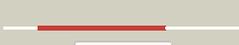


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1184c_(-)_1324538_1325617
Date	Wed Jul 31 22:05:27 BST 2019
Unique Job ID	0de7a7220dce547f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ajaA_	 Alignment		99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of msmeg_6394
2	c2czqB_	 Alignment		99.4	17	PDB header: hydrolase Chain: B: PDB Molecule: cutinase-like protein; PDBTitle: a novel cutinase-like protein from cryptococcus sp.
3	d1qoza_	 Alignment		99.4	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like
4	d1g66a_	 Alignment		99.4	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like
5	c3hc7A_	 Alignment		99.3	19	PDB header: cell adhesion Chain: A: PDB Molecule: gene 12 protein; PDBTitle: crystal structure of lysin b from mycobacteriophage d29
6	d1cexa_	 Alignment		99.1	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like
7	c3gbsA_	 Alignment		99.0	16	PDB header: hydrolase Chain: A: PDB Molecule: cutinase 1; PDBTitle: crystal structure of aspergillus oryzae cutinase
8	c3dd5F_	 Alignment		99.0	12	PDB header: hydrolase Chain: F: PDB Molecule: cutinase; PDBTitle: glomerella cingulata e600-cutinase complex
9	c5x88A_	 Alignment		98.8	22	PDB header: hydrolase Chain: A: PDB Molecule: cutinase; PDBTitle: a crystal structure of cutinases from malbranchea cinnamomea
10	c4oylC_	 Alignment		98.7	15	PDB header: hydrolase Chain: C: PDB Molecule: cutinase; PDBTitle: humicola insolens cutinase in complex with monoethylphosphate
11	c4psdA_	 Alignment		98.5	21	PDB header: hydrolase Chain: A: PDB Molecule: carbohydrate esterase family 5; PDBTitle: structure of trichoderma reesei cutinase native form.

12	c5xavB_	Alignment		95.3	13	PDB header: biosynthetic protein Chain: B: PDB Molecule: intracellular polyhydroxyalkanoate synthase; PDBTitle: structure of phac from chromobacterium sp. usm2
13	c3icvA_	Alignment		94.9	16	PDB header: hydrolase Chain: A: PDB Molecule: lipase b; PDBTitle: structural consequences of a circular permutation on lipase b from2 candida antartica
14	d1tcaa_	Alignment		94.4	11	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
15	c5t6oA_	Alignment		94.3	18	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
16	c3lp5A_	Alignment		93.2	18	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
17	c3ds8A_	Alignment		93.1	31	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin2722 protein; PDBTitle: the crysatl structure of the gene lin2722 products from listeria2 innocua
18	c2pplA_	Alignment		91.5	21	PDB header: hydrolase Chain: A: PDB Molecule: pancreatic lipase-related protein 1; PDBTitle: human pancreatic lipase-related protein 1
19	d1rp1a2	Alignment		91.2	22	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
20	c4qnnC_	Alignment		91.2	18	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
21	c1hplB_	Alignment	not modelled	90.6	20	PDB header: hydrolase(carboxylic esterase) Chain: B: PDB Molecule: lipase; PDBTitle: horse pancreatic lipase. the crystal structure at 2.3 angstroms2 resolution
22	d1bu8a2	Alignment	not modelled	89.5	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
23	d1ei9a_	Alignment	not modelled	89.1	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterases
24	d1lpbb2	Alignment	not modelled	88.1	23	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
25	d1jmkc_	Alignment	not modelled	88.0	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
26	d1ispa_	Alignment	not modelled	87.0	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
27	d1letha2	Alignment	not modelled	85.5	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
28	d2h7xa1	Alignment	not modelled	83.5	24	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
						Fold: alpha/beta-Hydrolases

29	d1hpla2	Alignment	not modelled	83.3	23	Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
30	d3b5ea1	Alignment	not modelled	82.8	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
31	d1gpla2	Alignment	not modelled	82.7	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
32	c1pjaA	Alignment	not modelled	82.6	12	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)
