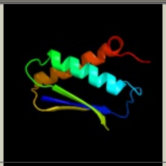
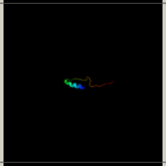
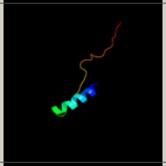
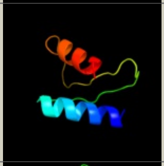
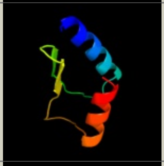
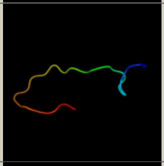
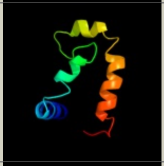
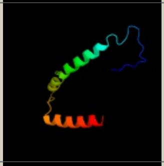
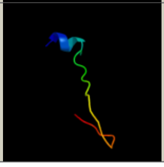
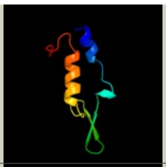
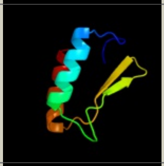
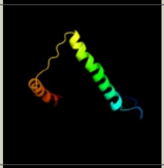
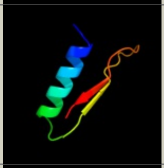
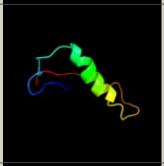
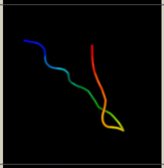
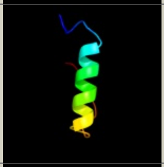
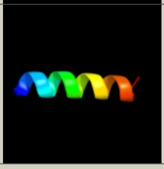
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P0ABR1
Date	Thu Jan 5 11:16:06 GMT 2012
Unique Job ID	dd7d17514b6a48f7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ghha_	Alignment		100.0	100	**Fold:**DNA damage-inducible protein DinI **Superfamily:**DNA damage-inducible protein DinI **Family:**DNA damage-inducible protein DinI
2	c2j58G_	Alignment		65.2	13	**PDB header:**membrane protein **Chain:** G: **PDB Molecule:**outer membrane lipoprotein wza; **PDBTitle:** the structure of wza
3	c2w8iG_	Alignment		56.1	13	**PDB header:**membrane protein **Chain:** G: **PDB Molecule:**putative outer membrane lipoprotein wza; **PDBTitle:** crystal structure of wza24-345.
4	c3gr0D_	Alignment		38.6	10	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**protein prgh; **PDBTitle:** periplasmic domain of the t3ss inner membrane protein prgh from2 s.typhimurium (fragment 170-362)
5	d1kn0a_	Alignment		38.6	21	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**The homologous-pairing domain of Rad52 recombinase
6	c3gr1A_	Alignment		35.3	8	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**protein prgh; **PDBTitle:** periplamic domain of the t3ss inner membrane protein prgh2 from s.typhimurium (fragment 170-392)
7	d2akja1	Alignment		23.9	19	**Fold:**Ferredoxin-like **Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like **Family:**Duplicated SiR/NiR-like domains 1 and 3
8	d1ciya1	Alignment		23.8	30	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**delta-Endotoxin, C-terminal domain
9	d1g5ma_	Alignment		23.7	18	**Fold:**Toxins' membrane translocation domains **Superfamily:**Bcl-2 inhibitors of programmed cell death **Family:**Bcl-2 inhibitors of programmed cell death
10	c2pfzA_	Alignment		23.7	25	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative exported protein; **PDBTitle:** crystal structure of dctp6, a bordetella pertussis2 extracytoplasmic solute receptor binding pyroglutamic acid
11	d1ji6a1	Alignment		23.3	30	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**delta-Endotoxin, C-terminal domain

12	c1h2iG_	Alignment		22.9	21	**PDB header:**dna-binding protein **Chain:** G: **PDB Molecule:**dna repair protein rad52 homolog; **PDBTitle:** human rad52 protein, n-terminal domain
13	d1zj8a1	Alignment		21.4	9	**Fold:**Ferredoxin-like **Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like **Family:**Duplicated SiR/NiR-like domains 1 and 3
14	c2zzxD_	Alignment		20.4	17	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**abc transporter, solute-binding protein; **PDBTitle:** crystal structure of a periplasmic substrate binding protein in2 complex with lactate
15	c2o90A_	Alignment		19.8	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydroneopterin aldolase; **PDBTitle:** atomic resolution crystal structure of e.coli2 dihydroneopterin aldolase in complex with neopterin
16	c2qfiB_	Alignment		19.3	16	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**ferrous-iron efflux pump fief; **PDBTitle:** structure of the zinc transporter yiip
17	d1aopa2	Alignment		19.0	23	**Fold:**Ferredoxin-like **Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like **Family:**Duplicated SiR/NiR-like domains 1 and 3
18	d1dlca1	Alignment		18.1	13	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**delta-Endotoxin, C-terminal domain
19	c2z51A_	Alignment		15.5	10	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**nifu-like protein 2, chloroplast; **PDBTitle:** crystal structure of arabidopsis cnfu involved in iron-2 sulfur cluster biosynthesis
20	c1usdA_	Alignment		15.1	28	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**vasodilator-stimulated phosphoprotein; **PDBTitle:** human vasp tetramerisation domain l352m
21	c2xa0A_	Alignment	not modelled	15.1	18	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**apoptosis regulator bcl-2; **PDBTitle:** crystal structure of bcl-2 in complex with a bax bh32 peptide
22	d1ev0a_	Alignment	not modelled	14.7	17	**Fold:**Cell division protein MinE topological specificity domain **Superfamily:**Cell division protein MinE topological specificity domain **Family:**Cell division protein MinE topological specificity domain
23	c2v4jE_	Alignment	not modelled	14.5	17	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit **PDBTitle:** the crystal structure of desulfovibrio vulgaris2 dissimilatory sulfite reductase bound to dsrc provides3 novel insights into the mechanism of sulfate respiration
24	c2kz0A_	Alignment	not modelled	12.7	27	**PDB header:**transcription **Chain:** A: **PDB Molecule:**bola family protein; **PDBTitle:** solution structure of a bola protein (ech_0303) from ehrlichia2 chaffeensis. seattle structural genomics center for infectious3 disease target ehcha.10365.a
25	c2dbiA_	Alignment	not modelled	12.3	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ybiu; **PDBTitle:** crystal structure of a hypothetical protein jw0805 from2 escherichia coli
26	c2cg8B_	Alignment	not modelled	11.8	21	**PDB header:**lyase/transferase **Chain:** B: **PDB Molecule:**dihydroneopterin aldolase 6-hydroxymethyl-7,8- **PDBTitle:** the bifunctional dihydroneopterin aldolase 6-hydroxymethyl-2 7,8-dihydropterin synthase from streptococcus pneumoniae
27	c1zj8B_	Alignment	not modelled	11.3	9	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable ferredoxin-dependent nitrite reductase nira;

						PDBTitle: structure of mycobacterium tuberculosis nira protein
28	c3u5gB_	Alignment	not modelled	10.7	23	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**40s ribosomal protein s1-a; **PDBTitle:** the structure of the eukaryotic ribosome at 3.0 a resolution
29	d2csga1	Alignment	not modelled	10.6	24	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**YbiU-like
30	d1b9la_	Alignment	not modelled	10.6	10	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**DHN aldolase/epimerase
31	c3tr3A_	Alignment	not modelled	10.2	10	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**bola; **PDBTitle:** structure of a bola protein homologue from coxiella burnetii
32	c2w7aA_	Alignment	not modelled	10.1	28	**PDB header:**rna-binding protein **Chain:** A: **PDB Molecule:**line-1 orf1p; **PDBTitle:** structure of the human line-1 orf1p central domain
33	c3d0wD_	Alignment	not modelled	9.9	46	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**yflh protein; **PDBTitle:** crystal structure of yflh protein from bacillus subtilis.2 northeast structural genomics consortium target sr326
34	c1xs3A_	Alignment	not modelled	9.7	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein xc975; **PDBTitle:** solution structure analysis of the xc975 protein
35	c2xzm4_	Alignment	not modelled	9.2	14	**PDB header:**ribosome **Chain:** 4: **PDB Molecule:**40s ribosomal protein s3a; **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 1
36	d1ekea_	Alignment	not modelled	9.2	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Ribonuclease H
37	d1izna_	Alignment	not modelled	8.9	22	**Fold:**Subunits of heterodimeric actin filament capping protein Capz **Superfamily:**Subunits of heterodimeric actin filament capping protein Capz **Family:**Capz alpha-1 subunit
38	d1pv0a_	Alignment	not modelled	8.5	29	**Fold:**Long alpha-hairpin **Superfamily:**Sporulation inhibitor Sda **Family:**Sporulation inhibitor Sda
39	c2kxoA_	Alignment	not modelled	8.4	7	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division topological specificity factor; **PDBTitle:** solution nmr structure of the cell division regulator mine protein2 from neisseria gonorrhoeae
40	c2yqrA_	Alignment	not modelled	8.2	16	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**kiaa0907 protein; **PDBTitle:** solution structure of the kh domain in kiaa0907 protein
41	c2jttD_	Alignment	not modelled	8.0	29	**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
42	d2qfia1	Alignment	not modelled	8.0	15	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Cation efflux protein cytoplasmic domain-like **Family:**Cation efflux protein cytoplasmic domain-like
43	c1sqlN_	Alignment	not modelled	7.8	12	**PDB header:**lyase **Chain:** N: **PDB Molecule:**dihydroneopterin aldolase; **PDBTitle:** crystal structure of 7,8-dihydroneopterin aldolase in2 complex with guanine
44	d1zbsa2	Alignment	not modelled	7.7	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
45	c2zztA_	Alignment	not modelled	7.7	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of the cytosolic domain of the cation2 diffusion facilitator family protein
46	c3r9jD_	Alignment	not modelled	7.7	12	**PDB header:**cell cycle,hydrolase/cell cycle **Chain:** D: **PDB Molecule:**cell division topological specificity factor; **PDBTitle:** 4.3a resolution structure of a mind-mine(i24n) protein complex
47	d2akja2	Alignment	not modelled	7.7	16	**Fold:**Ferredoxin-like **Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like **Family:**Duplicated SiR/NiR-like domains 1 and 3
48	d1a6qa1	Alignment	not modelled	7.5	17	**Fold:**Another 3-helical bundle **Superfamily:**Protein serine/threonine phosphatase 2C, C-terminal domain **Family:**Protein serine/threonine phosphatase 2C, C-terminal domain
49	d1k46a_	Alignment	not modelled	7.4	15	**Fold:**YopH tyrosine phosphatase N-terminal domain **Superfamily:**YopH tyrosine phosphatase N-terminal domain **Family:**YopH tyrosine phosphatase N-terminal domain
50	d2ponb1	Alignment	not modelled	7.3	20	**Fold:**Toxins' membrane translocation domains **Superfamily:**Bcl-2 inhibitors of programmed cell death **Family:**Bcl-2 inhibitors of programmed cell death
51	d1zj8a2	Alignment	not modelled	6.9	18	**Fold:**Ferredoxin-like **Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like **Family:**Duplicated SiR/NiR-like domains 1 and 3
52	c3c7bE_	Alignment	not modelled	6.9	15	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit beta; **PDBTitle:** structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
						PDB header:transcription regulator

53	c3oxnD_	Alignment	not modelled	6.9	14	**Chain:** D: **PDB Molecule:**putative transcriptional regulator, lysr family; **PDBTitle:** the crystal structure of a putative transcriptional regulator from2 vibrio parahaemolyticus
54	c2veqA_	Alignment	not modelled	6.7	35	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**centromere dna-binding protein complex cbf3 **PDBTitle:** insights into kinetochore-dna interactions from the2 structure of cep3p
55	c2kilA_	Alignment	not modelled	6.6	6	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** nmr structure of the h103g mutant so2144 h-nox domain from2 shewanella oneidensis in the fe(ii)co ligation state
56	d1d4ua1	Alignment	not modelled	6.5	31	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**DNA repair factor XPA DNA- and RPA-binding domain, C-terminal subdomain
57	d3bypa1	Alignment	not modelled	6.5	22	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Cation efflux protein cytoplasmic domain-like **Family:**Cation efflux protein cytoplasmic domain-like
58	c3fljA_	Alignment	not modelled	6.3	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein conserved in bacteria with a **PDBTitle:** crystal structure of uncharacterized protein conserved in bacteria2 with a cystatin-like fold (yp_168589.1) from silicibacter pomeroyi3 dss-3 at 2.00 a resolution
59	d1wjwa_	Alignment	not modelled	6.2	11	**Fold:**TBP-like **Superfamily:**Phosphoglucomutase, C-terminal domain **Family:**Phosphoglucomutase, C-terminal domain
60	d2esna2	Alignment	not modelled	6.1	19	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
61	c3dukD_	Alignment	not modelled	6.1	26	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**ntf2-like protein of unknown function; **PDBTitle:** crystal structure of a ntf2-like protein of unknown function2 (mfla_0564) from methylobacillus flagellatus kt at 2.200 a resolution
62	d1p90a_	Alignment	not modelled	6.1	32	**Fold:**Ribonuclease H-like motif **Superfamily:**Nitrogenase accessory factor-like **Family:**Nitrogenase accessory factor
63	d2pa2a1	Alignment	not modelled	6.0	17	**Fold:**alpha/beta-Hammerhead **Superfamily:**Ribosomal protein L16p/L10e **Family:**Ribosomal protein L10e
64	d1otka_	Alignment	not modelled	5.7	16	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ribonucleotide reductase-like
65	c3c66B_	Alignment	not modelled	5.7	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**poly(a) polymerase; **PDBTitle:** yeast poly(a) polymerase in complex with fip1 residues 80-105
66	c2akjA_	Alignment	not modelled	5.6	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ferredoxin--nitrite reductase, chloroplast; **PDBTitle:** structure of spinach nitrite reductase
67	d1fx0a1	Alignment	not modelled	5.4	20	**Fold:**Left-handed superhelix **Superfamily:**C-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**C-terminal domain of alpha and beta subunits of F1 ATP synthase
68	d1pjqa3	Alignment	not modelled	5.4	22	**Fold:**Siroheme synthase middle domains-like **Superfamily:**Siroheme synthase middle domains-like **Family:**Siroheme synthase middle domains-like
69	d3c7bb2	Alignment	not modelled	5.4	16	**Fold:**Ferredoxin-like **Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like **Family:**DsrA/DsrB N-terminal-domain-like
70	d1s3aa1	Alignment	not modelled	5.3	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Mitochondrial ribosomal protein L51/S25/CI-B8 domain
71	c2l82A_	Alignment	not modelled	5.2	33	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**designed protein or32; **PDBTitle:** solution nmr structure of de novo designed protein, p-loop ntpase2 fold, northeast structural genomics consortium target or32
72	d2ctja1	Alignment	not modelled	5.1	18	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
73	c2d4gA_	Alignment	not modelled	5.1	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein bsu11850; **PDBTitle:** structure of yjcg protein, a putative 2'-5' rna ligase from2 bacillus subtilis
74	d1q46a1	Alignment	not modelled	5.1	22	**Fold:**SAM domain-like **Superfamily:**eIF2alpha middle domain-like **Family:**eIF2alpha middle domain-like
75	d1q1oa_	Alignment	not modelled	5.0	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**PB1 domain
76	d1koya_	Alignment	not modelled	5.0	38	**Fold:**C-terminal domain of DFF45/ICAD (DFF-C domain) **Superfamily:**C-terminal domain of DFF45/ICAD (DFF-C domain) **Family:**C-terminal domain of DFF45/ICAD (DFF-C domain)