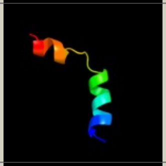
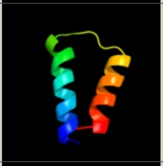
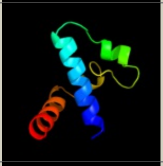
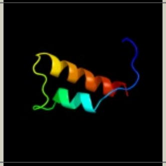
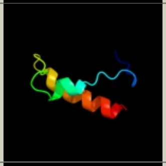
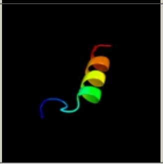
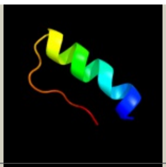
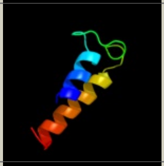
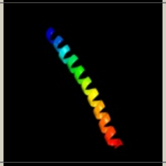
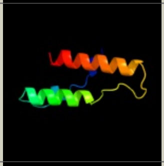
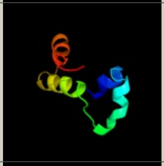
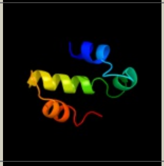
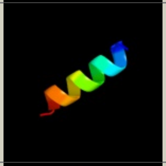
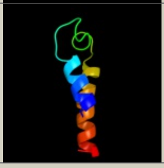
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P42911
Date	Thu Jan 5 12:02:08 GMT 2012
Unique Job ID	1632ff3e6c1753eb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2dmwA_	Alignment		42.3	18	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**synaptobrevin-like 1 variant; **PDBTitle:** solution structure of the longin domain of synaptobrevin-2 like protein 1
2	c2jttD_	Alignment		19.0	26	**PDB header:**calcium binding protein/antitumor protei **Chain:** D: **PDB Molecule:**calcyclin-binding protein; **PDBTitle:** solution structure of calcium loaded s100a6 bound to c-2 terminal siah-1 interacting protein
3	d1ljra1	Alignment		18.2	6	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
4	c3aqpB_	Alignment		17.7	11	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**probable secdf protein-export membrane protein; **PDBTitle:** crystal structure of secdf, a translocon-associated membrane protein,2 from thermus thrmophilus
5	c3ctvA_	Alignment		16.9	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-hydroxyacyl-coa dehydrogenase; **PDBTitle:** crystal structure of central domain of 3-hydroxyacyl-coa2 dehydrogenase from archaeoglobus fulgidus
6	c1l2aD_	Alignment		16.6	21	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**cellobiohydrolase; **PDBTitle:** the crystal structure and catalytic mechanism of2 cellobiohydrolase cels, the major enzymatic component of3 the clostridium thermocellum cellulosome
7	d1l1ya_	Alignment		16.6	21	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Cellulases catalytic domain
8	d1iyxa2	Alignment		16.2	14	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
9	d1t3qa1	Alignment		13.8	21	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
10	d1g9ga_	Alignment		13.4	16	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Cellulases catalytic domain
11	c3bd0D_	Alignment		12.9	26	**PDB header:**peptide binding protein **Chain:** D: **PDB Molecule:**protein memo1; **PDBTitle:** crystal structure of memo, form ii

12	d2i4ra1	Alignment		12.3	35	**Fold:**AtpF-like **Superfamily:**AtpF-like **Family:**AtpF-like
13	c1x1jA_	Alignment		12.2	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**xanthan lyase; **PDBTitle:** crystal structure of xanthan lyase (n194a) with a substrate.
