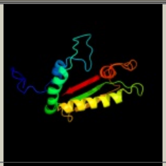
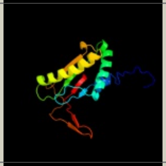
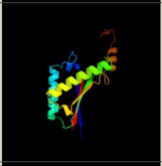
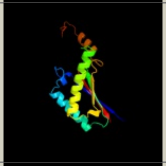
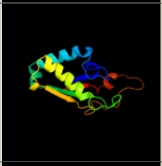
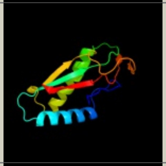
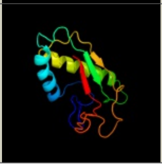
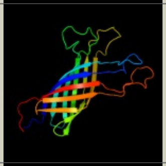
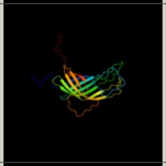
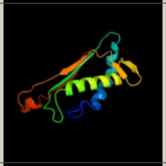
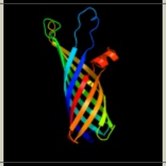
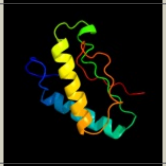
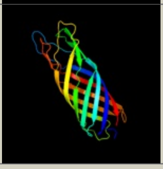
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0A910
Date	Thu Jan 5 11:09:07 GMT 2012
Unique Job ID	2ed792f147a7591f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2l26A_	Alignment		100.0	33	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**uncharacterized protein rv0899/mt0922; **PDBTitle:** rv0899 from mycobacterium tuberculosis contains two separated domains
2	d2aizp1	Alignment		100.0	27	**Fold:**Bacillus chorismate mutase-like **Superfamily:**OmpA-like **Family:**OmpA-like
3	c2kgwA_	Alignment		100.0	32	**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
4	c3td4D_	Alignment		100.0	26	**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
5	c1r1mA_	Alignment		100.0	40	**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
6	d1r1ma_	Alignment		100.0	40	**Fold:**Bacillus chorismate mutase-like **Superfamily:**OmpA-like **Family:**OmpA-like
7	c2k1sA_	Alignment		100.0	33	**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.
8	c3khnB_	Alignment		100.0	30	**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.
9	d2hqsc1	Alignment		100.0	30	**Fold:**Bacillus chorismate mutase-like **Superfamily:**OmpA-like **Family:**OmpA-like
10	c3cyqM_	Alignment		99.9	22	**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		99.9	22	**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	c3oonA_	Alignment		99.9	30	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein (tpn50); **PDBTitle:** the structure of an outer membrance protein from borrelia burgdorferi2 b31
13	c3ldtA_	Alignment		99.9	23	**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
14	d1g90a_	Alignment		99.9	98	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
15	c2k0lA_	Alignment		99.9	82	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein a; **PDBTitle:** nmr structure of the transmembrane domain of the outer2 membrane protein a from klebsiella pneumoniae in dhpc3 micelles.
