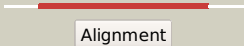

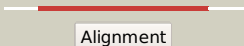

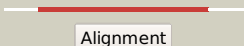







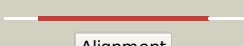




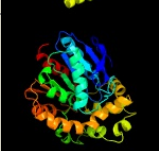






Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0134_(ephF)_161769_162671
Date	Tue Jul 23 14:50:17 BST 2019
Unique Job ID	ed23c763ceb94ca8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1cr6A_	 Alignment		100.0	23	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	23	PDB header: hydrolase Chain: A; PDB Molecule: epoxide hydrolase 2; PDBTitle: crystal structure of soluble epoxide hydrolase
3	d1zd3a2	 Alignment		100.0	23	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
4	d1cr6a2	 Alignment		100.0	23	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
5	c4d9jl_	 Alignment		100.0	23	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
6	c3u1tA_	 Alignment		100.0	20	PDB header: hydrolase Chain: A; PDB Molecule: dmma haloalkane dehalogenase; PDBTitle: haloalkane dehalogenase, dmma, of marine microbial origin
7	c5nfgA_	 Alignment		100.0	21	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	c4nvrC_	 Alignment		100.0	22	PDB header: transferase Chain: C; PDB Molecule: putative acyltransferase; PDBTitle: 2.22 angstrom resolution crystal structure of a putative2 acyltransferase from salmonella enterica
9	c3kdaB_	 Alignment		100.0	23	PDB header: hydrolase Chain: B; PDB Molecule: cftr inhibitory factor (cif); PDBTitle: crystal structure of the cftr inhibitory factor cif with the h269a2 mutation
10	c5yhpB_	 Alignment		100.0	15	PDB header: hydrolase Chain: B; PDB Molecule: cold active proline iminopeptidase; PDBTitle: proline iminopeptidase from psychrophilic yeast glaciozyma antarctica
11	c4b9aA_	 Alignment		100.0	24	PDB header: hydrolase Chain: A; PDB Molecule: probable epoxide hydrolase; PDBTitle: structure of a putative epoxide hydrolase from pseudomonas2 aeruginosa.

12	d1azwa_	Alignment		100.0	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Proline iminopeptidase-like
13	c3wibB_	Alignment		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
14	c4pw0A_	Alignment		100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase fold protein; PDBTitle: alpha/beta hydrolase fold protein from chitinophaga pinensis
15	c5xmdA_	Alignment		100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase a; PDBTitle: crystal structure of epoxide hydrolase vreh1 from vigna radiata
16	d1bn7a_	Alignment		100.0	22	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloalkane dehalogenase
17	c2e3jA_	Alignment		100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase ephb; PDBTitle: the crystal structure of epoxide hydrolase b (rv1938) from2 mycobacterium tuberculosis at 2.1 angstrom
18	d1b6ga_	Alignment		100.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloalkane dehalogenase
19	c3kxpD_	Alignment		100.0	19	PDB header: hydrolase Chain: D: PDB Molecule: alpha-(n-acetylamino)methylene)succinic acid hydrolase; PDBTitle: crystal structure of e-2-(acetamidomethylene)succinate hydrolase
20	c1zoiC_	Alignment		100.0	20	PDB header: hydrolase Chain: C: PDB Molecule: esterase; PDBTitle: crystal structure of a stereoselective esterase from2 pseudomonas putida ifo12996
21	d1q0ra_	Alignment	not modelled	100.0	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Aclacinomycin methylesterase RdmC
22	c3om8A_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: probable hydrolase; PDBTitle: the crystal structure of a hydrolase from pseudomonas aeruginosa pa01
23	c5h3hB_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: abhydrolase domain-containing protein; PDBTitle: esterase (eaest) from exiguobacterium antarcticum
24	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
25	c3a2nF_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: F: PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of dbja (wild type type ii p21)
26	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)
27	c4y7dA_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase fold protein; PDBTitle: alpha/beta hydrolase fold protein from nakamurella multipartita
28	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 gargasensis - crystal structure and activity profiles of3 carboxylesterases linked to their metabolic

