Phyre^2

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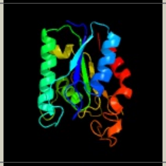
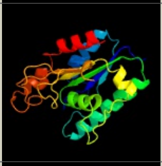
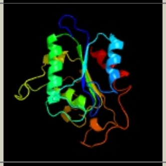
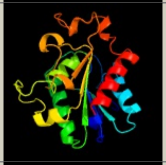
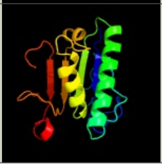
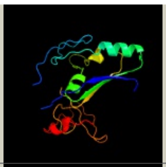
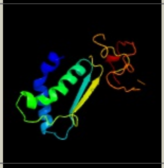
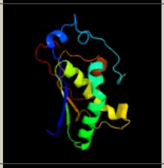
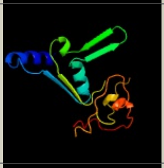
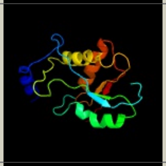
Description	RVBD3451_(cut3)_3872796_3873584
Date	Fri Aug 9 18:20:12 BST 2019
Unique Job ID	8121a7a81811a84b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4psdA_	Alignment		100.0	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**carbohydrate esterase family 5; **PDBTitle:** structure of trichoderma reesei cutinase native form.
2	d1qoza_	Alignment		100.0	30	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Cutinase-like
3	d1cexa_	Alignment		100.0	23	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Cutinase-like
4	d1g66a_	Alignment		100.0	29	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Cutinase-like
5	c5x88A_	Alignment		100.0	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cutinase; **PDBTitle:** a crystal structure of cutinases from malbranchea cinnamomea
6	c2czqB_	Alignment		100.0	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cutinase-like protein; **PDBTitle:** a novel cutinase-like protein from cryptococcus sp.
7	c3dd5F_	Alignment		100.0	26	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**cutinase; **PDBTitle:** glomerella cingulata e600-cutinase complex
8	c4oylC_	Alignment		100.0	29	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**cutinase; **PDBTitle:** humicola insolens cutinase in complex with mono-ethylphosphate
9	c3gbsA_	Alignment		100.0	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cutinase 1; **PDBTitle:** crystal structure of aspergillus oryzae cutinase
10	c3ajaA_	Alignment		100.0	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of msmeg_6394
11	c3hc7A_	Alignment		99.9	24	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**gene 12 protein; **PDBTitle:** crystal structure of lysin b from mycobacteriophage d29

12	c3g7nA_	Alignment		98.4	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipase; **PDBTitle:** crystal structure of a triacylglycerol lipase from penicillium2 expansum at 1.3
13	d1uwca_	Alignment		97.9	18	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
14	c3ngmB_	Alignment		97.7	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**extracellular lipase; **PDBTitle:** crystal structure of lipase from gibberella zeae
15	d3tgla_	Alignment		97.6	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
16	d1tiaa_	Alignment		97.6	20	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
17	c6qppA_	Alignment		97.5	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipase; **PDBTitle:** rhizomucor miehei lipase propeptide complex, native
18	c5xk2A_	Alignment		97.3	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**diacylglycerol lipase; **PDBTitle:** crystal structure of mono- and diacylglycerol lipase from aspergillus2 oryzae
19	d1mo2a_	Alignment		97.3	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Thioesterase domain of polypeptide, polyketide and fatty acid synthases
20	c1mo2A_	Alignment		97.3	16	**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
21	d1tcaa_	Alignment	not modelled	97.1	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
22	c5gw8A_	Alignment	not modelled	97.1	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hypothetical secretory lipase (family 3); **PDBTitle:** crystal structure of a putative dag-like lipase (mgmdl2) from2 malassezia globosa
23	c3icvA_	Alignment	not modelled	97.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipase b; **PDBTitle:** structural consequences of a circular permutation on lipase b from2 candida antartica
24	c3uueA_	Alignment	not modelled	97.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lip1, secretory lipase (family 3); **PDBTitle:** crystal structure of mono- and diacylglycerol lipase from malassezia2 globosa
25	d1ei9a_	Alignment	not modelled	96.9	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Thioesterases
26	d1tiba_	Alignment	not modelled	96.8	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
27	d1lgya_	Alignment	not modelled	96.6	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
28	c3lcrA_	Alignment	not modelled	96.5	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tautomycetin biosynthetic pks; **PDBTitle:** thioesterase from tautomycetin biosynthhetic pathway
29	c5f2hA_	Alignment	not modelled	96.5	13	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein;

