Phyre2

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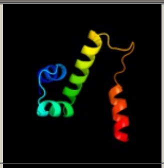
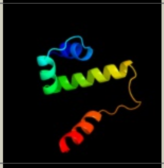
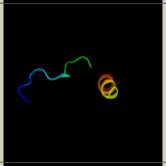
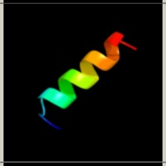
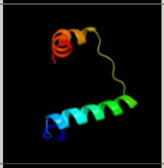
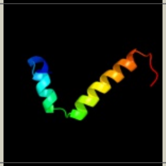
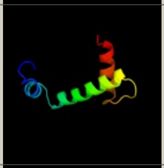
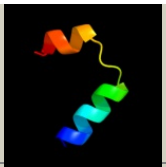
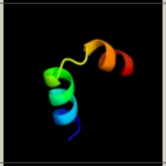
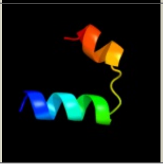
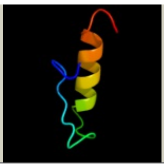
Description	P0AFX7
Date	Thu Jan 5 11:27:30 GMT 2012
Unique Job ID	8143756da6cb788a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1or7C_	 Alignment		100.0	100	**PDB header:**transcription **Chain:** C: **PDB Molecule:**sigma-e factor negative regulatory protein; **PDBTitle:** crystal structure of escherichia coli sigmae with the cytoplasmic2 domain of its anti-sigma rsea
2	d1or7c_	 Alignment		100.0	100	**Fold:**N-terminal, cytoplasmic domain of anti-sigmaE factor RseA **Superfamily:**N-terminal, cytoplasmic domain of anti-sigmaE factor RseA **Family:**N-terminal, cytoplasmic domain of anti-sigmaE factor RseA
3	c3m4wH_	 Alignment		97.3	100	**PDB header:**signaling protein/signaling protein **Chain:** H: **PDB Molecule:**sigma-e factor negative regulatory protein; **PDBTitle:** structural basis for the negative regulation of bacterial stress2 response by rseb
4	c2z2sD_	 Alignment		95.0	15	**PDB header:**transcription **Chain:** D: **PDB Molecule:**anti-sigma factor chrr, transcriptional activator chrr; **PDBTitle:** crystal structure of rhodobacter sphaeroides sige in complex with the2 anti-sigma chrr
5	c3hugJ_	 Alignment		94.8	16	**PDB header:**transcription/membrane protein **Chain:** J: **PDB Molecule:**probable conserved membrane protein; **PDBTitle:** crystal structure of mycobacterium tuberculosis anti-sigma factor rsla2 in complex with -35 promoter binding domain of sigl
6	d1t98a1	 Alignment		25.5	38	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MukF N-terminal domain-like
7	d1u04a1	 Alignment		19.8	50	**Fold:**SH3-like barrel **Superfamily:**PAZ domain **Family:**PAZ domain
8	d1m98a1	 Alignment		9.9	10	**Fold:**Orange carotenoid protein, N-terminal domain **Superfamily:**Orange carotenoid protein, N-terminal domain **Family:**Orange carotenoid protein, N-terminal domain
9	d1jhga_	 Alignment		7.3	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**Trp repressor, TrpR
10	d1trra_	 Alignment		7.1	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**Trp repressor, TrpR
11	c1yfnG_	 Alignment		6.5	100	**PDB header:**protein binding **Chain:** G: **PDB Molecule:**sigma-e factor negative regulatory protein; **PDBTitle:** versatile modes of peptide recognition by the aaa+ adaptor2 protein sspb- the crystal structure of a sspb-rsea complex

12	c1g2yC_	Alignment		6.3	30	**PDB header:**transcription **Chain:** C: **PDB Molecule:**hepatocyte nuclear factor 1-alpha; **PDBTitle:** hnf-1alpha dimerization domain, with selenomethionine2 substitued at leu 12
13	c1g2yD_	Alignment		6.0	30	**PDB header:**transcription **Chain:** D: **PDB Molecule:**hepatocyte nuclear factor 1-alpha; **PDBTitle:** hnf-1alpha dimerization domain, with selenomethionine2 substitued at leu 12
14	c1g2yB_	Alignment		6.0	30	**PDB header:**transcription **Chain:** B: **PDB Molecule:**hepatocyte nuclear factor 1-alpha; **PDBTitle:** hnf-1alpha dimerization domain, with selenomethionine2 substitued at leu 12
15	d1g2ya_	Alignment		5.9	30	**Fold:**Dimerisation interlock **Superfamily:**Dimerization cofactor of HNF-1 alpha **Family:**Dimerization cofactor of HNF-1 alpha
16	c1g2yA_	Alignment		5.9	30	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hepatocyte nuclear factor 1-alpha; **PDBTitle:** hnf-1alpha dimerization domain, with selenomethionine2 substitued at leu 12

17	c7ceiB_	Alignment		5.7	27	**PDB header:**immune system **Chain:** B: **PDB Molecule:**protein (colicin e7 immunity protein); **PDBTitle:** the endonuclease domain of colicin e7 in complex with its inhibitor2 im7 protein