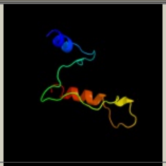
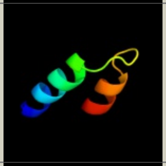
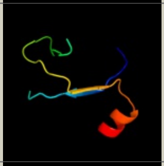
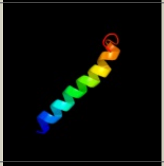
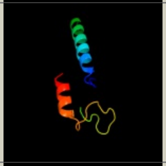
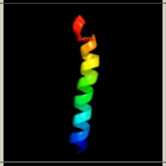
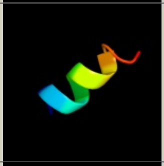
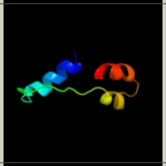
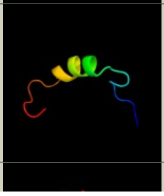
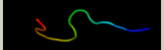
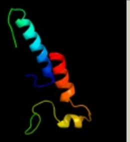
Email	l.a.kelley@imperial.ac.uk
Description	P41068
Date	Thu Jan 5 12:01:24 GMT 2012
Unique Job ID	b676cd525b8b591e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2v4jE_	Alignment		36.6	18	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit **PDBTitle:** the crystal structure of desulfovibrio vulgaris2 dissimilatory sulfite reductase bound to dsrc provides3 novel insights into the mechanism of sulfate respiration
2	d3c07a2	Alignment		31.2	17	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
3	c2jsoA_	Alignment		18.8	23	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**polymyxin resistance protein pmrd; **PDBTitle:** antimicrobial resistance protein
4	c2rqxA_	Alignment		13.1	23	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**polymyxin b resistance protein; **PDBTitle:** solution nmr structure of pmrd from klebsiella pneumoniae
5	d1oeda_	Alignment		12.2	17	**Fold:**Neurotransmitter-gated ion-channel transmembrane pore **Superfamily:**Neurotransmitter-gated ion-channel transmembrane pore **Family:**Neurotransmitter-gated ion-channel transmembrane pore
6	d1qjwa_	Alignment		9.7	21	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycosyl hydrolases family 6, cellulases **Family:**Glycosyl hydrolases family 6, cellulases
7	d1oede_	Alignment		8.5	13	**Fold:**Neurotransmitter-gated ion-channel transmembrane pore **Superfamily:**Neurotransmitter-gated ion-channel transmembrane pore **Family:**Neurotransmitter-gated ion-channel transmembrane pore
8	c3kdpG_	Alignment		7.2	42	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**na+/k+ atpase gamma subunit transcript variant a; **PDBTitle:** crystal structure of the sodium-potassium pump
9	c3kdpH_	Alignment		7.2	42	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**na+/k+ atpase gamma subunit transcript variant a; **PDBTitle:** crystal structure of the sodium-potassium pump
10	d2bida_	Alignment		7.0	11	**Fold:**Toxins' membrane translocation domains **Superfamily:**Bcl-2 inhibitors of programmed cell death **Family:**Bcl-2 inhibitors of programmed cell death
11	d1doab_	Alignment		6.6	32	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**RhoGDI-like

12	c2k58B_	Alignment		6.6	24	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**neuronal acetylcholine receptor subunit beta-2; **PDBTitle:** nmr structures of the first transmembrane domain of the2 neuronal acetylcholine receptor beta 2 subunit
13	c3heiI_	Alignment		6.5	40	**PDB header:**transferase/signaling protein **Chain:** I: **PDB Molecule:**ephrin type-a receptor 2; **PDBTitle:** ligand recognition by a-class eph receptors: crystal structures of the2 epha2 ligand-binding domain and the epha2/ephrin-a1 complex
14	d1oeyj_	Alignment		5.8	20	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**PB1 domain
15	d2gp4a2	Alignment		5.7	40	**Fold:**IlvD/EDD N-terminal domain-like **Superfamily:**IlvD/EDD N-terminal domain-like **Family:**IvD/EDD N-terminal domain-like
16	d2bodx1	Alignment		5.3	35	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycosyl hydrolases family 6, cellulases **Family:**Glycosyl hydrolases family 6, cellulases
17	d1dysa_	Alignment		5.3	24	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycosyl hydrolases family 6, cellulases **Family:**Glycosyl hydrolases family 6, cellulases
18	c2ytuA_	Alignment		5.2	40	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**friend leukemia integration 1 transcription **PDBTitle:** solution structure of the sam_pnt-domain of the human2 friend leukemiaintegration 1 transcription factor
19	d3bz6a2	Alignment		5.2	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PSPTO2686-like
20	c2kw3C_	Alignment		5.2	50	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**regulatory factor x-associated protein; **PDBTitle:** heterotrimeric interaction between rfx5 and rfxap
21	c3nctC_	Alignment	not modelled	5.1	33	**PDB header:**dna binding protein, chaperone **Chain:** C: **PDB Molecule:**protein psib; **PDBTitle:** x-ray crystal structure of the bacterial conjugation factor psib, a2 negative regulator of reca