29	c5f2hA_	Alignment	not modelled	[illegible]	[illegible]	**PDBTitle:** 2.75 angstrom resolution crystal structure of uncharacterized protein2 from bacillus cereus atcc 10987
30	d4lipd_	Alignment	not modelled	96.3	27	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Bacterial lipase
31	c6e6uA_	Alignment	not modelled	96.3	16	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**dieckmann cyclase, ncmc; **PDBTitle:** variant c89s of dieckmann cyclase, ncmc
32	c6cl4A_	Alignment	not modelled	96.2	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipase c12; **PDBTitle:** lipc12 - lipase from metagenomics
33	d1cvla_	Alignment	not modelled	96.2	21	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Bacterial lipase
34	c2zyiB_	Alignment	not modelled	96.2	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lipase, putative; **PDBTitle:** a. fulgidus lipase with fatty acid fragment and calcium
35	c3o0dF_	Alignment	not modelled	96.0	22	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**triacylglycerol lipase; **PDBTitle:** crystal structure of lip2 lipase from yarrowia lipolytica at 1.7 a2 resolution
36	c4zxiA_	Alignment	not modelled	95.9	14	**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
37	c2oryA_	Alignment	not modelled	95.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipase; **PDBTitle:** crystal structure of m37 lipase
38	d1ex9a_	Alignment	not modelled	95.9	23	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Bacterial lipase
39	c3og9A_	Alignment	not modelled	95.8	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein yahd a copper inducible hydrolase; **PDBTitle:** structure of yahd with malic acid
40	d2h1ia1	Alignment	not modelled	95.8	23	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase/thioesterase 1
41	c2r8bA_	Alignment	not modelled	95.6	17	**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
42	c1qgeD_	Alignment	not modelled	95.6	21	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**protein (triacylglycerol hydrolase); **PDBTitle:** new crystal form of pseudomonas glumae (formerly chromobacterium2 viscosum atcc 6918) lipase
43	d3b5ea1	Alignment	not modelled	95.5	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase/thioesterase 1
44	c3lp5A_	Alignment	not modelled	95.4	15	**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
45	d2r8ba1	Alignment	not modelled	95.2	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase/thioesterase 1
46	c2yijA_	Alignment	not modelled	95.2	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phospholipase a1-iigamma; **PDBTitle:** crystal structure of phospholipase a1
47	d1ispa_	Alignment	not modelled	95.1	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Bacterial lipase
48	c5d8mA_	Alignment	not modelled	95.1	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metagenomic carboxyl esterase mgs0156; **PDBTitle:** crystal structure of the metagenomic carboxyl esterase mgs0156
49	c4gw3A_	Alignment	not modelled	95.0	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative lipase; **PDBTitle:** crystal structure of the lipase from proteus mirabilis
50	c2qjwA_	Alignment	not modelled	95.0	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
51	c2q0xA_	Alignment	not modelled	94.9	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** alpha/beta hydrolase fold protein of unknown function
52	c4f21G_	Alignment	not modelled	94.9	14	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** G: **PDB Molecule:**carboxylesterase/phospholipase family protein; **PDBTitle:** crystal structure of carboxylesterase/phospholipase family protein2 from francisella tularensis
53	c2h7xA_	Alignment	not modelled	94.7	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**type i polyketide synthase pikaiv; **PDBTitle:** pikromycin thioesterase adduct with reduced triketide2 affinity label
54	c5xavB_	Alignment	not modelled	94.5	7	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**intracellular polyhydroxyalkanoate synthase; **PDBTitle:** structure of phac from chromobacterium sp. usm2
55	c5t6oA_	Alignment	not modelled	94.4	21	**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

56	d1jmkc_	Alignment	not modelled	94.3	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Thioesterase domain of polypeptide, polyketide and fatty acid synthases
57	d2h7xa1	Alignment	not modelled	94.3	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Thioesterase domain of polypeptide, polyketide and fatty acid synthases
58	c2veoA_	Alignment	not modelled	94.0	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipase a; **PDBTitle:** x-ray structure of candida antarctica lipase a in its closed state.
