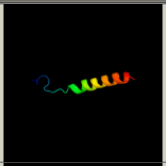
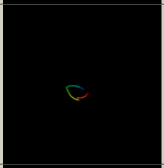
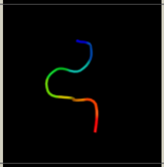
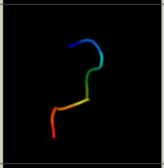
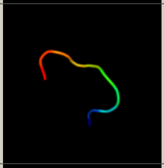
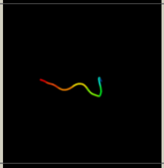
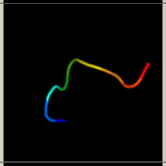
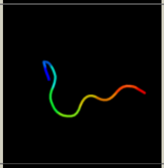
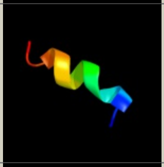
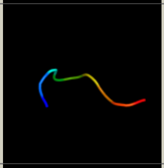
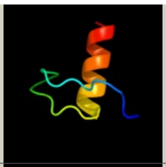
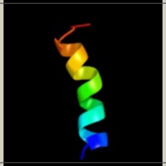
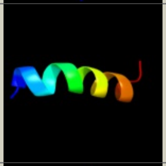
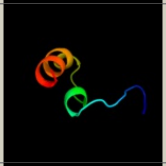
Email	l.a.kelley@imperial.ac.uk
Description	A5A630
Date	Thu Jan 5 10:55:32 GMT 2012
Unique Job ID	b11f8cc451fde165

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3kdpD_	Alignment		35.5	19	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**sodium/potassium-transporting atpase subunit beta-1; **PDBTitle:** crystal structure of the sodium-potassium pump
2	c2z8tX_	Alignment		21.5	70	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**protein-glutaminase; **PDBTitle:** crystal structure of protein-glutaminase of c.proteolyticum2 strain 9670
3	d8i1ba_	Alignment		20.0	33	**Fold:**beta-Trefoil **Superfamily:**Cytokine **Family:**Interleukin-1 (IL-1)
4	d1ilr1_	Alignment		19.9	56	**Fold:**beta-Trefoil **Superfamily:**Cytokine **Family:**Interleukin-1 (IL-1)
5	c3a56B_	Alignment		19.6	70	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein-glutaminase; **PDBTitle:** crystal structure of pro- protein-glutaminase
6	c2wryA_	Alignment		19.5	56	**PDB header:**immune system **Chain:** A: **PDB Molecule:**interleukin-1beta; **PDBTitle:** crystal structure of chicken cytokine interleukin 1 beta
7	d2ilaa_	Alignment		19.0	22	**Fold:**beta-Trefoil **Superfamily:**Cytokine **Family:**Interleukin-1 (IL-1)
8	d1l2ha_	Alignment		18.2	22	**Fold:**beta-Trefoil **Superfamily:**Cytokine **Family:**Interleukin-1 (IL-1)
9	c1cn3F_	Alignment		17.1	31	**PDB header:**viral protein **Chain:** F: **PDB Molecule:**fragment of coat protein vp2; **PDBTitle:** interaction of polyomavirus internal protein vp2 with major2 capsid protein vp1 and implications for participation of3 vp2 in viral entry
10	d1md6a_	Alignment		16.5	67	**Fold:**beta-Trefoil **Superfamily:**Cytokine **Family:**Interleukin-1 (IL-1)
11	c1afoB_	Alignment		13.0	31	**PDB header:**integral membrane protein **Chain:** B: **PDB Molecule:**glycophorin a; **PDBTitle:** dimeric transmembrane domain of human glycophorin a, nmr,2 20 structures

12	c1kveA_	Alignment		12.1	24	**PDB header:**toxin **Chain:** A: **PDB Molecule:**smk toxin; **PDBTitle:** killer toxin from halotolerant yeast
13	c3bz1y_	Alignment		7.7	16	**PDB header:**electron transport **Chain:** Y: **PDB Molecule:**photosystem ii protein y; **PDBTitle:** crystal structure of cyanobacterial photosystem ii (part 12 of 2). this file contains first monomer of psii dimer
14	c3a0by_	Alignment		7.7	16	**PDB header:**electron transport **Chain:** Y: **PDB Molecule:**photosystem ii reaction center protein ycf12; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
15	c3a0hy_	Alignment		7.7	16	**PDB header:**electron transport **Chain:** Y: **PDB Molecule:**photosystem ii reaction center protein ycf12; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
16	c3a0hY_	Alignment		7.7	16	**PDB header:**electron transport **Chain:** Y: **PDB Molecule:**photosystem ii reaction center protein ycf12; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
17	c3deeA_	Alignment		7.5	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative regulatory protein; **PDBTitle:** crystal structure of a putative regulatory protein involved in2 transcription (ngo1945) from neisseria gonorrhoeae fa 1090 at 2.25 a3 resolution
18	c3arcy_	Alignment		7.3	16	**PDB header:**electron transport, photosynthesis **Chain:** Y: **PDB Molecule:**protein ycf12; **PDBTitle:** crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution
19	c3arcY_	Alignment		7.3	16	**PDB header:**electron transport, photosynthesis **Chain:** Y: **PDB Molecule:**protein ycf12; **PDBTitle:** crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution
20	c3a0bY_	Alignment		7.3	16	**PDB header:**electron transport **Chain:** Y: **PDB Molecule:**photosystem ii reaction center protein ycf12; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
21	c1w2wA_	Alignment	not modelled	7.3	36	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**5-methylthioribose-1-phosphate isomerase; **PDBTitle:** crystal structure of yeast ypr118w, a methylthioribose-1-2 phosphate isomerase related to regulatory eif2b subunits