Phyre2

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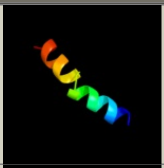
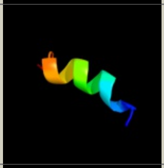
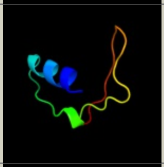
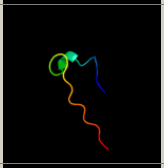
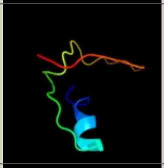
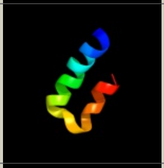
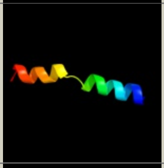
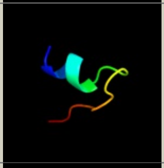
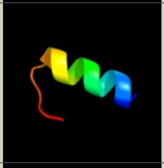
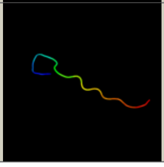
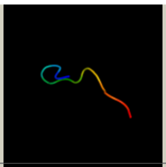
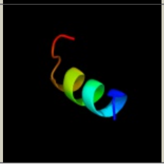
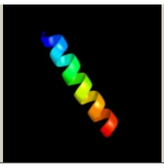
Description	P0AC92
Date	Thu Jan 5 11:17:37 GMT 2012
Unique Job ID	37b84844099e6b92

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1avoA_	Alignment		77.8	30	**PDB header:**proteasome activator **Chain:** A: **PDB Molecule:**11s regulator; **PDBTitle:** proteasome activator reg(alpha)
2	c2a7uA_	Alignment		42.5	53	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp synthase alpha chain; **PDBTitle:** nmr solution structure of the e.coli f-atpase delta subunit n-terminal2 domain in complex with alpha subunit n-terminal 22 residues
3	d1diva1	Alignment		27.3	21	**Fold:**Ribosomal protein L9 C-domain **Superfamily:**Ribosomal protein L9 C-domain **Family:**Ribosomal protein L9 C-domain
4	d1uwwa_	Alignment		14.9	41	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Family 28 carbohydrate binding module, CBM28
5	d2j01i1	Alignment		14.3	24	**Fold:**Ribosomal protein L9 C-domain **Superfamily:**Ribosomal protein L9 C-domain **Family:**Ribosomal protein L9 C-domain
6	c2x43S_	Alignment		10.5	37	**PDB header:**membrane protein **Chain:** S: **PDB Molecule:**sherp; **PDBTitle:** structural basis of molecular recognition by sherp at membrane2 surfaces
7	c2kwyA_	Alignment		10.1	42	**PDB header:**proton transport **Chain:** A: **PDB Molecule:**v-type proton atpase subunit g; **PDBTitle:** structure of g61-101
8	d1x6ma_	Alignment		8.3	60	**Fold:**Mss4-like **Superfamily:**Mss4-like **Family:**Glutathione-dependent formaldehyde-activating enzyme, Gfa
9	c3iwfA_	Alignment		8.0	25	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcription regulator rpir family; **PDBTitle:** the crystal structure of the n-terminal domain of a rpir2 transcriptional regulator from staphylococcus epidermidis to 1.4a
10	d1ybza1	Alignment		6.5	31	**Fold:**Chorismate mutase II **Superfamily:**Chorismate mutase II **Family:**Dimeric chorismate mutase
11	d1repc2	Alignment		6.4	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Replication initiation protein

12	d2nrac2	Alignment		6.4	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Replication initiation protein
13	c2qbvA_	Alignment		5.8	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**chorismate mutase; **PDBTitle:** crystal structure of intracellular chorismate mutase from2 mycobacterium tuberculosis

14	c2k88A_	Alignment		5.5	38	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**vacuolar proton pump subunit g; **PDBTitle:** association of subunit d (vma6p) and e (vma4p) with g2 (vma10p) and the nmr solution structure of subunit g (g1-3 59) of the saccharomyces cerevisiae v1vo atpase