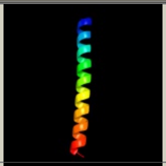
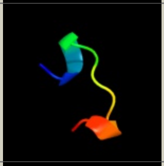
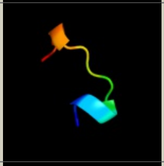
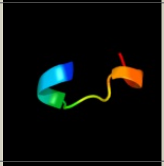
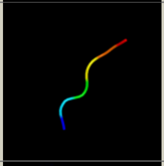
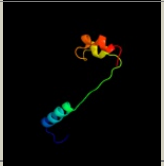
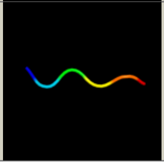
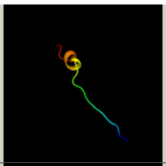
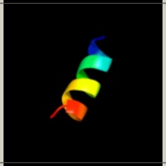
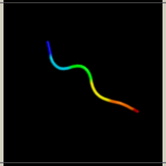
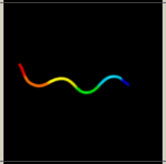
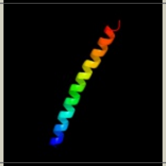
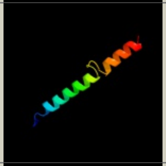
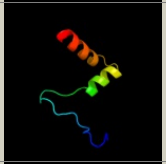
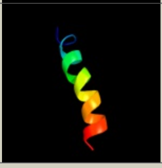
Email	l.a.kelley@imperial.ac.uk
Description	P71297
Date	Thu Jan 5 12:12:43 GMT 2012
Unique Job ID	daede93f31f498c3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1debA_	Alignment		48.0	29	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**adenomatous polyposis coli protein; **PDBTitle:** crystal structure of the n-terminal coiled coil domain from2 apc
2	d1v2za_	Alignment		29.2	67	**Fold:**KaiA/RbsU domain **Superfamily:**KaiA/RbsU domain **Family:**Circadian clock protein KaiA, C-terminal domain
3	d1sv1a_	Alignment		27.8	67	**Fold:**KaiA/RbsU domain **Superfamily:**KaiA/RbsU domain **Family:**Circadian clock protein KaiA, C-terminal domain
4	d1r8ja1	Alignment		27.7	50	**Fold:**KaiA/RbsU domain **Superfamily:**KaiA/RbsU domain **Family:**Circadian clock protein KaiA, C-terminal domain
5	d1r5qa_	Alignment		26.4	42	**Fold:**KaiA/RbsU domain **Superfamily:**KaiA/RbsU domain **Family:**Circadian clock protein KaiA, C-terminal domain
6	c1r8jB_	Alignment		18.9	50	**PDB header:**circadian clock protein **Chain:** B: **PDB Molecule:**kaia; **PDBTitle:** crystal structure of circadian clock protein kaia from2 synechococcus elongatus
7	c2kaoA_	Alignment		18.9	67	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methionine-r-sulfoxide reductase b1; **PDBTitle:** structure of reduced mouse methionine sulfoxide reductase b12 (sec95cys mutant)
8	c2fe9A_	Alignment		17.6	33	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**protein vts1; **PDBTitle:** solution structure of the vts1 sam domain in the presence2 of rna
9	c3zqoK_	Alignment		16.7	40	**PDB header:**dna-binding protein **Chain:** K: **PDB Molecule:**terminase small subunit; **PDBTitle:** crystal structure of the small terminase oligomerization2 core domain from a spp1-like bacteriophage (crystal form 3)
10	c3lupA_	Alignment		13.5	15	**PDB header:**structure genomics, unknown function **Chain:** A: **PDB Molecule:**degv family protein; **PDBTitle:** crystal structure of fatty acid binding degv family protein sag13422 from streptococcus agalactiae
11	c3hcjB_	Alignment		11.8	67	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**peptide methionine sulfoxide reductase; **PDBTitle:** structure of msrb from xanthomonas campestris (oxidized2 form)

12	c3iymA_	Alignment		11.6	45	**PDB header:**virus **Chain:** A: **PDB Molecule:**capsid protein; **PDBTitle:** backbone trace of the capsid protein dimer of a fungal partitivirus2 from electron cryomicroscopy and homology modeling
13	c2konA_	Alignment		11.5	62	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** nmr solution structure of cv_2116 from chromobacterium2 violaceum. northeast structural genomics consortium target3 cvt4(1-82)
14	d1xm0a1	Alignment		10.6	83	**Fold:**Mss4-like **Superfamily:**Mss4-like **Family:**SelR domain
15	c3e0mB_	Alignment		9.2	83	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**peptide methionine sulfoxide reductase msra/msrb **PDBTitle:** crystal structure of fusion protein of msra and msrb
16	c1junB_	Alignment		8.9	32	**PDB header:**transcription regulation **Chain:** B: **PDB Molecule:**c-jun homodimer; **PDBTitle:** nmr study of c-jun homodimer
17	c3q4fG_	Alignment		8.7	17	**PDB header:**dna binding protein/protein binding **Chain:** G: **PDB Molecule:**dna repair protein xrcc4; **PDBTitle:** crystal structure of xrcc4/xlf-cernunnos complex
18	c3mudA_	Alignment		7.2	23	**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
19	d1iica1	Alignment		6.8	25	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-myristoyl transferase, NMT
20	c1u2uB_	Alignment		5.9	43	**PDB header:**transcription **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** nmr solution structure of a designed heterodimeric leucine2 zipper
21	c3fovA_	Alignment	not modelled	5.4	41	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0102 protein rpa0323; **PDBTitle:** crystal structure of protein rpa0323 of unknown function from2 rhodopseudomonas palustris
22	d1hwxa2	Alignment	not modelled	5.3	13	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
23	c2d1lA_	Alignment	not modelled	5.2	18	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**metastasis suppressor protein 1; **PDBTitle:** structure of f-actin binding domain imd of mim (missing in metastasis)
24	c3fdjA_	Alignment	not modelled	5.1	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**degv family protein; **PDBTitle:** the structure of a degv family protein from eubacterium eligens.