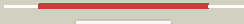

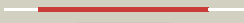










Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2928_(tesA)_3242208_3242993
Date	Thu Aug 8 16:20:08 BST 2019
Unique Job ID	fd1505b89929f560

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3flaB_	 Alignment		100.0	27	PDB header: hydrolase Chain: B: PDB Molecule: rifr; PDBTitle: rifr - type ii thioesterase from rifamycin nrps/pks biosynthetic2 pathway - form 1
2	c6fvjB_	 Alignment		100.0	99	PDB header: hydrolase Chain: B: PDB Molecule: thioesterase; PDBTitle: tesa a major thioesterase from mycobacterium tuberculosis
3	c6ba8A_	 Alignment		100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: iron aquisition yersiniabactin synthesis enzyme, ybtt; PDBTitle: ybtt - type ii thioesterase from yersiniabactin nrps/pks biosynthetic2 pathway
4	c3qmwD_	 Alignment		100.0	26	PDB header: hydrolase Chain: D: PDB Molecule: thioesterase; PDBTitle: redj with peg molecule bound in the active site
5	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
6	c3i28A_	 Alignment		100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase 2; PDBTitle: crystal structure of soluble epoxide hydrolase
7	c5ugzA_	 Alignment		100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: putative thioesterase; PDBTitle: crystal structure of clbq from the colibactin nrps/pks pathway
8	c2y6vB_	 Alignment		100.0	11	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	c5w8pA_	 Alignment		100.0	14	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: homoserine transacetylase meta from mycobacterium abscessus
10	c4d9jl_	 Alignment		100.0	11	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
11	c2ronA_	 Alignment		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: surfactin synthetase thioesterase subunit; PDBTitle: the external thioesterase of the surfactin-synthetase

12	c2qmqa_	Alignment		100.0	14	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
13	c2vavL_	Alignment		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)
14	d2b61a1	Alignment		100.0	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
15	c5d6oB_	Alignment		100.0	13	PDB header: transferase Chain: B: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: orthorhombic crystal structure of an acetyler hydrolase from2 corynebacterium glutamicum
16	c3i1iA_	Alignment		100.0	10	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: x-ray crystal structure of homoserine o-acetyltransferase from2 bacillus anthracis
17	c3om8A_	Alignment		100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: probable hydrolase; PDBTitle: the crystal structure of a hydrolase from pseudomonas aeruginosa pa01
18	c2h7xA_	Alignment		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: type i polyketide synthase pikaiv; PDBTitle: pikromycin thioesterase adduct with reduced triketide2 affinity label
19	c2r11D_	Alignment		100.0	12	PDB header: hydrolase Chain: D: PDB Molecule: carboxylesterase np; PDBTitle: crystal structure of putative hydrolase (2632844) from bacillus2 subtilis at 1.96 a resolution
20	c4qlaB_	Alignment		100.0	10	PDB header: hydrolase Chain: B: PDB Molecule: juvenile hormone epoxide hydrolase; PDBTitle: crystal structure of juvenile hormone epoxide hydrolase from the2 silkworm bombyx mori
21	c4qlaA_	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: A: PDB Molecule: juvenile hormone epoxide hydrolase; PDBTitle: crystal structure of juvenile hormone epoxide hydrolase from the2 silkworm bombyx mori
22	c3vv1A_	Alignment	not modelled	100.0	13	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
23	c4qloA_	Alignment	not modelled	100.0	12	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: crystal structure of homoserine o-acetyltransferase from2 staphylococcus aureus
24	c2xuaH_	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: H: PDB Molecule: 3-oxoadipate enol-lactonase; PDBTitle: crystal structure of the enol-lactonase from burkholderia2 xenovorans lb400
25	d2vata1	Alignment	not modelled	100.0	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
26	c3v48B_	Alignment	not modelled	100.0	11	PDB header: hydrolase Chain: B: PDB Molecule: putative aminoacrylate hydrolase rutd; PDBTitle: crystal structure of the putative alpha/beta hydrolase rutd from2 e.coli
27	c5esrA_	Alignment	not modelled	100.0	11	PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of haloalkane dehalogenase (dccca) from caulobacter2 crescentus
28	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 streptomycetes2 carzinostaticus subsp. neocarzinostaticus
						PDB header: hydrolase