16	c2zovA_	Alignment		99.9	23	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**chemotaxis protein motb; **PDBTitle:** structure of the periplasmic domain of motb from salmonella2 (crystal form i)
17	d1qjpa_	Alignment		99.8	99	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
18	c3nb3C_	Alignment		99.8	99	**PDB header:**virus **Chain:** C: **PDB Molecule:**outer membrane protein a; **PDBTitle:** the host outer membrane proteins ompa and ompc are packed at specific2 sites in the shigella phage sf6 virion as structural components
19	c2zf8A_	Alignment		99.8	30	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**component of sodium-driven polar flagellar motor; **PDBTitle:** crystal structure of moty
20	c2x27X_	Alignment		99.7	12	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**outer membrane protein oprg; **PDBTitle:** crystal structure of the outer membrane protein oprg from2 pseudomonas aeruginosa
21	d1p4ta_	Alignment	not modelled	99.7	17	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
22	c2f1tB_	Alignment	not modelled	99.7	13	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**outer membrane protein w; **PDBTitle:** outer membrane protein ompw
23	c2jmmA_	Alignment	not modelled	99.7	76	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein a; **PDBTitle:** nmr solution structure of a minimal transmembrane beta-2 barrel platform protein
24	c3qraA_	Alignment	not modelled	99.6	18	**PDB header:**cell invasion **Chain:** A: **PDB Molecule:**attachment invasion locus protein; **PDBTitle:** the crystal structure of ail, the attachment invasion locus protein of2 yersinia pestis
25	d1qj8a_	Alignment	not modelled	99.5	23	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane protein
26	c2lhfA_	Alignment	not modelled	99.4	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein h1; **PDBTitle:** solution structure of outer membrane protein h (oprh) from p.2 aeruginosa in dhpc micelles
27	d1uynx_	Alignment	not modelled	97.7	20	**Fold:**Transmembrane beta-barrels **Superfamily:**Autotransporter **Family:**Autotransporter
28	c3kvnA_	Alignment	not modelled	97.6	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase esta; **PDBTitle:** crystal structure of the full-length autotransporter esta from2 pseudomonas aeruginosa
						PDB header:hydrolase

29	c3aehB_	Alignment	not modelled	97.5	12	**Chain:** B: **PDB Molecule:**hemoglobin-binding protease hbp autotransporter; **PDBTitle:** integral membrane domain of autotransporter hbp
30	c2qomB_	Alignment	not modelled	97.2	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**serine protease espp; **PDBTitle:** the crystal structure of the e.coli espp autotransporter beta-domain.
31	c3sljA_	Alignment	not modelled	97.2	16	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**serine protease espp; **PDBTitle:** pre-cleavage structure of the autotransporter espp - n1023a mutant
32	c2x4mD_	Alignment	not modelled	97.0	12	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**coagulase/fibrinolysin; **PDBTitle:** yersinia pestis plasminogen activator pla
33	c3qq2C_	Alignment	not modelled	96.8	12	**PDB header:**membrane protein/protein transport **Chain:** C: **PDB Molecule:**brka autotransporter; **PDBTitle:** crystal structure of the beta domain of the bordetella autotransporter2 brka
34	c3dwoX_	Alignment	not modelled	96.1	11	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**probable outer membrane protein; **PDBTitle:** crystal structure of a pseudomonas aeruginosa fadl homologue
35	c2iwvD_	Alignment	not modelled	96.0	18	**PDB header:**ion channel **Chain:** D: **PDB Molecule:**outer membrane protein g; **PDBTitle:** structure of the monomeric outer membrane porin ompg in the2 open and closed conformation
36	c3brzA_	Alignment	not modelled	94.5	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**todx; **PDBTitle:** crystal structure of the pseudomonas putida toluene2 transporter todx
37	c3nsgA_	Alignment	not modelled	94.5	10	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein f; **PDBTitle:** crystal structure of ompf, an outer membrane protein from salmonella2 typhi
38	d1i78a_	Alignment	not modelled	91.3	19	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPT-like **Family:**Outer membrane protease OMPT
39	d1osma_	Alignment	not modelled	90.3	15	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
40	d1t16a_	Alignment	not modelled	89.1	10	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Outer membrane protein transport protein
41	c2ervA_	Alignment	not modelled	88.7	10	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**hypothetical protein paer03002360; **PDBTitle:** crystal structure of the outer membrane enzyme pagl
42	c2wjqA_	Alignment	not modelled	88.7	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**probable n-acetylneuraminic acid outer membrane channel **PDBTitle:** nanc porin structure in hexagonal crystal form.
43	d1phoa_	Alignment	not modelled	85.5	11	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
44	c3a2rX_	Alignment	not modelled	81.0	13	**PDB header:**membrane protein **Chain:** X: **PDB Molecule:**outer membrane protein ii; **PDBTitle:** crystal structure of outer membrane protein porb from neisseria2 meningitidis
45	d1gvha3	Alignment	not modelled	78.5	17	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Flavohemoglobin, C-terminal domain
46	d2zfga1	Alignment	not modelled	78.5	14	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
47	c1gvhA_	Alignment	not modelled	76.2	18	**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
48	c2r6hC_	Alignment	not modelled	75.8	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
49	c2iahA_	Alignment	not modelled	74.6	13	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**ferripyoverdine receptor; **PDBTitle:** crystal structure of the ferripyoverdine receptor of the outer2 membrane of pseudomonas aeruginosa bound to ferripyoverdine.
