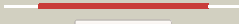



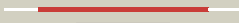



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3341_(metX)_3727659_3728798
Date	Thu Aug 8 16:20:55 BST 2019
Unique Job ID	5a2c125409806c5b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5w8pA_	 Alignment		100.0	77	PDB header: transferase Chain: A; PDB Molecule: homoserine o-acetyltransferase; PDBTitle: homoserine transacetylase meta from mycobacterium abscessus
2	c3i1iA_	 Alignment		100.0	20	PDB header: transferase Chain: A; PDB Molecule: homoserine o-acetyltransferase; PDBTitle: x-ray crystal structure of homoserine o-acetyltransferase from2 bacillus anthracis
3	c5ijkA_	 Alignment		100.0	23	PDB header: hydrolase Chain: A; PDB Molecule: esterase e22; PDBTitle: crystal structure of esterase e22 I374d mutant
4	d2pl5a1	 Alignment		100.0	36	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
5	d2b61a1	 Alignment		100.0	37	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
6	c3vvlA_	 Alignment		100.0	35	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
7	c2vavL_	 Alignment		100.0	34	PDB header: transferase Chain: L; PDB Molecule: acetyl-coa--deacetylcephalosporin c acetyltransferase; PDBTitle: crystal structure of deacetylcephalosporin c acetyltransferase (dac-2 soak)
8	d2vata1	 Alignment		100.0	34	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
9	c4qloA_	 Alignment		100.0	29	PDB header: transferase Chain: A; PDB Molecule: homoserine o-acetyltransferase; PDBTitle: crystal structure of homoserine o-acetyltransferase from2 staphylococcus aureus
10	c5d6oB_	 Alignment		100.0	26	PDB header: transferase Chain: B; PDB Molecule: homoserine o-acetyltransferase; PDBTitle: orthorhombic crystal structure of an acetylerster hydrolase from2 corynebacterium glutamicum
11	c5efzC_	 Alignment		100.0	24	PDB header: hydrolase Chain: C; PDB Molecule: homoserine o-acetyltransferase; PDBTitle: monoclinic structure of the acetyl esterase mekb

12	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
13	c3i28A_	Alignment		100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase 2; PDBTitle: crystal structure of soluble epoxide hydrolase
14	c4d9jl_	Alignment		100.0	17	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
15	c4qlaA_	Alignment		100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: juvenile hormone epoxide hydrolase; PDBTitle: crystal structure of juvenile hormone epoxide hydrolase from the2 silkworm bombyx mori
16	c5f4zB_	Alignment		100.0	15	PDB header: hydrolase Chain: B: PDB Molecule: epoxide hydrolase; PDBTitle: the crystal structure of an epoxide hydrolase from streptomycetes2 carzinostaticus subsp. neocarzinostaticus
17	d1k8qa_	Alignment		100.0	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Gastric lipase
18	c4i19A_	Alignment		100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: the crystal structure of juvenile epoxide hydrolase from streptomycetes2 carzinostaticus subsp. neocarzinostaticus.
19	c4qlaB_	Alignment		100.0	16	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	c5yhpB_	Alignment		100.0	14	PDB header: hydrolase Chain: B: PDB Molecule: cold active proline iminopeptidase; PDBTitle: proline iminopeptidase from psychrophilic yeast glaciozyma antarctica
21	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)
22	c2qmqA_	Alignment	not modelled	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
23	d1hlga_	Alignment	not modelled	100.0	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Gastric lipase
24	c5esrA_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of haloalkane dehalogenase (dcca) from caulobacter2 crescentus
25	c2e3jA_	Alignment	not modelled	100.0	16	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
26	d1azwa_	Alignment	not modelled	100.0	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Proline iminopeptidase-like
27	c3oosA_	Alignment	not modelled	100.0	17	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
28	d1b6ga_	Alignment	not modelled	100.0	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloalkane dehalogenase