33	d1pjaa	Alignment	not modelled	82.6	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterases
34	c2h7xA	Alignment	not modelled	82.5	26	PDB header: hydrolase Chain: A: PDB Molecule: type i polyketide synthase pikaiv; PDBTitle: pikromycin thioesterase adduct with reduced triketide2 affinity label
35	c3lcrA	Alignment	not modelled	80.5	21	PDB header: hydrolase Chain: A: PDB Molecule: tautomycetin biosynthetic pks; PDBTitle: thioesterase from tautomycetin biosynthetic pathway
36	c5f2hA	Alignment	not modelled	80.3	12	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
37	c6e7kB	Alignment	not modelled	79.9	22	PDB header: hydrolase Chain: B: PDB Molecule: lipoprotein lipase; PDBTitle: structure of the lipoprotein lipase gpibbp1 complex that mediates2 plasma triglyceride hydrolysis
38	c1mo2A	Alignment	not modelled	79.1	13	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
39	d1mo2a	Alignment	not modelled	79.1	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
40	c1gplA	Alignment	not modelled	78.6	21	PDB header: serine esterase Chain: A: PDB Molecule: rp2 lipase; PDBTitle: rp2 lipase
41	c2pvsB	Alignment	not modelled	76.7	19	PDB header: hydrolase Chain: B: PDB Molecule: pancreatic lipase-related protein 2; PDBTitle: structure of human pancreatic lipase related protein 22 mutant n336q
42	d3tgla	Alignment	not modelled	75.1	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
43	c2cbgA	Alignment	not modelled	74.7	11	PDB header: hydrolase Chain: A: PDB Molecule: fengycin synthetase; PDBTitle: crystal structure of the pmsf-inhibited thioesterase domain of the2 fengycin biosynthesis cluster
44	d1uxoa	Alignment	not modelled	74.6	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: YdeN-like
45	d1xkta	Alignment	not modelled	74.6	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
46	c6cl4A	Alignment	not modelled	74.2	13	PDB header: hydrolase Chain: A: PDB Molecule: lipase c12; PDBTitle: lipc12 - lipase from metagenomics
47	d2h1ia1	Alignment	not modelled	74.0	10	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
48	c4h0cA	Alignment	not modelled	73.2	18	PDB header: hydrolase Chain: A: PDB Molecule: phospholipase/carboxylesterase; PDBTitle: crystal structure of phospholipase/carboxylesterase from dyadobacter2 fermentans dsm 18053
49	c6qppA	Alignment	not modelled	72.1	16	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: rhizomucor miehei lipase propeptide complex, native
50	d1lgva	Alignment	not modelled	72.0	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
51	d2r8ba1	Alignment	not modelled	71.2	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
52	c1rp1A	Alignment	not modelled	71.1	24	PDB header: hydrolase Chain: A: PDB Molecule: pancreatic lipase related protein 1; PDBTitle: dog pancreatic lipase related protein 1
53	c3og9A	Alignment	not modelled	69.2	10	PDB header: hydrolase Chain: A: PDB Molecule: protein yahd a copper inducible hydrolase; PDBTitle: structure of yahd with malic acid
54	c4xjvA	Alignment	not modelled	67.9	23	PDB header: hydrolase Chain: A: PDB Molecule: s-acyl fatty acid synthase thioesterase, medium chain; PDBTitle: crystal structure of human thioesterase 2
55	c4f21G	Alignment	not modelled	66.2	19	PDB header: hydrolase/hydrolase inhibitor Chain: G: PDB Molecule: carboxylesterase/phospholipase family protein; PDBTitle: crystal structure of carboxylesterase/phospholipase

						family protein2 from francisella tularensis
56	c6n8eA_	Alignment	not modelled	65.8	15	PDB header: hydrolase Chain: A: PDB Molecule: holo-obif1; PDBTitle: crystal structure of holo-obif1, a five domain nonribosomal peptide2 synthetase from burkholderia diffusa
57	c2h1iA_	Alignment	not modelled	64.6	10	PDB header: hydrolase Chain: A: PDB Molecule: carboxylesterase; PDBTitle: crystal structure of the bacillus cereus carboxylesterase
58	c3h2iA_	Alignment	not modelled	64.2	17	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
59	c3fleB_	Alignment	not modelled	63.3	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: se_1780 protein; PDBTitle: se_1780 protein of unknown function from staphylococcus epidermidis.
60	c3bdvB_	Alignment	not modelled	63.2	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
61	c2r8bA_	Alignment	not modelled	60.6	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
62	c3p3dA_	Alignment	not modelled	60.2	15	PDB header: nuclear protein Chain: A: PDB Molecule: nucleoporin 53; PDBTitle: crystal structure of the nup53 rrm domain from pichia guilliermondii
63	c2qjwA_	Alignment	not modelled	57.3	20	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
64	d1ex9a_	Alignment	not modelled	56.8	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
65	c2veoA_	Alignment	not modelled	55.3	15	PDB header: hydrolase Chain: A: PDB Molecule: lipase a; PDBTitle: x-ray structure of candida antarctica lipase a in its closed state.
66	c4x91C_	Alignment	not modelled	54.9	16	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)
67	c4fleA_	Alignment	not modelled	54.2	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
68	c5uazB_	Alignment	not modelled	52.0	15	PDB header: protein transport Chain: B: PDB Molecule: nucleoporin nup53; PDBTitle: crystal structure of the yeast nucleoporin
69	c5d8mA_	Alignment	not modelled	51.8	10	PDB header: hydrolase Chain: A: PDB Molecule: metagenomic carboxyl esterase mgs0156; PDBTitle: crystal structure of the metagenomic carboxyl esterase mgs0156
70	c3flaB_	Alignment	not modelled	51.7	26	PDB header: hydrolase Chain: B: PDB Molecule: rifr; PDBTitle: rifr - type ii thioesterase from rifamycin nrps/pks biosynthetic2 pathway - form 1
71	c4x96B_	Alignment	not modelled	51.5	17	PDB header: transferase Chain: B: PDB Molecule: phosphatidylcholine-sterol acyltransferase; PDBTitle: low resolution crystal structure of lecithin:cholesterol2 acyltransferase (lcat; residues 21-397)
72	c4z8zA_	Alignment	not modelled	51.2	20	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the hypothetical protein from ruminiclostridium2 thermocellum atcc 27405
73	c2vsqA_	Alignment	not modelled	50.8	15	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
74	c5gw8A_	Alignment	not modelled	49.1	13	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
75	c2zyiB_	Alignment	not modelled	48.8	25	PDB header: hydrolase Chain: B: PDB Molecule: lipase, putative; PDBTitle: a. fulgidus lipase with fatty acid fragment and calcium
76	c4nfuB_	Alignment	not modelled	42.8	17	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
77	c5h3bA_	Alignment	not modelled	42.8	18	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein hi_1552; PDBTitle: crystal structure of semet-biog from haemophilus influenzae at 1.492 angstroms resolution
78	c5ja2A_	Alignment	not modelled	41.5	17	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
79	c4o5pB_	Alignment	not modelled	40.8	18	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein from pseudomonas2 aeruginosa
80	c3g7nA_	Alignment	not modelled	39.4	17	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: crystal structure of a triacylglycerol lipase from

						penicillium2 expansum at 1.3
81	c2vtvA	Alignment	not modelled	39.1	11	PDB header: hydrolase Chain: A: PDB Molecule: phb depolymerase phaz7; PDBTitle: phaz7 depolymerase from paucimonas lemoignei
82	c4zxiA	Alignment	not modelled	39.0	10	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
83	c2ronA	Alignment	not modelled	38.6	16	PDB header: hydrolase Chain: A: PDB Molecule: surfactin synthetase thioesterase subunit; PDBTitle: the external thioesterase of the surfactin-synthetase
84	c2q0xA	Alignment	not modelled	38.3	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: alpha/beta hydrolase fold protein of unknown function
85	c3uuuA	Alignment	not modelled	37.9	12	PDB header: hydrolase Chain: A: PDB Molecule: lip1, secretory lipase (family 3); PDBTitle: crystal structure of mono- and diacylglycerol lipase from malassezia2 globosa
86	c2m4mA	Alignment	not modelled	37.8	21	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: solution structure of the rrm domain of the hypothetical protein2 cagl0m09691g from candida glabrata
87	d4lipd	Alignment	not modelled	36.6	23	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
88	c4eziA	Alignment	not modelled	36.5	14	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
89	c3ilsA	Alignment	not modelled	35.9	20	PDB header: hydrolase Chain: A: PDB Molecule: afatoxin biosynthesis polyketide synthase; PDBTitle: the thioesterase domain from pksa
90	c4bipA	Alignment	not modelled	34.4	27	PDB header: virus Chain: A: PDB Molecule: vp1; PDBTitle: homology model of coxsackievirus a7 (cav7) full capsid proteins.
91	d1tiaa	Alignment	not modelled	33.8	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
92	c2rauA	Alignment	not modelled	33.8	13	PDB header: hydrolase Chain: A: PDB Molecule: putative esterase; PDBTitle: crystal structure of a putative lipase (np_343859.1) from sulfobolus2 solfataricus at 1.85 a resolution
93	c4gw3A	Alignment	not modelled	31.7	20	PDB header: hydrolase Chain: A: PDB Molecule: putative lipase; PDBTitle: crystal structure of the lipase from proteus mirabilis
94	c2oryA	Alignment	not modelled	31.1	14	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: crystal structure of m37 lipase
95	c3wydA	Alignment	not modelled	30.3	15	PDB header: hydrolase Chain: A: PDB Molecule: lc-est1c; PDBTitle: c-terminal esterase domain of lc-est1
96	c5xs5A	Alignment	not modelled	29.6	17	PDB header: virus Chain: A: PDB Molecule: genome polyprotein; PDBTitle: structure of coxsackievirus a6 (cva6) virus procapsid particle
97	c2vavL	Alignment	not modelled	29.4	13	PDB header: transferase Chain: L: PDB Molecule: acetyl-coa--deacetylcephalosporin c acetyltransferase; PDBTitle: crystal structure of deacetylcephalosporin c acetyltransferase (dac-2 soak)
98	c6fvjB	Alignment	not modelled	28.3	20	PDB header: hydrolase Chain: B: PDB Molecule: thioesterase; PDBTitle: tesa a major thioesterase from mycobacterium tuberculosis
99	c2qs9A	Alignment	not modelled	26.9	11	PDB header: structural protein Chain: A: PDB Molecule: retinoblastoma-binding protein 9; PDBTitle: crystal structure of the human retinoblastoma-binding2 protein 9 (rbbp-9). nesg target hr2978
100	c2y6vB	Alignment	not modelled	26.8	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)
101	c5ugzA	Alignment	not modelled	26.0	15	PDB header: hydrolase Chain: A: PDB Molecule: putative thioesterase; PDBTitle: crystal structure of clbq from the colibactin nrps/pks pathway
102	c6ijjA	Alignment	not modelled	25.9	19	PDB header: viral protein Chain: A: PDB Molecule: vp1; PDBTitle: cryo-em structure of cv-a10 mature virion
103	c3vbfA	Alignment	not modelled	25.8	16	PDB header: virus Chain: A: PDB Molecule: genome polyprotein, capsid protein vp1; PDBTitle: crystal structure of formaldehyde treated human enterovirus 71 (space2 group i23)
104	d1uwca	Alignment	not modelled	25.3	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
105	c3l80A	Alignment	not modelled	24.6	16	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein smu.1393c; PDBTitle: crystal structure of smu.1393c from streptococcus mutans ua159
106	c3qmwD	Alignment	not modelled	24.2	15	PDB header: hydrolase Chain: D: PDB Molecule: thioesterase;

					PDBTitle: redj with peg molecule bound in the active site
107	d1k8qa_	Alignment	not modelled	23.2	20 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Gastric lipase
108	d1tiba_	Alignment	not modelled	22.2	16 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
109	c5xk2A_	Alignment	not modelled	22.0	22 PDB header: hydrolase Chain: A: PDB Molecule: diacylglycerol lipase; PDBTitle: crystal structure of mono- and diacylglycerol lipase from aspergillus2 oryzae
110	c4fhzA_	Alignment	not modelled	22.0	18 PDB header: hydrolase Chain: A: PDB Molecule: phospholipase/carboxylesterase; PDBTitle: crystal structure of a carboxyl esterase at 2.0 angstrom resolution
111	d1cvla_	Alignment	not modelled	21.9	23 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase