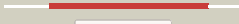



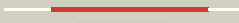



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3802c_(-)_4263533_4264543
Date	Fri Aug 9 18:20:51 BST 2019
Unique Job ID	4b42ed46e134820a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ajaA_	 Alignment		100.0	72	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of msmeg_6394
2	d1qoza_	 Alignment		100.0	23	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like
3	d1g66a_	 Alignment		100.0	23	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like
4	c2czqB_	 Alignment		100.0	22	PDB header: hydrolase Chain: B: PDB Molecule: cutinase-like protein; PDBTitle: a novel cutinase-like protein from cryptococcus sp.
5	c3dd5F_	 Alignment		100.0	23	PDB header: hydrolase Chain: F: PDB Molecule: cutinase; PDBTitle: glomerella cingulata e600-cutinase complex
6	d1cexa_	 Alignment		100.0	27	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like
7	c3gbsA_	 Alignment		100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: cutinase 1; PDBTitle: crystal structure of aspergillus oryzae cutinase
8	c5x88A_	 Alignment		100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: cutinase; PDBTitle: a crystal structure of cutinases from malbranchea cinnamomea
9	c4psdA_	 Alignment		100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: carbohydrate esterase family 5; PDBTitle: structure of trichoderma reesei cutinase native form.
10	c4oylC_	 Alignment		100.0	24	PDB header: hydrolase Chain: C: PDB Molecule: cutinase; PDBTitle: humicola insolens cutinase in complex with monoethylphosphate
11	c3hc7A_	 Alignment		100.0	19	PDB header: cell adhesion Chain: A: PDB Molecule: gene 12 protein; PDBTitle: crystal structure of lysin b from mycobacteriophage d29

12	d1tcaa_	Alignment		98.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
13	c5h6bA_	Alignment		97.5	20	PDB header: hydrolase Chain: A: PDB Molecule: putative secreted lipase; PDBTitle: crystal structure of a thermostable lipase from marine streptomyces
14	c3icvA_	Alignment		97.5	18	PDB header: hydrolase Chain: A: PDB Molecule: lipase b; PDBTitle: structural consequences of a circular permutation on lipase b from2 candida antartica
15	d2r8ba1	Alignment		97.3	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
16	c5t6oA_	Alignment		97.2	17	PDB header: biosynthetic protein Chain: A: PDB Molecule: poly-beta-hydroxybuterate polymerase; PDBTitle: structure of the catalytic domain of the class i polyhydroxybutyrate2 synthase from cupriavidus necator
17	c6cl4A_	Alignment		97.1	19	PDB header: hydrolase Chain: A: PDB Molecule: lipase c12; PDBTitle: lipc12 - lipase from metagenomics
18	c2rauA_	Alignment		97.1	19	PDB header: hydrolase Chain: A: PDB Molecule: putative esterase; PDBTitle: crystal structure of a putative lipase (np_343859.1) from sulfolobus2 solfataricus at 1.85 a resolution
19	c5xavB_	Alignment		97.0	13	PDB header: biosynthetic protein Chain: B: PDB Molecule: intracellular polyhydroxyalkanoate synthase; PDBTitle: structure of phac from chromobacterium sp. usm2
20	d1ex9a_	Alignment		97.0	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
21	c3lp5A_	Alignment	not modelled	97.0	14	PDB header: hydrolase Chain: A: PDB Molecule: putative cell surface hydrolase; PDBTitle: the crystal structure of the putative cell surface hydrolase from2 lactobacillus plantarum wcfs1
22	c2r8bA_	Alignment	not modelled	97.0	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atu2452; PDBTitle: the crystal structure of the protein atu2452 of unknown function from2 agrobacterium tumefaciens str. c58
23	c1qgeD_	Alignment	not modelled	96.9	25	PDB header: hydrolase Chain: D: PDB Molecule: protein (triacylglycerol hydrolase); PDBTitle: new crystal form of pseudomonas glumae (formerly chromobacterium2 viscosum atcc 6918) lipase
24	c3uuuA_	Alignment	not modelled	96.9	14	PDB header: hydrolase Chain: A: PDB Molecule: lip1, secretory lipase (family 3); PDBTitle: crystal structure of mono- and diacylglycerol lipase from malassezia2 globosa
25	c3ds8A_	Alignment	not modelled	96.9	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin2722 protein; PDBTitle: the crysatl structure of the gene lin2722 products from listeria2 innocua
