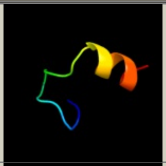
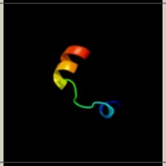
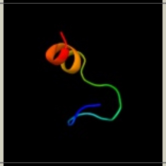
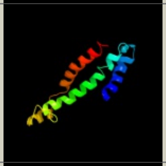
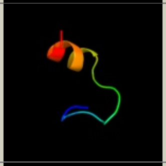
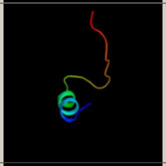
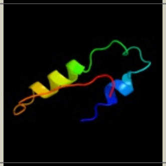
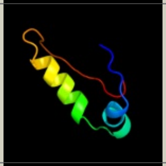
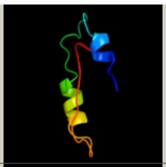
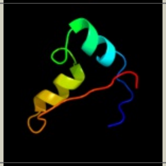
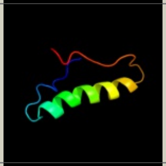
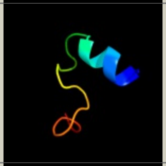
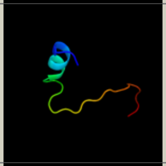
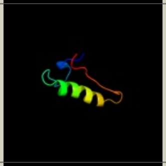
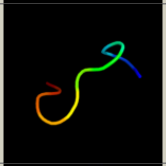
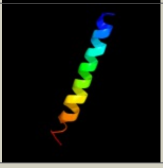
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P69831
Date	Thu Jan 5 12:12:12 GMT 2012
Unique Job ID	62e86fc840183265

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2nscA_	Alignment		40.8	25	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**trigger factor; **PDBTitle:** structures of and interactions between domains of trigger factor from2 themotoga maritima
2	d1w26a2	Alignment		35.3	20	**Fold:**Ribosome binding domain-like **Superfamily:**Trigger factor ribosome-binding domain **Family:**Trigger factor ribosome-binding domain
3	d1p9ya_	Alignment		34.3	20	**Fold:**Ribosome binding domain-like **Superfamily:**Trigger factor ribosome-binding domain **Family:**Trigger factor ribosome-binding domain
4	d1t11a2	Alignment		33.7	15	**Fold:**Ribosome binding domain-like **Superfamily:**Trigger factor ribosome-binding domain **Family:**Trigger factor ribosome-binding domain
5	c2d3o1_	Alignment		30.3	25	**PDB header:**ribosome **Chain:** 1: **PDB Molecule:**trigger factor; **PDBTitle:** structure of ribosome binding domain of the trigger factor2 on the 50s ribosomal subunit from d. radiodurans
6	c2yvxD_	Alignment		30.2	17	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**mg2+ transporter mgte; **PDBTitle:** crystal structure of magnesium transporter mgte
7	c1t11A_	Alignment		27.4	15	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**trigger factor; **PDBTitle:** trigger factor
8	c2qgoA_	Alignment		25.7	13	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**putative fe-s biosynthesis protein; **PDBTitle:** crystal structure of a putative fe-s biosynthesis protein from2 lactobacillus acidophilus
9	d1osda_	Alignment		21.7	21	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
10	d1cpza_	Alignment		20.6	21	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
11	c2k2pA_	Alignment		18.7	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu1203; **PDBTitle:** solution nmr structure of protein atu1203 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att10, ontario center for structural proteomics target atc1183

12	c1yg0A_	Alignment		18.7	24	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**cop associated protein; **PDBTitle:** solution structure of apo-copp from helicobacter pylori
13	d1mwza_	Alignment		18.7	21	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
14	c1y3kA_	Alignment		16.7	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 1; **PDBTitle:** solution structure of the apo form of the fifth domain of2 menkes protein
15	c2ga7A_	Alignment		16.3	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 1; **PDBTitle:** solution structure of the copper(i) form of the third metal-2 binding domain of atp7a protein (menkes disease protein)
16	d1qb2a_	Alignment		16.2	25	**Fold:**Signal peptide-binding domain **Superfamily:**Signal peptide-binding domain **Family:**Signal peptide-binding domain
17	d2p2ea1	Alignment		15.5	19	**Fold:**HesB-like domain **Superfamily:**HesB-like domain **Family:**HesB-like domain
18	d1p6ta1	Alignment		14.0	18	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
19	d1jw2a_	Alignment		13.9	27	**Fold:**Open three-helical up-and-down bundle **Superfamily:**Hemolysin expression modulating protein HHA **Family:**Hemolysin expression modulating protein HHA