59	c2rauA_	Alignment	not modelled	93.7	15	**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
60	c2cbgA_	Alignment	not modelled	93.5	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**fengycin synthetase; **PDBTitle:** crystal structure of the pmsf-inhibited thioesterase domain of the2 fengycin biosynthesis cluster
61	c4nfuB_	Alignment	not modelled	93.4	10	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**senescence-associated carboxylesterase 101; **PDBTitle:** structure of the central plant immunity signaling node eds1 in complex2 with its interaction partner sag101
62	d1etha2	Alignment	not modelled	93.3	12	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Pancreatic lipase, N-terminal domain
63	c3ds8A_	Alignment	not modelled	92.8	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin2722 protein; **PDBTitle:** the crysatl structure of the gene lin2722 products from listeria2 innocua
64	c2y6vB_	Alignment	not modelled	92.7	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**peroxisomal membrane protein lpx1; **PDBTitle:** peroxisomal alpha-beta-hydrolase lpx1 (yor084w) from saccharomyces2 cerevisiae (crystal form i)
65	c4eziA_	Alignment	not modelled	92.3	20	**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
66	c6e7kB_	Alignment	not modelled	92.2	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lipoprotein lipase; **PDBTitle:** structure of the lipoprotein lipase gpihbp1 complex that mediates2 plasma triglyceride hydrolysis
67	d1rp1a2	Alignment	not modelled	91.6	12	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Pancreatic lipase, N-terminal domain
68	c4h0cA_	Alignment	not modelled	91.5	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phospholipase/carboxylesterase; **PDBTitle:** crystal structure of phospholipase/carboxylesterase from dyadobacter2 fermentans dsm 18053
69	d1hpla2	Alignment	not modelled	91.5	10	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Pancreatic lipase, N-terminal domain
70	d1lpbb2	Alignment	not modelled	91.4	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Pancreatic lipase, N-terminal domain
71	c1hplB_	Alignment	not modelled	91.4	13	**PDB header:**hydrolase(carboxylic esterase) **Chain:** B: **PDB Molecule:**lipase; **PDBTitle:** horse pancreatic lipase. the crystal structure at 2.3 angstroms2 resolution
72	c2h1iA_	Alignment	not modelled	91.3	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**carboxylesterase; **PDBTitle:** crystal structure of the bacillus cereus carboxylesterase
73	c2pvsB_	Alignment	not modelled	91.3	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**pancreatic lipase-related protein 2; **PDBTitle:** structure of human pancreatic lipase related protein 22 mutant n336q
74	c1gplA_	Alignment	not modelled	91.3	11	**PDB header:**serine esterase **Chain:** A: **PDB Molecule:**rp2 lipase; **PDBTitle:** rp2 lipase
75	d1gpla2	Alignment	not modelled	90.4	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Pancreatic lipase, N-terminal domain
76	c5h6bA_	Alignment	not modelled	90.1	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative secreted lipase; **PDBTitle:** crystal structure of a thermostable lipase from marine streptomyces
77	c3h2iA_	Alignment	not modelled	89.7	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase; **PDBTitle:** crystal structure of n228w mutant of the rice cell wall2 degrading esterase lipa from xanthomonas oryzae
78	d1k8qa_	Alignment	not modelled	89.4	21	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Gastric lipase
79	c2vavL_	Alignment	not modelled	89.1	8	**PDB header:**transferase **Chain:** L: **PDB Molecule:**acetyl-coa--deacetylcephalosporin c acetyltransferase; **PDBTitle:** crystal structure of deacetylcephalosporin c acetyltransferase (dac-2 soak)
80	c2vsqA_	Alignment	not modelled	89.0	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
81	d1bu8a2	Alignment	not modelled	88.6	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases

						Family: Pancreatic lipase, N-terminal domain
82	c4nfuA_	Alignment	not modelled	88.4	11	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**eds1; **PDBTitle:** structure of the central plant immunity signaling node eds1 in complex2 with its interaction partner sag101
83	c4qnnC_	Alignment	not modelled	87.2	15	**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
84	c3ilsA_	Alignment	not modelled	87.2	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aflatoxin biosynthesis polyketide synthase; **PDBTitle:** the thioesterase domain from pksa
85	c3l80A_	Alignment	not modelled	87.2	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein smu.1393c; **PDBTitle:** crystal structure of smu.1393c from streptococcus mutans ua159
86	c5ja2A_	Alignment	not modelled	87.2	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**enterobactin synthase component f; **PDBTitle:** entf, a terminal nonribosomal peptide synthetase module bound to the2 non-native mbth-like protein pa2412
87	d1xkta_	Alignment	not modelled	87.0	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Thioesterase domain of polypeptide, polyketide and fatty acid synthases
88	c1rp1A_	Alignment	not modelled	86.4	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pancreatic lipase related protein 1; **PDBTitle:** dog pancreatic lipase related protein 1
89	c4xjvA_	Alignment	not modelled	86.0	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**s-acyl fatty acid synthase thioesterase, medium chain; **PDBTitle:** crystal structure of human thioesterase 2
90	c5ugzA_	Alignment	not modelled	85.4	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative thioesterase; **PDBTitle:** crystal structure of clbq from the colibactin nrps/pks pathway