29	c4pw0A_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase fold protein; PDBTitle: alpha/beta hydrolase fold protein from chitinophaga pinensis
30	d1wm1a_	Alignment	not modelled	100.0	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Proline iminopeptidase-like
31	d1cr6a2	Alignment	not modelled	100.0	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
32	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
33	d1zd3a2	Alignment	not modelled	100.0	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
34	c2xt0A_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase; PDBTitle: dehalogenase dppa from pliesicystis pacifica sir-i
35	c5xmdA_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase a; PDBTitle: crystal structure of epoxide hydrolase vreh1 from vigna radiata
36	c5uroA_	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: A: PDB Molecule: predicted protein; PDBTitle: structure of a soluble epoxide hydrolase identified in trichoderma2 reesei
37	c4f0jA_	Alignment	not modelled	100.0	14	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
38	d1qo7a_	Alignment	not modelled	100.0	10	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
39	c2r11D_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: D: PDB Molecule: carboxylesterase np; PDBTitle: crystal structure of putative hydrolase (2632844) from bacillus2 subtilis at 1.96 a resolution
40	c2xuaH_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: H: PDB Molecule: 3-oxoadipate enol-lactonase; PDBTitle: crystal structure of the enol-lactonase from burkholderia2 xenovorans lb400
41	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
42	c3v48B_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: putative aminoacrylate hydrolase rutt; PDBTitle: crystal structure of the putative alpha/beta hydrolase rutt from2 e.coli
43	d1mtza_	Alignment	not modelled	100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Proline iminopeptidase-like
44	c2cjpA_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: structure of potato (solanum tuberosum) epoxide hydrolase i (steh1)
45	c4nvrC_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: C: PDB Molecule: putative acyltransferase; PDBTitle: 2.22 angstrom resolution crystal structure of a putative2 acyltransferase from salmonella enterica
46	c4oseA_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: putative hydrolase; PDBTitle: x-ray crystal structure of a putative hydrolase from rickettsia typhi
47	c3qvmA_	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: olei00960; PDBTitle: the structure of olei00960, a hydrolase from oleispira antarctica
48	c5nfqA_	Alignment	not modelled	100.0	15	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
49	c1y37A_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: fluoroacetate dehalogenase; PDBTitle: structure of fluoroacetate dehalogenase from burkholderia sp. fa1
50	c3u1tA_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: dmma haloalkane dehalogenase; PDBTitle: haloalkane dehalogenase, dmma, of marine microbial origin
51	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 from2 agrobacterium tumefaciens c58
52	c6brtB_	Alignment	not modelled	100.0	18	PDB header: ligase Chain: B: PDB Molecule: d3-cth-d14-d-ring; PDBTitle: f-box protein cth with hydrolase
53	c6f9oA_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of cold-adapted haloalkane dehalogenase dpca from2 psychrobacter cryohalolentis k5
54	d1q0ra_	Alignment	not modelled	100.0	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Aclacinomycin methylesterase RdmC

55	c4mj3B	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: haloalkane dehalogenase; PDBTitle: haloalkane dehalogenase dmra from mycobacterium rhodesiae js60
56	c3fsgC	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: C: PDB Molecule: alpha/beta superfamily hydrolase; PDBTitle: crystal structure of alpha/beta superfamily hydrolase from oenococcus2 oeni psu-1
57	c4y7dA	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase fold protein; PDBTitle: alpha/beta hydrolase fold protein from nakamurella multipartita
58	c4l0cA	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: A: PDB Molecule: deformylase; PDBTitle: crystal structure of the n-fopmylmaeamic acid deformylase nfo(s94a)2 from pseudomonas putida s16
59	c4opmB	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: B: PDB Molecule: lipase; PDBTitle: crystal structure of a putative lipase (lip1) from acinetobacter2 baumannii aye at 1.70 a resolution
60	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
61	c5cw2C	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: C: PDB Molecule: putative epoxide hydrolase epha; PDBTitle: crystal structure of epoxide hydrolase a from mycobacterium2 thermoresistibile
62	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)
63	c2vysA	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
64	c5mxbB	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: B: PDB Molecule: alpha/beta hydrolase; PDBTitle: haloalkane dehalogenase dmxa from marinobacter sp. elb17 possessing a2 unique catalytic residue
65	c3ibtA	Alignment	not modelled	100.0	14	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)
66	c4b9aA	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: probable epoxide hydrolase; PDBTitle: structure of a putative epoxide hydrolase from pseudomonas2 aeruginosa.
67	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
68	c5egnB	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: B: PDB Molecule: esterase; PDBTitle: est816 as an n-acyl homoserine lactone degrading enzyme
69	d1mj5a	Alignment	not modelled	100.0	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloalkane dehalogenase
70	c5bovD	Alignment	not modelled	100.0	14	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	c4uhhA	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: structural studies of a thermophilic esterase from2 thermogutta terrifontis (cacodylate complex)
72	d1c4xa	Alignment	not modelled	100.0	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase
73	c4psuA	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase; PDBTitle: crystal structure of alpha/beta hydrolase from rhodopseudomonas2 palustris cga009
74	c3kxpD	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: D: PDB Molecule: alpha-(n-acetylamino)methylene)succinic acid hydrolase; PDBTitle: crystal structure of e-2-(acetamidomethylene)succinate hydrolase
75	c3l80A	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein smu.1393c; PDBTitle: crystal structure of smu.1393c from streptococcus mutans ua159
76	c3r3xA	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: fluoroacetate dehalogenase; PDBTitle: crystal structure of the fluoroacetate dehalogenase rpa1163 -2 asp110asn/bromoacetate
77	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)
78	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

79	c4inzB	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: B: PDB Molecule: soluble epoxide hydrolase; PDBTitle: the crystal structure of m145a mutant of an epoxide hydrolase from2 bacillus megaterium
80	c4q3IC	Alignment	not modelled	100.0	17	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	c3e3aA	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: possible peroxidase bpoC; PDBTitle: the structure of rv0554 from mycobacterium tuberculosis
82	d1ehya	Alignment	not modelled	100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Epoxide hydrolase
83	c3bwxA	Alignment	not modelled	100.0	15	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
84	c3p2mA	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: possible hydrolase; PDBTitle: crystal structure of a novel esterase rv0045c from mycobacterium2 tuberculosis
85	c4i3fA	Alignment	not modelled	100.0	17	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
86	c4c6hA	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase; PDBTitle: haloalkane dehalogenase with 1-hexanol
87	c3nwoA	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: proline iminopeptidase; PDBTitle: crystal structure of proline iminopeptidase mycobacterium smegmatis
88	c3wzIB	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: B: PDB Molecule: zearealenone hydrolase; PDBTitle: zen lactonase
89	d2rhwa1	Alignment	not modelled	100.0	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase
90	c5w15D	Alignment	not modelled	100.0	18	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.
91	c5dnvA	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: shkai2ib; PDBTitle: crystal structure of kai2-like protein from striga (apo state 2)
92	d1uk8a	Alignment	not modelled	100.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carbon-carbon bond hydrolase
93	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
94	c3qyIB	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: B: PDB Molecule: alr0039 protein; PDBTitle: crystal structure of alr0039, a putative alpha/beta hydrolase from2 nostoc sp pcc 7120.
95	c2qvBA	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase 3; PDBTitle: crystal structure of haloalkane dehalogenase rv2579 from mycobacterium2 tuberculosis
96	c1u2eA	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: 2-hydroxy-6-ketona-2,4-dienedioic acid PDBTitle: crystal structure of the c-c bond hydrolase mhpc
97	c3e0xB	Alignment	not modelled	100.0	16	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
98	d1bn7a	Alignment	not modelled	100.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloalkane dehalogenase
99	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 renilla reniformis
100	d3c70a1	Alignment	not modelled	100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hydroxynitrile lyase-like
101	c2vf2A	Alignment	not modelled	100.0	18	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
102	c3flaB	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: B: PDB Molecule: rifr; PDBTitle: rifr - type ii thioesterase from rifamycin nrps/pks biosynthetic2 pathway - form 1
103	c5h3hB	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: B: PDB Molecule: abhydrolase domain-containing protein; PDBTitle: esterase (eaest) from exigubacterium antarcticum
104	c4dnqA	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: dad2; PDBTitle: crystal structure of dad2 s96a mutant

105	d1e89a_	Alignment	not modelled	100.0	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hydroxynitrile lyase-like
106	c3wwoA_	Alignment	not modelled	100.0	10	PDB header: lyase Chain: A: PDB Molecule: (s)-hydroxynitrile lyase; PDBTitle: s-selective hydroxynitrile lyase from baliospermum montanum (apo1)
107	c5a62A_	Alignment	not modelled	100.0	18	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 of 3 carboxylesterases linked to their metabolic function
108	d1a8qa_	Alignment	not modelled	100.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
109	d1brta_	Alignment	not modelled	100.0	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
110	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
111	d1xkla_	Alignment	not modelled	100.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hydroxynitrile lyase-like
112	c5cbkA_	Alignment	not modelled	100.0	16	PDB header: signaling protein Chain: A: PDB Molecule: shht15; PDBTitle: crystal structure of the strigolactone receptor shht15 from striga2 hermonthica
113	d1m33a_	Alignment	not modelled	100.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Biotin biosynthesis protein BioH
114	d1a88a_	Alignment	not modelled	100.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
115	c4lxgA_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: mcp hydrolase; PDBTitle: crystal structure of dxnb2, a carbon - carbon bond hydrolase from2 sphingomonas wittichii rw1
116	d1hkha_	Alignment	not modelled	100.0	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Haloperoxidase
117	c3fobA_	Alignment	not modelled	100.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: bromoperoxidase; PDBTitle: crystal structure of bromoperoxidase from bacillus anthracis
118	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
119	c3jw8A_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: mgll protein; PDBTitle: crystal structure of human mono-glyceride lipase
120	c3stxB_	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: B: PDB Molecule: methylketone synthase 1; PDBTitle: crystal structure of tomato methylketone synthase i h243a variant2 complexed with beta-ketoheptanoate