14	d1oaia_	Alignment		12.1	16	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TAP-C domain-like
15	c3htkB_	Alignment		11.5	15	**PDB header:**recombination/replication/ligase **Chain:** B: **PDB Molecule:**structural maintenance of chromosomes protein 5; **PDBTitle:** crystal structure of mms21 and smc5 complex
16	c1zroB_	Alignment		11.2	15	**PDB header:**cell invasion **Chain:** B: **PDB Molecule:**erythrocyte binding antigen region ii; **PDBTitle:** crystal structure of eba-175 region ii (rii) crystallized2 in the presence of (alpha)2,3-sialyllactose
17	d1v97a1	Alignment		11.1	19	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
18	d1rm6c1	Alignment		11.1	21	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
19	d1s29a_	Alignment		10.0	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**La domain
20	d1x1ia1	Alignment		9.5	18	**Fold:**alpha/alpha toroid **Superfamily:**Chondroitin AC/alginate lyase **Family:**Hyaluronate lyase-like catalytic, N-terminal domain
21	c2cfhD_	Alignment	not modelled	9.5	16	**PDB header:**transport **Chain:** D: **PDB Molecule:**trafficking protein particle complex subunit 6b; **PDBTitle:** structure of the bet3-tpc6b core of trapp
22	d2cqka1	Alignment	not modelled	9.4	33	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**La domain
23	d1ffva1	Alignment	not modelled	9.2	17	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
24	c2j96B_	Alignment	not modelled	9.1	11	**PDB header:**photosynthesis **Chain:** B: **PDB Molecule:**phycoerythrocyanin alpha chain; **PDBTitle:** the e-configuration of alfa-phycoerythrocyanin
25	d1j2za_	Alignment	not modelled	8.9	19	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**UDP N-acetylglucosamine acyltransferase
26	d1k3ra2	Alignment	not modelled	8.5	35	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**Hypothetical protein MTH1 (MT0001), dimerisation domain
27	d1cb8a1	Alignment	not modelled	8.4	9	**Fold:**alpha/alpha toroid **Superfamily:**Chondroitin AC/alginate lyase **Family:**Hyaluronate lyase-like catalytic, N-terminal domain
28	c2vh3B_	Alignment	not modelled	8.4	24	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**ranasmurfin; **PDBTitle:** ranasmurfin
29	d1w6ta2	Alignment	not modelled	8.4	14	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like

						Family: Enolase N-terminal domain-like
30	c3cloC_	Alignment	not modelled	8.0	10	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of putative transcriptional regulator containing a2 luxr dna binding domain (np_811094.1) from bacteroides3 thetaiotaomicron vpi-5482 at 2.04 a resolution
31	c2kdtA_	Alignment	not modelled	7.9	50	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**neuroendocrine convertase 1; **PDBTitle:** pc1/3 dcsg sorting domain structure in dpc
32	c1cb8A_	Alignment	not modelled	7.9	5	**PDB header:**lyase **Chain:** A: **PDB Molecule:**protein (chondroitinase ac); **PDBTitle:** chondroitinase ac lyase from flavobacterium heparinum
33	c2rrfA_	Alignment	not modelled	7.8	35	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**zinc finger fyve domain-containing protein 21; **PDBTitle:** the solution structure of the c-terminal region of zinc finger fyve2 domain-containing protein 21
34	d1zxia1	Alignment	not modelled	7.4	13	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
35	d1n62a1	Alignment	not modelled	7.3	13	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
36	c1t3qD_	Alignment	not modelled	7.3	21	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**quinoline 2-oxidoreductase small subunit; **PDBTitle:** crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
37	c2jp7A_	Alignment	not modelled	7.0	21	**PDB header:**translation **Chain:** A: **PDB Molecule:**mrna export factor mex67; **PDBTitle:** nmr structure of the mex67 uba domain
38	d2j0wa3	Alignment	not modelled	7.0	0	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Aspartokinase allosteric domain-like
39	d1go5a_	Alignment	not modelled	7.0	20	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TAP-C domain-like
40	c1q0wA_	Alignment	not modelled	6.9	30	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**vacuolar protein sorting-associated protein **PDBTitle:** solution structure of vps27 amino-terminal uim-ubiquitin2 complex
41	c1bm4A_	Alignment	not modelled	6.8	15	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protein (moloney murine leukemia virus capsid); **PDBTitle:** momlv capsid protein major homology region peptide analog
42	c3hrdH_	Alignment	not modelled	6.8	17	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**nicotinate dehydrogenase small fes subunit; **PDBTitle:** crystal structure of nicotinate dehydrogenase
43	c1rm6F_	Alignment	not modelled	6.8	21	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**4-hydroxybenzoyl-coa reductase gamma subunit; **PDBTitle:** structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
44	d3hdha1	Alignment	not modelled	6.6	20	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**HCDH C-domain-like
45	c1yx5A_	Alignment	not modelled	6.5	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**26s proteasome non-atpase regulatory subunit 4; **PDBTitle:** solution structure of s5a uim-1/ubiquitin complex
46	d1jroa1	Alignment	not modelled	6.2	19	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
47	c3c9pA_	Alignment	not modelled	6.0	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein sp1917; **PDBTitle:** crystal structure of uncharacterized protein sp1917
48	d1f0ya1	Alignment	not modelled	6.0	23	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**HCDH C-domain-like
49	c3n8bB_	Alignment	not modelled	6.0	9	**PDB header:**nucleic acid binding protein **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of borrelia burgdorferi pur-alpha
50	c3snhA_	Alignment	not modelled	6.0	30	**PDB header:**endocytosis **Chain:** A: **PDB Molecule:**dynamin-1; **PDBTitle:** crystal structure of nucleotide-free human dynamin1
51	c3zvrA_	Alignment	not modelled	6.0	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dynamin-1; **PDBTitle:** crystal structure of dynamin
52	c3pf6C_	Alignment	not modelled	5.9	22	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein pp-luz7_gp033; **PDBTitle:** the structure of uncharacterized protein pp-luz7_gp033 from2 pseudomonas phage luz7.
53	d2h8aa1	Alignment	not modelled	5.9	9	**Fold:**MAPEG domain-like **Superfamily:**MAPEG domain-like **Family:**MAPEG domain
54	d1r2za1	Alignment	not modelled	5.8	36	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins

55	d1q33a_	Alignment	not modelled	5.7	8	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
56	c3fseB_	Alignment	not modelled	5.6	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**two-domain protein containing dj-1/thij/pfpi-like and **PDBTitle:** crystal structure of a two-domain protein containing dj-1/thij/pfpi-2 like and ferritin-like domains (ava_4496) from anabaena variabilis3 atcc 29413 at 1.90 a resolution
57	c3nm7D_	Alignment	not modelled	5.6	9	**PDB header:**nucleic acid binding protein **Chain:** D: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of borrelia burgdorferi pur-alpha
58	d1dq3a2	Alignment	not modelled	5.6	14	**Fold:**dsRBD-like **Superfamily:**YcfA/nrd intein domain **Family:**PI-Pfui intein middle domain
59	d1u7ka_	Alignment	not modelled	5.6	26	**Fold:**Retrovirus capsid protein, N-terminal core domain **Superfamily:**Retrovirus capsid protein, N-terminal core domain **Family:**Retrovirus capsid protein, N-terminal core domain
60	c3juiA_	Alignment	not modelled	5.6	14	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor eif-2b subunit epsilon; **PDBTitle:** crystal structure of the c-terminal domain of human translation2 initiation factor eif2b epsilon subunit
61	c1bb1B_	Alignment	not modelled	5.5	21	**PDB header:**de novo protein design **Chain:** B: **PDB Molecule:**designed, thermostable heterotrimeric coiled **PDBTitle:** crystal structure of a designed, thermostable2 heterotrimeric coiled coil
62	d1utga_	Alignment	not modelled	5.5	9	**Fold:**Uteroglobin-like **Superfamily:**Uteroglobin-like **Family:**Uteroglobin-like
63	d1jqna_	Alignment	not modelled	5.4	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate carboxylase
64	d2gena2	Alignment	not modelled	5.4	15	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
65	d1l2la_	Alignment	not modelled	5.4	43	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**ADP-specific Phosphofructokinase/Glucokinase
66	d1zh5a1	Alignment	not modelled	5.3	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**La domain
67	d1ee8a1	Alignment	not modelled	5.3	43	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
68	d1su3a1	Alignment	not modelled	5.3	26	**Fold:**PGBD-like **Superfamily:**PGBD-like **Family:**MMP N-terminal domain
69	c1ffuA_	Alignment	not modelled	5.3	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cuts, iron-sulfur protein of carbon monoxide **PDBTitle:** carbon monoxide dehydrogenase from hydrogenophaga2 pseudoflava which lacks the mo-pyranopterin moiety of the3 molybdenum cofactor
70	c3b9jI_	Alignment	not modelled	5.2	19	**PDB header:**oxidoreductase **Chain:** I: **PDB Molecule:**xanthine oxidase; **PDBTitle:** structure of xanthine oxidase with 2-hydroxy-6-methylpurine
71	c2bbjB_	Alignment	not modelled	5.2	17	**PDB header:**metal transport/membrane protein **Chain:** B: **PDB Molecule:**divalent cation transport-related protein; **PDBTitle:** crystal structure of the cora mg2+ transporter
72	c1k3rA_	Alignment	not modelled	5.2	35	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein mt0001; **PDBTitle:** crystal structure of the methyltransferase with a knot from2 methanobacterium thermoautotrophicum
73	d1hh4e_	Alignment	not modelled	5.2	28	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**RhoGDI-like
74	d1seda_	Alignment	not modelled	5.1	12	**Fold:**Hypothetical protein YhaI **Superfamily:**Hypothetical protein YhaI **Family:**Hypothetical protein YhaI