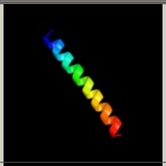
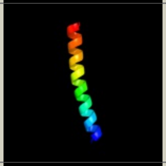
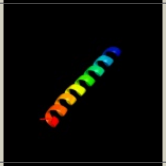
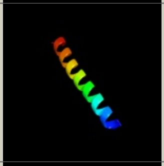
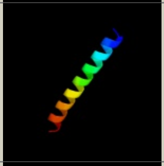
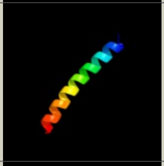
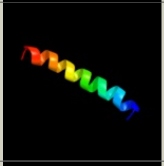
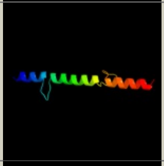
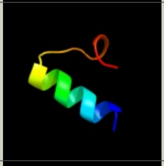
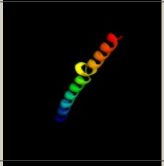
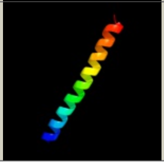
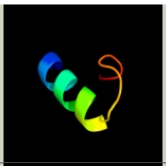
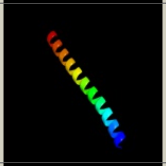
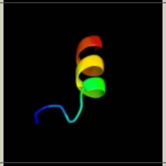
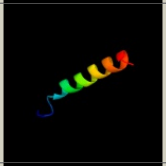
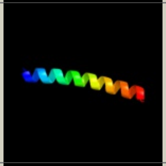
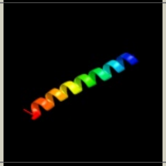
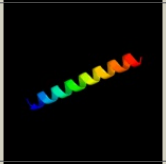
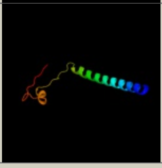
Email	l.a.kelley@imperial.ac.uk
Description	P0AEN4
Date	Thu Jan 5 11:23:47 GMT 2012
Unique Job ID	d3466d2c70603d08

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1kddC_	Alignment		21.8	31	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**gcn4 acid base heterodimer acid-d12la16i; **PDBTitle:** x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16i base-d12la16l
2	c1kddA_	Alignment		21.4	31	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**gcn4 acid base heterodimer acid-d12la16i; **PDBTitle:** x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16i base-d12la16l
3	c1kddF_	Alignment		21.4	31	**PDB header:**de novo protein **Chain:** F: **PDB Molecule:**gcn4 acid base heterodimer acid-d12la16i; **PDBTitle:** x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16i base-d12la16l
4	c1kd9F_	Alignment		21.4	31	**PDB header:**de novo protein **Chain:** F: **PDB Molecule:**gcn4 acid base heterodimer acid-d12la16l; **PDBTitle:** x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16l base-d12la16l
5	c1kd9C_	Alignment		21.4	31	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**gcn4 acid base heterodimer acid-d12la16l; **PDBTitle:** x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16l base-d12la16l
6	c1kd9A_	Alignment		21.4	31	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**gcn4 acid base heterodimer acid-d12la16l; **PDBTitle:** x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16l base-d12la16l
7	c1u2uA_	Alignment		21.3	31	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** nmr solution structure of a designed heterodimeric leucine2 zipper
8	c3mudA_	Alignment		19.4	15	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**dna repair protein xrcc4, tropomyosin alpha-1 chain; **PDBTitle:** structure of the tropomyosin overlap complex from chicken smooth2 muscle
9	d1gyxa_	Alignment		15.3	14	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**4-oxalocrotonate tautomerase-like
10	c1debA_	Alignment		14.8	28	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**adenomatous polyposis coli protein; **PDBTitle:** crystal structure of the n-terminal coiled coil domain from2 apc
11	c3q4fG_	Alignment		9.9	11	**PDB header:**dna binding protein/protein binding **Chain:** G: **PDB Molecule:**dna repair protein xrcc4; **PDBTitle:** crystal structure of xrcc4/xlf-cernunnos complex

12	c3m20A_	Alignment		9.3	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**4-oxalocrotonate tautomerase, putative; **PDBTitle:** crystal structure of dmpi from archaeoglobus fulgidus determined to2 2.37 angstroms resolution
13	c2w6aB_	Alignment		9.0	17	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**arf gtpase-activating protein git1; **PDBTitle:** x-ray structure of the dimeric git1 coiled-coil domain
14	d2csba3	Alignment		8.7	40	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Topoisomerase V repeat domain
15	c2kncB_	Alignment		8.2	16	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-3; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
16	c2j5uB_	Alignment		7.1	24	**PDB header:**cell shape regulation **Chain:** B: **PDB Molecule:**mrec protein; **PDBTitle:** mrec lysteria monocytogenes
17	c1kd8A_	Alignment		7.1	28	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**gcn4 acid base heterodimer acid-d12ia16v; **PDBTitle:** x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12ia16v base-d12la16l
18	c1kd8F_	Alignment		7.1	28	**PDB header:**de novo protein **Chain:** F: **PDB Molecule:**gcn4 acid base heterodimer acid-d12ia16v; **PDBTitle:** x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12ia16v base-d12la16l
19	c1kd8C_	Alignment		7.1	28	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**gcn4 acid base heterodimer acid-d12ia16v; **PDBTitle:** x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12ia16v base-d12la16l
20	d2azeb1	Alignment		6.8	18	**Fold:**E2F-DP heterodimerization region **Superfamily:**E2F-DP heterodimerization region **Family:**E2F dimerization segment
21	c2jeeA_	Alignment	not modelled	6.7	15	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**yiiu; **PDBTitle:** xray structure of e. coli yiiu
22	c3htkB_	Alignment	not modelled	6.7	14	**PDB header:**recombination/replication/ligase **Chain:** B: **PDB Molecule:**structural maintenance of chromosomes protein 5; **PDBTitle:** crystal structure of mms21 and smc5 complex
23	c2gd7B_	Alignment	not modelled	6.5	31	**PDB header:**transcription **Chain:** B: **PDB Molecule:**hexim1 protein; **PDBTitle:** the structure of the cyclin t-binding domain of hexim12 reveals the molecular basis for regulation of3 transcription elongation
24	c2voyB_	Alignment	not modelled	6.4	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**sarcoplasmic/endoplasmic reticulum calcium **PDBTitle:** cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
25	d1b0nb_	Alignment	not modelled	5.8	55	**Fold:**Dimerisation interlock **Superfamily:**SinR repressor dimerisation domain-like **Family:**SinR repressor dimerisation domain-like
26	c1b0nB_	Alignment	not modelled	5.8	55	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**protein (sini protein); **PDBTitle:** sinr protein/sini protein complex
27	c3o2iB_	Alignment	not modelled	5.8	33	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of a functionally unknown protein from2 leptospirillum sp. group ii uba