50	d2fgqx1	Alignment	not modelled	70.6	10	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
51	c1xkhC_	Alignment	not modelled	64.7	13	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**ferripyoverdine receptor; **PDBTitle:** pyoverdine outer membrane receptor fpva from pseudomonas aeruginosa2 pao1 bound to pyoverdine
52	c2hdiA_	Alignment	not modelled	64.4	14	**PDB header:**protein transport,antimicrobial protein **Chain:** A: **PDB Molecule:**colicin i receptor; **PDBTitle:** crystal structure of the colicin i receptor cir from e.coli in complex2 with receptor binding domain of colicin ia.
53	c1cqxB_	Alignment	not modelled	63.9	23	**PDB header:**lipid binding protein **Chain:** B: **PDB Molecule:**flavohemoprotein; **PDBTitle:** crystal structure of the flavohemoglobin from alcaligenes eutrophus at2 1.75 a resolution
						Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain

54	d1cqxa3	Alignment	not modelled	62.8	20	**Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Flavohemoglobin, C-terminal domain
55	d1tvca2	Alignment	not modelled	60.4	18	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Aromatic dioxygenase reductase-like
56	c1tvcA_	Alignment	not modelled	55.9	19	**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)
57	d1krha2	Alignment	not modelled	54.4	15	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Aromatic dioxygenase reductase-like
58	c2gpjA_	Alignment	not modelled	47.5	4	**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
59	c2oghA_	Alignment	not modelled	43.7	27	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor eif-1; **PDBTitle:** solution structure of yeast eif1
60	c3dzmB_	Alignment	not modelled	41.7	10	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hypothetical conserved protein; **PDBTitle:** crystal structure of a major outer membrane protein from thermus2 thermophilus hb27
61	d2gdga1	Alignment	not modelled	40.6	13	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
62	d2vdfa1	Alignment	not modelled	40.3	10	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPT-like **Family:**Outer membrane adhesin/invasin OpcA
63	d1gd0a_	Alignment	not modelled	39.8	13	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
64	c3t5sA_	Alignment	not modelled	38.9	21	**PDB header:**immune system **Chain:** A: **PDB Molecule:**macrophage migration inhibitory factor; **PDBTitle:** structure of macrophage migration inhibitory factor from giardia2 lamblia
65	c3b64A_	Alignment	not modelled	38.0	29	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**macrophage migration inhibitory factor-like **PDBTitle:** macrophage migration inhibitory factor (mif) from2 /leishmania major
66	c1xkwA_	Alignment	not modelled	34.7	13	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**fe(iii)-pyochelin receptor; **PDBTitle:** pyochelin outer membrane receptor fpta from pseudomonas2 aeruginosa
67	d1hfoa_	Alignment	not modelled	33.6	25	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
68	c3ct5A_	Alignment	not modelled	33.6	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**morphogenesis protein 1; **PDBTitle:** crystal and cryoem structural studies of a cell wall degrading enzyme2 in the bacteriophage phi29 tail
69	d1fima_	Alignment	not modelled	33.1	12	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
70	c3fwtA_	Alignment	not modelled	32.2	21	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**macrophage migration inhibitory factor-like **PDBTitle:** crystal structure of leishmania major mif2
71	c3o0dF_	Alignment	not modelled	31.0	20	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**triacylglycerol lipase; **PDBTitle:** crystal structure of lip2 lipase from yarrowia lipolytica at 1.7 a2 resolution
72	d2jnaa1	Alignment	not modelled	30.8	33	**Fold:**Dodecin subunit-like **Superfamily:**YdgH-like **Family:**YdgH-like
73	c3k13A_	Alignment	not modelled	30.1	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**5-methyltetrahydrofolate-homocysteine methyltransferase; **PDBTitle:** structure of the pterin-binding domain metr of 5-2 methyltetrahydrofolate-homocysteine methyltransferase from3 bacteroides thetaiotaomicron
74	d2pora_	Alignment	not modelled	29.4	20	**Fold:**Transmembrane beta-barrels **Superfamily:**Porins **Family:**Porin
75	c3l7pA_	Alignment	not modelled	29.4	28	**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
76	d1jmxa1	Alignment	not modelled	29.1	21	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
77	c2bgjB_	Alignment	not modelled	28.7	22	**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
78	c3pohA_	Alignment	not modelled	28.6	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endo-beta-n-acetylglucosaminidase f1; **PDBTitle:** crystal structure of an endo-beta-n-acetylglucosaminidase (bt_3987)2 from bacteroides thetaiotaomicron vpi-5482 at 1.55 a resolution
						Fold:eIF1-like

79	d2if1a_	Alignment	not modelled	28.3	14	**Superfamily:**eIF1-like **Family:**eIF1-like
80	c2os5C_	Alignment	not modelled	28.3	20	**PDB header:**cytokine **Chain:** C: **PDB Molecule:**acemif; **PDBTitle:** macrophage migration inhibitory factor from ancylostoma ceylanicum
81	c1krhA_	Alignment	not modelled	27.9	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**benzoate 1,2-dioxygenase reductase; **PDBTitle:** x-ray stucture of benzoate dioxygenase reductase
82	c2rd5D_	Alignment	not modelled	26.7	27	**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
83	c3g40A_	Alignment	not modelled	26.6	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**na-k-cl cotransporter; **PDBTitle:** crystal structure of the cytoplasmic domain of a2 prokaryotic cation chloride cotransporter
84	c2yciX_	Alignment	not modelled	26.5	17	**PDB header:**transferase **Chain:** X: **PDB Molecule:**5-methyltetrahydrofolate corrinoid/iron sulfur protein **PDBTitle:** methyltransferase native
85	c3bryB_	Alignment	not modelled	26.1	14	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**tbux; **PDBTitle:** crystal structure of the ralstonia pickettii toluene2 transporter tbux
86	c3ca8B_	Alignment	not modelled	25.6	29	**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
87	d2nvma1	Alignment	not modelled	24.9	35	**Fold:**XisI-like **Superfamily:**XisI-like **Family:**XisI-like
88	d1f6ya_	Alignment	not modelled	24.4	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Methyltetrahydrofolate-utiluzing methyltransferases
89	c2xczA_	Alignment	not modelled	24.0	29	**PDB header:**immune system **Chain:** A: **PDB Molecule:**possible atls1-like light-inducible protein; **PDBTitle:** crystal structure of macrophage migration inhibitory factor2 homologue from prochlorococcus marinus
90	d2nlva1	Alignment	not modelled	23.9	24	**Fold:**XisI-like **Superfamily:**XisI-like **Family:**XisI-like
91	c3gacD_	Alignment	not modelled	23.0	13	**PDB header:**cytokine **Chain:** D: **PDB Molecule:**macrophage migration inhibitory factor-like **PDBTitle:** structure of mif with hpp
92	c3efmA_	Alignment	not modelled	22.0	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**ferric alcaligin siderophore receptor; **PDBTitle:** structure of the alcaligin outer membrane recepteur faua from2 bordetella pertussis
93	c2xznF_	Alignment	not modelled	21.7	29	**PDB header:**ribosome **Chain:** F: **PDB Molecule:**eif1; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
94	c3d7qB_	Alignment	not modelled	21.5	24	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**xisi protein-like; **PDBTitle:** crystal structure of a xisi-like protein (npun_ar114) from nostoc2 punctiforme pcc 73102 at 2.30 a resolution
95	d1uwca_	Alignment	not modelled	20.9	21	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
96	d2piia_	Alignment	not modelled	20.7	20	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
97	c3ce8A_	Alignment	not modelled	20.4	20	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative pii-like nitrogen regulatory protein; **PDBTitle:** crystal structure of a duf3240 family protein (sbal_0098) from2 shewanella baltica os155 at 2.40 a resolution
98	d1pbya1	Alignment	not modelled	20.1	14	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
99	d3tgla_	Alignment	not modelled	19.9	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases