c4y7dA	Alignment	not modelled	99.7	19	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase fold protein; PDBTitle: alpha/beta hydrolase fold protein from nakamurella multipartita
32	c4pw0A	Alignment	not modelled	99.6	18	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase fold protein; PDBTitle: alpha/beta hydrolase fold protein from chitinophaga pinensis
33	c5nfgA	Alignment	not modelled	99.6	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
34	c3qvmA	Alignment	not modelled	99.6	14	PDB header: hydrolase Chain: A: PDB Molecule: olei00960; PDBTitle: the structure of olei00960, a hydrolase from oleispira antarctica
35	c5uroA	Alignment	not modelled	99.6	16	PDB header: hydrolase Chain: A: PDB Molecule: predicted protein; PDBTitle: structure of a soluble epoxide hydrolase identified in trichoderma2 reesei
36	c4f0jA	Alignment	not modelled	99.6	18	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
37	c2yysA	Alignment	not modelled	99.6	21	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
38	c5xmdA	Alignment	not modelled	99.6	13	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase a; PDBTitle: crystal structure of epoxide hydrolase vreh1 from vigna radiata
39	c3om8A	Alignment	not modelled	99.6	20	PDB header: hydrolase Chain: A: PDB Molecule: probable hydrolase; PDBTitle: the crystal structure of a hydrolase from pseudomonas aeruginosa pa01
40	c2r11D	Alignment	not modelled	99.6	16	PDB header: hydrolase Chain: D: PDB Molecule: carboxylesterase np; PDBTitle: crystal structure of putative hydrolase (2632844) from bacillus2 subtilis at 1.96 a resolution
41	c2y6vB	Alignment	not modelled	99.6	18	PDB header: hydrolase Chain: B: PDB Molecule: peroxisomal membrane protein lpx1; PDBTitle: peroxisomal alpha-beta-hydrolase lpx1 (yor084w) from saccharomyces2 cerevisiae (crystal form i)
42	d1zd3a2	Alignment	not modelled	99.6	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
43	c5esrA	Alignment	not modelled	99.6	18	PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of haloalkane dehalogenase (dcca) from caulobacter2 crescentus
44	d1mtza	Alignment	not modelled	99.6	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Proline iminopeptidase-like
45	c4oseA	Alignment	not modelled	99.6	11	PDB header: hydrolase Chain: A: PDB Molecule: putative hydrolase; PDBTitle: x-ray crystal structure of a putative hydrolase from rickettsia typhi
46	d1q0ra	Alignment	not modelled	99.6	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Aclacinomycin methylesterase RdmC
47	d1c4xa	Alignment	not modelled	99.6	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase
48	d1b6ga	Alignment	not modelled	99.5	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloalkane dehalogenase
49	c4l0cA	Alignment	not modelled	99.5	17	PDB header: hydrolase Chain: A: PDB Molecule: deformylase; PDBTitle: crystal structure of the n-fopmylmaeamic acid deformylase nfo(s94a)2 from pseudomonas putida s16
50	c1u2eA	Alignment	not modelled	99.5	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
51	c6brtB	Alignment	not modelled	99.5	17	PDB header: ligase Chain: B: PDB Molecule: d3-cth-d14-d-ring; PDBTitle: f-box protein cth with hydrolase
52	c4rpcA	Alignment	not modelled	99.5	18	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
53	c3bwxA	Alignment	not modelled	99.5	16	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
54	c2vf2A	Alignment	not modelled	99.5	13	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
55	c2wj4B_	Alignment	not modelled	99.5	17	PDB header: oxidoreductase Chain: B: PDB Molecule: 1h-3-hydroxy-4-oxoquinoline 2,4-dioxygenase; PDBTitle: 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
56	c3flaB_	Alignment	not modelled	99.5	21	PDB header: hydrolase Chain: B: PDB Molecule: rifr; PDBTitle: rifr - type ii thioesterase from rifamycin nrps/pks biosynthetic2 pathway - form 1
57	c2cjpA_	Alignment	not modelled	99.5	11	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: structure of potato (solanum tuberosum) epoxide hydrolase i (steh1)
58	d1ehya_	Alignment	not modelled	99.5	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
59	c3fsgC_	Alignment	not modelled	99.5	15	PDB header: hydrolase Chain: C: PDB Molecule: alpha/beta superfamily hydrolase; PDBTitle: crystal structure of alpha/beta superfamily hydrolase from oenococcus2 oeni psu-1
60	c2xmzA_	Alignment	not modelled	99.5	13	PDB header: lyase Chain: A: PDB Molecule: hydrolase, alpha/beta hydrolase fold family; PDBTitle: structure of menh from s. aureus
61	c4inzB_	Alignment	not modelled	99.5	14	PDB header: hydrolase Chain: B: PDB Molecule: soluble epoxide hydrolase; PDBTitle: the crystal structure of m145a mutant of an epoxide hydrolase from2 bacillus megaterium
62	c5egnB_	Alignment	not modelled	99.5	20	PDB header: hydrolase Chain: B: PDB Molecule: esterase; PDBTitle: est816 as an n-acyl homoserine lactone degrading enzyme
63	c5hdfB_	Alignment	not modelled	99.5	20	PDB header: hydrolase Chain: B: PDB Molecule: hydrolase; PDBTitle: hydrolase semet-stna
64	c3e3aA_	Alignment	not modelled	99.5	21	PDB header: oxidoreductase Chain: A: PDB Molecule: possible peroxidase bpc; PDBTitle: the structure of rv0554 from mycobacterium tuberculosis
65	d2rhw1	Alignment	not modelled	99.5	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase
66	c3h04A_	Alignment	not modelled	99.4	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of the protein with unknown function from2 staphylococcus aureus subsp. aureus mu50
67	c5bovD_	Alignment	not modelled	99.4	16	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
68	c5cw2C_	Alignment	not modelled	99.4	14	PDB header: hydrolase Chain: C: PDB Molecule: putative epoxide hydrolase epha; PDBTitle: crystal structure of epoxide hydrolase a from mycobacterium2 thermoresistibile
69	c2hu7A_	Alignment	not modelled	99.4	22	PDB header: hydrolase Chain: A: PDB Molecule: acylamino-acid-releasing enzyme; PDBTitle: binding of inhibitors by acylaminoacyl peptidase
70	c4nvrC_	Alignment	not modelled	99.4	16	PDB header: transferase Chain: C: PDB Molecule: putative acyltransferase; PDBTitle: 2.22 angstrom resolution crystal structure of a putative2 acyltransferase from salmonella enterica
71	d1qo7a_	Alignment	not modelled	99.4	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
72	c3nwoA_	Alignment	not modelled	99.4	19	PDB header: hydrolase Chain: A: PDB Molecule: proline iminopeptidase; PDBTitle: crystal structure of proline iminopeptidase mycobacterium smegmatis
73	d1m33a_	Alignment	not modelled	99.4	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Biotin biosynthesis protein BioH
74	c1y37A_	Alignment	not modelled	99.4	19	PDB header: hydrolase Chain: A: PDB Molecule: fluoroacetate dehalogenase; PDBTitle: structure of fluoroacetate dehalogenase from burkholderia sp. fa1
75	c4psuA_	Alignment	not modelled	99.4	19	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase; PDBTitle: crystal structure of alpha/beta hydrolase from rhodospseudomonas2 palustris cga009
76	c3u1tA_	Alignment	not modelled	99.4	15	PDB header: hydrolase Chain: A: PDB Molecule: dmma haloalkane dehalogenase; PDBTitle: haloalkane dehalogenase, dmma, of marine microbial origin
77	c3a2nF_	Alignment	not modelled	99.4	16	PDB header: hydrolase Chain: F: PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of dbja (wild type type ii p21)
