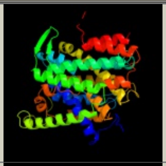
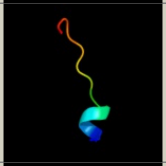
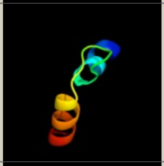
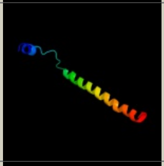
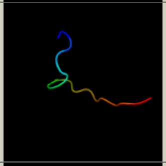
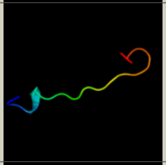
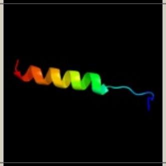
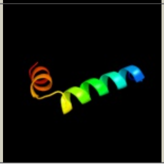
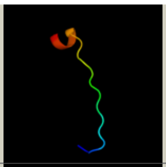
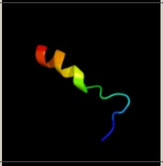
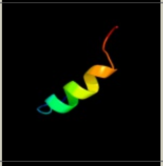
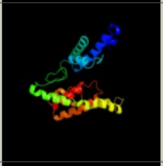
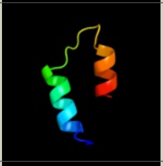
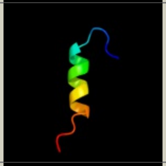
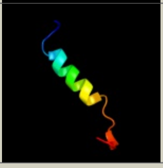
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P31440
Date	Thu Jan 5 11:47:30 GMT 2012
Unique Job ID	ea340db96a41ad1b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3qe7A_	Alignment		100.0	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**uracil permease; **PDBTitle:** crystal structure of uracil transporter--uraa
2	c3lpzA_	Alignment		15.7	14	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**get4 (yor164c homolog); **PDBTitle:** crystal structure of c. therm. get4
3	c2dmeA_	Alignment		15.5	16	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**phd finger protein 3; **PDBTitle:** solution structure of the tfiis domain ii of human phd2 finger protein 3
4	d1w7ca3	Alignment		11.2	23	**Fold:**Cystatin-like **Superfamily:**Amine oxidase N-terminal region **Family:**Amine oxidase N-terminal region
5	c2elpA_	Alignment		10.9	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 406; **PDBTitle:** solution structure of the 13th c2h2 zinc finger of human2 zinc finger protein 406
6	c3dinD_	Alignment		10.1	10	**PDB header:**membrane protein, protein transport **Chain:** D: **PDB Molecule:**preprotein translocase subunit sece; **PDBTitle:** crystal structure of the protein-translocation complex formed by the2 secy channel and the seca atpase
7	c2jqoA_	Alignment		9.5	16	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**hypothetical protein yoba; **PDBTitle:** nmr solution structure of bacillus subtilis yoba 21-120:2 northeast structural genomics consortium target sr547
8	d1enwa_	Alignment		9.4	6	**Fold:**RuvA C-terminal domain-like **Superfamily:**Elongation factor TFIIS domain 2 **Family:**Elongation factor TFIIS domain 2
9	c1w3gA_	Alignment		9.0	16	**PDB header:**toxin/lectin **Chain:** A: **PDB Molecule:**hemolytic lectin from laetiporus sulphureus; **PDBTitle:** hemolytic lectin from the mushroom laetiporus sulphureus2 complexed with two n-acetyllactosamine molecules.
10	d2axtf1	Alignment		7.9	24	**Fold:**Single transmembrane helix **Superfamily:**Cytochrome b559 subunits **Family:**Cytochrome b559 subunits
11	c3ndqA_	Alignment		7.8	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor a protein 1; **PDBTitle:** structure of human tfiis domain ii

12	d1xsza2	Alignment		6.9	16	**Fold:**TBP-like **Superfamily:**RalF, C-terminal domain **Family:**RalF, C-terminal domain
13	c3arcl_	Alignment		6.7	29	**PDB header:**electron transport, photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution
14	c3e5aB_	Alignment		6.5	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**targeting protein for xklp2; **PDBTitle:** crystal structure of aurora a in complex with vx-680 and tpx2
15	d1p7ga2	Alignment		6.3	5	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), C-terminal domain
16	d3er7a1	Alignment		6.1	28	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Exig0174-like
17	c2ht2B_	Alignment		5.9	13	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**h(+)/cl(-) exchange transporter clca; **PDBTitle:** structure of the escherichia coli clc chloride channel2 y445h mutant and fab complex
18	c3bu8B_	Alignment		5.5	13	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**telomeric repeat-binding factor 2; **PDBTitle:** crystal structure of trf2 trfh domain and tin2 peptide2 complex
19	d1dt0a2	Alignment		5.4	15	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), C-terminal domain
20	c2aexA_	Alignment		5.4	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**coproporphyrinogen iii oxidase, mitochondrial; **PDBTitle:** the 1.58a crystal structure of human coproporphyrinogen oxidase2 reveals the structural basis of hereditary coproporphyria
21	d1txna_	Alignment	not modelled	5.3	8	**Fold:**Coproporphyrinogen III oxidase **Superfamily:**Coproporphyrinogen III oxidase **Family:**Coproporphyrinogen III oxidase