Phyre²

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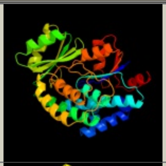
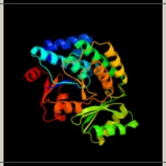
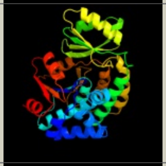
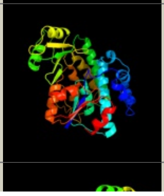
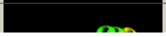
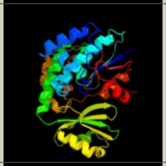
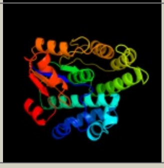
Description	P0AAI9
Date	Thu Jan 5 11:13:02 GMT 2012
Unique Job ID	67b84eb8ab23ea25

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2g2oA_	Alignment		100.0	100	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malonyl coa-acyl carrier protein transacylase; **PDBTitle:** structure of e.coli fabd complexed with sulfate
2	c3eenA_	Alignment		100.0	54	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malonyl coa-acp transacylase; **PDBTitle:** crystal structure of malonyl-coa:acyl carrier protein transacylase2 (fabd), xoo0880, from xanthomonas oryzae pv. oryzae kacc10331
3	c3im8A_	Alignment		100.0	45	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malonyl acyl carrier protein transacylase; **PDBTitle:** crystal structure of mcat from streptococcus pneumoniae
4	c3ezoA_	Alignment		100.0	55	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malonyl coa-acyl carrier protein transacylase; **PDBTitle:** crystal structure of acyl-carrier-protein s-2 malonyltransferase from burkholderia pseudomallei 1710b
5	c3tqeA_	Alignment		100.0	54	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malonyl-coa-[acyl-carrier-protein] transacylase; **PDBTitle:** structure of the malonyl coa-acyl carrier protein transacylase (fabd)2 from coxiella burnetii
6	c3qatB_	Alignment		100.0	43	**PDB header:**transferase **Chain:** B: **PDB Molecule:**malonyl coa-acyl carrier protein transacylase; **PDBTitle:** crystal structure of acyl-carrier-protein-s-malonyltransferase from2 bartonella henselae
7	c3ptwA_	Alignment		100.0	39	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malonyl coa-acyl carrier protein transacylase; **PDBTitle:** crystal structure of malonyl coa-acyl carrier protein transacylase2 from clostridium perfringens atcc 13124
8	c3im9A_	Alignment		100.0	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malonyl coa-acyl carrier protein transacylase; **PDBTitle:** crystal structure of mcat from staphylococcus aureus
9	c2qj3B_	Alignment		100.0	32	**PDB header:**transferase **Chain:** B: **PDB Molecule:**malonyl coa-acyl carrier protein transacylase; **PDBTitle:** mycobacterium tuberculosis fabd
10	c2cuyA_	Alignment		100.0	44	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malonyl coa-[acyl carrier protein] transacylase; **PDBTitle:** crystal structure of malonyl coa-acyl carrier protein transacylase2 from thermus thermophilus hb8
11	c2cdh9_	Alignment		100.0	36	**PDB header:**transferase **Chain:** 9: **PDB Molecule:**acetyl transferase; **PDBTitle:** architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
						

12	c2h1yA_	Alignment		100.0	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malonyl coenzyme a-acyl carrier protein transacylase; **PDBTitle:** crystal structure of malonyl-coa:acyl carrier protein transacylase2 (mcat) from helicobacter pylori
13	c3rgiA_	Alignment		100.0	40	**PDB header:**transferase **Chain:** A: **PDB Molecule:**disd protein; **PDBTitle:** trans-acting transferase from disorazole synthase
14	c2qo3A_	Alignment		100.0	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**eryaii erythromycin polyketide synthase modules 3 and 4; **PDBTitle:** crystal structure of [ks3][at3] didomain from module 3 of 6-2 deoxyerthronolide b synthase
15	c2c2nA_	Alignment		100.0	34	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malonyl coa-acyl carrier protein transacylase; **PDBTitle:** structure of human mitochondrial malonyltransferase
16	c3g87A_	Alignment		100.0	37	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malonyl coa-acyl carrier protein transacylase; **PDBTitle:** crystal structure of malonyl coa-acyl carrier protein transacylase2 from burkholderia pseudomallei using dried seaweed as nucleant or3 protease
17	c2hg4A_	Alignment		100.0	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**6-deoxyerythronolide b synthase; **PDBTitle:** structure of the ketosynthase-acyltransferase didomain of module 52 from debs.
18	c3hhdC_	Alignment		100.0	21	**PDB header:**transferase, hydrolase **Chain:** C: **PDB Molecule:**fatty acid synthase; **PDBTitle:** structure of the human fatty acid synthase ks-mat didomain2 as a framework for inhibitor design.
19	c2jfkD_	Alignment		100.0	20	**PDB header:**transferase **Chain:** D: **PDB Molecule:**fatty acid synthase; **PDBTitle:** structure of the mat domain of human fas with malonyl-coa
20	d1mlaa1	Alignment		100.0	100	**Fold:**FabD/lysophospholipase-like **Superfamily:**FabD/lysophospholipase-like **Family:**FabD-like
21	c2vz8B_	Alignment	not modelled	100.0	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**fatty acid synthase; **PDBTitle:** crystal structure of mammalian fatty acid synthase
22	d1nm2a1	Alignment	not modelled	100.0	41	**Fold:**FabD/lysophospholipase-like **Superfamily:**FabD/lysophospholipase-like **Family:**FabD-like
23	c2vkzH_	Alignment	not modelled	100.0	24	**PDB header:**transferase **Chain:** H: **PDB Molecule:**fatty acid synthase subunit beta; **PDBTitle:** structure of the cerulenin-inhibited fungal fatty acid2 synthase type i multienzyme complex
24	c2uvaI_	Alignment	not modelled	100.0	22	**PDB header:**transferase **Chain:** I: **PDB Molecule:**fatty acid synthase beta subunits; **PDBTitle:** crystal structure of fatty acid synthase from thermomyces2 lanuginosus at 3.1 angstrom resolution. this file contains3 the beta subunits of the fatty acid synthase. the entire4 crystal structure consists of one heterododecameric fatty5 acid synthase and is described in remark 400
25	d1mlaa2	Alignment	not modelled	99.3	100	**Fold:**Ferredoxin-like **Superfamily:**Probable ACP-binding domain of malonyl-CoA ACP transacylase **Family:**Probable ACP-binding domain of malonyl-CoA ACP transacylase
26	d1nm2a2	Alignment	not modelled	98.7	27	**Fold:**Ferredoxin-like **Superfamily:**Probable ACP-binding domain of malonyl-CoA ACP transacylase **Family:**Probable ACP-binding domain of malonyl-CoA ACP transacylase
27	c2uv9B_	Alignment	not modelled	98.7	28	**PDB header:**transferase **Chain:** B: **PDB Molecule:**fatty acid synthase alpha subunits; **PDBTitle:** crystal structure of fatty acid synthase from thermomyces2 lanuginosus at 3.1 angstrom resolution. this file contains3 the alpha subunits of the fatty acid synthase. the entire4

						crystal structure consists of one heterododecameric fatty5 acid synthase and is described in remark 400
28	c2vkzC_	Alignment	not modelled	98.5	26	**PDB header:**transferase **Chain:** C: **PDB Molecule:**fatty acid synthase subunit alpha; **PDBTitle:** structure of the cerulenin-inhibited fungal fatty acid2 synthase type i multienzyme complex
29	c2uv8C_	Alignment	not modelled	98.5	26	**PDB header:**transferase **Chain:** C: **PDB Molecule:**fatty acid synthase subunit alpha (fas2); **PDBTitle:** crystal structure of yeast fatty acid synthase with stalled2 acyl carrier protein at 3.1 angstrom resolution
30	c3iraA_	Alignment	not modelled	83.7	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein; **PDBTitle:** the crystal structure of one domain of the conserved protein from2 methanosarcina mazei go1
31	c3i1iA_	Alignment	not modelled	79.7	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**homoserine o-acetyltransferase; **PDBTitle:** x-ray crystal structure of homoserine o-acetyltransferase from2 bacillus anthracis
32	c3ds8A_	Alignment	not modelled	78.4	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin2722 protein; **PDBTitle:** the crysatl structure of the gene lin2722 products from listeria2 innocua
33	d2vata1	Alignment	not modelled	73.8	22	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**O-acetyltransferase
34	d2b61a1	Alignment	not modelled	72.6	20	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**O-acetyltransferase
35	c1cr6A_	Alignment	not modelled	71.7	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**epoxide hydrolase; **PDBTitle:** crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
36	d2pl5a1	Alignment	not modelled	71.4	22	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**O-acetyltransferase
37	d1ex9a_	Alignment	not modelled	71.1	23	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Bacterial lipase
38	c2vavL_	Alignment	not modelled	70.2	20	**PDB header:**transferase **Chain:** L: **PDB Molecule:**acetyl-coa--deacetylcephalosporin c **PDBTitle:** crystal structure of deacetylcephalosporin c2 acetyltransferase (dac-soak)
39	c3lp5A_	Alignment	not modelled	69.6	13	**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
40	d1xkta_	Alignment	not modelled	67.8	23	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Thioesterase domain of polypeptide, polyketide and fatty acid synthases
41	c3bdvB_	Alignment	not modelled	67.8	28	**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
42	c1qgeD_	Alignment	not modelled	67.3	28	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**protein (triacylglycerol hydrolase); **PDBTitle:** new crystal form of pseudomonas glumae (formerly chromobacterium2 viscosum atcc 6918) lipase
43	c1mo2A_	Alignment	not modelled	66.8	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**erythronolide synthase, modules 5 and 6; **PDBTitle:** thioesterase domain from 6-deoxyerythronolide synthase2 (debs te), ph 8.5
44	d1mo2a_	Alignment	not modelled	66.8	24	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Thioesterase domain of polypeptide, polyketide and fatty acid synthases
45	c2q0xA_	Alignment	not modelled	66.7	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** alpha/beta hydrolase fold protein of unknown function
46	c3lcrA_	Alignment	not modelled	64.5	32	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tautomycetin biosynthetic pks; **PDBTitle:** thioesterase from tautomycetin biosynthhetic pathway
47	d1ispa_	Alignment	not modelled	64.4	23	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Bacterial lipase
48	d1zkda1	Alignment	not modelled	63.3	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**RPA4359-like
49	c3l80A_	Alignment	not modelled	62.5	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein smu.1393c; **PDBTitle:** crystal structure of smu.1393c from streptococcus mutans ua159
50	c3giwA_	Alignment	not modelled	61.9	16	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**protein of unknown function duf574; **PDBTitle:** crystal structure of a duf574 family protein (sav_2177) from2 streptomyces avermitilis ma-4680 at 1.45 a resolution
51	c2h7xA_	Alignment	not modelled	61.0	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**type i polyketide synthase pikaiv; **PDBTitle:** pikromycin thioesterase adduct with reduced triketide2 affinity label
52	d1lpbb2	Alignment	not modelled	59.9	21	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Pancreatic lipase, N-terminal domain
						PDB header:hydrolase

53	c2zyiB_	Alignment	not modelled	58.7	20	**Chain:** B: **PDB Molecule:**lipase, putative; **PDBTitle:** a. fulgidus lipase with fatty acid fragment and calcium
54	c3qmwD_	Alignment	not modelled	58.0	20	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**thioesterase; **PDBTitle:** redj with peg molecule bound in the active site
55	d1bu8a2	Alignment	not modelled	57.2	30	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Pancreatic lipase, N-terminal domain
56	d4lipd_	Alignment	not modelled	56.7	28	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Bacterial lipase
57	c2y6vB_	Alignment	not modelled	56.4	42	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**peroxisomal membrane protein lpx1; **PDBTitle:** peroxisomal alpha-beta-hydrolase lpx1 (yor084w) from2 saccharomyces cerevisiae (crystal form i)
58	c3fleB_	Alignment	not modelled	55.9	23	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**se_1780 protein; **PDBTitle:** se_1780 protein of unknown function from staphylococcus epidermidis.
59	d1k8qa_	Alignment	not modelled	55.1	19	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Gastric lipase
60	c2qs9A_	Alignment	not modelled	54.6	23	**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
61	c3flaB_	Alignment	not modelled	53.9	34	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**rifr; **PDBTitle:** rifr - type ii thioesterase from rifamycin nrps/pks biosynthetic2 pathway - form 1
62	c2qmqA_	Alignment	not modelled	53.6	17	**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
63	d2h7xa1	Alignment	not modelled	53.6	38	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Thioesterase domain of polypeptide, polyketide and fatty acid synthases
64	d1hlga_	Alignment	not modelled	52.6	20	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Gastric lipase
65	c1i4wA_	Alignment	not modelled	52.1	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**mitochondrial replication protein mtf1; **PDBTitle:** the crystal structure of the transcription factor sc-mttfb2 offers intriguing insights into mitochondrial transcription
66	d1i4wa_	Alignment	not modelled	52.1	12	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**rRNA adenine dimethylase-like
67	d1cvla_	Alignment	not modelled	52.0	28	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Bacterial lipase
68	c2cbgA_	Alignment	not modelled	50.5	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**fengycin synthetase; **PDBTitle:** crystal structure of the pmsf-inhibited thioesterase domain2 of the fengycin biosynthesis cluster
69	d1uxoa_	Alignment	not modelled	49.7	26	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**YdeN-like
70	d1rp1a2	Alignment	not modelled	49.6	27	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Pancreatic lipase, N-terminal domain
71	c3qvmA_	Alignment	not modelled	48.7	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**olei00960; **PDBTitle:** the structure of olei00960, a hydrolase from oleispira antarctica
72	c1pjaA_	Alignment	not modelled	47.8	6	**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)
73	d1pjaa_	Alignment	not modelled	47.8	6	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Thioesterases
74	d1jmkc_	Alignment	not modelled	46.8	23	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Thioesterase domain of polypeptide, polyketide and fatty acid synthases
75	c1gplA_	Alignment	not modelled	46.5	29	**PDB header:**serine esterase **Chain:** A: **PDB Molecule:**rp2 lipase; **PDBTitle:** rp2 lipase
76	c2rauA_	Alignment	not modelled	45.2	23	**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
77	d1etha2	Alignment	not modelled	45.1	32	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Pancreatic lipase, N-terminal domain
78	d1tcaa_	Alignment	not modelled	45.0	18	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
						PDB header:transferase

79	c2qe6B_	Alignment	not modelled	44.9	12	**Chain:** B: **PDB Molecule:**uncharacterized protein tfu_2867; **PDBTitle:** crystal structure of a putative methyltransferase (tfu_2867) from2 thermobifida fusca yx at 1.95 a resolution
80	c2qjwA_	Alignment	not modelled	44.7	32	**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
81	d2dsta1	Alignment	not modelled	42.5	7	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**TTHA1544-like
82	c1hplB_	Alignment	not modelled	41.9	32	**PDB header:**hydrolase(carboxylic esterase) **Chain:** B: **PDB Molecule:**lipase; **PDBTitle:** horse pancreatic lipase. the crystal structure at 2.32 angstroms resolution
83	d1gpla2	Alignment	not modelled	39.3	23	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Pancreatic lipase, N-terminal domain
84	c3h04A_	Alignment	not modelled	39.1	25	**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
85	d1hpla2	Alignment	not modelled	38.5	27	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Pancreatic lipase, N-terminal domain
86	c3ilsA_	Alignment	not modelled	35.7	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aflatoxin biosynthesis polyketide synthase; **PDBTitle:** the thioesterase domain from pksa
87	d1r88a_	Alignment	not modelled	34.8	30	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Mycobacterial antigens
88	c2vtvA_	Alignment	not modelled	32.7	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phb depolymerase phaz7; **PDBTitle:** phaz7 depolymerase from paucimonas lemoignei
89	d1uwca_	Alignment	not modelled	32.4	28	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
90	c2pvsB_	Alignment	not modelled	29.7	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**pancreatic lipase-related protein 2; **PDBTitle:** structure of human pancreatic lipase related protein 22 mutant n336q
91	d1dqza_	Alignment	not modelled	29.1	30	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Mycobacterial antigens
92	d1ei9a_	Alignment	not modelled	28.8	11	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Thioesterases
93	d1sfra_	Alignment	not modelled	27.9	30	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Mycobacterial antigens
94	c2veoA_	Alignment	not modelled	27.7	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipase a; **PDBTitle:** x-ray structure of candida antarctica lipase a in its2 closed state.
95	c1rp1A_	Alignment	not modelled	27.5	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pancreatic lipase related protein 1; **PDBTitle:** dog pancreatic lipase related protein 1
96	c3og9A_	Alignment	not modelled	27.5	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein yahd a copper inducible hydrolase; **PDBTitle:** structure of yahd with malic acid
97	c2pplA_	Alignment	not modelled	27.4	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pancreatic lipase-related protein 1; **PDBTitle:** human pancreatic lipase-related protein 1
98	c3uzuA_	Alignment	not modelled	27.1	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribosomal rna small subunit methyltransferase a; **PDBTitle:** the structure of the ribosomal rna small subunit methyltransferase a2 from burkholderia pseudomallei
99	c2jbwB_	Alignment	not modelled	26.5	29	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**2,6-dihydroxy-pseudo-oxynicotine hydrolase; **PDBTitle:** crystal structure of the 2,6-dihydroxy-pseudo-oxynicotine2 hydrolase.
100	d2jbwa1	Alignment	not modelled	25.9	29	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**2,6-dihydropseudooxynicotine hydrolase-like
101	c2r11D_	Alignment	not modelled	25.8	22	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**carboxylesterase np; **PDBTitle:** crystal structure of putative hydrolase (2632844) from2 bacillus subtilis at 1.96 a resolution
102	d3b5ea1	Alignment	not modelled	25.7	19	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase/thioesterase 1
103	d3tgla_	Alignment	not modelled	25.5	34	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
104	c3o0dF_	Alignment	not modelled	25.3	25	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**triacylglycerol lipase; **PDBTitle:** crystal structure of lip2 lipase from yarrowia lipolytica at 1.7 a2 resolution
						PDB header:hydrolase

105	c3d59B_	Alignment	not modelled	25.2	25	**Chain:** B: **PDB Molecule:**platelet-activating factor acetylhydrolase; **PDBTitle:** crystal structure of human plasma platelet activating2 factor acetylhydrolase
106	c2ecfA_	Alignment	not modelled	25.0	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dipeptidyl peptidase iv; **PDBTitle:** crystal structure of dipeptidyl aminopeptidase iv from2 stenotrophomonas maltophilia
107	c3fnbB_	Alignment	not modelled	24.2	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**acylaminoacyl peptidase smu_737; **PDBTitle:** crystal structure of acylaminoacyl peptidase smu_737 from2 streptococcus mutans ua159
108	c2fx5A_	Alignment	not modelled	23.7	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipase; **PDBTitle:** pseudomonas mendocina lipase
109	c3fuxB_	Alignment	not modelled	22.8	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dimethyladenosine transferase; **PDBTitle:** t. thermophilus 16s rrna a1518 and a1519 methyltransferase (ksga) in2 complex with 5'-methylthioadenosine in space group p212121
110	d1jqna_	Alignment	not modelled	21.7	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate carboxylase
111	c2hu7A_	Alignment	not modelled	21.3	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acylamino-acid-releasing enzyme; **PDBTitle:** binding of inhibitors by acylaminoacyl peptidase
112	c3g7nA_	Alignment	not modelled	21.1	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipase; **PDBTitle:** crystal structure of a triacylglycerol lipase from2 penicillium expansum at 1.3
113	d3c8da2	Alignment	not modelled	21.0	30	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase
114	c3grrA_	Alignment	not modelled	20.6	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dimethyladenosine transferase; **PDBTitle:** crystal structure of the complex between s-adenosyl homocysteine and2 methanocaldococcus jannaschi dim1.
115	c3fydA_	Alignment	not modelled	20.6	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable dimethyladenosine transferase; **PDBTitle:** crystal structure of dim1 from the thermophilic archeon,2 methanocaldococcus jannaschi
116	d1ku0a_	Alignment	not modelled	20.5	19	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Bacterial lipase
117	c3azqA_	Alignment	not modelled	20.5	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aminopeptidase; **PDBTitle:** crystal structure of puromycin hydrolase s511a mutant complexed with2 pgg
118	d1tiaa_	Alignment	not modelled	20.3	25	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
119	d1tiba_	Alignment	not modelled	20.1	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases