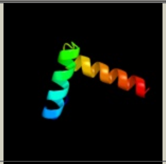
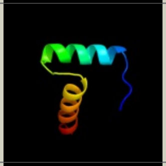
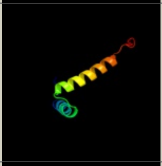
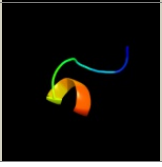
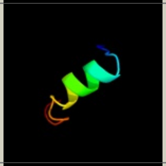
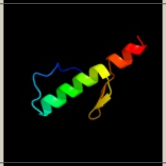
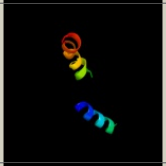
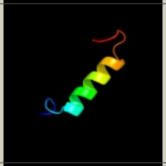
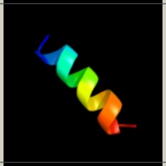
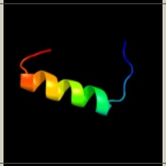
Email	l.a.kelley@imperial.ac.uk
Description	A5A607
Date	Thu Jan 5 10:55:15 GMT 2012
Unique Job ID	6729257cc7d75a0e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2bj7a1	Alignment		77.6	20	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
2	d2hzab1	Alignment		70.4	21	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
3	d2hzaa1	Alignment		67.6	20	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
4	c2ca9B_	Alignment		61.4	12	**PDB header:**transcriptional regulation **Chain:** B: **PDB Molecule:**putative nickel-responsive regulator; **PDBTitle:** apo-nikr from helicobacter pylori in closed trans-2 conformation
5	c2bj3D_	Alignment		51.2	20	**PDB header:**transcription **Chain:** D: **PDB Molecule:**nickel responsive regulator; **PDBTitle:** nikr-apo
6	c1q5vB_	Alignment		46.1	20	**PDB header:**transcription **Chain:** B: **PDB Molecule:**nickel responsive regulator; **PDBTitle:** apo-nikr
7	c2lf0A_	Alignment		18.8	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein yibl; **PDBTitle:** solution structure of sf3636, a two-domain unknown function protein2 from shigella flexneri 2a, determined by joint refinement of nmr,3 residual dipolar couplings and small-angle x-ray scatting, nesg4 target sfr339/ocsp target sf3636
8	d1y9ba1	Alignment		17.4	14	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**VCA0319-like
9	d1ku2a1	Alignment		15.6	50	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma3 domain
10	c1wn4A_	Alignment		14.3	35	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**vontr protein; **PDBTitle:** nmr structure of vontr
11	d2c5ra1	Alignment		14.1	50	**Fold:**Phage replication organizer domain **Superfamily:**Phage replication organizer domain **Family:**Phage replication organizer domain

12	c2agaA_	Alignment		12.5	38	**PDB header:**transcription **Chain:** A: **PDB Molecule:**machado-joseph disease protein 1; **PDBTitle:** de-ubiquitinating function of ataxin-3: insights from the2 solution structure of the josephin domain
13	d1mnta_	Alignment		11.8	27	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Arc/Mnt-like phage repressors
14	c2l3yA_	Alignment		10.9	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**interleukin-6; **PDBTitle:** solution structure of mouse il-6
15	d1pd3a_	Alignment		9.5	55	**Fold:**ROP-like **Superfamily:**Nonstructural protein ns2, Nep, M1-binding domain **Family:**Nonstructural protein ns2, Nep, M1-binding domain
16	d1qu3a1	Alignment		9.3	11	**Fold:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Superfamily:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Family:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
17	d1mg7a2	Alignment		9.0	27	**Fold:**Ferredoxin-like **Superfamily:**GHMP Kinase, C-terminal domain **Family:**Early switch protein XOL-1
18	c2k53A_	Alignment		8.7	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**a3dk08 protein; **PDBTitle:** nmr solution structure of a3dk08 protein from clostridium2 thermocellum: northeast structural genomics consortium3 target cmr9
19	c1u9pA_	Alignment		8.2	23	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**parc; **PDBTitle:** permuted single-chain arc
20	d1yzma1	Alignment		8.1	18	**Fold:**Long alpha-hairpin **Superfamily:**Rabenosyn-5 Rab-binding domain-like **Family:**Rabenosyn-5 Rab-binding domain-like
21	d1i1rb_	Alignment	not modelled	7.0	55	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Long-chain cytokines
22	d3saka_	Alignment	not modelled	6.8	42	**Fold:**p53 tetramerization domain **Superfamily:**p53 tetramerization domain **Family:**p53 tetramerization domain
23	d1kkea1	Alignment	not modelled	6.4	41	**Fold:**Triple beta-spiral **Superfamily:**Fibre shaft of virus attachment proteins **Family:**Reovirus attachment protein sigma 1
24	c3kk4B_	Alignment	not modelled	6.3	22	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein bp1543; **PDBTitle:** uncharacterized protein bp1543 from bordetella pertussis tohama i
25	d1z0kb1	Alignment	not modelled	6.1	25	**Fold:**Long alpha-hairpin **Superfamily:**Rabenosyn-5 Rab-binding domain-like **Family:**Rabenosyn-5 Rab-binding domain-like
26	d1mvfd_	Alignment	not modelled	5.8	16	**Fold:**Double-split beta-barrel **Superfamily:**AbrB/MazE/MraZ-like **Family:**Kis/PemI addiction antidote
27	d2i5ua1	Alignment	not modelled	5.5	10	**Fold:**DnaD domain-like **Superfamily:**DnaD domain-like **Family:**DnaD domain
28	c2y0fD_	Alignment	not modelled	5.3	12	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; **PDBTitle:** structure of gcpe (ispg) from thermus thermophilus hb27
						Fold: Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain

29	d1hska2	Alignment	not modelled	5.2	27	**Superfamily:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain **Family:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain