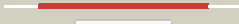



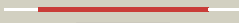



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1124_(ephC)_1247132_1248082
Date	Wed Jul 31 22:05:20 BST 2019
Unique Job ID	c5a7017806c85adf

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	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
2	c3i28A_	 Alignment		100.0	19	PDB header: hydrolase Chain: A; PDB Molecule: epoxide hydrolase 2; PDBTitle: crystal structure of soluble epoxide hydrolase
3	d1b6ga_	 Alignment		100.0	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloalkane dehalogenase
4	c5esrA_	 Alignment		100.0	20	PDB header: hydrolase Chain: A; PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of haloalkane dehalogenase (dccca) from caulobacter2 crescentus
5	c5xmdA_	 Alignment		100.0	25	PDB header: hydrolase Chain: A; PDB Molecule: epoxide hydrolase a; PDBTitle: crystal structure of epoxide hydrolase vreh1 from vigna radiata
6	c2e3jA_	 Alignment		100.0	24	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
7	c5nfgA_	 Alignment		100.0	19	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
8	c5uroA_	 Alignment		100.0	18	PDB header: hydrolase Chain: A; PDB Molecule: predicted protein; PDBTitle: structure of a soluble epoxide hydrolase identified in trichoderma2 reesei
9	c2r11D_	 Alignment		100.0	17	PDB header: hydrolase Chain: D; PDB Molecule: carboxylesterase np; PDBTitle: crystal structure of putative hydrolase (2632844) from bacillus2 subtilis at 1.96 a resolution
10	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
11	c4d9jl_	 Alignment		100.0	16	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

12	c5w8pA_	Alignment		100.0	16	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: homoserine transacetylase meta from mycobacterium abscessus
13	c4pw0A_	Alignment		100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase fold protein; PDBTitle: alpha/beta hydrolase fold protein from chitinophaga pinensis
14	d2b61a1	Alignment		100.0	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
15	c6f9oA_	Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of cold-adapted haloalkane dehalogenase dpca from2 psychrobacter cryohalolentis k5
16	d1cr6a2	Alignment		100.0	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
17	c4y7dA_	Alignment		100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase fold protein; PDBTitle: alpha/beta hydrolase fold protein from nakamuraella multipartita
18	c5d6oB_	Alignment		100.0	14	PDB header: transferase Chain: B: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: orthorhombic crystal structure of an acylester hydrolase from2 corynebacterium glutamicum
19	c2xt0A_	Alignment		100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase; PDBTitle: dehalogenase dpca from plesiocystis pacifica sir-i
20	c4mj3B_	Alignment		100.0	18	PDB header: hydrolase Chain: B: PDB Molecule: haloalkane dehalogenase; PDBTitle: haloalkane dehalogenase dmra from mycobacterium rhodesiae js60
21	d1zd3a2	Alignment	not modelled	100.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
22	c4qlaA_	Alignment	not modelled	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
23	c4f0jA_	Alignment	not modelled	100.0	21	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
24	c2vavL_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: L: PDB Molecule: acetyl-coa--deacetylcephalosporin c acetyltransferase; PDBTitle: crystal structure of deacetylcephalosporin c acetyltransferase (dac-2 soak)
25	c3oosA_	Alignment	not modelled	100.0	13	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
26	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
27	d2vata1	Alignment	not modelled	100.0	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
28	c5f4zB_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: B: PDB Molecule: epoxide hydrolase; PDBTitle: the crystal structure of an epoxide hydrolase from streptomyces2 carzinostaticus subsp. neocarzinostaticus

