Email	l.a.kelley@imperial.ac.uk
Description	P64499
Date	Thu Jan 5 12:08:57 GMT 2012
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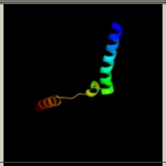
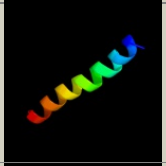
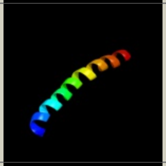
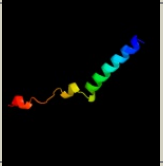
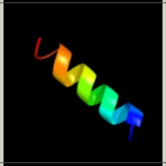
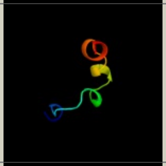
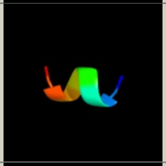
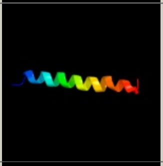
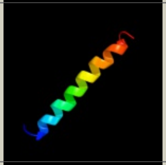
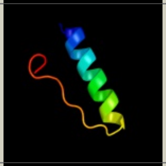
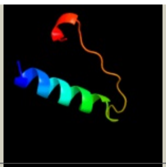
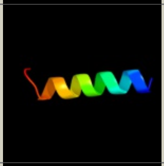
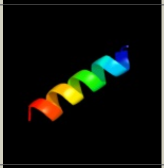
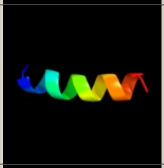
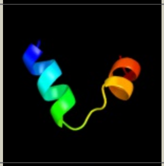
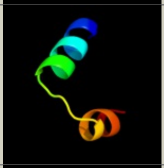
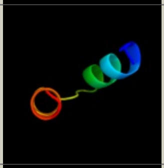
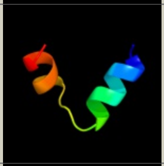
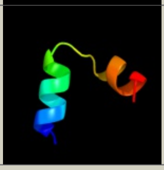
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2oarA_	Alignment		78.7	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**large-conductance mechanosensitive channel; **PDBTitle:** mechanosensitive channel of large conductance (mscl)
2	c2rddB_	Alignment		54.6	40	**PDB header:**membrane protein/transport protein **Chain:** B: **PDB Molecule:**upf0092 membrane protein yajc; **PDBTitle:** x-ray crystal structure of acrb in complex with a novel2 transmembrane helix.
3	c2ifoA_	Alignment		39.9	19	**PDB header:**virus **Chain:** A: **PDB Molecule:**inovirus; **PDBTitle:** model-building studies of inovirus: genetic variations on a2 geometric theme
4	d2oara1	Alignment		35.7	12	**Fold:**Gated mechanosensitive channel **Superfamily:**Gated mechanosensitive channel **Family:**Gated mechanosensitive channel
5	c3hd7A_	Alignment		20.0	35	**PDB header:**exocytosis **Chain:** A: **PDB Molecule:**vesicle-associated membrane protein 2; **PDBTitle:** helical extension of the neuronal snare complex into the membrane,2 spacegroup c 1 2 1
6	c3lm3A_	Alignment		17.5	32	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a putative glycoside hydrolase/deacetylase2 (bdi_3119) from parabacteroides distasonis at 1.44 a resolution
7	c3fd9C_	Alignment		15.2	55	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the transcriptional anti-activator exsd2 from pseudomonas aeruginosa
8	c2k9yB_	Alignment		14.1	43	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ephrin type-a receptor 2; **PDBTitle:** epha2 dimeric structure in the lipidic bicelle at ph 5.0
9	c2k9yA_	Alignment		12.0	43	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ephrin type-a receptor 2; **PDBTitle:** epha2 dimeric structure in the lipidic bicelle at ph 5.0
10	c3l4qA_	Alignment		11.5	34	**PDB header:**viral protein/protein binding **Chain:** A: **PDB Molecule:**non-structural protein 1; **PDBTitle:** structural insights into phosphoinositide 3-kinase2 activation by the influenza a virus ns1 protein
11	c2a93B_	Alignment		11.0	50	**PDB header:**leucine zippers **Chain:** B: **PDB Molecule:**c-myc-max heterodimeric leucine zipper; **PDBTitle:** nmr solution structure of the c-myc-max heterodimeric2 leucine zipper, 40 structures

12	d2gx9a1	Alignment		9.5	34	**Fold:**Ns1 effector domain-like **Superfamily:**Ns1 effector domain-like **Family:**Ns1 effector domain-like
13	d2r6gf1	Alignment		8.8	30	**Fold:**MalF N-terminal region-like **Superfamily:**MalF N-terminal region-like **Family:**MalF N-terminal region-like
14	c2kubA_	Alignment		6.8	29	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**fimbriae-associated protein fap1; **PDBTitle:** solution structure of the alpha subdomain of the major non-repeat unit2 of fap1 fimbriae of streptococcus parasanguis
15	c3rguA_	Alignment		6.6	29	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**fimbriae-associated protein fap1; **PDBTitle:** structure of fap-nra at ph 5.0
16	c1f93H_	Alignment		6.2	45	**PDB header:**transcription **Chain:** H: **PDB Molecule:**hepatocyte nuclear factor 1-alpha; **PDBTitle:** crystal structure of a complex between the dimerization2 domain of hnf-1 alpha and the coactivator dcoh
17	c1g39B_	Alignment		6.2	45	**PDB header:**transcription **Chain:** B: **PDB Molecule:**hepatocyte nuclear factor 1-alpha; **PDBTitle:** wild-type hnf-1alpha dimerization domain
18	c1g39D_	Alignment		6.2	45	**PDB header:**transcription **Chain:** D: **PDB Molecule:**hepatocyte nuclear factor 1-alpha; **PDBTitle:** wild-type hnf-1alpha dimerization domain
19	c1f93F_	Alignment		6.1	45	**PDB header:**transcription **Chain:** F: **PDB Molecule:**hepatocyte nuclear factor 1-alpha; **PDBTitle:** crystal structure of a complex between the dimerization2 domain of hnf-1 alpha and the coactivator dcoh
20	d1f93f_	Alignment		6.1	45	**Fold:**Dimerisation interlock **Superfamily:**Dimerization cofactor of HNF-1 alpha **Family:**Dimerization cofactor of HNF-1 alpha
21	c1dipA_	Alignment	not modelled	6.1	30	**PDB header:**acetylation **Chain:** A: **PDB Molecule:**delta-sleep-inducing peptide immunoreactive **PDBTitle:** the solution structure of porcine delta-sleep-inducing2 peptide immunoreactive peptide, nmr, 10 structures
22	c1f93E_	Alignment	not modelled	6.1	45	**PDB header:**transcription **Chain:** E: **PDB Molecule:**hepatocyte nuclear factor 1-alpha; **PDBTitle:** crystal structure of a complex between the dimerization2 domain of hnf-1 alpha and the coactivator dcoh
23	c1f93G_	Alignment	not modelled	6.0	45	**PDB header:**transcription **Chain:** G: **PDB Molecule:**hepatocyte nuclear factor 1-alpha; **PDBTitle:** crystal structure of a complex between the dimerization2 domain of hnf-1 alpha and the coactivator dcoh