



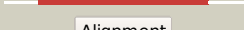



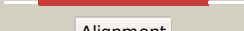

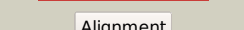

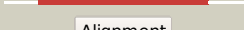

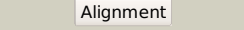



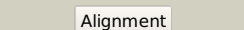

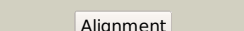









Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3473c_(bpoA)_3890127_3890912
 Date Fri Aug 9 18:20:14 BST 2019
 Unique Job ID 09dffbeb90e28d76

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3i28A_	 Alignment		100.0	15	PDB header: hydrolase Chain: A; PDB Molecule: epoxide hydrolase 2; PDBTitle: crystal structure of soluble epoxide hydrolase
2	c1cr6A_	 Alignment		100.0	15	PDB header: hydrolase Chain: A; PDB Molecule: epoxide hydrolase; PDBTitle: crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
3	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
4	d3c70a1	 Alignment		100.0	11	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hydroxynitrile lyase-like
5	d1e89a_	 Alignment		100.0	10	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hydroxynitrile lyase-like
6	c2vavL_	 Alignment		100.0	11	PDB header: transferase Chain: L; PDB Molecule: acetyl-coa--deacetylcephalosporin c acetyltransferase; PDBTitle: crystal structure of deacetylcephalosporin c acetyltransferase (dac-2 soak)
7	c3i1iA_	 Alignment		100.0	13	PDB header: transferase Chain: A; PDB Molecule: homoserine o-acetyltransferase; PDBTitle: x-ray crystal structure of homoserine o-acetyltransferase from2 bacillus anthracis
8	c2y6vB_	 Alignment		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)
9	c3v48B_	 Alignment		100.0	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
10	d1b6ga_	 Alignment		100.0	11	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloalkane dehalogenase
11	c3wwoA_	 Alignment		100.0	12	PDB header: lyase Chain: A; PDB Molecule: (s)-hydroxynitrile lyase; PDBTitle: s-selective hydroxynitrile lyase from baliospermum montanum (apo1)

12	d2vata1	Alignment		100.0	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
13	d1xkla_	Alignment		100.0	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hydroxynitrile lyase-like
14	c4f0jA_	Alignment		100.0	17	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
15	d2b61a1	Alignment		100.0	10	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
16	c3u1tA_	Alignment		100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: dmma haloalkane dehalogenase; PDBTitle: haloalkane dehalogenase, dmma, of marine microbial origin
17	d1zd3a2	Alignment		100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
18	c4qlaA_	Alignment		100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: juvenile hormone epoxide hydrolase; PDBTitle: crystal structure of juvenile hormone epoxide hydrolase from the2 silkworm bombyx mori
19	c4qlaB_	Alignment		100.0	13	PDB header: hydrolase Chain: B: PDB Molecule: juvenile hormone epoxide hydrolase; PDBTitle: crystal structure of juvenile hormone epoxide hydrolase from the2 silkworm bombyx mori
20	c3dqzB_	Alignment		100.0	10	PDB header: lyase Chain: B: PDB Molecule: alpha-hydroxynitrile lyase-like protein; PDBTitle: structure of the hydroxynitrile lyase from arabidopsis thaliana
21	c4y7dA_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase fold protein; PDBTitle: alpha/beta hydrolase fold protein from nakamurella multipartita
22	c3qvmA_	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: A: PDB Molecule: olei00960; PDBTitle: the structure of olei00960, a hydrolase from oleispira antarctica
23	c3stxB_	Alignment	not modelled	100.0	11	PDB header: hydrolase Chain: B: PDB Molecule: methylketone synthase 1; PDBTitle: crystal structure of tomato methylketone synthase i h243a variant2 complexed with beta-ketoheptanoate
24	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
25	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
26	c4qloA_	Alignment	not modelled	100.0	11	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: crystal structure of homoserine o-acetyltransferase from2 staphylococcus aureus
27	c4uhhA_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: structural studies of a thermophilic esterase from2 thermogutta terrifontis (cacodylate complex)
						PDB header: hydrolase