26	c4h0cA_	Alignment	not modelled	96.9	14	PDB header: hydrolase Chain: A: PDB Molecule: phospholipase/carboxylesterase; PDBTitle: crystal structure of phospholipase/carboxylesterase from dyadobacter2 fermentans dsm 18053
27	d1ispa_	Alignment	not modelled	96.9	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
28	c5f2hA_	Alignment	not modelled	96.8	14	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: 2.75 angstrom resolution crystal structure of uncharacterized protein2 from bacillus cereus atcc 10987 PDB header: hydrolase

29	c3h2iA_	Alignment	not modelled	96.8	16	Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of n228w mutant of the rice cell wall2 degrading esterase lipa from xanthomonas oryzae
30	c4eziA_	Alignment	not modelled	96.8	17	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative hydrolase (lpg1103) from legionella2 pneumophila subsp. pneumophila str. philadelphia 1 at 1.15 a3 resolution
31	d1cvla_	Alignment	not modelled	96.7	22	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
32	d1ei9a_	Alignment	not modelled	96.7	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterases
33	c4gw3A_	Alignment	not modelled	96.6	21	PDB header: hydrolase Chain: A: PDB Molecule: putative lipase; PDBTitle: crystal structure of the lipase from proteus mirabilis
34	d4lipd_	Alignment	not modelled	96.5	22	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
35	c3og9A_	Alignment	not modelled	96.5	12	PDB header: hydrolase Chain: A: PDB Molecule: protein yahd a copper inducible hydrolase; PDBTitle: structure of yahd with malic acid
36	c2q0xA_	Alignment	not modelled	96.5	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: alpha/beta hydrolase fold protein of unknown function
37	d3tgla_	Alignment	not modelled	96.3	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
38	c2veoA_	Alignment	not modelled	96.2	17	PDB header: hydrolase Chain: A: PDB Molecule: lipase a; PDBTitle: x-ray structure of candida antarctica lipase a in its closed state.
39	c6e6uA_	Alignment	not modelled	96.1	13	PDB header: biosynthetic protein Chain: A: PDB Molecule: dieckmann cyclase, ncmc; PDBTitle: variant c89s of dieckmann cyclase, ncmc
40	d1etha2	Alignment	not modelled	96.1	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
41	d3b5ea1	Alignment	not modelled	96.0	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
42	d2h1ia1	Alignment	not modelled	96.0	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
43	c6qppA_	Alignment	not modelled	95.9	22	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: rhizomucor miehei lipase propeptide complex, native
44	c3g7nA_	Alignment	not modelled	95.9	9	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: crystal structure of a triacylglycerol lipase from penicillium2 expansum at 1.3
45	d1lppb2	Alignment	not modelled	95.8	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
46	d1gp1a2	Alignment	not modelled	95.8	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
47	d1bu8a2	Alignment	not modelled	95.7	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
48	c2y6vB_	Alignment	not modelled	95.7	16	PDB header: hydrolase Chain: B: PDB Molecule: peroxisomal membrane protein lpx1; PDBTitle: peroxisomal alpha-beta-hydrolase lpx1 (yor084w) from saccharomyces2 cerevisiae (crystal form i)
49	c5hdfB_	Alignment	not modelled	95.6	14	PDB header: hydrolase Chain: B: PDB Molecule: hydrolase; PDBTitle: hydrolase semet-stna
50	c5gw8A_	Alignment	not modelled	95.6	18	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical secretory lipase (family 3); PDBTitle: crystal structure of a putative dag-like lipase (mgmd12) from2 malassezia globosa
51	d1tiaa_	Alignment	not modelled	95.3	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
52	c2h1iA_	Alignment	not modelled	95.3	15	PDB header: hydrolase Chain: A: PDB Molecule: carboxylesterase; PDBTitle: crystal structure of the bacillus cereus carboxylesterase
53	c2qjwA_	Alignment	not modelled	95.1	16	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein xcc1541; PDBTitle: crystal structure of a putative hydrolase of the alpha/beta2 superfamily (xcc1541) from xanthomonas campestris pv. campestris at3 1.35 a resolution