29	c3lcrA_	Alignment	not modelled	100.0	16	Chain: A: PDB Molecule: tautomycetin biosynthetic pks; PDBTitle: thioesterase from tautomycetin biosynthetic pathway
30	c5lkiA_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: esterase e22; PDBTitle: crystal structure of esterase e22 I374d mutant
31	d2h7xa1	Alignment	not modelled	100.0	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
32	c4i19A_	Alignment	not modelled	100.0	11	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: the crystal structure of an epoxide hydrolase from streptomyces2 carzinostaticus subsp. neocarzinostaticus.
33	c5uroA_	Alignment	not modelled	100.0	11	PDB header: hydrolase Chain: A: PDB Molecule: predicted protein; PDBTitle: structure of a soluble epoxide hydrolase identified in trichoderma2 reesei
34	c5efzC_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: C: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: monoclinic structure of the acetyl esterase mekb
35	c4l0cA_	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: deformylase; PDBTitle: crystal structure of the n-fopmylmaaleamic acid deformylase nfo(s94a)2 from pseudomonas putida s16
36	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
37	d1xkta_	Alignment	not modelled	100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
38	c6brtB_	Alignment	not modelled	100.0	8	PDB header: ligase Chain: B: PDB Molecule: d3-cth-d14-d-ring; PDBTitle: f-box protein cth with hydrolase
39	d2pl5a1	Alignment	not modelled	100.0	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
40	c3l80A_	Alignment	not modelled	100.0	11	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein smu.1393c; PDBTitle: crystal structure of smu.1393c from streptococcus mutans ua159
41	c2e3jA_	Alignment	not modelled	100.0	14	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
42	c4rpcA_	Alignment	not modelled	100.0	11	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
43	d1mo2a_	Alignment	not modelled	100.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
44	c1mo2A_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: erythronolide synthase, modules 5 and 6; PDBTitle: thioesterase domain from 6-deoxyerythronolide synthase (debs te), ph2 8.5
45	c4pw0A_	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase fold protein; PDBTitle: alpha/beta hydrolase fold protein from chitinophaga pinensis
46	c1y37A_	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: A: PDB Molecule: fluoroacetate dehalogenase; PDBTitle: structure of fluoroacetate dehalogenase from burkholderia sp. fa1
47	d1b6ga_	Alignment	not modelled	100.0	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloalkane dehalogenase
48	c2cjpA_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: structure of potato (solanum tuberosum) epoxide hydrolase i (steh1)
49	c5xmdA_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase a; PDBTitle: crystal structure of epoxide hydrolase vreh1 from vigna radiata
50	c3oosA_	Alignment	not modelled	100.0	12	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
51	c3ibtA_	Alignment	not modelled	100.0	12	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)
52	c2wj4B_	Alignment	not modelled	100.0	11	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
53	d1e89a_	Alignment	not modelled	100.0	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hydroxynitrile lyase-like
						PDB header: hydrolase