29	c3i1a_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: x-ray crystal structure of homoserine o-acetyltransferase from2 bacillus anthracis
30	c5yhpB_	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: B: PDB Molecule: cold active proline iminopeptidase; PDBTitle: proline iminopeptidase from psychrophilic yeast glaciozyma antarctica
31	c2cjpA_	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: structure of potato (solanum tuberosum) epoxide hydrolase i (steh1)
32	c5cw2C_	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: C: PDB Molecule: putative epoxide hydrolase epha; PDBTitle: crystal structure of epoxide hydrolase a from mycobacterium2 thermoresistibile
33	d1mtza_	Alignment	not modelled	100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Proline iminopeptidase-like
34	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)
35	c4i19A_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: the crystal structure of an epoxide hydrolase from streptomyces2 carzinostaticus subsp. neocarzinostaticus.
36	c3kdaB_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: B: PDB Molecule: cftr inhibitory factor (cif); PDBTitle: crystal structure of the cftr inhibitory factor cif with the h269a2 mutation
37	c4opmB_	Alignment	not modelled	100.0	19	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
38	c2qmqa_	Alignment	not modelled	100.0	15	PDB header: signaling protein Chain: A: PDB Molecule: protein ndr2; 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
39	c4inzB_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: B: PDB Molecule: soluble epoxide hydrolase; PDBTitle: the crystal structure of m145a mutant of an epoxide hydrolase from2 bacillus megaterium
40	c5efzC_	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: C: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: monoclinic structure of the acetyl esterase mekb
41	c3u1ta_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: dmma haloalkane dehalogenase; PDBTitle: haloalkane dehalogenase, dmma, of marine microbial origin
42	c3vv1A_	Alignment	not modelled	100.0	15	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
43	c5bovd_	Alignment	not modelled	100.0	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
44	c5jkjA_	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: A: PDB Molecule: esterase e22; PDBTitle: crystal structure of esterase e22 l374d mutant
45	c4rncB_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: esterase; PDBTitle: crystal structure of an esterase rhest1 from rhodococcus sp. ecu1013
46	c2y6vB_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: B: PDB Molecule: peroxisomal membrane protein lpx1; PDBTitle: peroxisomal alpha-beta-hydrolase lpx1 (yor084w) from saccharomyces2 cerevisiae (crystal form i)
47	d1c4xa_	Alignment	not modelled	100.0	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase
48	c5ng7B_	Alignment	not modelled	100.0	23	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
49	d1q0ra_	Alignment	not modelled	100.0	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Aclacinomycin methylesterase RdmC
50	d2pl5a1	Alignment	not modelled	100.0	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
51	c3om8A_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: probable hydrolase; PDBTitle: the crystal structure of a hydrolase from pseudomonas aeruginosa pa01
52	c2vf2A_	Alignment	not modelled	100.0	17	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
53	d1azwa_	Alignment	not modelled	100.0	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Proline iminopeptidase-like
54	c4ocpA_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: putative hydrolase;

54	c405aA	Alignment	not modelled	100.0	15	PDBTitle: x-ray crystal structure of a putative hydrolase from rickettsia typhi PDB header: hydrolase
55	c4psuA	Alignment	not modelled	100.0	16	Chain: A; PDB Molecule: alpha/beta hydrolase; PDBTitle: crystal structure of alpha/beta hydrolase from rhodopseudomonas2 palustris cga009
56	c5mxB	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: B; PDB Molecule: alpha/beta hydrolase; PDBTitle: haloalkane dehalogenase dmxa from marinobacter sp. elb17 possessing a2 unique catalytic residue
57	c4ccyA	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A; PDB Molecule: carboxylesterase ybfk; PDBTitle: crystal structure of carboxylesterase cesb (ybfk) from bacillus2 subtilis
58	c3wibB	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: B; PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of y109w mutant haloalkane dehalogenase data from2 agrobacterium tumefaciens c58
59	c4b9aA	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A; PDB Molecule: probable epoxide hydrolase; PDBTitle: structure of a putative epoxide hydrolase from pseudomonas2 aeruginosa.
60	d1qo7a	Alignment	not modelled	100.0	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
61	c2pseA	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: A; PDB Molecule: renilla-luciferin 2-monooxygenase; PDBTitle: crystal structures of the luciferase and green fluorescent2 protein from renilla reniformis
62	c2wj4B	Alignment	not modelled	100.0	13	PDB header: oxidoreductase Chain: B; PDB Molecule: 1h-3-hydroxy-4-oxoquinaldine 2,4-dioxygenase; 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
63	d1bn7a	Alignment	not modelled	100.0	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloalkane dehalogenase
64	c4l0cA	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A; PDB Molecule: deformylase; PDBTitle: crystal structure of the n-fopmylmaleamic acid deformylase nfo(s94a)2 from pseudomonas putida s16
65	d1ehya	Alignment	not modelled	100.0	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
66	c3v48B	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: B; PDB Molecule: putative aminoacrylate hydrolase rutt; PDBTitle: crystal structure of the putative alpha/beta hydrolase rutt from2 e.coli
67	d2rhwa1	Alignment	not modelled	100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase
68	d1wm1a	Alignment	not modelled	100.0	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Proline iminopeptidase-like
69	c6g75B	Alignment	not modelled	100.0	18	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)
70	c4x00D	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: D; PDB Molecule: putative hydrolase; PDBTitle: x-ray crystal structure of a putative aryl esterase from burkholderia2 cenocepacia
71	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
72	c5a62A	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A; PDB Molecule: putative alpha/beta hydrolase fold protein; PDBTitle: hydrolytic potential of the ammonia-oxidizing thaumarchaeon2 nitrososphaera gargensis - crystal structure and activity profiles of3 carboxylesterases linked to their metabolic function
73	c1u2eA	Alignment	not modelled	100.0	15	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
74	c4i3fA	Alignment	not modelled	100.0	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
75	c3p2mA	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: A; PDB Molecule: possible hydrolase; PDBTitle: crystal structure of a novel esterase rv0045c from mycobacterium2 tuberculosis
76	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)
77	c1y37A	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A; PDB Molecule: fluoroacetate dehalogenase; PDBTitle: structure of fluoroacetate dehalogenase from burkholderia sp. fa1
78	c1zoiC	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: C; PDB Molecule: esterase; PDBTitle: crystal structure of a stereoselective esterase from2 pseudomonas putida ifo12996

79	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
80	c3ibtA_	Alignment	not modelled	100.0	13	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)
81	d1hlga_	Alignment	not modelled	100.0	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Gastric lipase
82	c3kxpD_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: D: PDB Molecule: alpha-(n-acetylamino)methylene)succinic acid hydrolase; PDBTitle: crystal structure of e-2-(acetamidomethylene)succinate hydrolase
83	d1k8qa_	Alignment	not modelled	100.0	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Gastric lipase
84	d1a88a_	Alignment	not modelled	100.0	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
85	d1va4a_	Alignment	not modelled	100.0	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
86	d1xkla_	Alignment	not modelled	100.0	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hydroxynitrile lyase-like
87	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
88	c3qitB_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: polyketide synthase; PDBTitle: thioesterase domain from curacin biosynthetic pathway
89	c3nwoA_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: proline iminopeptidase; PDBTitle: crystal structure of proline iminopeptidase mycobacterium smegmatis
90	c3qvmA_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: olei00960; PDBTitle: the structure of olei00960, a hydrolase from oleispira antarctica
91	c3fsgC_	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: C: PDB Molecule: alpha/beta superfamily hydrolase; PDBTitle: crystal structure of alpha/beta superfamily hydrolase from oenococcus2 oeni psu-1
92	c3bwxA_	Alignment	not modelled	100.0	23	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
93	c2xuaH_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: H: PDB Molecule: 3-oxoadipate enol-lactonase; PDBTitle: crystal structure of the enol-lactonase from burkholderia2 xenovorans lb400
94	d1a8sa_	Alignment	not modelled	100.0	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
95	c5h3hB_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: abhydrolase domain-containing protein; PDBTitle: esterase (eaest) from exigubacterium antarcticum
96	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.
97	c2yysA_	Alignment	not modelled	100.0	16	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
98	d3c70a1	Alignment	not modelled	100.0	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hydroxynitrile lyase-like
99	c4ns4A_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase fold protein; PDBTitle: crystal structure of cold-active esterase from psychrobacter2 cryohalolentis k5t
100	d1brta_	Alignment	not modelled	100.0	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
101	c5egnB_	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: B: PDB Molecule: esterase; PDBTitle: est816 as an n-acyl homoserine lactone degrading enzyme
102	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
103	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 desulfotobacterium hafniense
104	d1hkha_	Alignment	not modelled	100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase

105	d1e89a_	Alignment	not modelled	100.0	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hydroxynitrile lyase-like
106	d1mj5a_	Alignment	not modelled	100.0	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloalkane dehalogenase
107	c3fobA_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: bromoperoxidase; PDBTitle: crystal structure of bromoperoxidase from bacillus anthracis
108	c4zwnD_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: D: PDB Molecule: monoglyceride lipase; PDBTitle: crystal structure of a soluble variant of the monoglyceride lipase2 from saccharomyces cerevisiae
109	c3jw8A_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: mgll protein; PDBTitle: crystal structure of human mono-glyceride lipase
110	c3qyjB_	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: B: PDB Molecule: alr0039 protein; PDBTitle: crystal structure of alr0039, a putative alpha/beta hydrolase from2 nostoc sp pcc 7120.
111	d1a8qa_	Alignment	not modelled	100.0	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
112	d1uk8a_	Alignment	not modelled	100.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase
113	c3wzIB_	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: B: PDB Molecule: zearalenone hydrolase; PDBTitle: zen lactonase
114	c1wprA_	Alignment	not modelled	100.0	17	PDB header: signaling protein Chain: A: PDB Molecule: sigma factor sigb regulation protein rsbq; PDBTitle: crystal structure of rsbq inhibited by pmsf
115	d1m33a_	Alignment	not modelled	100.0	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Biotin biosynthesis protein BioH
116	c3e3aA_	Alignment	not modelled	100.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: possible peroxidase bpoc; PDBTitle: the structure of rv0554 from mycobacterium tuberculosis
117	c3dqzB_	Alignment	not modelled	100.0	13	PDB header: lyase Chain: B: PDB Molecule: alpha-hydroxynitrile lyase-like protein; PDBTitle: structure of the hydroxynitrile lyase from arabidopsis thaliana
118	c4c6hA_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase; PDBTitle: haloalkane dehalogenase with 1-hexanol
119	c3wwoA_	Alignment	not modelled	100.0	13	PDB header: lyase Chain: A: PDB Molecule: (s)-hydroxynitrile lyase; PDBTitle: s-selective hydroxynitrile lyase from baliospermum montanum (apo1)
120	c6azdA_	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: ppkai2-like h; PDBTitle: crystal structure of physcomitrella patens kai2-like h