78	c4q31C_	Alignment	not modelled	99.4	18	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
79	c3e0xB_	Alignment	not modelled	99.4	19	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: lipase-esterase related protein; PDBTitle: the crystal structure of a lipase-esterase related protein2

						from clostridium acetobutylicum atcc 824
80	c6f9oA	Alignment	not modelled	99.4	13	PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of cold-adapted haloalkane dehalogenase dpca from2 psychrobacter cryohalolentis k5
81	c5ng7B	Alignment	not modelled	99.4	18	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
82	c3bf7B	Alignment	not modelled	99.4	21	PDB header: hydrolase Chain: B: PDB Molecule: esterase ybff; PDBTitle: 1.1 resolution structure of ybff, a new esterase from escherichia2 coli: a unique substrate-binding crevice generated by domain3 arrangement
83	c4dnqA	Alignment	not modelled	99.4	18	PDB header: hydrolase Chain: A: PDB Molecule: dad2; PDBTitle: crystal structure of dad2 s96a mutant
84	c5mxbB	Alignment	not modelled	99.4	21	PDB header: hydrolase Chain: B: PDB Molecule: alpha/beta hydrolase; PDBTitle: haloalkane dehalogenase dmxa from marinobacter sp. elb17 possessing a2 unique catalytic residue
85	c4i3fA	Alignment	not modelled	99.4	18	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
86	c3fobA	Alignment	not modelled	99.4	17	PDB header: oxidoreductase Chain: A: PDB Molecule: bromoperoxidase; PDBTitle: crystal structure of bromoperoxidase from bacillus anthracis
87	d1uk8a	Alignment	not modelled	99.4	22	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase
88	c3kdaB	Alignment	not modelled	99.4	13	PDB header: hydrolase Chain: B: PDB Molecule: cfr inhibitory factor (cif); PDBTitle: crystal structure of the cfr inhibitory factor cif with the h269a2 mutation
89	c3wibB	Alignment	not modelled	99.4	12	PDB header: hydrolase Chain: B: PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of y109w mutant haloalkane dehalogenase data from2 agrobacterium tumefaciens c58
90	d1imja	Alignment	not modelled	99.4	23	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Ccg1/TafII250-interacting factor B (Cib)
91	c2xt0A	Alignment	not modelled	99.4	15	PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase; PDBTitle: dehalogenase dpqa from plesiocystis pacifica sir-i
92	c3jw8A	Alignment	not modelled	99.4	15	PDB header: hydrolase Chain: A: PDB Molecule: mgll protein; PDBTitle: crystal structure of human mono-glyceride lipase
93	c6g75B	Alignment	not modelled	99.4	12	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 (anchI-d-luc)
94	c5dnvA	Alignment	not modelled	99.4	13	PDB header: hydrolase Chain: A: PDB Molecule: shkai2ib; PDBTitle: crystal structure of kai2-like protein from striga (apo state 2)
95	c3kxpD	Alignment	not modelled	99.4	20	PDB header: hydrolase Chain: D: PDB Molecule: alpha-(n-acetylamino)methylene)succinic acid hydrolase; PDBTitle: crystal structure of e-2-(acetamidomethylene)succinate hydrolase
96	c1wprA	Alignment	not modelled	99.4	19	PDB header: signaling protein Chain: A: PDB Molecule: sigma factor sigb regulation protein rsbq; PDBTitle: crystal structure of rsbq inhibited by pmsf
97	c3ibtA	Alignment	not modelled	99.4	16	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)
98	c5ugzA	Alignment	not modelled	99.3	14	PDB header: hydrolase Chain: A: PDB Molecule: putative thioesterase; PDBTitle: crystal structure of clbq from the colibactin nrps/pks pathway
99	c4uhhA	Alignment	not modelled	99.3	20	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: structural studies of a thermophilic esterase from2 thermogutta terrifontis (cacodylate complex)