					function
29	c4psuA_	Alignment	not modelled	100.0	21 PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase; PDBTitle: crystal structure of alpha/beta hydrolase from rhodospseudomonas2 palustris cga009
30	c5uroA_	Alignment	not modelled	100.0	19 PDB header: hydrolase Chain: A: PDB Molecule: predicted protein; PDBTitle: structure of a soluble epoxide hydrolase identified in trichoderma2 reesei
31	d1wm1a_	Alignment	not modelled	100.0	17 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Proline iminopeptidase-like
32	c2xt0A_	Alignment	not modelled	100.0	22 PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase; PDBTitle: dehalogenase dppa from pliesocystis pacifica sir-i
33	c5esrA_	Alignment	not modelled	100.0	19 PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of haloalkane dehalogenase (dcca) from caulobacter2 crescentus
34	c5mxbB_	Alignment	not modelled	100.0	19 PDB header: hydrolase Chain: B: PDB Molecule: alpha/beta hydrolase; PDBTitle: haloalkane dehalogenase dmxa from marinobacter sp. elb17 possessing a2 unique catalytic residue
35	d1a88a_	Alignment	not modelled	100.0	21 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
36	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
37	d1c4xa_	Alignment	not modelled	100.0	17 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase
38	c1y37A_	Alignment	not modelled	100.0	24 PDB header: hydrolase Chain: A: PDB Molecule: fluoroacetate dehalogenase; PDBTitle: structure of fluoroacetate dehalogenase from burkholderia sp. fa1
39	c3qy1B_	Alignment	not modelled	100.0	22 PDB header: hydrolase Chain: B: PDB Molecule: alr0039 protein; PDBTitle: crystal structure of alr0039, a putative alpha/beta hydrolase from2 nostoc sp pcc 7120.
40	c3oosA_	Alignment	not modelled	100.0	15 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
41	c5egnB_	Alignment	not modelled	100.0	24 PDB header: hydrolase Chain: B: PDB Molecule: esterase; PDBTitle: est816 as an n-acyl homoserine lactone degrading enzyme
42	c4i3fA_	Alignment	not modelled	100.0	14 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
43	d1ehya_	Alignment	not modelled	100.0	25 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
44	d1brta_	Alignment	not modelled	100.0	21 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
45	c5cw2C_	Alignment	not modelled	100.0	25 PDB header: hydrolase Chain: C: PDB Molecule: putative epoxide hydrolase epha; PDBTitle: crystal structure of epoxide hydrolase a from mycobacterium2 thermoresistibile
46	c2vf2A_	Alignment	not modelled	100.0	15 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
47	c4ql0A_	Alignment	not modelled	100.0	13 PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: crystal structure of homoserine o-acetyltransferase from2 staphylococcus aureus
48	c4f0jA_	Alignment	not modelled	100.0	22 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
49	d1mtza_	Alignment	not modelled	100.0	14 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Proline iminopeptidase-like
50	c4rncB_	Alignment	not modelled	100.0	18 PDB header: hydrolase Chain: B: PDB Molecule: esterase; PDBTitle: crystal structure of an esterase rhest1 from rhodococcus sp. ecu1013
51	c2r11D_	Alignment	not modelled	100.0	20 PDB header: hydrolase Chain: D: PDB Molecule: carboxylesterase np; PDBTitle: crystal structure of putative hydrolase (2632844) from bacillus2 subtilis at 1.96 a resolution
52	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
53	d1a8qa_	Alignment	not modelled	100.0	19 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
54	c5w15D_	Alignment	not modelled	100.0	22 PDB header: hydrolase Chain: D: PDB Molecule: alpha/beta hydrolase fold protein;

