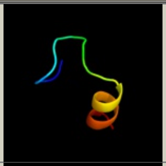
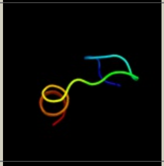
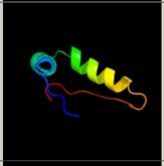
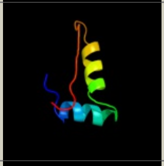
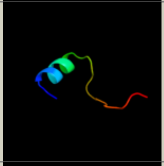
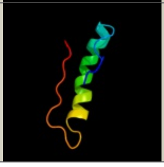
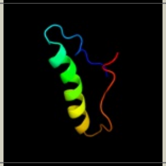
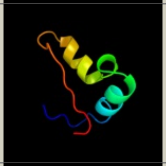
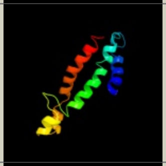
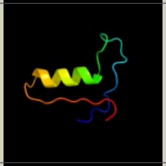
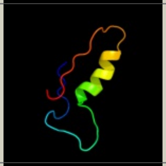
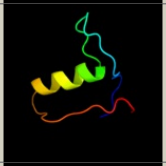
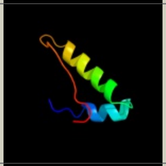
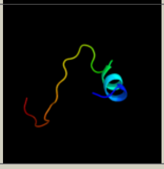
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P39365
Date	Thu Jan 5 11:59:56 GMT 2012
Unique Job ID	7b2c078e2a315500

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2nscA_	Alignment		41.6	20	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**trigger factor; **PDBTitle:** structures of and interactions between domains of trigger factor from2 themotoga maritima
2	c3k3gA_	Alignment		40.5	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
3	d1w26a2	Alignment		36.2	20	**Fold:**Ribosome binding domain-like **Superfamily:**Trigger factor ribosome-binding domain **Family:**Trigger factor ribosome-binding domain
4	d1p9ya_	Alignment		35.0	20	**Fold:**Ribosome binding domain-like **Superfamily:**Trigger factor ribosome-binding domain **Family:**Trigger factor ribosome-binding domain
5	d1t11a2	Alignment		34.6	15	**Fold:**Ribosome binding domain-like **Superfamily:**Trigger factor ribosome-binding domain **Family:**Trigger factor ribosome-binding domain
6	c2d3o1_	Alignment		31.1	20	**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
7	c1t11A_	Alignment		28.2	15	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**trigger factor; **PDBTitle:** trigger factor
8	d1cpza_	Alignment		27.7	12	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
9	d1osda_	Alignment		27.6	6	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
10	c2qgoA_	Alignment		25.8	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
11	c1yg0A_	Alignment		25.5	6	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**cop associated protein; **PDBTitle:** solution structure of apo-copp from helicobacter pylori

12	d1p6ta2	Alignment		24.5	12	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
13	c1y3kA_	Alignment		24.5	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
14	d1mwza_	Alignment		24.4	3	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
15	c2yvxD_	Alignment		24.1	18	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**mg2+ transporter mgte; **PDBTitle:** crystal structure of magnesium transporter mgte
16	c2k2pA_	Alignment		21.6	12	**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
17	c2ga7A_	Alignment		21.3	12	**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)
18	c2ofhX_	Alignment		18.7	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
19	d2qifa1	Alignment		18.5	9	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
20	d2p2ea1	Alignment		18.1	26	**Fold:**HesB-like domain **Superfamily:**HesB-like domain **Family:**HesB-like domain
21	c2aj1A_	Alignment	not modelled	18.0	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable cadmium-transporting atpase; **PDBTitle:** solution structure of apocada
22	d2aw0a_	Alignment	not modelled	17.2	21	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
23	d1afia_	Alignment	not modelled	16.4	6	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
24	d1p6ta1	Alignment	not modelled	15.9	9	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
25	d1qb2a_	Alignment	not modelled	15.8	17	**Fold:**Signal peptide-binding domain **Superfamily:**Signal peptide-binding domain **Family:**Signal peptide-binding domain
26	c3dxsX_	Alignment	not modelled	15.8	12	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**copper-transporting atpase ran1; **PDBTitle:** crystal structure of a copper binding domain from hma7, a p-2 type atpase
27	c2kt2A_	Alignment	not modelled	15.1	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**mercuric reductase; **PDBTitle:** structure of nmera, the n-terminal hma domain of tn501 mercuric2 reductase
28	d1vyva2	Alignment	not modelled	14.2	29	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
						Fold: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex

29	d1w4ha1	Alignment	not modelled	14.2	29	**Superfamily:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Family:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
30	c3bdlA_	Alignment	not modelled	14.2	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**staphylococcal nuclease domain-containing **PDBTitle:** crystal structure of a truncated human tudor-sn
31	d1kvja_	Alignment	not modelled	13.9	21	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
32	d1qzxa2	Alignment	not modelled	13.8	21	**Fold:**Signal peptide-binding domain **Superfamily:**Signal peptide-binding domain **Family:**Signal peptide-binding domain
33	c2kkhA_	Alignment	not modelled	13.8	21	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**putative heavy metal transporter; **PDBTitle:** structure of the zinc binding domain of the atpase hma4
34	d1jw2a_	Alignment	not modelled	13.8	36	**Fold:**Open three-helical up-and-down bundle **Superfamily:**Hemolysin expression modulating protein HHA **Family:**Hemolysin expression modulating protein HHA
35	c2e75E_	Alignment	not modelled	13.7	29	**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
36	c2e74E_	Alignment	not modelled	13.7	29	**PDB header:**photosynthesis **Chain:** E: **PDB Molecule:**cytochrome b6-f complex subunit 6; **PDBTitle:** crystal structure of the cytochrome b6f complex from m.laminosus
37	c2e76E_	Alignment	not modelled	13.7	29	**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
38	d2e74e1	Alignment	not modelled	13.7	29	**Fold:**Single transmembrane helix **Superfamily:**PetL subunit of the cytochrome b6f complex **Family:**PetL subunit of the cytochrome b6f complex
39	c1vf5R_	Alignment	not modelled	13.7	29	**PDB header:**photosynthesis **Chain:** R: **PDB Molecule:**protein pet l; **PDBTitle:** crystal structure of cytochrome b6f complex from m.laminosus
40	d2aq0a1	Alignment	not modelled	13.6	10	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
41	d1uwda_	Alignment	not modelled	13.0	11	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**PaaD-like
42	d1s6ua_	Alignment	not modelled	12.3	18	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
43	d2cyua1	Alignment	not modelled	12.1	29	**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
44	c2rogA_	Alignment	not modelled	10.5	12	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**heavy metal binding protein; **PDBTitle:** solution structure of thermus thermophilus hb8 ttha17182 protein in living e. coli cells
45	d2ffha2	Alignment	not modelled	10.2	17	**Fold:**Signal peptide-binding domain **Superfamily:**Signal peptide-binding domain **Family:**Signal peptide-binding domain
46	c1yjrA_	Alignment	not modelled	10.1	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 1; **PDBTitle:** solution structure of the apo form of the sixth soluble2 domain a69p mutant of menkes protein
47	c1w26B_	Alignment	not modelled	10.0	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
48	c2iy3A_	Alignment	not modelled	9.9	21	**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
49	d1sb6a_	Alignment	not modelled	9.5	6	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
50	c2l3mA_	Alignment	not modelled	9.4	12	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**copper-ion-binding protein; **PDBTitle:** solution structure of the putative copper-ion-binding protein from2 bacillus anthracis str. ames
51	d1vs6z1	Alignment	not modelled	9.2	25	**Fold:**L28p-like **Superfamily:**L28p-like **Family:**Ribosomal protein L31p
52	d3elga1	Alignment	not modelled	8.8	31	**Fold:**BLIP-like **Superfamily:**BT0923-like **Family:**BT0923-like
53	d1x2ia1	Alignment	not modelled	8.7	29	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
54	d1ftra1	Alignment	not modelled	8.6	16	**Fold:**Ferredoxin-like **Superfamily:**Formylmethanofuran:tetrahydromethanopterin formyltransferase **Family:**Formylmethanofuran:tetrahydromethanopterin formyltransferase

55	c2vzkD_	Alignment	not modelled	8.0	32	**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
56	c1qzwC_	Alignment	not modelled	7.5	21	**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
57	d1q8la_	Alignment	not modelled	7.5	18	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
58	d2ggpb1	Alignment	not modelled	7.4	6	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
59	d2a1jb1	Alignment	not modelled	7.3	14	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
60	c3j09A_	Alignment	not modelled	7.1	6	**PDB header:**hydrolase, metal transport **Chain:** A: **PDB Molecule:**copper-exporting p-type atpase a; **PDBTitle:** high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa
61	c2ksdA_	Alignment	not modelled	6.8	14	**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
62	c2dbcA_	Alignment	not modelled	6.7	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**unnamed protein product; **PDBTitle:** solution structure of the thioredoxin-like domain of2 phosducin-like protein 2(pdcl2)
63	c1vf5E_	Alignment	not modelled	6.7	27	**PDB header:**photosynthesis **Chain:** E: **PDB Molecule:**protein pet l; **PDBTitle:** crystal structure of cytochrome b6f complex from m.laminosus
64	c1xbsA_	Alignment	not modelled	6.6	8	**PDB header:**transcription, cell cycle **Chain:** A: **PDB Molecule:**dim1-like protein; **PDBTitle:** crystal structure of human dim2: a dim1-like protein
65	c2kncA_	Alignment	not modelled	6.5	23	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
66	c3dv0I_	Alignment	not modelled	6.4	11	**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
67	c2ldiA_	Alignment	not modelled	6.4	6	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zinc-transporting atpase; **PDBTitle:** nmr solution structure of ziaan sub mutant
68	c3bvsA_	Alignment	not modelled	6.4	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alkylpurine dna glycosylase alkd; **PDBTitle:** crystal structure of bacillus cereus alkylpurine dna glycosylase alkd
69	d3duea1	Alignment	not modelled	6.3	25	**Fold:**BLIP-like **Superfamily:**BT0923-like **Family:**BT0923-like
70	c2kelB_	Alignment	not modelled	6.1	21	**PDB header:**transcription repressor **Chain:** B: **PDB Molecule:**uncharacterized protein 56b; **PDBTitle:** structure of the transcription regulator svtr from the2 hyperthermophilic archaeal virus sirv1
71	c2q9rA_	Alignment	not modelled	6.1	7	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**protein of unknown function; **PDBTitle:** crystal structure of a duf416 family protein (sbal_3149) from2 shewanella baltica os155 at 1.91 a resolution
72	d1nyta2	Alignment	not modelled	6.0	33	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Shikimate dehydrogenase-like
73	d1w85i_	Alignment	not modelled	5.8	13	**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
74	c3b1qD_	Alignment	not modelled	5.6	22	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ribokinase, putative; **PDBTitle:** structure of burkholderia thailandensis nucleoside kinase (bthnk) in2 complex with inosine
75	c2eq9C_	Alignment	not modelled	5.6	11	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**pyruvate dehydrogenase complex, dihydrolipoamide **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdb
76	c2wwaJ_	Alignment	not modelled	5.6	14	**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
77	d2c4ka1	Alignment	not modelled	5.6	27	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
78	d1vyua2	Alignment	not modelled	5.5	29	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
79	d1xs5a_	Alignment	not modelled	5.5	18	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II

						Family: Phosphate binding protein-like
80	c2eq7C_	Alignment	not modelled	5.5	13	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**2-oxoglutarate dehydrogenase e2 component; **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdo
81	c2gcfA_	Alignment	not modelled	5.5	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cation-transporting atpase pacs; **PDBTitle:** solution structure of the n-terminal domain of the coppper(i) atpase2 pacs in its apo form
82	c3tqwA_	Alignment	not modelled	5.4	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**methionine-binding protein; **PDBTitle:** structure of a abc transporter, periplasmic substrate-binding protein2 from coxiella burnetii
83	c1w3dA_	Alignment	not modelled	5.4	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydrolipoyllysine-residue acetyltransferase **PDBTitle:** nmr structure of the peripheral-subunit binding domain of2 bacillus stearothermophilus e2p
84	d1bala_	Alignment	not modelled	5.4	26	**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
85	d1vkpa_	Alignment	not modelled	5.3	15	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Porphyromonas-type peptidylarginine deiminase
86	d2axoa1	Alignment	not modelled	5.2	44	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Atu2684-like
87	c3pwzA_	Alignment	not modelled	5.2	44	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**shikimate dehydrogenase 3; **PDBTitle:** crystal structure of an ael1 enzyme from pseudomonas putida
88	d2brja1	Alignment	not modelled	5.2	25	**Fold:**AOC barrel-like **Superfamily:**Allene oxide cyclase-like **Family:**Allene oxide cyclase-like