54	c4opmB_	Alignment	not modelled	100.0	11	Chain: B; PDB Molecule: lipase; PDBTitle: crystal structure of a putative lipase (lip1) from acinetobacter2 baumannii aye at 1.70 a resolution
55	d1qo7a_	Alignment	not modelled	100.0	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
56	c3kdaB_	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: B; PDB Molecule: cftr inhibitory factor (cif); PDBTitle: crystal structure of the cftr inhibitory factor cif with the h269a2 mutation
57	c6ecfB_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: B; PDB Molecule: vlm2; PDBTitle: vlm2 thioesterase domain with genetically encoded 2,3-diaminopropionic2 acid bound with a dodecadesipeptide, space group p1
58	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
59	c5dnvA_	Alignment	not modelled	100.0	7	PDB header: hydrolase Chain: A; PDB Molecule: shkai2ib; PDBTitle: crystal structure of kai2-like protein from striga (apo state 2)
60	d3c70a1	Alignment	not modelled	100.0	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hydroxynitrile lyase-like
61	c3e0xB_	Alignment	not modelled	100.0	14	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: lipase-esterase related protein; PDBTitle: the crystal structure of a lipase-esterase related protein2 from clostridium acetobutylicum atcc 824
62	c4uhhA_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A; PDB Molecule: esterase; PDBTitle: structural studies of a thermophilic esterase from2 thermogutta terrifontis (cacodylate complex)
63	c4f0jA_	Alignment	not modelled	100.0	16	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
64	c5egnB_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: B; PDB Molecule: esterase; PDBTitle: est816 as an n-acyl homoserine lactone degrading enzyme
65	c3a2nF_	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: F; PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of dbja (wild type type ii p21)
66	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 oenococcus2 oeni psu-1
67	c3dqzB_	Alignment	not modelled	100.0	10	PDB header: lyase Chain: B; PDB Molecule: alpha-hydroxynitrile lyase-like protein; PDBTitle: structure of the hydroxynitrile lyase from arabidopsis thaliana
68	c5yhpB_	Alignment	not modelled	100.0	11	PDB header: hydrolase Chain: B; PDB Molecule: cold active proline iminopeptidase; PDBTitle: proline iminopeptidase from psychrophilic yeast glaciozyma antarctica
69	c4oseA_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A; PDB Molecule: putative hydrolase; PDBTitle: x-ray crystal structure of a putative hydrolase from rickettsia typhi
70	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)
71	c3wwoA_	Alignment	not modelled	100.0	11	PDB header: lyase Chain: A; PDB Molecule: (s)-hydroxynitrile lyase; PDBTitle: s-selective hydroxynitrile lyase from baliospermum montanum (apo1)
72	c3wzIB_	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: B; PDB Molecule: zearealenone hydrolase; PDBTitle: zen lactonase
73	d1xkla_	Alignment	not modelled	100.0	10	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hydroxynitrile lyase-like
74	c3wibB_	Alignment	not modelled	100.0	9	PDB header: hydrolase Chain: B; PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of y109w mutant haloalkane dehalogenase data from2 agrobacterium tumefaciens c58
75	d1mj5a_	Alignment	not modelled	100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloalkane dehalogenase
76	d1m33a_	Alignment	not modelled	100.0	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Biotin biosynthesis protein BioH
77	c4nvrC_	Alignment	not modelled	100.0	11	PDB header: transferase Chain: C; PDB Molecule: putative acyltransferase; PDBTitle: 2.22 angstrom resolution crystal structure of a putative2 acyltransferase from salmonella enterica
78	d1mtza_	Alignment	not modelled	100.0	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Proline iminopeptidase-like
79	c3stxB_	Alignment	not modelled	100.0	7	PDB header: hydrolase Chain: B; PDB Molecule: methylketone synthase 1; PDBTitle: crystal structure of tomato methylketone synthase i h243a variant2 complexed with beta-ketoheptanoate