54	c2zyiB_	Alignment	not modelled	95.1	13	PDB header: hydrolase Chain: B: PDB Molecule: lipase, putative; PDBTitle: a. fulgidus lipase with fatty acid fragment and calcium
55	d1mo2a_	Alignment	not modelled	95.1	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases

56	c1mo2A_	Alignment	not modelled	95.1	19	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
57	d1lgva_	Alignment	not modelled	95.0	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
58	d1tiba_	Alignment	not modelled	94.9	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
59	c3ngmB_	Alignment	not modelled	94.6	24	PDB header: hydrolase Chain: B: PDB Molecule: extracellular lipase; PDBTitle: crystal structure of lipase from gibberella zeae
60	c4qnnC_	Alignment	not modelled	94.6	16	PDB header: hydrolase Chain: C: PDB Molecule: phospholipase a 1 from hornet(vespa basalis) venom; PDBTitle: crystal structure of phospholipase a 1 from hornet(vespa basalis)2 venom
61	c3o0dF_	Alignment	not modelled	94.6	14	PDB header: hydrolase Chain: F: PDB Molecule: triacylglycerol lipase; PDBTitle: crystal structure of lip2 lipase from yarrowia lipolytica at 1.7 a2 resolution
62	d1rp1a2	Alignment	not modelled	94.4	22	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
63	d1hlga_	Alignment	not modelled	94.4	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Gastric lipase
64	d1hpla2	Alignment	not modelled	94.3	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
65	c5xk2A_	Alignment	not modelled	94.3	17	PDB header: hydrolase Chain: A: PDB Molecule: diacylglycerol lipase; PDBTitle: crystal structure of mono- and diacylglycerol lipase from aspergillus2 oryzae
66	d1uwca_	Alignment	not modelled	94.2	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
67	c2pvsB_	Alignment	not modelled	94.1	16	PDB header: hydrolase Chain: B: PDB Molecule: pancreatic lipase-related protein 2; PDBTitle: structure of human pancreatic lipase related protein 22 mutant n336q
68	d2h7xa1	Alignment	not modelled	94.0	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
69	c2oryA_	Alignment	not modelled	93.6	10	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: crystal structure of m37 lipase
70	c5d8mA_	Alignment	not modelled	93.4	14	PDB header: hydrolase Chain: A: PDB Molecule: metagenomic carboxyl esterase mgs0156; PDBTitle: crystal structure of the metagenomic carboxyl esterase mgs0156
71	c6gupB_	Alignment	not modelled	93.3	15	PDB header: hydrolase Chain: B: PDB Molecule: siderophore biosynthesis lipase/esterase, putative; PDBTitle: siderophore hydrolase estb from aspergillus fumigatus
72	d1jmkc_	Alignment	not modelled	93.1	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
73	c2h7xA_	Alignment	not modelled	93.0	19	PDB header: hydrolase Chain: A: PDB Molecule: type i polyketide synthase pikaiv; PDBTitle: pikromycin thioesterase adduct with reduced triketide2 affinity label
74	c1hplB_	Alignment	not modelled	93.0	16	PDB header: hydrolase(carboxylic esterase) Chain: B: PDB Molecule: lipase; PDBTitle: horse pancreatic lipase. the crystal structure at 2.3 angstroms2 resolution
75	d1k8qa_	Alignment	not modelled	93.0	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Gastric lipase
76	c3lcrA_	Alignment	not modelled	92.7	19	PDB header: hydrolase Chain: A: PDB Molecule: tautomycin biosynthetic pks; PDBTitle: thioesterase from tautomycin biosynthetic pathway
77	c3qmwD_	Alignment	not modelled	92.6	16	PDB header: hydrolase Chain: D: PDB Molecule: thioesterase; PDBTitle: redj with peg molecule bound in the active site
78	c1cr6A_	Alignment	not modelled	92.6	13	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
79	c2vavL_	Alignment	not modelled	92.5	15	PDB header: transferase Chain: L: PDB Molecule: acetyl-coa--deacetylcephalosporin c acetyltransferase; PDBTitle: crystal structure of deacetylcephalosporin c acetyltransferase (dac-2 soak)
80	c2jwbB_	Alignment	not modelled	92.5	15	PDB header: hydrolase Chain: B: PDB Molecule: 2,6-dihydroxy-pseudo-oxynicotine hydrolase; PDBTitle: crystal structure of the 2,6-dihydroxy-pseudo-oxynicotine hydrolase.
81	c2vsqA_	Alignment	not modelled	92.3	18	PDB header: ligase Chain: A: PDB Molecule: surfactin synthetase subunit 3; PDBTitle: structure of surfactin a synthetase c (srfa-c), a

						nonribosomal peptide2 synthetase termination module
82	d2jbwa1	Alignment	not modelled	92.2	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: 2,6-dihydropseudooxynicotine hydrolase-like
83	c6e7kB	Alignment	not modelled	92.1	24	PDB header: hydrolase Chain: B: PDB Molecule: lipoprotein lipase; PDBTitle: structure of the lipoprotein lipase gpibp1 complex that mediates2 plasma triglyceride hydrolysis
84	c3l80A	Alignment	not modelled	91.0	16	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein smu.1393c; PDBTitle: crystal structure of smu.1393c from streptococcus mutans ua159
85	c2vtvA	Alignment	not modelled	91.0	10	PDB header: hydrolase Chain: A: PDB Molecule: phb depolymerase phaz7; PDBTitle: phaz7 depolymerase from paucimonas lemoignei
86	c5ugzA	Alignment	not modelled	90.8	10	PDB header: hydrolase Chain: A: PDB Molecule: putative thioesterase; PDBTitle: crystal structure of clbq from the colibactin nrps/pks pathway
87	c3i28A	Alignment	not modelled	90.7	14	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase 2; PDBTitle: crystal structure of soluble epoxide hydrolase
88	c1gplA	Alignment	not modelled	90.7	17	PDB header: serine esterase Chain: A: PDB Molecule: rp2 lipase; PDBTitle: rp2 lipase
89	c2cbgA	Alignment	not modelled	90.7	19	PDB header: hydrolase Chain: A: PDB Molecule: fengycin synthetase; PDBTitle: crystal structure of the pmsf-inhibited thioesterase domain of the2 fengycin biosynthesis cluster
90	c4f21G	Alignment	not modelled	90.7	21	PDB header: hydrolase/hydrolase inhibitor Chain: G: PDB Molecule: carboxylesterase/phospholipase family protein; PDBTitle: crystal structure of carboxylesterase/phospholipase family protein2 from francisella tularensis
91	c1pjaA	Alignment	not modelled	90.6	17	PDB header: hydrolase Chain: A: PDB Molecule: palmitoyl-protein thioesterase 2 precursor; PDBTitle: the crystal structure of palmitoyl protein thioesterase-2 reveals the2 basis for divergent substrate specificities of the two lysosomal3 thioesterases (ppt1 and ppt2)
92	d1pjaa	Alignment	not modelled	90.6	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterases
93	d1uxoa	Alignment	not modelled	90.3	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: YdeN-like
94	c4zxiA	Alignment	not modelled	90.3	25	PDB header: biosynthetic protein Chain: A: PDB Molecule: tyrocidine synthetase 3; PDBTitle: crystal structure of holo-ab3403 a four domain nonribosomal peptide2 synthetase bound to amp and glycine
95	c4wfiA	Alignment	not modelled	90.1	16	PDB header: hydrolase Chain: A: PDB Molecule: cutinase; PDBTitle: crystal structure of pet-degrading cutinase cut190 s226p mutant in2 ca(2+)-free state
96	c3fleB	Alignment	not modelled	90.0	10	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: se_1780 protein; PDBTitle: se_1780 protein of unknown function from staphylococcus epidermidis.
