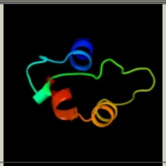
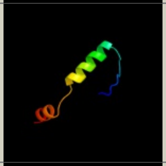
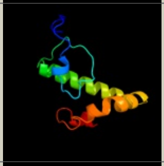
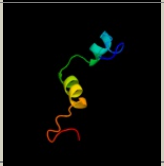
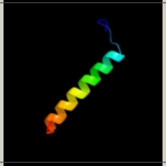
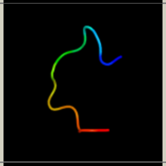
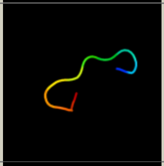
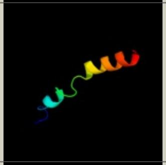
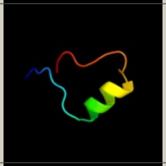
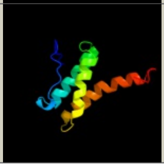
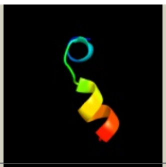
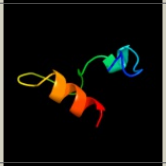
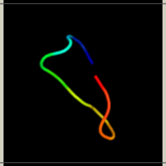
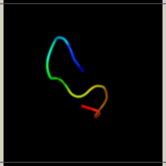
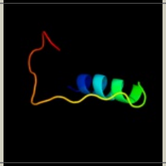
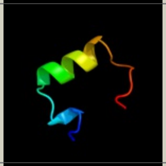
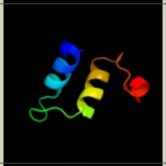
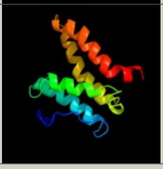
Email	l.a.kelley@imperial.ac.uk
Description	P32694
Date	Thu Jan 5 11:50:16 GMT 2012
Unique Job ID	38820bd8ae5a2616

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2k5eA_	Alignment		28.3	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of putative uncharacterized protein2 gsu1278 from methanocaldococcus jannaschii, northeast3 structural genomics consortium (nesg) target gsr195
2	d2uube1	Alignment		20.1	19	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Translational machinery components
3	c2pr1B_	Alignment		18.0	50	**PDB header:**transferase **Chain:** B: **PDB Molecule:**uncharacterized n-acetyltransferase ylbp; **PDBTitle:** crystal structure of the bacillus subtilis n-acetyltransferase ylbp2 protein in complex with coenzyme-a
4	c1y6zA_	Alignment		13.6	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**heat shock protein, putative; **PDBTitle:** middle domain of plasmodium falciparum putative heat shock protein2 pf14_0417
5	c2jugB_	Alignment		11.9	21	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**tubc protein; **PDBTitle:** multienzyme docking in hybrid megasynthetases
6	d2gu2a1	Alignment		11.1	23	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**AstE/AspA-like
7	d1ci4a_	Alignment		10.4	15	**Fold:**SAM domain-like **Superfamily:**Barrier-to-autointegration factor, BAF **Family:**Barrier-to-autointegration factor, BAF
8	c2f2iA_	Alignment		10.1	50	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**kalata-b1; **PDBTitle:** solution structure of [p20d,v21k]-kalata b1
9	c2kn8A_	Alignment		9.4	24	**PDB header:**protein binding, dna binding protein **Chain:** A: **PDB Molecule:**dna cleavage and packaging protein large subunit, ul89; **PDBTitle:** nmr structure of the c-terminal domain of pul89
10	d3elga1	Alignment		9.1	29	**Fold:**BLIP-like **Superfamily:**BT0923-like **Family:**BT0923-like
11	c3mdjB_	Alignment		8.9	19	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** B: **PDB Molecule:**endoplasmic reticulum aminopeptidase 1; **PDBTitle:** er aminopeptidase, erap1, bound to the zinc aminopeptidase inhibitor,2 bestatin

12	c1kdxB_	Alignment		8.4	40	**PDB header:**transcription regulation complex **Chain:** B: **PDB Molecule:**creb; **PDBTitle:** kix domain of mouse cbp (creb binding protein) in complex2 with phosphorylated kinase inducible domain (pkid) of rat3 creb (cyclic amp response element binding protein), nmr 174 structures
13	d1cuka1	Alignment		8.2	19	**Fold:**RuvA C-terminal domain-like **Superfamily:**DNA helicase RuvA subunit, C-terminal domain **Family:**DNA helicase RuvA subunit, C-terminal domain
14	c3e4hA_	Alignment		7.8	42	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**varv peptide f; **PDBTitle:** crystal structure of the cyclotide varv f
15	c2jwmA_	Alignment		7.6	33	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**kalata-b7; **PDBTitle:** nmr spatial srtucture of ternary complex kalata b7/mn2+/dpc2 micelle
16	c3di3A_	Alignment		7.5	19	**PDB header:**cytokine/cytokine receptor **Chain:** A: **PDB Molecule:**interleukin-7; **PDBTitle:** crystal structure of the complex of human interleukin-7 with2 glycosylated human interleukin-7 receptor alpha ectodomain
17	d3duea1	Alignment		6.8	25	**Fold:**BLIP-like **Superfamily:**BT0923-like **Family:**BT0923-like
18	c2qfaC_	Alignment		6.6	55	**PDB header:**cell cycle/cell cycle/cell cycle **Chain:** C: **PDB Molecule:**inner centromere protein; **PDBTitle:** crystal structure of a survivin-borealin-incenp core complex
19	c2kzvA_	Alignment		6.5	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of cv_0373(175-257) protein from2 chromobacterium violaceum, northeast structural genomics consortium3 target cvr118a
20	c3rjoA_	Alignment		6.3	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoplasmic reticulum aminopeptidase 1; **PDBTitle:** crystal structure of erap1 peptide binding domain
21	d1pt4a_	Alignment	not modelled	6.3	42	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Cyclotides **Family:**Kalata B1
22	d1tyka_	Alignment	not modelled	5.7	44	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**omega toxin-like **Family:**Spider toxins
23	d1nb1a_	Alignment	not modelled	5.5	50	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Cyclotides **Family:**Kalata B1
24	d2e1ba1	Alignment	not modelled	5.4	24	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**AlaX-M N-terminal domain-like
25	c1k0rB_	Alignment	not modelled	5.3	13	**PDB header:**transcription **Chain:** B: **PDB Molecule:**nusa; **PDBTitle:** crystal structure of mycobacterium tuberculosis nusa