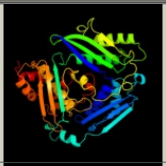
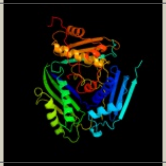
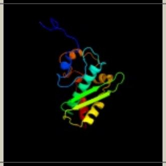
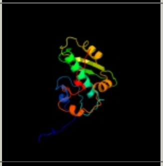
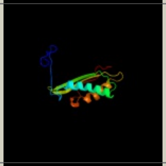
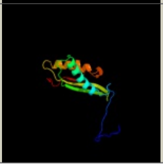
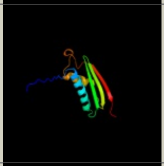
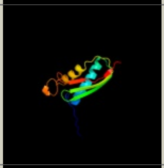
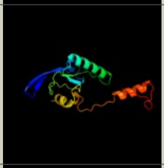
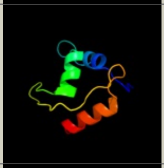
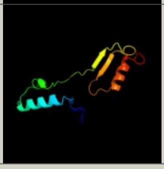
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P0A817
Date	Thu Jan 5 11:06:38 GMT 2012
Unique Job ID	880a708c72f867e0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1rg9D_	Alignment		100.0	100	**PDB header:**transferase **Chain:** D: **PDB Molecule:**s-adenosylmethionine synthetase; **PDBTitle:** s-adenosylmethionine synthetase complexed with sam and ppnp
2	c2obvA_	Alignment		100.0	57	**PDB header:**transferase **Chain:** A: **PDB Molecule:**s-adenosylmethionine synthetase isoform type-1; **PDBTitle:** crystal structure of the human s-adenosylmethionine synthetase 1 in2 complex with the product
3	c3so4C_	Alignment		100.0	52	**PDB header:**transferase **Chain:** C: **PDB Molecule:**methionine-adenosyltransferase; **PDBTitle:** methionine-adenosyltransferase from entamoeba histolytica
4	c3imlB_	Alignment		100.0	72	**PDB header:**transferase **Chain:** B: **PDB Molecule:**s-adenosylmethionine synthetase; **PDBTitle:** crystal structure of s-adenosylmethionine synthetase from burkholderia2 pseudomallei
5	c3rv2B_	Alignment		100.0	62	**PDB header:**transferase **Chain:** B: **PDB Molecule:**s-adenosylmethionine synthase; **PDBTitle:** crystal structure of s-adenosylmethionine synthetase from2 mycobacterium marinum
6	d1mxaa3	Alignment		100.0	100	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase
7	d2p02a3	Alignment		100.0	62	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase
8	d1qm4a3	Alignment		100.0	64	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase
9	d1mxaa2	Alignment		100.0	100	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase
10	d2p02a2	Alignment		100.0	48	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase
11	d1qm4a2	Alignment		100.0	49	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase

12	d2p02a1	Alignment		100.0	61	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase
13	d1mxaa1	Alignment		100.0	100	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase
14	d1qm4a1	Alignment		100.0	62	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase
15	c3k8zD_	Alignment		82.9	13	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**nad-specific glutamate dehydrogenase; **PDBTitle:** crystal structure of gudb1 a decryptified secondary glutamate2 dehydrogenase from b. subtilis
16	d2dt5a1	Alignment		82.1	28	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcriptional repressor Rex, N-terminal domain
17	c2bmaA_	Alignment		56.4	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutamate dehydrogenase (nadp+); **PDBTitle:** the crystal structure of plasmodium falciparum glutamate2 dehydrogenase, a putative target for novel antimalarial3 drugs
18	d1w9ha1	Alignment		54.5	23	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**PIWI domain
19	c3lvtA_	Alignment		51.4	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycosyl hydrolase, family 38; **PDBTitle:** the crystal structure of a protein in the glycosyl hydrolase2 family 38 from enterococcus faecalis to 2.55a
20	c2inrA_	Alignment		48.9	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dna topoisomerase 4 subunit a; **PDBTitle:** crystal structure of a 59 kda fragment of topoisomerase iv subunit a2 (grla) from staphylococcus aureus
21	c2w42A_	Alignment	not modelled	40.4	24	**PDB header:**protein/dna complex **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** the structure of a piwi protein from archaeoglobus fulgidus2 complexed with a 16nt dna duplex.
