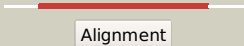

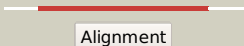

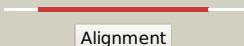







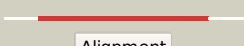











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3177 (-) _3545444_3546304
Date	Thu Aug 8 16:20:36 BST 2019
Unique Job ID	752dc00ae6856773

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1cr6A_	 Alignment		100.0	14	PDB header: hydrolase Chain: A; PDB Molecule: epoxide hydrolase; PDBTitle: crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
2	c3i28A_	 Alignment		100.0	16	PDB header: hydrolase Chain: A; PDB Molecule: epoxide hydrolase 2; PDBTitle: crystal structure of soluble epoxide hydrolase
3	c4pw0A_	 Alignment		100.0	35	PDB header: hydrolase Chain: A; PDB Molecule: alpha/beta hydrolase fold protein; PDBTitle: alpha/beta hydrolase fold protein from chitinophaga pinensis
4	c4d9jl_	 Alignment		100.0	22	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	c4y7dA_	 Alignment		100.0	15	PDB header: hydrolase Chain: A; PDB Molecule: alpha/beta hydrolase fold protein; PDBTitle: alpha/beta hydrolase fold protein from nakamurella multipartita
6	d1q0ra_	 Alignment		100.0	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Aclacinomycin methylesterase RdmC
7	c4psuA_	 Alignment		100.0	15	PDB header: hydrolase Chain: A; PDB Molecule: alpha/beta hydrolase; PDBTitle: crystal structure of alpha/beta hydrolase from rhodopseudomonas2 palustris cga009
8	c3kxpD_	 Alignment		100.0	16	PDB header: hydrolase Chain: D; PDB Molecule: alpha-(n-acetylaminomethylene)succinic acid hydrolase; PDBTitle: crystal structure of e-2-(acetamidomethylene)succinate hydrolase
9	d1c4xa_	 Alignment		100.0	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase
10	c4opmB_	 Alignment		100.0	14	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
11	c4i3fA_	 Alignment		100.0	20	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

12	c4rncB_	Alignment		100.0	20	PDB header: hydrolase Chain: B: PDB Molecule: esterase; PDBTitle: crystal structure of an esterase rhest1 from rhodococcus sp. ecu1013
13	d2rhwa1	Alignment		100.0	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase
14	c3kdaB_	Alignment		100.0	13	PDB header: hydrolase Chain: B: PDB Molecule: cftr inhibitory factor (cif); PDBTitle: crystal structure of the cftr inhibitory factor cif with the h269a2 mutation
15	c2vf2A_	Alignment		100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate PDBTitle: x-ray crystal structure of hsad from mycobacterium2 tuberculosis
16	d1cr6a2	Alignment		100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
17	c4lxgA_	Alignment		100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: mcp hydrolase; PDBTitle: crystal structure of dxnb2, a carbon - carbon bond hydrolase from2 sphingomonas wittichii rw1
18	d1bn7a_	Alignment		100.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloalkane dehalogenase
19	c5egnB_	Alignment		100.0	23	PDB header: hydrolase Chain: B: PDB Molecule: esterase; PDBTitle: est816 as an n-acyl homoserine lactone degrading enzyme
20	c5h3hB_	Alignment		100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: abhydrolase domain-containing protein; PDBTitle: esterase (eaest) from exiguobacterium antarcticum
21	c4f0jA_	Alignment	not modelled	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
22	c5xmdA_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase a; PDBTitle: crystal structure of epoxide hydrolase vreh1 from vigna radiata
23	c3oosA_	Alignment	not modelled	100.0	20	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
24	c2e3jA_	Alignment	not modelled	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
25	c3a2nF_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: F: PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of dbja (wild type type ii p21)
26	d1b6ga_	Alignment	not modelled	100.0	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloalkane dehalogenase
27	c3u1tA_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: dmma haloalkane dehalogenase; PDBTitle: haloalkane dehalogenase, dmma, of marine microbial origin
28	c5cw2C_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: C: PDB Molecule: putative epoxide hydrolase epha; PDBTitle: crystal structure of epoxide hydrolase a from mycobacterium2 thermoresistibile
						PDB header: hydrolase

29	c2cjpA_	Alignment	not modelled	100.0	13	Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: structure of potato (solanum tuberosum) epoxide hydrolase i (steh1)
30	d1zd3a2	Alignment	not modelled	100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
31	c3e3aA_	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: possible peroxidase bpoc; PDBTitle: the structure of rv0554 from mycobacterium tuberculosis
32	d1ehya_	Alignment	not modelled	100.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
33	c3wibB_	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: B: PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of y109w mutant haloalkane dehalogenase data from2 agrobacterium tumefaciens c58
34	c2yysA_	Alignment	not modelled	100.0	18	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
35	c1zoiC_	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: C: PDB Molecule: esterase; PDBTitle: crystal structure of a stereoselective esterase from2 pseudomonas putida ifo12996
36	c3ibtA_	Alignment	not modelled	100.0	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)
37	c5w15D_	Alignment	not modelled	100.0	15	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.
38	c1u2eA_	Alignment	not modelled	100.0	21	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
39	c5a62A_	Alignment	not modelled	100.0	13	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
40	d1uk8a_	Alignment	not modelled	100.0	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase
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	c5nfgA_	Alignment	not modelled	100.0	17	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
43	c4uhhA_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: structural studies of a thermophilic esterase from2 thermogutta terrifontis (cacodylate complex)
44	c3om8A_	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: probable hydrolase; PDBTitle: the crystal structure of a hydrolase from pseudomonas aeruginosa pa01
45	c4qloA_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: crystal structure of homoserine o-acetyltransferase from2 staphylococcus aureus
46	c4inzB_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: B: PDB Molecule: soluble epoxide hydrolase; PDBTitle: the crystal structure of m145a mutant of an epoxide hydrolase from2 bacillus megaterium
47	c5esrA_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of haloalkane dehalogenase (dcca) from caulobacter2 crescentus
48	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
49	d1mtza_	Alignment	not modelled	100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Proline iminopeptidase-like
50	c2xt0A_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase; PDBTitle: dehalogenase dppa from plesiocystis pacifica sir-i
51	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)
52	c5mxbB_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: alpha/beta hydrolase; PDBTitle: haloalkane dehalogenase dmxa from marinobacter sp. elb17 possessing a2 unique catalytic residue
53	c4l0cA_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: deformylase; PDBTitle: crystal structure of the n-fopmylmaeamic acid deformylase nfo(s94a)2 from pseudomonas putida s16
54	c4nseA_	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: putative hydrolase;

54	c405aA	Alignment	not modelled	100.0	13	PDBTitle: x-ray crystal structure of a putative hydrolase from rickettsia typhi PDB header: hydrolase
55	c2r11D	Alignment	not modelled	100.0	14	Chain: D; PDB Molecule: carboxylesterase np; PDBTitle: crystal structure of putative hydrolase (2632844) from bacillus2 subtilis at 1.96 a resolution
56	c4q3lC	Alignment	not modelled	100.0	15	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
57	d1a8sa	Alignment	not modelled	100.0	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
58	c5yhpB	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: B; PDB Molecule: cold active proline iminopeptidase; PDBTitle: proline iminopeptidase from psychrophilic yeast glaciozyma antarctica
59	d1va4a	Alignment	not modelled	100.0	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
60	d1a88a	Alignment	not modelled	100.0	22	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
61	d1azwa	Alignment	not modelled	100.0	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Proline iminopeptidase-like
62	c4b9aA	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A; PDB Molecule: probable epoxide hydrolase; PDBTitle: structure of a putative epoxide hydrolase from pseudomonas2 aeruginosa.
63	d1brta	Alignment	not modelled	100.0	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
64	c2xuaH	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: H; PDB Molecule: 3-oxoadipate enol-lactonase; PDBTitle: crystal structure of the enol-lactonase from burkholderia2 xenovorans lb400
65	c4x00D	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: D; PDB Molecule: putative hydrolase; PDBTitle: x-ray crystal structure of a putative aryl esterase from burkholderia2 cenocepacia
66	c5bovD	Alignment	not modelled	100.0	17	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
67	c2qmqa	Alignment	not modelled	100.0	13	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
68	c2wj4B	Alignment	not modelled	100.0	14	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
69	c2vavL	Alignment	not modelled	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)
70	c3qyjB	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: B; PDB Molecule: alr0039 protein; PDBTitle: crystal structure of alr0039, a putative alpha/beta hydrolase from2 nostoc sp pcc 7120.
71	c3p2mA	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A; PDB Molecule: possible hydrolase; PDBTitle: crystal structure of a novel esterase rv0045c from mycobacterium2 tuberculosis
72	c2ockA	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A; PDB Molecule: valacyclovir hydrolase; PDBTitle: crystal structure of valacyclovir hydrolase d123n mutant
73	d2b61a1	Alignment	not modelled	100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
74	c5d6oB	Alignment	not modelled	100.0	14	PDB header: transferase Chain: B; PDB Molecule: homoserine o-acetyltransferase; PDBTitle: orthorhombic crystal structure of an acylester hydrolase from2 corynebacterium glutamicum
75	c3r3xA	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A; PDB Molecule: fluoroacetate dehalogenase; PDBTitle: crystal structure of the fluoroacetate dehalogenase rpa1163 -2 asp110asn/bromoacetate
76	d2vata1	Alignment	not modelled	100.0	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
77	c3qitB	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B; PDB Molecule: polyketide synthase; PDBTitle: thioesterase domain from curacin biosynthetic pathway
78	c5efzC	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: C; PDB Molecule: homoserine o-acetyltransferase; PDBTitle: monoclinic structure of the acetyl esterase mekb
79	c1nc4A	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A; PDB Molecule: alpha/beta hydrolase fold protein;

79	c4189A_	Alignment	not modelled	100.0	10	PDBTitle: crystal structure of cold-active esterase from psychrobacter2 cryohalolentis k5t PDB header: hydrolase
80	c4ccyA_	Alignment	not modelled	100.0	13	Chain: A; PDB Molecule: carboxylesterase ybfk; PDBTitle: crystal structure of carboxylesterase cesb (ybfk) from bacillus2 subtilis
81	c3nwoA_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A; PDB Molecule: proline iminopeptidase; PDBTitle: crystal structure of proline iminopeptidase mycobacterium smegmatis
82	c6f9oA_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A; PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of cold-adapted haloalkane dehalogenase dpca from2 psychrobacter cryohalolentis k5
83	c4nvrC_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: C; PDB Molecule: putative acyltransferase; PDBTitle: 2.22 angstrom resolution crystal structure of a putative2 acyltransferase from salmonella enterica
84	c4c6hA_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A; PDB Molecule: haloalkane dehalogenase; PDBTitle: haloalkane dehalogenase with 1-hexanol
85	d1j1ia_	Alignment	not modelled	100.0	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase
86	c1j1iA_	Alignment	not modelled	100.0	20	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)
87	c1y37A_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A; PDB Molecule: fluoroacetate dehalogenase; PDBTitle: structure of fluoroacetate dehalogenase from burkholderia sp. fa1
88	c5f4zB_	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: B; PDB Molecule: epoxide hydrolase; PDBTitle: the crystal structure of an epoxide hydrolase from streptomyces2 carzinostaticus subsp. neocarzinostaticus
89	c4rpcA_	Alignment	not modelled	100.0	14	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
90	c4qlaA_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A; PDB Molecule: juvenile hormone epoxide hydrolase; PDBTitle: crystal structure of juvenile hormone epoxide hydrolase from the2 silkworm bombyx mori
91	c5kja_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A; PDB Molecule: esterase e22; PDBTitle: crystal structure of esterase e22 I374d mutant
92	c4qlaB_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: B; PDB Molecule: juvenile hormone epoxide hydrolase; PDBTitle: crystal structure of juvenile hormone epoxide hydrolase from the2 silkworm bombyx mori
93	d1a8qa_	Alignment	not modelled	100.0	22	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
94	c4mj3B_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: B; PDB Molecule: haloalkane dehalogenase; PDBTitle: haloalkane dehalogenase dmra from mycobacterium rhodesiae js60
95	d1mj5a_	Alignment	not modelled	100.0	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloalkane dehalogenase
96	c2pseA_	Alignment	not modelled	100.0	12	PDB header: oxidoreductase Chain: A; PDB Molecule: renilla-luciferin 2-monooxygenase; PDBTitle: crystal structures of the luciferase and green fluorescent2 protein from renilla reniformis
97	d1hkha_	Alignment	not modelled	100.0	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
98	c3i1iA_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A; PDB Molecule: homoserine o-acetyltransferase; PDBTitle: x-ray crystal structure of homoserine o-acetyltransferase from2 bacillus anthracis
99	c2qvba_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A; PDB Molecule: haloalkane dehalogenase 3; PDBTitle: crystal structure of haloalkane dehalogenase rv2579 from mycobacterium2 tuberculosis
100	c4i19A_	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: A; PDB Molecule: epoxide hydrolase; PDBTitle: the crystal structure of an epoxide hydrolase from streptomyces2 carzinostaticus subsp. neocarzinostaticus.
101	d1wm1a_	Alignment	not modelled	100.0	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Proline iminopeptidase-like
102	c3bwxA_	Alignment	not modelled	100.0	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
103	c3jw8A_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A; PDB Molecule: mgll protein; PDBTitle: crystal structure of human mono-glyceride lipase
104	c5w8pA_	Alignment	not modelled	100.0	21	PDB header: transferase Chain: A; PDB Molecule: homoserine o-acetyltransferase; PDBTitle: homoserine transacetylase meta from mycobacterium abscessus
105	d1m33a_	Alignment	not modelled	100.0	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases

				Family: Biotin biosynthesis protein BioH	
106	c3v48B_	Alignment	not modelled	100.0	20 PDB header: hydrolase Chain: B: PDB Molecule: putative aminoacrylate hydrolase rutd; PDBTitle: crystal structure of the putative alpha/beta hydrolase rutd from 2 e.coli
107	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.
108	c6g75B_	Alignment	not modelled	100.0	13 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	c6ra2E_	Alignment	not modelled	100.0	16 PDB header: hydrolase Chain: E: PDB Molecule: putative dioxygenase (1h-3-hydroxy-4-oxoquinoline 2,4- PDBTitle: structural basis for recognition and ring-cleavage of the pseudomonas2 quinolone signal (pqs) by aqdc
110	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
111	c5frdA_	Alignment	not modelled	100.0	15 PDB header: hydrolase Chain: A: PDB Molecule: carboxylesterase (est-2); PDBTitle: structure of a thermophilic esterase
112	c4zwnD_	Alignment	not modelled	100.0	15 PDB header: hydrolase Chain: D: PDB Molecule: monoglyceride lipase; PDBTitle: crystal structure of a soluble variant of the monoglyceride lipase2 from saccharomyces cerevisiae
113	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
114	c3bf7B_	Alignment	not modelled	100.0	16 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
115	c3vv1A_	Alignment	not modelled	100.0	19 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
116	c3fobA_	Alignment	not modelled	100.0	18 PDB header: oxidoreductase Chain: A: PDB Molecule: bromoperoxidase; PDBTitle: crystal structure of bromoperoxidase from bacillus anthracis
117	c3bdiA_	Alignment	not modelled	100.0	24 PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ta0194; PDBTitle: crystal structure of predicted cib-like hydrolase (np_393672.1) from 2 thermoplasma acidophilum at 1.45 a resolution
118	c3wz1B_	Alignment	not modelled	100.0	14 PDB header: hydrolase Chain: B: PDB Molecule: zearalenone hydrolase; PDBTitle: zen lactonase
119	c3hjuB_	Alignment	not modelled	100.0	15 PDB header: hydrolase Chain: B: PDB Molecule: monoglyceride lipase; PDBTitle: crystal structure of human monoglyceride lipase
120	d2pl5a1	Alignment	not modelled	100.0	15 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase