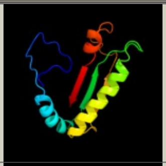
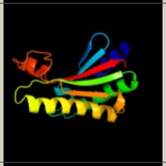
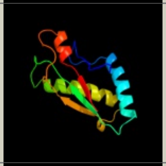
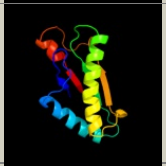
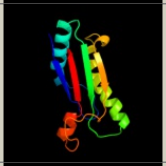
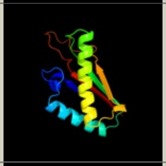
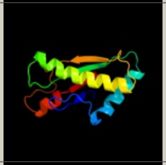
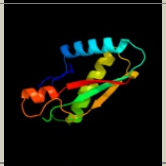
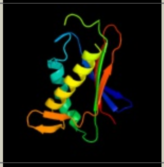
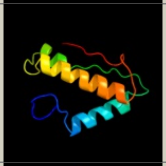
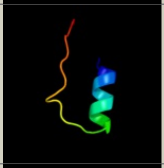
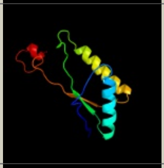
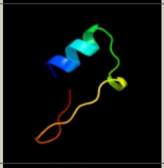
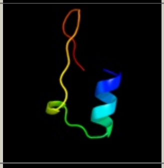
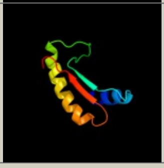
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P37665
Date	Wed Jan 25 15:20:53 GMT 2012
Unique Job ID	8b52b1282e6cc1ad

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2l26A_	Alignment		100.0	46	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**uncharacterized protein rv0899/mt0922; **PDBTitle:** rv0899 from mycobacterium tuberculosis contains two separated domains
2	c2k1sA_	Alignment		100.0	100	**PDB header:**lipoprotein **Chain:** A: **PDB Molecule:**inner membrane lipoprotein yiad; **PDBTitle:** solution nmr structure of the folded c-terminal fragment of yiad from2 escherichia coli. northeast structural genomics consortium target3 er553.
3	c3khnB_	Alignment		100.0	22	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**motb protein, putative; **PDBTitle:** crystal structure of putative motb like protein dvu_22282 from desulfovibrio vulgaris.
4	c2kgwA_	Alignment		100.0	47	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein a; **PDBTitle:** solution structure of the carboxy-terminal domain of ompatb, a pore2 forming protein from mycobacterium tuberculosis
5	d2aizp1	Alignment		100.0	30	**Fold:**Bacillus chorismate mutase-like **Superfamily:**OmpA-like **Family:**OmpA-like
6	c3td4D_	Alignment		100.0	46	**PDB header:**membrane protein,peptide binding protein **Chain:** D: **PDB Molecule:**outer membrane protein omp38; **PDBTitle:** crystal structure of ompa-like domain from acinetobacter baumannii in2 complex with diaminopimelate
7	d1r1ma_	Alignment		100.0	27	**Fold:**Bacillus chorismate mutase-like **Superfamily:**OmpA-like **Family:**OmpA-like
8	c1r1mA_	Alignment		100.0	27	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein class 4; **PDBTitle:** structure of the ompa-like domain of rmpm from neisseria2 meningitidis
9	d2hqsc1	Alignment		100.0	28	**Fold:**Bacillus chorismate mutase-like **Superfamily:**OmpA-like **Family:**OmpA-like
10	c3cyqM_	Alignment		100.0	30	**PDB header:**membrane protein **Chain:** M: **PDB Molecule:**chemotaxis protein motb; **PDBTitle:** the crystal structure of the complex of the c-terminal domain of2 helicobacter pylori motb (residues 125-256) with n-acetylmuramic acid
11	c2zvyB_	Alignment		100.0	21	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**chemotaxis protein motb; **PDBTitle:** structure of the periplasmic domain of motb from salmonella2 (crystal form ii)

12	c3ldtA_	Alignment		100.0	28	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein, ompa family protein; **PDBTitle:** crystal structure of an outer membrane protein(ompa)from2 legionella pneumophila
13	c3oonA_	Alignment		99.9	28	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein (tpn50); **PDBTitle:** the structure of an outer membrance protein from borrelia burgdorferi2 b31
14	c2zovA_	Alignment		99.9	24	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**chemotaxis protein motb; **PDBTitle:** structure of the periplasmic domain of motb from salmonella2 (crystal form i)
15	c2zf8A_	Alignment		99.8	25	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**component of sodium-driven polar flagellar motor; **PDBTitle:** crystal structure of moty
16	c2r6hC_	Alignment		60.8	25	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nadh:ubiquinone oxidoreductase, na translocating, f **PDBTitle:** crystal structure of the domain comprising the nad binding and the fad2 binding regions of the nadh:ubiquinone oxidoreductase, na3 translocating, f subunit from porphyromonas gingivalis
17	c2qw5B_	Alignment		55.6	11	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**xylose isomerase-like tim barrel; **PDBTitle:** crystal structure of a putative sugar phosphate isomerase/epimerase2 (ava4194) from anabaena variabilis atcc 29413 at 1.78 a resolution
18	d1gvha3	Alignment		51.9	24	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Flavohemoglobin, C-terminal domain
19	c1gvhA_	Alignment		51.9	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**flavohemoprotein; **PDBTitle:** the x-ray structure of ferric escherichia coli2 flavohemoglobin reveals an unespected geometry of the3 distal heme pocket
20	d1tiaa_	Alignment		49.4	21	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
21	c3cqyA_	Alignment	not modelled	44.1	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**anhydro-n-acetylmuramic acid kinase; **PDBTitle:** crystal structure of a functionally unknown protein (so_1313) from2 shewanella oneidensis mr-1
22	d1tiba_	Alignment	not modelled	42.9	25	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
23	d1cqxa3	Alignment	not modelled	38.9	25	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Flavohemoglobin, C-terminal domain
24	c3ngmB_	Alignment	not modelled	38.6	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**extracellular lipase; **PDBTitle:** crystal structure of lipase from gibberella zeae
25	c1cqxB_	Alignment	not modelled	33.4	25	**PDB header:**lipid binding protein **Chain:** B: **PDB Molecule:**flavohemoprotein; **PDBTitle:** crystal structure of the flavohemoglobin from alcaligenes eutrophus at2 1.75 a resolution
26	c2gpjA_	Alignment	not modelled	33.3	9	**PDB header:**fad-binding protein **Chain:** A: **PDB Molecule:**siderophore-interacting protein; **PDBTitle:** crystal structure of a siderophore-interacting protein (sputcn32_0076)2 from shewanella putrefaciens cn-32 at 2.20 a resolution
27	c3qbwA_	Alignment	not modelled	32.6	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**anhydro-n-acetylmuramic acid kinase; **PDBTitle:** crystal structure of pseudomonas aeruginosa 1,6-anhydro-n-2 actetylmuramic acid kinase (anmk) bound to adenosine diphosphate
28	c3g7nA_	Alignment	not modelled	32.6	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipase; **PDBTitle:** crystal structure of a triacylglycerol lipase from2 penicillium expansum at 1.3

29	d1krha2	Alignment	not modelled	31.3	23	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Aromatic dioxygenase reductase-like
30	c3o0dF_	Alignment	not modelled	30.9	25	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**triacylglycerol lipase; **PDBTitle:** crystal structure of lip2 lipase from yarrowia lipolytica at 1.7 a2 resolution
31	c1tvcA_	Alignment	not modelled	30.7	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methane monooxygenase component c; **PDBTitle:** fad and nadh binding domain of methane monooxygenase2 reductase from methylococcus capsulatus (bath)
32	d1tvca2	Alignment	not modelled	29.9	11	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Aromatic dioxygenase reductase-like
33	d1uzhc1	Alignment	not modelled	26.3	15	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
34	d1uwca_	Alignment	not modelled	25.2	25	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
35	d1rbli_	Alignment	not modelled	25.0	22	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
36	d1bxni_	Alignment	not modelled	24.7	16	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
37	c1amuB_	Alignment	not modelled	23.7	14	**PDB header:**peptide synthetase **Chain:** B: **PDB Molecule:**gramicidin synthetase 1; **PDBTitle:** phenylalanine activating domain of gramicidin synthetase 12 in a complex with amp and phenylalanine
38	c3pe3D_	Alignment	not modelled	22.4	18	**PDB header:**transferase **Chain:** D: **PDB Molecule:**udp-n-acetylglucosamine--peptide n- **PDBTitle:** structure of human o-glcnac transferase and its complex with a peptide2 substrate
39	d1svdm1	Alignment	not modelled	21.2	24	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
40	c3pa8A_	Alignment	not modelled	20.6	16	**PDB header:**toxin/peptide inhibitor **Chain:** A: **PDB Molecule:**toxin b; **PDBTitle:** structure of the c. difficile tcdb cysteine protease domain in complex2 with a peptide inhibitor
41	c3iteB_	Alignment	not modelled	20.2	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**sidn siderophore synthetase; **PDBTitle:** the third adenylation domain of the fungal sidn non-2 ribosomal peptide synthetase
42	d2axla1	Alignment	not modelled	20.1	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**RecQ helicase DNA-binding domain-like
43	d8ruci_	Alignment	not modelled	16.2	31	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
44	d1xdpa4	Alignment	not modelled	15.0	18	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Polyphosphate kinase C-terminal domain
45	c1krhA_	Alignment	not modelled	14.9	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**benzoate 1,2-dioxygenase reductase; **PDBTitle:** x-ray stucture of benzoate dioxygenase reductase
46	d2o8ra4	Alignment	not modelled	14.9	24	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Polyphosphate kinase C-terminal domain
47	c1jrjA_	Alignment	not modelled	14.8	17	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**exendin-4; **PDBTitle:** solution structure of exendin-4 in 30-vol% trifluoroethanol
48	d1bwvs_	Alignment	not modelled	14.5	19	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
49	d1ir1s_	Alignment	not modelled	14.3	22	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
50	d1wdds_	Alignment	not modelled	14.3	27	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
51	d1jmxa1	Alignment	not modelled	14.3	18	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
52	d1i4ua_	Alignment	not modelled	14.2	22	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
53	d1r3na1	Alignment	not modelled	13.9	8	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
54	c3ds8A_	Alignment	not modelled	13.4	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin2722 protein; **PDBTitle:** the crysatl structure of the gene lin2722 products from listeria2 innocua
55	d1d4oa_	Alignment	not modelled	13.4	16	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Transhydrogenase domain III (dIII)

56	c1pt9B_	Alignment	not modelled	12.6	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nad(p) transhydrogenase, mitochondrial; **PDBTitle:** crystal structure analysis of the diii component of transhydrogenase2 with a thio-nicotinamide nucleotide analogue
57	c3og9A_	Alignment	not modelled	12.4	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein yahd a copper inducible hydrolase; **PDBTitle:** structure of yahd with malic acid
58	c3a9lB_	Alignment	not modelled	12.2	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**poly-gamma-glutamate hydrolase; **PDBTitle:** structure of bacteriophage poly-gamma-glutamate hydrolase
59	c1nauA_	Alignment	not modelled	12.1	18	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**glucagon; **PDBTitle:** nmr solution structure of the glucagon antagonist [deshis1,2 desphe6, glu9]glucagon amide in the presence of3 perdeuterated dodecylphosphocholine micelles
60	d3tgla_	Alignment	not modelled	12.1	25	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
61	c2bgjB_	Alignment	not modelled	12.0	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ferredoxin-nadp(h) reductase; **PDBTitle:** x-ray structure of the ferredoxin-nadp(h) reductase from2 rhodobacter capsulatus at 2.1 angstroms
62	c3iibA_	Alignment	not modelled	12.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidase m28; **PDBTitle:** crystal structure of peptidase m28 precursor (yp_926796.1) from2 shewanella amazonensis sb2b at 1.70 a resolution
63	c3l7pA_	Alignment	not modelled	11.7	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative nitrogen regulatory protein pii; **PDBTitle:** crystal structure of smu.1657c, putative nitrogen regulatory protein2 pii from streptococcus mutans
64	d1tkja1	Alignment	not modelled	10.9	17	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
65	d1lgya_	Alignment	not modelled	10.8	20	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
66	c3ca8B_	Alignment	not modelled	10.7	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein ydcf; **PDBTitle:** crystal structure of escherichia coli ydcf, an s-adenosyl-l-methionine2 utilizing enzyme
67	c2rd5D_	Alignment	not modelled	10.5	20	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**pii protein; **PDBTitle:** structural basis for the regulation of n-acetylglutamate kinase by pii2 in arabidopsis thaliana
68	d1saza1	Alignment	not modelled	10.2	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Acetokinase-like
69	c1gplA_	Alignment	not modelled	10.0	18	**PDB header:**serine esterase **Chain:** A: **PDB Molecule:**rp2 lipase; **PDBTitle:** rp2 lipase
70	c2ckcA_	Alignment	not modelled	9.9	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chromodomain-helicase-dna-binding protein 7; **PDBTitle:** solution structures of the brk domains of the human chromo2 helicase domain 7 and 8, reveals structural similarity3 with gyf domain suggesting a role in protein interaction
71	d2ckca1	Alignment	not modelled	9.9	23	**Fold:**GYF/BRK domain-like **Superfamily:**BRK domain-like **Family:**BRK domain-like
72	c2ogsA_	Alignment	not modelled	9.9	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**thermostable carboxylesterase est50; **PDBTitle:** crystal structure of the geobacillus stearothermophilus2 carboxylesterase est55 at ph 6.2
73	c3b9eA_	Alignment	not modelled	9.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitinase a; **PDBTitle:** crystal structure of inactive mutant e315m chitinase a from2 vibrio harveyi
74	c2oghA_	Alignment	not modelled	9.9	27	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor eif-1; **PDBTitle:** solution structure of yeast eif1
75	d1e32a3	Alignment	not modelled	9.8	18	**Fold:**Cdc48 domain 2-like **Superfamily:**Cdc48 domain 2-like **Family:**Cdc48 domain 2-like
76	d1amua_	Alignment	not modelled	9.8	13	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
77	d1pbya1	Alignment	not modelled	9.7	11	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
78	d1ej7s_	Alignment	not modelled	9.3	23	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
79	d2v0ea1	Alignment	not modelled	9.2	25	**Fold:**GYF/BRK domain-like **Superfamily:**BRK domain-like **Family:**BRK domain-like
80	d2nvma1	Alignment	not modelled	9.0	13	**Fold:**XisI-like **Superfamily:**XisI-like **Family:**XisI-like
81	d1wfya_	Alignment	not modelled	9.0	9	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like

						Family: Ras-binding domain, RBD
82	c3eyiB_	Alignment	not modelled	8.9	33	**PDB header:**dna binding protein/dna **Chain:** B: **PDB Molecule:**z-dna-binding protein 1; **PDBTitle:** the crystal structure of the second z-dna binding domain of2 human dai (zbp1) in complex with z-dna
83	d1gk8i_	Alignment	not modelled	8.8	13	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
84	c3mxoB_	Alignment	not modelled	8.8	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**serine/threonine-protein phosphatase pgam5, mitochondrial; **PDBTitle:** crystal structure oh human phosphoglycerate mutase family member 52 (pgam5)
85	d1uzdc1	Alignment	not modelled	8.6	13	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
86	c1f8uA_	Alignment	not modelled	8.5	18	**PDB header:**hydrolase/toxin **Chain:** A: **PDB Molecule:**acetylcholinesterase; **PDBTitle:** crystal structure of mutant e202q of human acetylcholinesterase2 complexed with green mamba venom peptide fasciculin-ii
87	d1f8ua_	Alignment	not modelled	8.5	18	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetylcholinesterase-like
88	c2apnA_	Alignment	not modelled	8.5	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein hi1723; **PDBTitle:** hi1723 solution structure
89	c1hplB_	Alignment	not modelled	8.3	12	**PDB header:**hydrolase(carboxylic esterase) **Chain:** B: **PDB Molecule:**lipase; **PDBTitle:** horse pancreatic lipase. the crystal structure at 2.32 angstroms resolution
90	c2el7A_	Alignment	not modelled	7.9	12	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of tryptophanyl-trna synthetase from thermus2 thermophilus
91	d2nlva1	Alignment	not modelled	7.9	33	**Fold:**XisI-like **Superfamily:**XisI-like **Family:**XisI-like
92	d1u5ta2	Alignment	not modelled	7.8	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
93	d1o57a1	Alignment	not modelled	7.7	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**N-terminal domain of Bacillus PurR
94	d2v6ai1	Alignment	not modelled	7.6	13	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
95	d1qy7a_	Alignment	not modelled	7.4	14	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
96	c3b64A_	Alignment	not modelled	7.3	25	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**macrophage migration inhibitory factor-like **PDBTitle:** macrophage migration inhibitory factor (mif) from2 /leishmania major
97	d1rp1a2	Alignment	not modelled	7.3	10	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Pancreatic lipase, N-terminal domain
98	c2pfuA_	Alignment	not modelled	7.2	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**biopolymer transport exbd protein; **PDBTitle:** nmr strcuture determination of the periplasmic domain of exbd from2 e.coli
99	d2ha2a1	Alignment	not modelled	7.0	21	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetylcholinesterase-like