22	d1u04a2	Alignment	not modelled	39.0	31	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**PIWI domain
23	d1euza2	Alignment	not modelled	36.1	18	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
24	c3ketA_	Alignment	not modelled	34.9	17	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**redox-sensing transcriptional repressor rex; **PDBTitle:** crystal structure of a rex-family transcriptional regulatory protein2 from streptococcus agalactiae bound to a palindromic operator
25	d1kjna_	Alignment	not modelled	34.4	29	**Fold:**Hypothetical protein MTH777 (MT0777) **Superfamily:**Hypothetical protein MTH777 (MT0777) **Family:**Hypothetical protein MTH777 (MT0777)
26	c3aoeC_	Alignment	not modelled	31.1	20	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**glutamate dehydrogenase; **PDBTitle:** crystal structure of hetero-hexameric glutamate dehydrogenase from2 thermus thermophilus (leu bound form)
27	d2fiqa1	Alignment	not modelled	28.4	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**GatZ-like
28	c2dt5A_	Alignment	not modelled	27.9	28	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**at-rich dna-binding protein; **PDBTitle:** crystal structure of ttha1657 (at-rich dna-binding protein) from2 thermus thermophilus hb8

29	d1to0a_	Alignment	not modelled	24.0	60	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YbeA-like
30	d2fm8a1	Alignment	not modelled	23.6	22	**Fold:**Secretion chaperone-like **Superfamily:**Type III secretory system chaperone-like **Family:**Type III secretory system chaperone
31	c2vofA_	Alignment	not modelled	22.7	8	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**bcl-2-related protein a1; **PDBTitle:** structure of mouse a1 bound to the puma bh3-domain
32	d1vh0a_	Alignment	not modelled	22.7	75	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YbeA-like
33	c1hrdA_	Alignment	not modelled	22.2	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutamate dehydrogenase; **PDBTitle:** glutamate dehydrogenase
34	d1ns5a_	Alignment	not modelled	22.0	50	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YbeA-like
35	d1o6da_	Alignment	not modelled	21.3	63	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YbeA-like
36	d1b26a2	Alignment	not modelled	20.9	23	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
37	c2z51A_	Alignment	not modelled	20.1	20	**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
38	d1vkha_	Alignment	not modelled	19.8	19	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Putative serine hydrolase Ydr428c
39	d1azpa_	Alignment	not modelled	17.4	40	**Fold:**SH3-like barrel **Superfamily:**Chromo domain-like **Family:**"Histone-like" proteins from archaea
40	c1u04A_	Alignment	not modelled	17.3	46	**PDB header:**hydrolase/gene regulation **Chain:** A: **PDB Molecule:**hypothetical protein pf0537; **PDBTitle:** crystal structure of full length argonaute from pyrococcus furiosus
41	c1v57A_	Alignment	not modelled	16.5	26	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbg; **PDBTitle:** crystal structure of the disulfide bond isomerase dsbg
42	c2jvfA_	Alignment	not modelled	15.4	9	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**de novo protein m7; **PDBTitle:** solution structure of m7, a computationally-designed2 artificial protein
43	d1q33a_	Alignment	not modelled	15.3	60	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
44	c2bh7A_	Alignment	not modelled	14.4	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**n-acetylmuramoyl-l-alanine amidase; **PDBTitle:** crystal structure of a semet derivative of amid at 2.22 angstroms
45	d1gtma2	Alignment	not modelled	14.1	13	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
46	c3lwaA_	Alignment	not modelled	13.9	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**secreted thiol-disulfide isomerase; **PDBTitle:** the crystal structure of a secreted thiol-disulfide2 isomerase from corynebacterium glutamicum to 1.75a
47	c3h6nA_	Alignment	not modelled	13.7	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**plexin-d1; **PDBTitle:** crystal structure of the ubiquitin-like domain of plexin d1
48	d2f9wa2	Alignment	not modelled	13.5	50	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**CoaX-like
49	c2gjhA_	Alignment	not modelled	13.1	18	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**designed protein; **PDBTitle:** nmr structure of cfr (c-terminal fragment of2 computationally designed novel-topology protein top7)
50	c2fmmE_	Alignment	not modelled	13.0	21	**PDB header:**transcription **Chain:** E: **PDB Molecule:**protein emsy; **PDBTitle:** crystal structure of emsy-hp1 complex
51	d1lfda_	Alignment	not modelled	12.9	17	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ras-binding domain, RBD
52	d2fmme1	Alignment	not modelled	12.9	21	**Fold:**ENT-like **Superfamily:**ENT-like **Family:**Emsy N terminal (ENT) domain-like
53	d1vhfa_	Alignment	not modelled	12.8	11	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Divalent ion tolerance proteins CutA (CutA1)
54	d1t0ga_	Alignment	not modelled	12.7	39	**Fold:**Cytochrome b5-like heme/steroid binding domain **Superfamily:**Cytochrome b5-like heme/steroid binding domain **Family:**Steroid-binding domain
55	c1wnkA_	Alignment	not modelled	12.4	50	**PDB header:**transcription **Chain:** A: **PDB Molecule:**fibroin-modulator-binding-protein-1; **PDBTitle:** nmr structure of fmbp-1 tandem repeat 3 in 30%(v/v) tfe2 solution
						Fold:ENT-like

56	d1uz3a1	Alignment	not modelled	12.3	21	**Superfamily:**ENT-like **Family:**Emsy N terminal (ENT) domain-like
57	d1knga_	Alignment	not modelled	12.2	8	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
58	d1ztpa1	Alignment	not modelled	12.0	16	**Fold:**eIF4e-like **Superfamily:**eIF4e-like **Family:**BLES03-like
59	c2jkzB_	Alignment	not modelled	12.0	44	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hypoxanthine-guanine phosphoribosyltransferase; **PDBTitle:** saccharomyces cerevisiae hypoxanthine-guanine2 phosphoribosyltransferase in complex with gmp (guanosine 5'3 - monophosphate) (orthorhombic crystal form)
60	d1p1la_	Alignment	not modelled	11.5	32	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Divalent ion tolerance proteins CutA (CutA1)
61	d1yvua2	Alignment	not modelled	11.5	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**PIWI domain
62	c2tmgD_	Alignment	not modelled	11.4	18	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**protein (glutamate dehydrogenase); **PDBTitle:** thermotoga maritima glutamate dehydrogenase mutant s128r,2 t158e, n117r, s160e
63	d2bu3a1	Alignment	not modelled	11.2	26	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Phytochelatin synthase
64	c2zfhA_	Alignment	not modelled	11.1	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**cuta; **PDBTitle:** crystal structure of putative cuta1 from homo sapiens at 2.05a2 resolution
65	c3kh0A_	Alignment	not modelled	11.1	19	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ral guanine nucleotide dissociation stimulator; **PDBTitle:** crystal structure of the ras-association (ra) domain of2 ralgds
66	c2zomC_	Alignment	not modelled	11.0	26	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**protein cuta, chloroplast, putative, expressed; **PDBTitle:** crystal structure of cuta1 from oryza sativa
67	d1ah4a_	Alignment	not modelled	11.0	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
68	c1qysA_	Alignment	not modelled	10.6	25	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**top7; **PDBTitle:** crystal structure of top7: a computationally designed2 protein with a novel fold
69	c2wl2B_	Alignment	not modelled	10.6	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna gyrase subunit a; **PDBTitle:** crystal structure of n-terminal domain of gyra with the2 antibiotic simocyclinone d8
70	d2bgxa2	Alignment	not modelled	10.5	26	**Fold:**N-acetylmuramoyl-L-alanine amidase-like **Superfamily:**N-acetylmuramoyl-L-alanine amidase-like **Family:**N-acetylmuramoyl-L-alanine amidase-like
71	d1naqa_	Alignment	not modelled	10.1	26	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Divalent ion tolerance proteins CutA (CutA1)
72	d1bf4a_	Alignment	not modelled	10.0	48	**Fold:**SH3-like barrel **Superfamily:**Chromo domain-like **Family:**"Histone-like" proteins from archaea
73	d1rlfa_	Alignment	not modelled	9.5	24	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ras-binding domain, RBD
74	d1nzaa_	Alignment	not modelled	9.4	42	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Divalent ion tolerance proteins CutA (CutA1)
75	c2btwA_	Alignment	not modelled	9.2	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**alr0975 protein; **PDBTitle:** crystal structure of alr0975
76	c3ag7A_	Alignment	not modelled	9.0	35	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein f9e10.5; **PDBTitle:** an auxilin-like j-domain containing protein, jac1 j-domain
77	d2rgfa_	Alignment	not modelled	9.0	19	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ras-binding domain, RBD
78	c2nuhA_	Alignment	not modelled	8.9	21	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**periplasmic divalent cation tolerance protein; **PDBTitle:** crystal structure of cuta from the phytopathgen bacterium xylella2 fastidiosa
79	c3gdeA_	Alignment	not modelled	8.9	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dna ligase; **PDBTitle:** the closed conformation of atp-dependent dna ligase from2 archaeoglobus fulgidus
80	d3c9fa1	Alignment	not modelled	8.8	16	**Fold:**5'-nucleotidase (syn. UDP-sugar hydrolase), C-terminal domain **Superfamily:**5'-nucleotidase (syn. UDP-sugar hydrolase), C-terminal domain **Family:**5'-nucleotidase (syn. UDP-sugar hydrolase), C-terminal domain
81	c2kucA_	Alignment	not modelled	8.7	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative disulphide-isomerase;

81	c2kdcA_	Alignment	not modelled	8.7	13	**PDBTitle:** solution structure of a putative disulphide-isomerase from bacteroides2 thetaiotaomicron
82	d1osce_	Alignment	not modelled	8.7	26	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Divalent ion tolerance proteins CutA (CutA1)
83	c3b6nA_	Alignment	not modelled	8.7	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**2-c-methyl-d-erythritol 2,4-cyclodiphosphate **PDBTitle:** crystal structure of 2c-methyl-d-erythritol 2,4-2 cyclodiphosphate synthase pv003920 from plasmodium vivax
84	c3lorB_	Alignment	not modelled	8.6	14	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**thiol-disulfide isomerase and thioredoxins; **PDBTitle:** the crystal structure of a thiol-disulfide isomerase from2 corynebacterium glutamicum to 2.2a
85	d1j03a_	Alignment	not modelled	8.4	39	**Fold:**Cytochrome b5-like heme/steroid binding domain **Superfamily:**Cytochrome b5-like heme/steroid binding domain **Family:**Steroid-binding domain
86	d1hkoa_	Alignment	not modelled	8.4	36	**Fold:**Cytochrome b5-like heme/steroid binding domain **Superfamily:**Cytochrome b5-like heme/steroid binding domain **Family:**Cytochrome b5
87	d2zfha1	Alignment	not modelled	8.4	26	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Divalent ion tolerance proteins CutA (CutA1)
88	c1xk8A_	Alignment	not modelled	8.4	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**divalent cation tolerant protein cuta; **PDBTitle:** divalent cation tolerant protein cuta from homo sapiens2 o60888
89	d1ukua_	Alignment	not modelled	8.4	21	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Divalent ion tolerance proteins CutA (CutA1)
90	c2wnyB_	Alignment	not modelled	8.2	17	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**conserved protein mth689; **PDBTitle:** structure of mth689, a duf54 protein from methanothermobacter2 thermautotrophicus
91	d1c9ka_	Alignment	not modelled	8.2	86	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
92	c3d4oA_	Alignment	not modelled	8.1	44	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dipicolinate synthase subunit a; **PDBTitle:** crystal structure of dipicolinate synthase subunit a (np_243269.1)2 from bacillus halodurans at 2.10 a resolution
93	d1mhyd_	Alignment	not modelled	8.0	35	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ribonucleotide reductase-like
94	d1vjpa1	Alignment	not modelled	7.9	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
95	c2hw2A_	Alignment	not modelled	7.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rifampin adp-ribosyl transferase; **PDBTitle:** crystal structure of rifampin adp-ribosyl transferase in2 complex with rifampin
96	c3s5pA_	Alignment	not modelled	7.9	22	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase b rpib from giardia2 lamblia
97	c3ga2A_	Alignment	not modelled	7.8	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endonuclease v; **PDBTitle:** crystal structure of the endonuclease_v (bsu36170) from2 bacillus subtilis, northeast structural genomics3 consortium target sr624
98	d1kr4a_	Alignment	not modelled	7.8	11	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Divalent ion tolerance proteins CutA (CutA1)
99	d1mtyd_	Alignment	not modelled	7.7	41	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ribonucleotide reductase-like