54	c3w13D	Alignment	not modelled	100.0	22	PDBTitle: crystal structure of an alpha/beta hydrolase fold protein from2 burkholderia ambifaria. PDB header: transferase
55	c3i1iA	Alignment	not modelled	100.0	15	Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: x-ray crystal structure of homoserine o-acetyltransferase from2 bacillus anthracis
56	c3r3xA	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: fluoroacetate dehalogenase; PDBTitle: crystal structure of the fluoroacetate dehalogenase rpa1163 -2 asp110asn/bromoacetate
57	c6f9oA	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of cold-adapted haloalkane dehalogenase dpca from2 psychrobacter cryohalolentis k5
58	c4ns4A	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase fold protein; PDBTitle: crystal structure of cold-active esterase from psychrobacter2 cryohalolentis k5t
59	c1u2eA	Alignment	not modelled	100.0	14	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
60	c4q3C	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
61	d1va4a	Alignment	not modelled	100.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
62	d2rhwa1	Alignment	not modelled	100.0	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase
63	c4mj3B	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: B: PDB Molecule: haloalkane dehalogenase; PDBTitle: haloalkane dehalogenase dmra from mycobacterium rhodesiae js60
64	c4lxgA	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: mcp hydrolase; PDBTitle: crystal structure of dxnb2, a carbon - carbon bond hydrolase from2 sphingomonas wittichii rw1
65	c2wj4B	Alignment	not modelled	100.0	20	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
66	c2vavL	Alignment	not modelled	100.0	16	PDB header: transferase Chain: L: PDB Molecule: acetyl-coa--deacetylcephalosporin c acetyltransferase; PDBTitle: crystal structure of deacetylcephalosporin c acetyltransferase (dac-2 soak)
67	d2b61a1	Alignment	not modelled	100.0	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
68	c4inzB	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: B: PDB Molecule: soluble epoxide hydrolase; PDBTitle: the crystal structure of m145a mutant of an epoxide hydrolase from2 bacillus megaterium
69	c4q1aB	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: B: PDB Molecule: juvenile hormone epoxide hydrolase; PDBTitle: crystal structure of juvenile hormone epoxide hydrolase from the2 silkworm bombyx mori
70	c5bovD	Alignment	not modelled	100.0	20	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
71	d1a8sa	Alignment	not modelled	100.0	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
72	c4q1aA	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
73	c3qitB	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: polyketide synthase; PDBTitle: thioesterase domain from curacin biosynthetic pathway
74	c4uhhA	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: structural studies of a thermophilic esterase from2 thermogutta terrifontis (cacodylate complex)
75	c5d6oB	Alignment	not modelled	100.0	12	PDB header: transferase Chain: B: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: orthorhombic crystal structure of an acetyler hydrolase from2 corynebacterium glutamicum
76	c410cA	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: deformylase; PDBTitle: crystal structure of the n-fopmylmaaleamic acid deformylase nfo(s94a)2 from pseudomonas putida s16
77	c3ibtA	Alignment	not modelled	100.0	15	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)
78	c2xuaH	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: H: PDB Molecule: 3-oxoadipate enol-lactonase; PDBTitle: crystal structure of the enol-lactonase from burkholderia2 xenovorans lb400

79	d1uk8a_	Alignment	not modelled	100.0	22	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase
80	c3bwxA_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase; PDBTitle: crystal structure of an alpha/beta hydrolase (yp_496220.1) from <i>Novosphingobium aromaticivorans</i> DSM 12444 at 1.50 Å resolution
81	c5w8pA_	Alignment	not modelled	100.0	21	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: homoserine transacetylase meta from <i>Mycobacterium abscessus</i>
82	c3nwoA_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: proline iminopeptidase; PDBTitle: crystal structure of proline iminopeptidase <i>Mycobacterium smegmatis</i>
83	c2qmqa_	Alignment	not modelled	100.0	12	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 <i>Mus musculus</i> at 1.70 Å resolution
84	c4ccyA_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: carboxylesterase ybfk; PDBTitle: crystal structure of carboxylesterase cesb (ybfk) from <i>Bacillus subtilis</i>
85	d2vata1	Alignment	not modelled	100.0	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
86	c5efzC_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: C: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: monoclinic structure of the acetyl esterase mekb
87	c3fobA_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: bromoperoxidase; PDBTitle: crystal structure of bromoperoxidase from <i>Bacillus anthracis</i>
88	d1hkha_	Alignment	not modelled	100.0	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
89	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 involved in the carbazole degradation (carc enzyme)
90	d1j1ia_	Alignment	not modelled	100.0	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase
91	c5jkjA_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: esterase e22; PDBTitle: crystal structure of esterase e22 I374d mutant
92	c5f4zB_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: epoxide hydrolase; PDBTitle: the crystal structure of an epoxide hydrolase from <i>Streptomyces2 carzinostaticus</i> subsp. <i>neocarzinostaticus</i>
93	c4oseA_	Alignment	not modelled	100.0	11	PDB header: hydrolase Chain: A: PDB Molecule: putative hydrolase; PDBTitle: x-ray crystal structure of a putative hydrolase from <i>Rickettsia typhi</i>
94	d1mj5a_	Alignment	not modelled	100.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloalkane dehalogenase
95	c2y6vB_	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: B: PDB Molecule: peroxisomal membrane protein lpx1; PDBTitle: peroxisomal alpha-beta-hydrolase lpx1 (yor084w) from <i>Saccharomyces2 cerevisiae</i> (crystal form I)
96	c3e3aA_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: possible peroxidase bpoc; PDBTitle: the structure of rv0554 from <i>Mycobacterium tuberculosis</i>
97	c3wz1B_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: B: PDB Molecule: zearalenone hydrolase; PDBTitle: zen lactonase
98	c2yysA_	Alignment	not modelled	100.0	22	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 <i>Thermus thermophilus</i> hb8
99	c5xo6F_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: F: PDB Molecule: lactonase for protein; PDBTitle: crystal structure of a novel zen lactonase mutant
100	c3fsgC_	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: C: PDB Molecule: alpha/beta superfamily hydrolase; PDBTitle: crystal structure of alpha/beta superfamily hydrolase from <i>Oenococcus2 oeni</i> psu-1
101	c2pseA_	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: renilla-luciferin 2-monooxygenase; PDBTitle: crystal structures of the luciferase and green fluorescent2 protein from <i>Renilla reniformis</i>
102	c4i19A_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: the crystal structure of an epoxide hydrolase from <i>Streptomyces2 carzinostaticus</i> subsp. <i>neocarzinostaticus</i> .
103	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 <i>Mycobacterium2 tuberculosis</i>
104	c3vvlA_	Alignment	not modelled	100.0	18	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

105	c2ockA_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: valacyclovir hydrolase; PDBTitle: crystal structure of valacyclovir hydrolase d123n mutant
106	c4g9gA_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase fold protein; PDBTitle: crystal structures of n-acyl homoserine lactonase aidh e219g mutant
107	c3jw8A_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: mgll protein; PDBTitle: crystal structure of human mono-glyceride lipase
108	c6g75B_	Alignment	not modelled	100.0	19	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 (anchIId-rluc)
109	d1hlga_	Alignment	not modelled	100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Gastric lipase
110	c3v48B_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: B: PDB Molecule: putative aminoacrylate hydrolase rutt; PDBTitle: crystal structure of the putative alpha/beta hydrolase rutt from2 e.coli
111	c4rpcA_	Alignment	not modelled	100.0	16	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
112	d2pl5a1	Alignment	not modelled	100.0	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
113	c3r0vA_	Alignment	not modelled	100.0	14	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.
114	c3p2mA_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: possible hydrolase; PDBTitle: crystal structure of a novel esterase rv0045c from mycobacterium2 tuberculosis
115	d1qo7a_	Alignment	not modelled	100.0	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
116	c4c6hA_	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase; PDBTitle: haloalkane dehalogenase with 1-hexanol
117	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
118	d1k8qa_	Alignment	not modelled	100.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Gastric lipase
119	c6ra2E_	Alignment	not modelled	100.0	17	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
120	c5frdA_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: carboxylesterase (est-2); PDBTitle: structure of a thermophilic esterase