80	c4q3IC	Alignment	not modelled	100.0	11	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
81	c5mxbB	Alignment	not modelled	100.0	11	PDB header: hydrolase Chain: B: PDB Molecule: alpha/beta hydrolase; PDBTitle: haloalkane dehalogenase dmxa from marinobacter sp. elb17 possessing a2 unique catalytic residue
82	c3kxpD	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: D: PDB Molecule: alpha-(n-acetylaminomethylene)succinic acid hydrolase; PDBTitle: crystal structure of e-2-(acetamidomethylene)succinate hydrolase
83	c4dngA	Alignment	not modelled	100.0	9	PDB header: hydrolase Chain: A: PDB Molecule: dad2; PDBTitle: crystal structure of dad2 s96a mutant
84	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
85	c3w06A	Alignment	not modelled	100.0	9	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase, alpha/beta fold family protein; PDBTitle: crystal structure of arabidopsis thaliana dwarf14 like (atd14l)
86	c5xo6F	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: F: PDB Molecule: lactonase for protein; PDBTitle: crystal structure of a novel zen lactonase mutant
87	c4psuA	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase; PDBTitle: crystal structure of alpha/beta hydrolase from rhodospseudomonas2 palustris cga009
88	d1hlga	Alignment	not modelled	100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Gastric lipase
89	c5w15D	Alignment	not modelled	100.0	11	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.
90	c3u1tA	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: dmma haloalkane dehalogenase; PDBTitle: haloalkane dehalogenase, dmma, of marine microbial origin
91	c2yysA	Alignment	not modelled	100.0	13	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
92	c2xt0A	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase; PDBTitle: dehalogenase dpca from plesiocystis pacifica sir-i
93	c6f9oA	Alignment	not modelled	100.0	11	PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of cold-adapted haloalkane dehalogenase dpca from2 psychrobacter cryohalolentis k5
94	d1zd3a2	Alignment	not modelled	100.0	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
95	c3gzjB	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: B: PDB Molecule: polyneuridine-aldehyde esterase; PDBTitle: crystal structure of polyneuridine aldehyde esterase complexed with2 16-epi-vellosimine
96	c2px6A	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: thioesterase domain; PDBTitle: crystal structure of the thioesterase domain of human fatty2 acid synthase inhibited by orlistat
97	c4y7dA	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 nakamurella multipartita
98	c5y51F	Alignment	not modelled	100.0	11	PDB header: hydrolase Chain: F: PDB Molecule: pyrethroid hydrolase; PDBTitle: crystal structure of pyth_h230a
99	d1ehya	Alignment	not modelled	100.0	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
100	c3bf7B	Alignment	not modelled	100.0	10	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
101	c5cbkA	Alignment	not modelled	100.0	10	PDB header: signaling protein Chain: A: PDB Molecule: shhtl5; PDBTitle: crystal structure of the strigolactone receptor shhtl5 from striga2 hermonthica
102	d1k8qa	Alignment	not modelled	100.0	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Gastric lipase
103	c4zwnD	Alignment	not modelled	100.0	11	PDB header: hydrolase Chain: D: PDB Molecule: monoglyceride lipase; PDBTitle: crystal structure of a soluble variant of the monoglyceride lipase2 from saccharomyces cerevisiae
104	c5hdfB	Alignment	not modelled	100.0	10	PDB header: hydrolase Chain: B: PDB Molecule: hydrolase; PDBTitle: hydrolase semet-stna
105	c4b9aA	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: probable epoxide hydrolase; PDBTitle: structure of a putative epoxide hydrolase from

					pseudomonas2 aeruginosa.
106	d1c4xa_	Alignment	not modelled	100.0	11 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase
107	c5ng7B_	Alignment	not modelled	100.0	15 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
108	c3ilsA_	Alignment	not modelled	100.0	18 PDB header: hydrolase Chain: A: PDB Molecule: afatoxin biosynthesis polyketide synthase; PDBTitle: the thioesterase domain from pksa
109	c5bovD_	Alignment	not modelled	100.0	12 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
110	d1cr6a2	Alignment	not modelled	100.0	13 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
111	c2xmzA_	Alignment	not modelled	100.0	12 PDB header: lyase Chain: A: PDB Molecule: hydrolase, alpha/beta hydrolase fold family; PDBTitle: structure of menh from s. aureus
112	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
113	c4mj3B_	Alignment	not modelled	100.0	12 PDB header: hydrolase Chain: B: PDB Molecule: haloalkane dehalogenase; PDBTitle: haloalkane dehalogenase dmra from mycobacterium rhodesiae js60
114	c3bwxA_	Alignment	not modelled	100.0	14 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
115	d1bn7a_	Alignment	not modelled	100.0	10 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloalkane dehalogenase
116	c4ccyA_	Alignment	not modelled	100.0	10 PDB header: hydrolase Chain: A: PDB Molecule: carboxylesterase ybfk; PDBTitle: crystal structure of carboxylesterase cesb (ybfk) from bacillus2 subtilis
117	c6ra2E_	Alignment	not modelled	100.0	11 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
118	c3r3xA_	Alignment	not modelled	100.0	15 PDB header: hydrolase Chain: A: PDB Molecule: fluoroacetate dehalogenase; PDBTitle: crystal structure of the fluoroacetate dehalogenase rpa1163 -2 asp110asn/bromoacetate
119	c3jw8A_	Alignment	not modelled	100.0	13 PDB header: hydrolase Chain: A: PDB Molecule: mgll protein; PDBTitle: crystal structure of human mono-glyceride lipase
120	c6azdA_	Alignment	not modelled	100.0	11 PDB header: hydrolase Chain: A: PDB Molecule: ppkai2-like h; PDBTitle: crystal structure of physcomitrella patens kai2-like h