20	c1vf5R_	Alignment		13.5	26	**PDB header:**photosynthesis **Chain:** R: **PDB Molecule:**protein pet l; **PDBTitle:** crystal structure of cytochrome b6f complex from m.laminosus
21	c2e75E_	Alignment	not modelled	13.5	26	**PDB header:**photosynthesis **Chain:** E: **PDB Molecule:**cytochrome b6-f complex subunit 6; **PDBTitle:** crystal structure of the cytochrome b6f complex with 2-nonyl-4-2 hydroxyquinoline n-oxide (nqno) from m.laminosus
22	c2e74E_	Alignment	not modelled	13.5	26	**PDB header:**photosynthesis **Chain:** E: **PDB Molecule:**cytochrome b6-f complex subunit 6; **PDBTitle:** crystal structure of the cytochrome b6f complex from m.laminosus
23	c2e76E_	Alignment	not modelled	13.5	26	**PDB header:**photosynthesis **Chain:** E: **PDB Molecule:**cytochrome b6-f complex subunit 6; **PDBTitle:** crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
24	d2e74e1	Alignment	not modelled	13.5	26	**Fold:**Single transmembrane helix **Superfamily:**PetL subunit of the cytochrome b6f complex **Family:**PetL subunit of the cytochrome b6f complex
25	d1qzxa2	Alignment	not modelled	13.2	25	**Fold:**Signal peptide-binding domain **Superfamily:**Signal peptide-binding domain **Family:**Signal peptide-binding domain
26	c2ofhX_	Alignment	not modelled	13.1	15	**PDB header:**hydrolase, membrane protein **Chain:** X: **PDB Molecule:**zinc-transporting atpase; **PDBTitle:** solution structure of the n-terminal domain of the zinc(ii) atpase2 ziaa in its apo form
27	c2aj1A_	Alignment	not modelled	13.1	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable cadmium-transporting atpase; **PDBTitle:** solution structure of apocada
28	d2aw0a_	Alignment	not modelled	12.6	26	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
						Fold: Peripheral subunit-binding domain of 2-oxo acid

29	d1w4ha1	Alignment	not modelled	12.1	19	dehydrogenase complex **Superfamily:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Family:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
30	d1afia_	Alignment	not modelled	11.7	18	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
31	c3bdlA_	Alignment	not modelled	11.2	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**staphylococcal nuclease domain-containing **PDBTitle:** crystal structure of a truncated human tudor-sn
32	d1vyva2	Alignment	not modelled	11.1	29	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
33	d2cyua1	Alignment	not modelled	10.8	18	**Fold:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Superfamily:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Family:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
34	d2c4ka1	Alignment	not modelled	10.7	27	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
35	c2kt2A_	Alignment	not modelled	10.2	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**mercuric reductase; **PDBTitle:** structure of nmera, the n-terminal hma domain of tn501 mercuric2 reductase
36	d2ffha2	Alignment	not modelled	9.9	29	**Fold:**Signal peptide-binding domain **Superfamily:**Signal peptide-binding domain **Family:**Signal peptide-binding domain
37	c2kkhA_	Alignment	not modelled	9.8	21	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**putative heavy metal transporter; **PDBTitle:** structure of the zinc binding domain of the atpase hma4
38	c1w26B_	Alignment	not modelled	9.8	20	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**trigger factor; **PDBTitle:** trigger factor in complex with the ribosome forms a2 molecular cradle for nascent proteins
39	c2iy3A_	Alignment	not modelled	9.6	25	**PDB header:**rna-binding **Chain:** A: **PDB Molecule:**signal recognition particle protein ffh; **PDBTitle:** structure of the e. coli signal recognition particle2 bound to a translating ribosome
40	d1kvja_	Alignment	not modelled	9.3	29	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
41	d1vs6z1	Alignment	not modelled	9.3	25	**Fold:**L28p-like **Superfamily:**L28p-like **Family:**Ribosomal protein L31p
42	c2vzkD_	Alignment	not modelled	8.8	26	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glutamate n-acetyltransferase 2 beta chain; **PDBTitle:** structure of the acyl-enzyme complex of an n-terminal2 nucleophile (ntn) hydrolase, oat2
43	c2oarA_	Alignment	not modelled	8.6	18	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**large-conductance mechanosensitive channel; **PDBTitle:** mechanosensitive channel of large conductance (mscl)
44	d1sb6a_	Alignment	not modelled	8.6	15	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
45	d1s6ua_	Alignment	not modelled	8.4	35	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
46	d1uwda_	Alignment	not modelled	8.4	25	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**PaaD-like
47	d1p6ta2	Alignment	not modelled	8.3	21	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
48	d2oara1	Alignment	not modelled	7.5	18	**Fold:**Gated mechanosensitive channel **Superfamily:**Gated mechanosensitive channel **Family:**Gated mechanosensitive channel
49	c3bvsA_	Alignment	not modelled	7.4	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alkylpurine dna glycosylase alkd; **PDBTitle:** crystal structure of bacillus cereus alkylpurine dna glycosylase alkd
50	c2kelB_	Alignment	not modelled	7.2	29	**PDB header:**transcription repressor **Chain:** B: **PDB Molecule:**uncharacterized protein 56b; **PDBTitle:** structure of the transcription regulator svtr from the2 hyperthermophilic archaeal virus sirv1
51	c1vf5E_	Alignment	not modelled	7.2	23	**PDB header:**photosynthesis **Chain:** E: **PDB Molecule:**protein pet l; **PDBTitle:** crystal structure of cytochrome b6f complex from m.laminosus
52	c1qzwC_	Alignment	not modelled	7.1	25	**PDB header:**signaling protein/rna **Chain:** C: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** crystal structure of the complete core of archaeal srp and2 implications for inter-domain communication
53	c3k3gA_	Alignment	not modelled	7.1	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**urea transporter; **PDBTitle:** crystal structure of the urea transporter from desulfovibrio vulgaris2 bound to 1,3-dimethylurea
54	d2qifa1	Alignment	not modelled	7.1	13	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain

						Family:HMA, heavy metal-associated domain
55	d3elga1	Alignment	not modelled	7.0	19	**Fold:**BLIP-like **Superfamily:**BT0923-like **Family:**BT0923-like
56	d1mn8a_	Alignment	not modelled	7.0	21	**Fold:**Retroviral matrix proteins **Superfamily:**Retroviral matrix proteins **Family:**MMLV matrix protein-like
57	d2aq0a1	Alignment	not modelled	6.8	24	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
58	c2ksdA_	Alignment	not modelled	6.6	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aerobic respiration control sensor protein arcb; **PDBTitle:** backbone structure of the membrane domain of e. coli2 histidine kinase receptor arcb, center for structures of3 membrane proteins (csmp) target 4310c
59	d1ftra1	Alignment	not modelled	6.1	24	**Fold:**Ferredoxin-like **Superfamily:**Formylmethanofuran:tetrahydromethanopterin formyltransferase **Family:**Formylmethanofuran:tetrahydromethanopterin formyltransferase
60	d1t3la2	Alignment	not modelled	5.6	29	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
61	d1nyta2	Alignment	not modelled	5.3	33	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Shikimate dehydrogenase-like
62	d3duea1	Alignment	not modelled	5.1	13	**Fold:**BLIP-like **Superfamily:**BT0923-like **Family:**BT0923-like
63	c2wwaJ_	Alignment	not modelled	5.1	7	**PDB header:**ribosome **Chain:** J: **PDB Molecule:**60s ribosomal protein l19; **PDBTitle:** cryo-em structure of idle yeast ssh1 complex bound to the2 yeast 80s ribosome
64	c3dv0I_	Alignment	not modelled	5.1	13	**PDB header:**oxidoreductase/transferase **Chain:** I: **PDB Molecule:**dihydrolipoyllysine-residue acetyltransferase **PDBTitle:** snapshots of catalysis in the e1 subunit of the pyruvate2 dehydrogenase multi-enzyme complex