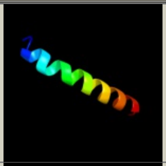
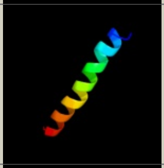
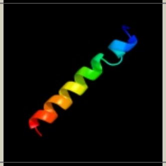
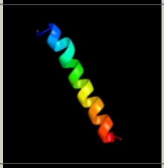
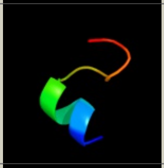
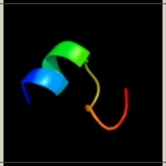
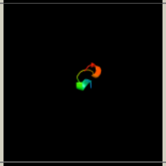
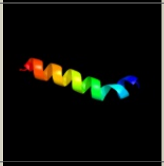
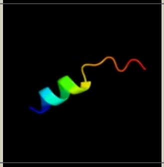
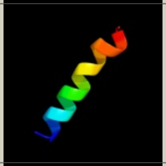
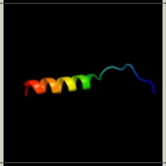
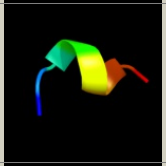
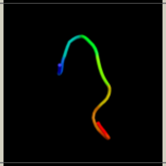
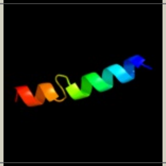
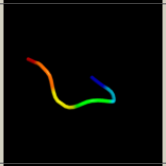
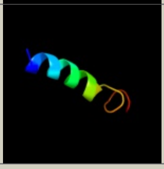
Email	l.a.kelley@imperial.ac.uk
Description	P64445
Date	Thu Jan 5 12:08:23 GMT 2012
Unique Job ID	a970fb54627e4712

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2ka1B_	Alignment		28.4	42	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles
2	c2ka2A_	Alignment		28.4	42	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles with his173-ser172 intermonomer3 hydrogen bond restraints
3	c2ka1A_	Alignment		24.9	42	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles
4	c2ka2B_	Alignment		24.9	42	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles with his173-ser172 intermonomer3 hydrogen bond restraints
5	c2o35A_	Alignment		22.0	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein duf1244; **PDBTitle:** protein of unknown function (duf1244) from sinorhizobium meliloti
6	d2o35a1	Alignment		22.0	29	**Fold:**SMc04008-like **Superfamily:**SMc04008-like **Family:**SMc04008-like
7	c3fybA_	Alignment		21.4	36	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein of unknown function (duf1244); **PDBTitle:** crystal structure of a protein of unknown function (duf1244) from2 alcanivorax borkumensis
8	c2j5dA_	Alignment		17.6	48	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** nmr structure of bnip3 transmembrane domain in lipid2 bicelles
9	c3r45C_	Alignment		13.8	31	**PDB header:**nuclear protein **Chain:** C: **PDB Molecule:**holliday junction recognition protein; **PDBTitle:** structure of a cenp-a-histone h4 heterodimer in complex with chaperone2 hjurp
10	c1vzjB_	Alignment		12.4	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**acetylcholinesterase; **PDBTitle:** structure of the tetramerization domain of2 acetylcholinesterase: four-fold interaction of a www motif3 with a left-handed polyproline helix
11	d1g4us1	Alignment		8.9	38	**Fold:**Four-helical up-and-down bundle **Superfamily:**Bacterial GAP domain **Family:**Bacterial GAP domain

12	c2ksdA_	Alignment		8.7	41	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aerobic respiration control sensor protein arcb; **PDBTitle:** backbone structure of the membrane domain of e. coli2 histidine kinase receptor arcb, center for structures of3 membrane proteins (csmp) target 4310c
13	c3mk7F_	Alignment		7.5	27	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**cytochrome c oxidase, cbb3-type, subunit p; **PDBTitle:** the structure of cbb3 cytochrome oxidase
14	d1pk1c1	Alignment		7.2	38	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
15	d1he1a_	Alignment		7.1	50	**Fold:**Four-helical up-and-down bundle **Superfamily:**Bacterial GAP domain **Family:**Bacterial GAP domain
16	d1te7a_	Alignment		6.7	56	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**yqfB-like
17	c2l35B_	Alignment		6.5	59	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**tyro protein tyrosine kinase-binding protein; **PDBTitle:** structure of the dap12-nkg2c transmembrane heterotrimer
18	d1hy5a_	Alignment		6.5	63	**Fold:**Four-helical up-and-down bundle **Superfamily:**Bacterial GAP domain **Family:**Bacterial GAP domain
19	d2idob1	Alignment		6.1	67	**Fold:**DNA polymerase III theta subunit-like **Superfamily:**DNA polymerase III theta subunit-like **Family:**DNA polymerase III theta subunit-like
20	c2l34B_	Alignment		6.0	59	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**tyro protein tyrosine kinase-binding protein; **PDBTitle:** structure of the dap12 transmembrane homodimer
21	c2l34A_	Alignment	not modelled	6.0	59	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**tyro protein tyrosine kinase-binding protein; **PDBTitle:** structure of the dap12 transmembrane homodimer
22	d2ae9a1	Alignment	not modelled	6.0	67	**Fold:**DNA polymerase III theta subunit-like **Superfamily:**DNA polymerase III theta subunit-like **Family:**DNA polymerase III theta subunit-like
23	c1m56G_	Alignment	not modelled	5.5	33	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**cytochrome c oxidase; **PDBTitle:** structure of cytochrome c oxidase from rhodobactor2 sphaeroides (wild type)
24	c3bq7A_	Alignment	not modelled	5.5	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**diacylglycerol kinase delta; **PDBTitle:** sam domain of diacylglycerol kinase delta1 (e35g)
25	d1se7a_	Alignment	not modelled	5.4	67	**Fold:**DNA polymerase III theta subunit-like **Superfamily:**DNA polymerase III theta subunit-like **Family:**DNA polymerase III theta subunit-like