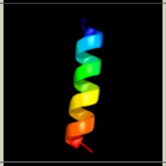
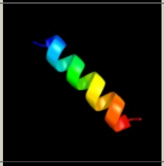
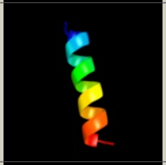
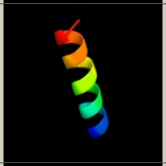
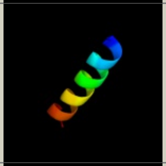
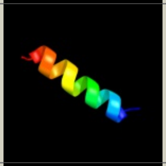
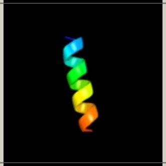
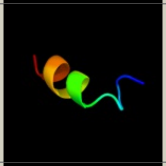
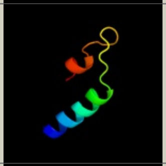
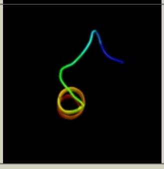
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P15068
Date	Thu Jan 5 11:34:31 GMT 2012
Unique Job ID	149c06ae9eb4ca9a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3bz1L_	Alignment		34.5	33	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of cyanobacterial photosystem ii (part 12 of 2). this file contains first monomer of psii dimer
2	c3kziL_	Alignment		34.5	33	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of monomeric form of cyanobacterial photosystem ii
3	c1s5lI_	Alignment		34.5	33	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein; **PDBTitle:** architecture of the photosynthetic oxygen evolving center
4	c1s5lL_	Alignment		34.5	33	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein; **PDBTitle:** architecture of the photosynthetic oxygen evolving center
5	c3prrL_	Alignment		34.5	33	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of cyanobacterial photosystem ii in complex with2 terbutryn (part 2 of 2). this file contains second monomer of psii3 dimer
6	d2axtl1	Alignment		34.5	33	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction center protein L, PsbL **Family:**PsbL-like
7	c3arcL_	Alignment		34.5	33	**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
8	c2axtI_	Alignment		34.5	33	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein; **PDBTitle:** crystal structure of photosystem ii from thermosynechococcus elongatus
9	c2axtL_	Alignment		34.5	33	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein; **PDBTitle:** crystal structure of photosystem ii from thermosynechococcus elongatus
10	c3prqL_	Alignment		34.5	33	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of cyanobacterial photosystem ii in complex with2 terbutryn (part 1 of 2). this file contains first monomer of psii3 dimer
11	c3bz2L_	Alignment		34.5	33	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of cyanobacterial photosystem ii (part 22 of 2). this file contains second monomer of psii dimer

12	c3a0bl_	Alignment		30.6	33	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
13	c3a0hl_	Alignment		30.6	33	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
14	c3a0hL_	Alignment		30.6	33	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
15	c3a0bL_	Alignment		29.1	33	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
16	d2foka1	Alignment		19.8	47	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Restriction endonuclease FokI, N-terminal (recognition) domain
17	c3hosA_	Alignment		17.4	29	**PDB header:**transferase, dna binding protein/dna **Chain:** A: **PDB Molecule:**transposable element mariner, complete cds; **PDBTitle:** crystal structure of the mariner mos1 paired end complex with mg
18	c2f7tA_	Alignment		15.9	29	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**mos1 transposase; **PDBTitle:** crystal structure of the catalytic domain of mos1 mariner2 transposase
19	c3n1bA_	Alignment		14.2	23	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**vacuolar protein sorting-associated protein 54; **PDBTitle:** c-terminal domain of vps54 subunit of the garp complex
20	d2e29a1	Alignment		11.1	25	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**GUCT domain
21	c3f2kB_	Alignment	not modelled	10.8	29	**PDB header:**transferase **Chain:** B: **PDB Molecule:**histone-lysine n-methyltransferase setmar; **PDBTitle:** structure of the transposase domain of human histone-lysine2 n-methyltransferase setmar
22	d1nb5i_	Alignment	not modelled	9.2	7	**Fold:**Cystatin-like **Superfamily:**Cystatin/monellin **Family:**Cystatins
23	d1d2zb_	Alignment	not modelled	7.7	40	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
24	d1eu3a1	Alignment	not modelled	7.1	29	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Superantigen toxins, N-terminal domain
25	c2rlfA_	Alignment	not modelled	6.3	21	**PDB header:**proton transport **Chain:** A: **PDB Molecule:**matrix protein 2; **PDBTitle:** proton channel m2 from influenza a in complex with2 inhibitor rimantadine
26	d2ihoa2	Alignment	not modelled	6.2	71	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**MOA C-terminal domain-like
27	d1stfi_	Alignment	not modelled	6.0	11	**Fold:**Cystatin-like **Superfamily:**Cystatin/monellin **Family:**Cystatins
28	d2jnwa1	Alignment	not modelled	6.0	21	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**XPF/Rad1/Mus81 nuclease
						PDB header:membrane protein

29	c1yceD_	Alignment	not modelled	5.7	19	**Chain:** D: **PDB Molecule:**subunit c; **PDBTitle:** structure of the rotor ring of f-type na+-atpase from ilyobacter2 tartaricus
30	c3zv0A_	Alignment	not modelled	5.3	13	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**protein shq1; **PDBTitle:** structure of the shq1p-cbf5p complex