28	c5h3hB_	Alignment	not modelled	100.0	14	Chain: B; PDB Molecule: abhydrolase domain-containing protein; PDBTitle: esterase (eaest) from <i>exiguobacterium antarcticum</i>
29	d2rhwa1	Alignment	not modelled	100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase
30	d1brta_	Alignment	not modelled	100.0	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
31	c3gzjB_	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: B; PDB Molecule: polyneuridine-aldehyde esterase; PDBTitle: crystal structure of polyneuridine aldehyde esterase complexed with 2 16-epi-vellosimine
32	c5d6oB_	Alignment	not modelled	100.0	11	PDB header: transferase Chain: B; PDB Molecule: homoserine o-acetyltransferase; PDBTitle: orthorhombic crystal structure of an acylester hydrolase from <i>2 corynebacterium glutamicum</i>
33	c2e3jA_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A; PDB Molecule: epoxide hydrolase ephb; PDBTitle: the crystal structure of epoxide hydrolase b (rv1938) from <i>2 mycobacterium tuberculosis</i> at 2.1 angstrom
34	c3kdaB_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B; PDB Molecule: cfr inhibitory factor (cif); PDBTitle: crystal structure of the cfr inhibitory factor cif with the h269a2 mutation
35	c4pw0A_	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: A; PDB Molecule: alpha/beta hydrolase fold protein; PDBTitle: alpha/beta hydrolase fold protein from <i>chitinophaga pinensis</i>
36	c5esrA_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A; PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of haloalkane dehalogenase (dcca) from <i>caulobacter 2 crescentus</i>
37	d1cr6a2	Alignment	not modelled	100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
38	c4oseA_	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: A; PDB Molecule: putative hydrolase; PDBTitle: x-ray crystal structure of a putative hydrolase from <i>rickettsia typhi</i>
39	c5uroA_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A; PDB Molecule: predicted protein; PDBTitle: structure of a soluble epoxide hydrolase identified in <i>trichoderma 2 reesei</i>
40	c2xt0A_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A; PDB Molecule: haloalkane dehalogenase; PDBTitle: dehalogenase dpaa from <i>pleisiocystis pacifica sir-i</i>
41	d1hkha_	Alignment	not modelled	100.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
42	c5efzC_	Alignment	not modelled	100.0	11	PDB header: hydrolase Chain: C; PDB Molecule: homoserine o-acetyltransferase; PDBTitle: monoclinic structure of the acetyl esterase mekb
43	c1u2eA_	Alignment	not modelled	100.0	19	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
44	c3wibB_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: B; PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of y109w mutant haloalkane dehalogenase data from <i>2 agrobacterium tumefaciens c58</i>
45	c5xmdA_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A; PDB Molecule: epoxide hydrolase a; PDBTitle: crystal structure of epoxide hydrolase vreh1 from <i>vigna radiata</i>
46	c5ijkA_	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: A; PDB Molecule: esterase e22; PDBTitle: crystal structure of esterase e22 l374d mutant
47	d1va4a_	Alignment	not modelled	100.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
48	d1q0ra_	Alignment	not modelled	100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Aclacinomycin methylesterase RdmC
49	c4psuA_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A; PDB Molecule: alpha/beta hydrolase; PDBTitle: crystal structure of alpha/beta hydrolase from <i>rhodospseudomonas 2 palustris cga009</i>
50	c5nfgA_	Alignment	not modelled	100.0	16	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
51	d1mtza_	Alignment	not modelled	100.0	11	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Proline iminopeptidase-like
52	c6f9oA_	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: A; PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of cold-adapted haloalkane dehalogenase dpca from <i>2 psychrobacter cryohalolentis k5</i>
53	c4rncB_	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: B; PDB Molecule: esterase; PDBTitle: crystal structure of an esterase rhest1 from <i>rhodococcus sp. ecu1013</i>
54	c2qmqA_	Alignment	not modelled	100.0	15	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
55	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
56	c2r11D_	Alignment	not modelled	100.0	13 PDB header: hydrolase Chain: D: PDB Molecule: carboxylesterase np; PDBTitle: crystal structure of putative hydrolase (2632844) from bacillus2 subtilis at 1.96 a resolution
57	c5w8pA_	Alignment	not modelled	100.0	15 PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: homoserine transacetylase meta from mycobacterium abscessus
58	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
59	d1a8sa_	Alignment	not modelled	100.0	17 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
60	c3oosA_	Alignment	not modelled	100.0	10 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
61	d1c4xa_	Alignment	not modelled	100.0	19 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase
62	d1a8qa_	Alignment	not modelled	100.0	17 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
63	c4q3lC_	Alignment	not modelled	100.0	13 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
64	c4mj3B_	Alignment	not modelled	100.0	16 PDB header: hydrolase Chain: B: PDB Molecule: haloalkane dehalogenase; PDBTitle: haloalkane dehalogenase dmra from mycobacterium rhodesiae js60
65	c2vf2A_	Alignment	not modelled	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 hsd from mycobacterium2 tuberculosis
66	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)
67	c6brtB_	Alignment	not modelled	100.0	14 PDB header: ligase Chain: B: PDB Molecule: d3-cth-d14-d-ring; PDBTitle: f-box protein cth with hydrolase
68	c4opmB_	Alignment	not modelled	100.0	15 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
69	c5a62A_	Alignment	not modelled	100.0	15 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
70	c5mxbB_	Alignment	not modelled	100.0	13 PDB header: hydrolase Chain: B: PDB Molecule: alpha/beta hydrolase; PDBTitle: haloalkane dehalogenase dmxa from marinobacter sp. elb17 possessing a2 unique catalytic residue
71	c4rpcA_	Alignment	not modelled	100.0	12 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
72	c4inzB_	Alignment	not modelled	100.0	13 PDB header: hydrolase Chain: B: PDB Molecule: soluble epoxide hydrolase; PDBTitle: the crystal structure of m145a mutant of an epoxide hydrolase from2 bacillus megaterium
73	c5hk8A_	Alignment	not modelled	100.0	13 PDB header: hydrolase Chain: A: PDB Molecule: probable pheophorbidase; PDBTitle: crystal structure of a methylsterase protein mes16 from arabidopsis
74	c3vvlA_	Alignment	not modelled	100.0	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
75	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)
76	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
77	c3kxpD_	Alignment	not modelled	100.0	22 PDB header: hydrolase Chain: D: PDB Molecule: alpha-(n-acetylamino)methylene)succinic acid hydrolase; PDBTitle: crystal structure of e-2-(acetamidomethylene)succinate hydrolase
78	c3om8A_	Alignment	not modelled	100.0	18 PDB header: hydrolase Chain: A: PDB Molecule: probable hydrolase; PDBTitle: the crystal structure of a hydrolase from pseudomonas aeruginosa pa01
79	d1ehya_	Alignment	not modelled	100.0	13 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases

						Family: Epoxide hydrolase
80	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
81	c3fobA	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: bromoperoxidase; PDBTitle: crystal structure of bromoperoxidase from bacillus anthracis
82	d1uk8a	Alignment	not modelled	100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase
83	c5w15D	Alignment	not modelled	100.0	24	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.
84	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.
85	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
86	d2pl5a1	Alignment	not modelled	100.0	9	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
87	c3bwxA	Alignment	not modelled	100.0	19	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
88	c3e3aA	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: possible peroxidase bpoc; PDBTitle: the structure of rv0554 from mycobacterium tuberculosis
89	c4nvrC	Alignment	not modelled	100.0	16	PDB header: transferase Chain: C: PDB Molecule: putative acyltransferase; PDBTitle: 2.22 angstrom resolution crystal structure of a putative2 acyltransferase from salmonella enterica
90	c3fsgC	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: C: PDB Molecule: alpha/beta superfamily hydrolase; PDBTitle: crystal structure of alpha/beta superfamily hydrolase from oenococcus2 oeni psu-1
91	c5dnvA	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: A: PDB Molecule: shkai2ib; PDBTitle: crystal structure of kai2-like protein from striga (apo state 2)
92	c2xuaH	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: H: PDB Molecule: 3-oxoadipate enol-lactonase; PDBTitle: crystal structure of the enol-lactonase from burkholderia2 xenovorans lb400
93	c4b9aA	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: probable epoxide hydrolase; PDBTitle: structure of a putative epoxide hydrolase from pseudomonas2 aeruginosa.
94	d1m33a	Alignment	not modelled	100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Biotin biosynthesis protein BioH
95	c5cbkA	Alignment	not modelled	100.0	12	PDB header: signaling protein Chain: A: PDB Molecule: shht15; PDBTitle: crystal structure of the strigolactone receptor shht15 from striga2 hermonthica
96	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)
97	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
98	c3jw8A	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: mgll protein; PDBTitle: crystal structure of human mono-glyceride lipase
99	c5y51F	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: F: PDB Molecule: pyrethroid hydrolase; PDBTitle: crystal structure of pyth_h230a
100	c6azdA	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: ppkai2-like h; PDBTitle: crystal structure of physcomitrella patens kai2-like h
101	c1zoiC	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: C: PDB Molecule: esterase; PDBTitle: crystal structure of a stereoselective esterase from2 pseudomonas putida ifo12996
102	d1bn7a	Alignment	not modelled	100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloalkane dehalogenase
103	c3nwoA	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: proline iminopeptidase; PDBTitle: crystal structure of proline iminopeptidase mycobacterium smegmatis
104	c3p2mA	Alignment	not modelled	100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: possible hydrolase; PDBTitle: crystal structure of a novel esterase rv0045c from mycobacterium2 tuberculosis
						Fold: alpha/beta-Hydrolases

105	d1a88a_	Alignment	not modelled	100.0	19	Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
106	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
107	c3w06A_	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase, alpha/beta fold family protein; PDBTitle: crystal structure of arabidopsis thaliana dwarf14 like (atd14l)
108	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
109	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
110	c4ixgA_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: mcp hydrolase; PDBTitle: crystal structure of dxnb2, a carbon - carbon bond hydrolase from2 sphingomonas wittichii rw1
111	c3bf7B_	Alignment	not modelled	100.0	22	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
112	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.
113	c3c5wP_	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: P: PDB Molecule: pp2a-specific methylesterase pme-1; PDBTitle: complex between pp2a-specific methylesterase pme-1 and pp2a core2 enzyme
114	c5yhpB_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: cold active proline iminopeptidase; PDBTitle: proline iminopeptidase from psychrophilic yeast glaciozyma antarctica
115	c3hjuB_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: B: PDB Molecule: monoglyceride lipase; PDBTitle: crystal structure of human monoglyceride lipase
116	c5oluA_	Alignment	not modelled	100.0	12	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
117	c2yysA_	Alignment	not modelled	100.0	17	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
118	c4l0cA_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: deformylase; PDBTitle: crystal structure of the n-fopmylmaaleamic acid deformylase nfo(s94a)2 from pseudomonas putida s16
119	c1y37A_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: fluoroacetate dehalogenase; PDBTitle: structure of fluoroacetate dehalogenase from burkholderia sp. fa1
120	c4g9gA_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase fold protein; PDBTitle: crystal structures of n-acyl homoserine lactonase aidh e219g mutant