97	c2o2gA	Alignment	not modelled	89.5	13	PDB header: hydrolase Chain: A: PDB Molecule: dienelactone hydrolase; PDBTitle: crystal structure of dienelactone hydrolase (yp_324580.1) from2 anabaena variabilis atcc 29413 at 1.92 a resolution
98	c3qvmA	Alignment	not modelled	89.3	16	PDB header: hydrolase Chain: A: PDB Molecule: olei00960; PDBTitle: the structure of olei00960, a hydrolase from oleispira antarctica
99	c2hu7A	Alignment	not modelled	89.1	15	PDB header: hydrolase Chain: A: PDB Molecule: acylamino-acid-releasing enzyme; PDBTitle: binding of inhibitors by acylaminoacyl peptidase
100	c5x6sB	Alignment	not modelled	88.8	16	PDB header: hydrolase Chain: B: PDB Molecule: acetylxylyan esterase a; PDBTitle: acetyl xylyan esterase from aspergillus awamori
101	c1rp1A	Alignment	not modelled	88.0	22	PDB header: hydrolase Chain: A: PDB Molecule: pancreatic lipase related protein 1; PDBTitle: dog pancreatic lipase related protein 1
102	c3flaB	Alignment	not modelled	87.4	20	PDB header: hydrolase Chain: B: PDB Molecule: rifr; PDBTitle: rifr - type ii thioesterase from rifamycin nrps/pks biosynthetic2 pathway - form 1
103	c2pplA	Alignment	not modelled	85.7	18	PDB header: hydrolase Chain: A: PDB Molecule: pancreatic lipase-related protein 1; PDBTitle: human pancreatic lipase-related protein 1
104	c4fleA	Alignment	not modelled	85.7	13	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of the esterase yqia (ye3661) from yersinia2 enterocolitica, northeast structural genomics consortium target yer85
105	c2hihB	Alignment	not modelled	85.6	19	PDB header: hydrolase Chain: B: PDB Molecule: lipase 46 kda form; PDBTitle: crystal structure of staphylococcus hyicus lipase
106	c2r11D	Alignment	not modelled	85.3	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
						PDB header: hydrolase

107	c3v48B_	Alignment	not modelled	85.1	16	Chain: B: PDB Molecule: putative aminoacrylate hydrolase rutd; PDBTitle: crystal structure of the putative alpha/beta hydrolase rutd from 2 e.coli
108	c2ecfA_	Alignment	not modelled	84.8	12	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl peptidase iv; PDBTitle: crystal structure of dipeptidyl aminopeptidase iv from 2 stenotrophomonas maltophilia
109	c2qs9A_	Alignment	not modelled	84.7	16	PDB header: structural protein Chain: A: PDB Molecule: retinoblastoma-binding protein 9; PDBTitle: crystal structure of the human retinoblastoma-binding 2 protein 9 (rbbp-9). nesg target hr2978
110	c3mveB_	Alignment	not modelled	84.4	12	PDB header: lyase Chain: B: PDB Molecule: upf0255 protein vv1_0328; PDBTitle: crystal structure of a novel pyruvate decarboxylase
111	c2ronA_	Alignment	not modelled	84.3	14	PDB header: hydrolase Chain: A: PDB Molecule: surfactin synthetase thioesterase subunit; PDBTitle: the external thioesterase of the surfactin-synthetase
112	d1xkta_	Alignment	not modelled	84.1	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
113	c3bdvB_	Alignment	not modelled	83.8	20	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein duf1234; PDBTitle: crystal structure of a putative yden-like hydrolase (eca3091) from 2 pectobacterium atrosepticum scri1043 at 1.66 a resolution
114	c3d0kA_	Alignment	not modelled	83.3	13	PDB header: hydrolase Chain: A: PDB Molecule: putative poly(3-hydroxybutyrate) depolymerase lpqc; PDBTitle: crystal structure of the lpqc, poly(3-hydroxybutyrate) depolymerase 2 from bordetella parapertussis
115	c4nfuA_	Alignment	not modelled	83.3	18	PDB header: signaling protein Chain: A: PDB Molecule: eds1; PDBTitle: structure of the central plant immunity signaling node eds1 in complex 2 with its interaction partner sag101
116	c5ah0B_	Alignment	not modelled	82.9	18	PDB header: hydrolase Chain: B: PDB Molecule: lipase; PDBTitle: structure of lipase 1 from pelosinus fermentans
117	c3wz1B_	Alignment	not modelled	82.4	15	PDB header: hydrolase Chain: B: PDB Molecule: zearealenone hydrolase; PDBTitle: zen lactonase
118	c4x91C_	Alignment	not modelled	81.9	7	PDB header: transferase Chain: C: PDB Molecule: group xv phospholipase a2; PDBTitle: crystal structure of lysosomal phospholipase a2 in complex with 2 isopropyl dodec-11-enylfluorophosphonate (idfp)
119	c5w8pA_	Alignment	not modelled	81.6	17	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: homoserine transacetylase meta from mycobacterium abscessus
120	c4z8zA_	Alignment	not modelled	81.3	18	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the hypothetical protein from ruminiclostridium 2 thermocellum atcc 27405