100	d1a8sa	Alignment	not modelled	99.3	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
101	c1zoiC	Alignment	not modelled	99.3	17	PDB header: hydrolase Chain: C: PDB Molecule: esterase; PDBTitle: crystal structure of a stereoselective esterase from2 pseudomonas putida ifo12996
102	c2ockA	Alignment	not modelled	99.3	23	PDB header: hydrolase Chain: A: PDB Molecule: valacyclovir hydrolase; PDBTitle: crystal structure of valacyclovir hydrolase d123n mutant
103	d1xkta	Alignment	not modelled	99.3	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
104	c4mj3B	Alignment	not modelled	99.3	17	PDB header: hydrolase Chain: B: PDB Molecule: haloalkane dehalogenase; PDBTitle: haloalkane dehalogenase dmra from mycobacterium

					rhodesiae js60
105	c3w06A_	Alignment	not modelled	99.3	15 PDB header: hydrolase Chain: A: PDB Molecule: hydrolase, alpha/beta fold family protein; PDBTitle: crystal structure of arabidopsis thaliana dwarf14 like (atd14l)
106	c3bdiA_	Alignment	not modelled	99.3	19 PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ta0194; PDBTitle: crystal structure of predicted cib-like hydrolase (np_393672.1) from2 thermoplasma acidophilum at 1.45 a resolution
107	c3mveB_	Alignment	not modelled	99.3	14 PDB header: lyase Chain: B: PDB Molecule: upf0255 protein vv1_0328; PDBTitle: crystal structure of a novel pyruvate decarboxylase
108	c6eicA_	Alignment	not modelled	99.3	18 PDB header: hydrolase Chain: A: PDB Molecule: mycobacterium tuberculosis monoglyceride lipase; PDBTitle: crystal structure of rv0183, a monoglyceride lipase from mycobacterium2 tuberculosis
109	c4b9aA_	Alignment	not modelled	99.3	23 PDB header: hydrolase Chain: A: PDB Molecule: probable epoxide hydrolase; PDBTitle: structure of a putative epoxide hydrolase from pseudomonas2 aeruginosa.
110	c3wzjB_	Alignment	not modelled	99.3	21 PDB header: hydrolase Chain: B: PDB Molecule: zearealenone hydrolase; PDBTitle: zen lactonase
111	c3qitB_	Alignment	not modelled	99.3	20 PDB header: hydrolase Chain: B: PDB Molecule: polyketide synthase; PDBTitle: thioesterase domain from curacin biosynthetic pathway
112	d1bn7a_	Alignment	not modelled	99.3	22 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloalkane dehalogenase
113	d1hkha_	Alignment	not modelled	99.3	15 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
114	c6ba8A_	Alignment	not modelled	99.3	19 PDB header: hydrolase Chain: A: PDB Molecule: iron aquisition yersiniabactin synthesis enzyme, ybtt; PDBTitle: ybtt - type ii thioesterase from yersiniabactin nrps/pks biosynthetic2 pathway
115	d1a8qa_	Alignment	not modelled	99.3	16 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
116	c5cbkA_	Alignment	not modelled	99.3	13 PDB header: signaling protein Chain: A: PDB Molecule: shhtl5; PDBTitle: crystal structure of the strigolactone receptor shhtl5 from striga2 hermonthica
117	c4opmB_	Alignment	not modelled	99.3	20 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
118	c2wtmC_	Alignment	not modelled	99.3	16 PDB header: hydrolase Chain: C: PDB Molecule: est1e; PDBTitle: est1e from butyrivibrio proteoclasticus
119	c3l80A_	Alignment	not modelled	99.3	13 PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein smu.1393c; PDBTitle: crystal structure of smu.1393c from streptococcus mutans ua159
120	c5oluA_	Alignment	not modelled	99.3	16 PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase family protein; PDBTitle: the crystal structure of a highly thermostable carboxyl esterase from2 bacillus coagulans in complex with glycerol