91	c2pplA_	Alignment	not modelled	84.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pancreatic lipase-related protein 1; **PDBTitle:** human pancreatic lipase-related protein 1
92	c3bdvB_	Alignment	not modelled	84.3	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**uncharacterized protein duf1234; **PDBTitle:** crystal structure of a putative yden-like hydrolase (eca3091) from2 pectobacterium atrosepticum scri1043 at 1.66 a resolution
93	c5x6sB_	Alignment	not modelled	84.2	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**acetylxylan esterase a; **PDBTitle:** acetyl xylan esterase from aspergillus awamori
94	c3qmwD_	Alignment	not modelled	83.8	18	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**thioesterase; **PDBTitle:** redj with peg molecule bound in the active site
95	d1hlga_	Alignment	not modelled	83.4	20	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Gastric lipase
96	c4pf1D_	Alignment	not modelled	78.8	23	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**peptidase s15/coce/nond; **PDBTitle:** crystal structure of aminopeptidase from marine sediment archaeon2 thaumarchaeota archaeon
97	c3flaB_	Alignment	not modelled	77.9	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**rifr; **PDBTitle:** rifr - type ii thioesterase from rifamycin nrps/pks biosynthetic2 pathway - form 1
98	c4fleA_	Alignment	not modelled	77.0	14	**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
99	c4x91C_	Alignment	not modelled	76.9	22	**PDB header:**transferase **Chain:** C: **PDB Molecule:**group xv phospholipase a2; **PDBTitle:** crystal structure of lysosomal phospholipase a2 in complex with2 isopropyl dodec-11-enylfluorophosphonate (idfp)
100	c5w8pA_	Alignment	not modelled	76.2	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**homoserine o-acetyltransferase; **PDBTitle:** homoserine transacetylase meta from mycobacterium abscessus
101	c6gupB_	Alignment	not modelled	75.7	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**siderophore biosynthesis lipase/esterase, putative; **PDBTitle:** siderophore hydrolase estb from aspergillus fumigatus
102	d1ji3a_	Alignment	not modelled	75.4	19	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Bacterial lipase
103	c4x96B_	Alignment	not modelled	74.0	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphatidylcholine-sterol acyltransferase; **PDBTitle:** low resolution crystal structure of lecithin:cholesterol2 acyltransferase (lcat; residues 21-397)
104	c5ah0B_	Alignment	not modelled	72.7	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lipase; **PDBTitle:** structure of lipase 1 from pelosinus fermentans
105	c2b9vB_	Alignment	not modelled	71.8	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-amino acid ester hydrolase; **PDBTitle:** acetobacter turbidans alpha-amino acid ester hydrolase
106	c3fleB_	Alignment	not modelled	70.3	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**se_1780 protein; **PDBTitle:** se_1780 protein of unknown function from staphylococcus epidermidis.

107	c2ronA_	Alignment	not modelled	70.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**surfactin synthetase thioesterase subunit; **PDBTitle:** the external thioesterase of the surfactin-synthetase
108	c4c87A_	Alignment	not modelled	69.3	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase; **PDBTitle:** esterase lpest1 from lactobacillus plantarum wcfs1
109	d1ku0a_	Alignment	not modelled	68.5	19	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Bacterial lipase
110	d2nn6i2	Alignment	not modelled	67.6	19	**Fold:**Barrel-sandwich hybrid **Superfamily:**Ribosomal L27 protein-like **Family:**ECR1 N-terminal domain-like
111	c2qruA_	Alignment	not modelled	67.2	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an alpha/beta hydrolase superfamily protein from2 enterococcus faecalis
112	c3h04A_	Alignment	not modelled	66.6	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of the protein with unknown function from2 staphylococcus aureus subsp. aureus mu50
113	c3v48B_	Alignment	not modelled	66.1	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative aminoacrylate hydrolase rutd; **PDBTitle:** crystal structure of the putative alpha/beta hydrolase rutd from2 e.coli
114	c4wfiA_	Alignment	not modelled	66.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cutinase; **PDBTitle:** crystal structure of pet-degrading cutinase cut190 s226p mutant in2 ca(2+)-free state
115	c4ao6A_	Alignment	not modelled	65.5	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase; **PDBTitle:** native structure of a novel cold-adapted esterase from an2 arctic intertidal metagenomic library
116	c4fhzA_	Alignment	not modelled	64.4	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phospholipase/carboxylesterase; **PDBTitle:** crystal structure of a carboxyl esterase at 2.0 angstrom resolution
117	c3mveB_	Alignment	not modelled	64.4	21	**PDB header:**lyase **Chain:** B: **PDB Molecule:**upf0255 protein vv1_0328; **PDBTitle:** crystal structure of a novel pyruvate decarboxylase
118	c5ah1A_	Alignment	not modelled	63.8	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**triacylglycerol lipase; **PDBTitle:** structure of esta from clostridium botulinum
119	c3d0kA_	Alignment	not modelled	62.7	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative poly(3-hydroxybutyrate) depolymerase lpqc; **PDBTitle:** crystal structure of the lpqc, poly(3-hydroxybutyrate) depolymerase2 from bordetella parapertussis
120	d2jbwa1	Alignment	not modelled	62.4	28	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**2,6-dihydropseudooxynicotine hydrolase-like