





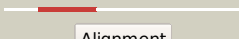



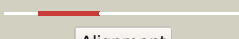











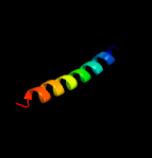

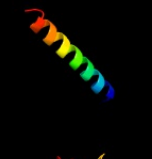
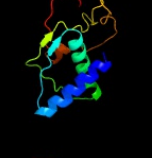



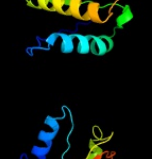
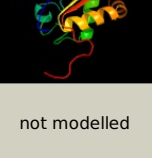


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0152c_(PE2)_179317_180894
 Date Tue Jul 23 14:50:19 BST 2019
 Unique Job ID d5cd724edb3a6dae

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ajaA_	 Alignment		99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of msmeg_6394
2	d1qoza_	 Alignment		99.3	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like
3	c3hc7A_	 Alignment		99.3	20	PDB header: cell adhesion Chain: A: PDB Molecule: gene 12 protein; PDBTitle: crystal structure of lysin b from mycobacteriophage d29
4	d1g66a_	 Alignment		99.3	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like
5	c2czqB_	 Alignment		99.1	17	PDB header: hydrolase Chain: B: PDB Molecule: cutinase-like protein; PDBTitle: a novel cutinase-like protein from cryptococcus sp.
6	c3dd5F_	 Alignment		99.0	12	PDB header: hydrolase Chain: F: PDB Molecule: cutinase; PDBTitle: glomerella cingulata e600-cutinase complex
7	d1cexa_	 Alignment		99.0	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like
8	c5x88A_	 Alignment		98.9	14	PDB header: hydrolase Chain: A: PDB Molecule: cutinase; PDBTitle: a crystal structure of cutinases from malbranchea cinnamomea
9	c3gbsA_	 Alignment		98.8	17	PDB header: hydrolase Chain: A: PDB Molecule: cutinase 1; PDBTitle: crystal structure of aspergillus oryzae cutinase
10	c4psdA_	 Alignment		98.7	17	PDB header: hydrolase Chain: A: PDB Molecule: carbohydrate esterase family 5; PDBTitle: structure of trichoderma reesei cutinase native form.
11	c4oylC_	 Alignment		98.6	12	PDB header: hydrolase Chain: C: PDB Molecule: cutinase; PDBTitle: humicola insolens cutinase in complex with monoethylphosphate

12	c5xfsA	Alignment		97.5	19	PDB header: protein transport Chain: A: PDB Molecule: pe family protein pe8; PDBTitle: crystal structure of pe8-ppe15 in complex with esp95 from m.2 tuberculosis
13	d2g38a1	Alignment		97.5	23	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PE
14	c2g38A	Alignment		97.5	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: pe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
15	c3icvA	Alignment		96.1	20	PDB header: hydrolase Chain: A: PDB Molecule: lipase b; PDBTitle: structural consequences of a circular permutation on lipase b from2 candida antarctica
16	d1tcaa	Alignment		94.6	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
17	c5xavB	Alignment		94.2	14	PDB header: biosynthetic protein Chain: B: PDB Molecule: intracellular polyhydroxyalkanoate synthase; PDBTitle: structure of phac from chromobacterium sp. usm2
18	c5t6oA	Alignment		94.2	14	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
19	d1jmkc	Alignment		93.9	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
20	d1ei9a	Alignment		92.3	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterases
21	c3lp5A	Alignment	not modelled	90.4	16	PDB header: hydrolase Chain: A: PDB Molecule: putative cell surface hydrolase; PDBTitle: the crystal structure of the putative cell surface hydrolase from2 lactobacillus plantarum wcf51
22	c2q0xA	Alignment	not modelled	89.1	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: alpha/beta hydrolase fold protein of unknown function
23	d2h7xa1	Alignment	not modelled	88.6	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
24	c3ds8A	Alignment	not modelled	88.2	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin2722 protein; PDBTitle: the crystal structure of the gene lin2722 products from listeria2 innocua
25	d1mo2a	Alignment	not modelled	87.5	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
26	c1mo2A	Alignment	not modelled	87.5	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
27	c2cbgA	Alignment	not modelled	87.3	14	PDB header: hydrolase Chain: A: PDB Molecule: fengycin synthetase; PDBTitle: crystal structure of the pmf-inhibited thioesterase domain of the2 fengycin biosynthesis cluster
28	c4qnnC	Alignment	not modelled	86.9	10	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

29	c4xjvA	Alignment	not modelled	85.7	15	PDB header: hydrolase Chain: A: PDB Molecule: s-acyl fatty acid synthase thioesterase, medium chain; PDBTitle: crystal structure of human thioesterase 2
30	c2h7xA	Alignment	not modelled	84.9	20	PDB header: hydrolase Chain: A: PDB Molecule: type i polyketide synthase pikaiv; PDBTitle: pikromycin thioesterase adduct with reduced triketide2 affinity label
31	c5d8mA	Alignment	not modelled	84.3	15	PDB header: hydrolase Chain: A: PDB Molecule: metagenomic carboxyl esterase mgs0156; PDBTitle: crystal structure of the metagenomic carboxyl esterase mgs0156
32	c2vsqA	Alignment	not modelled	82.3	17	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
33	c2zyiB	Alignment	not modelled	80.3	20	PDB header: hydrolase Chain: B: PDB Molecule: lipase, putative; PDBTitle: a. fulgidus lipase with fatty acid fragment and calcium
34	c5f2hA	Alignment	not modelled	80.0	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
35	c3lcrA	Alignment	not modelled	79.9	18	PDB header: hydrolase Chain: A: PDB Molecule: tautomycetin biosynthetic pks; PDBTitle: thioesterase from tautomycetin biosynthetic pathway
36	c4zxiA	Alignment	not modelled	77.9	18	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	c4x96B	Alignment	not modelled	76.2	23	PDB header: transferase Chain: B: PDB Molecule: phosphatidylcholine-sterol acyltransferase; PDBTitle: low resolution crystal structure of lecithin:cholesterol2 acyltransferase (lcat; residues 21-397)
38	c4x91C	Alignment	not modelled	73.1	21	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)
39	d3b5ea1	Alignment	not modelled	72.0	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
40	d1xkta	Alignment	not modelled	71.1	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
41	c6cl4A	Alignment	not modelled	70.4	15	PDB header: hydrolase Chain: A: PDB Molecule: lipase c12; PDBTitle: lipc12 - lipase from metagenomics
42	c3og9A	Alignment	not modelled	69.4	14	PDB header: hydrolase Chain: A: PDB Molecule: protein yahd a copper inducible hydrolase; PDBTitle: structure of yahd with malic acid
43	c2h1iA	Alignment	not modelled	68.6	25	PDB header: hydrolase Chain: A: PDB Molecule: carboxylesterase; PDBTitle: crystal structure of the bacillus cereus carboxylesterase
44	d1uxoa	Alignment	not modelled	67.4	9	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: YdeN-like
45	d1ispa	Alignment	not modelled	67.3	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
46	d2h1ia1	Alignment	not modelled	67.0	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
47	c4f21G	Alignment	not modelled	65.6	29	PDB header: hydrolase/hydrolase inhibitor Chain: G: PDB Molecule: carboxylesterase/phospholipase family protein; PDBTitle: crystal structure of carboxylesterase/phospholipase family protein2 from francisella tularensis
48	c2veoA	Alignment	not modelled	65.5	21	PDB header: hydrolase Chain: A: PDB Molecule: lipase a; PDBTitle: x-ray structure of candida antarctica lipase a in its closed state.
49	c3h2iA	Alignment	not modelled	65.4	13	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
50	d2r8ba1	Alignment	not modelled	63.8	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
51	d1lppb2	Alignment	not modelled	61.6	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
52	d1bu8a2	Alignment	not modelled	57.7	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
53	c2oryA	Alignment	not modelled	55.7	14	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: crystal structure of m37 lipase
54	c3p3dA	Alignment	not modelled	55.4	26	PDB header: nuclear protein Chain: A: PDB Molecule: nucleoporin 53; PDBTitle: crystal structure of the nup53 rrm domain from pichia guilliermondii
55	c4b0cA	Alignment	not modelled	55.2	12	PDB header: hydrolase Chain: A: PDB Molecule: phospholipase/carboxylesterase;

55	c410cA_	Alignment	not modelled	53.2	14	PDBTitle: crystal structure of phospholipase/carboxylesterase from dyadobacter2 fermentans dsm 18053 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
56	c2r8bA_	Alignment	not modelled	54.6	15	PDB header: hydrolase Chain: A: PDB Molecule: phb depolymerase phaz7; PDBTitle: phaz7 depolymerase from paucimonas lemoignei
57	c2vtvA_	Alignment	not modelled	54.4	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
58	d1gp1a2	Alignment	not modelled	54.2	20	PDB header: hydrolase Chain: A: PDB Molecule: putative lipase; PDBTitle: crystal structure of the lipase from proteus mirabilis
59	c4gw3A_	Alignment	not modelled	53.9	19	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
60	c4fleA_	Alignment	not modelled	53.0	22	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
61	d1etha2	Alignment	not modelled	51.8	18	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the hypothetical protein from ruminiclostridium2 thermocellum atcc 27405
62	c4z8zA_	Alignment	not modelled	50.9	7	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
63	c4nfvB_	Alignment	not modelled	50.5	19	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
64	c4eziA_	Alignment	not modelled	50.3	9	PDB header: protein transport Chain: B: PDB Molecule: nucleoporin nup53; PDBTitle: crystal structure of the yeast nucleoporin
65	c5uazB_	Alignment	not modelled	49.7	30	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
66	c2qjwA_	Alignment	not modelled	48.8	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
67	d1cv1a_	Alignment	not modelled	48.5	20	PDB header: hydrolase Chain: B: PDB Molecule: siderophore biosynthesis lipase/esterase, putative; PDBTitle: siderophore hydrolase estb from aspergillus fumigatus
68	c6gupB_	Alignment	not modelled	47.6	12	PDB header: hydrolase Chain: D: PDB Molecule: thioesterase; PDBTitle: redj with peg molecule bound in the active site
69	c3qmwD_	Alignment	not modelled	44.9	20	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
70	c5h3bA_	Alignment	not modelled	44.7	18	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: se_1780 protein; PDBTitle: se_1780 protein of unknown function from staphylococcus epidermidis.
71	c3fleB_	Alignment	not modelled	44.6	5	PDB header: hydrolase Chain: B: PDB Molecule: lipase 46 kda form; PDBTitle: crystal structure of staphylococcus hyicus lipase
72	c2h1hB_	Alignment	not modelled	43.4	23	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
73	d1rp1a2	Alignment	not modelled	42.5	16	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
74	c2m4mA_	Alignment	not modelled	42.3	30	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
75	d1thga_	Alignment	not modelled	40.1	29	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
76	d4lipd_	Alignment	not modelled	39.5	20	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: rhizomucor miehei lipase propeptide complex, native
77	c6qppA_	Alignment	not modelled	39.4	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
78	d1hplA2	Alignment	not modelled	38.4	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
79	d3tglA_	Alignment	not modelled	36.9	16	PDB header: hydrolase Chain: B: PDB Molecule: rifr; PDBTitle: rifr - type ii thioesterase from rifamycin nrps/pks biosynthetic2 pathway - form 1
80	c3flaB_	Alignment	not modelled	36.8	23	PDB header: hydrolase

81	c3bdvB_	Alignment	not modelled	35.1	30	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
82	d1tiaa_	Alignment	not modelled	33.3	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
83	c2y6vB_	Alignment	not modelled	32.8	18	PDB header: hydrolase Chain: B: PDB Molecule: peroxisomal membrane protein lpx1; PDBTitle: peroxisomal alpha-beta-hydrolase lpx1 (yor084w) from saccharomyces2 cerevisiae (crystal form i)
84	c4r1dA_	Alignment	not modelled	31.8	19	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of tle4-tli4 complex
85	c5xk2A_	Alignment	not modelled	31.5	13	PDB header: hydrolase Chain: A: PDB Molecule: diacylglycerol lipase; PDBTitle: crystal structure of mono- and diacylglycerol lipase from aspergillus2 oryzae
86	c5gw8A_	Alignment	not modelled	31.1	17	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
87	c2pvsB_	Alignment	not modelled	31.1	26	PDB header: hydrolase Chain: B: PDB Molecule: pancreatic lipase-related protein 2; PDBTitle: structure of human pancreatic lipase related protein 22 mutant n336q
88	c3ilsA_	Alignment	not modelled	30.6	13	PDB header: hydrolase Chain: A: PDB Molecule: afatoxin biosynthesis polyketide synthase; PDBTitle: the thioesterase domain from pksa
89	c4o5pB_	Alignment	not modelled	28.3	17	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein from pseudomonas2 aeruginosa
90	d1ex9a_	Alignment	not modelled	27.9	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
91	d1lghb_	Alignment	not modelled	27.5	20	Fold: Light-harvesting complex subunits Superfamily: Light-harvesting complex subunits Family: Light-harvesting complex subunits
92	c5ja2A_	Alignment	not modelled	26.5	13	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
93	c5d6oB_	Alignment	not modelled	25.3	15	PDB header: transferase Chain: B: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: orthorhombic crystal structure of an acetyler hydrolase from2 corynebacterium glutamicum
94	c4qwwA_	Alignment	not modelled	25.0	42	PDB header: hydrolase/immune system Chain: A: PDB Molecule: acetylcholinesterase; PDBTitle: crystal structure of the fab410-bfache complex
95	c5ugzA_	Alignment	not modelled	24.9	20	PDB header: hydrolase Chain: A: PDB Molecule: putative thioesterase; PDBTitle: crystal structure of clbq from the colibactin nrps/pks pathway
96	c1gplA_	Alignment	not modelled	23.7	21	PDB header: serine esterase Chain: A: PDB Molecule: rp2 lipase; PDBTitle: rp2 lipase
97	d2ha2a1	Alignment	not modelled	23.5	32	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like
98	c1qgeD_	Alignment	not modelled	23.5	19	PDB header: hydrolase Chain: D: PDB Molecule: protein (triacylglycerol hydrolase); PDBTitle: new crystal form of pseudomonas glumae (formerly chromobacterium2 viscosum atcc 6918) lipase
99	c3g7nA_	Alignment	not modelled	23.1	8	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: crystal structure of a triacylglycerol lipase from penicillium2 expansum at 1.3
100	d1dx4a_	Alignment	not modelled	22.7	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like
101	d1pjaa_	Alignment	not modelled	22.5	10	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterases
102	c1pjaA_	Alignment	not modelled	22.5	10	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)
103	c3uuuA_	Alignment	not modelled	22.3	16	PDB header: hydrolase Chain: A: PDB Molecule: lip1, secretory lipase (family 3); PDBTitle: crystal structure of mono- and diacylglycerol lipase from malassezia2 globosa
104	c2w6cX_	Alignment	not modelled	20.9	26	PDB header: hydrolase Chain: X: PDB Molecule: acetylcholinesterase; PDBTitle: ache in complex with a bis(-)-nor-meptazinol derivative
105	c3fkeB_	Alignment	not modelled	20.9	38	PDB header: rna binding protein Chain: B: PDB Molecule: polymerase cofactor vp35; PDBTitle: structure of the ebola vp35 interferon inhibitory domain
106	c5w8pA_	Alignment	not modelled	20.5	20	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: homoserine transacetylase meta from mycobacterium abscessus
						PDB header: hydrolase

107	c2pplA_	Alignment	not modelled	20.3	19	Chain: A: PDB Molecule: pancreatic lipase-related protein 1; PDBTitle: human pancreatic lipase-related protein 1
108	c1hplB_	Alignment	not modelled	20.3	16	PDB header: hydrolase(carboxylic esterase) Chain: B: PDB Molecule: lipase; PDBTitle: horse pancreatic lipase. the crystal structure at 2.3 angstroms2 resolution