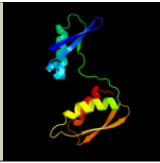


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1jyha_	 Alignment		100.0	100	Fold: Probable bacterial effector-binding domain Superfamily: Probable bacterial effector-binding domain Family: Gyrase inhibitory protein Gyrl (SbmC, YeeB)
2	c3lurB_	 Alignment		100.0	13	PDB header: transcription activator Chain: B: PDB Molecule: putative bacterial transcription regulation protein; PDBTitle: crystal structure of putative bacterial transcription regulation2 protein (np_372959.1) from staphylococcus aureus mu50 at 1.81 a3 resolution
3	d1d5ya3	 Alignment		100.0	8	Fold: Probable bacterial effector-binding domain Superfamily: Probable bacterial effector-binding domain Family: Rob transcription factor, C-terminal domain
4	c1d5yD_	 Alignment		100.0	8	PDB header: transcription/dna Chain: D: PDB Molecule: rob transcription factor; PDBTitle: crystal structure of the e. coli rob transcription factor2 in complex with dna
5	c3gk6A_	 Alignment		100.0	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: integron cassette protein vch_cass2; PDBTitle: crystal structure from the mobile metagenome of vibrio cholerae.2 integron cassette protein vch_cass2.
6	c2kcuA_	 Alignment		100.0	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein ctr107; PDBTitle: nmr solution structure of an uncharacterized protein from2 chlorobium tepidum. northeast structural genomics target3 ctr107
7	c3b49A_	 Alignment		99.9	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin2189 protein; PDBTitle: crystal structure of an uncharacterized conserved protein from2 listeria innocua
8	d1r8ea2	 Alignment		99.8	11	Fold: Probable bacterial effector-binding domain Superfamily: Probable bacterial effector-binding domain Family: Multidrug-binding domain of transcription activator BmrR
9	c3d6zA_	 Alignment		99.7	11	PDB header: transcription regulator/dna Chain: A: PDB Molecule: multidrug-efflux transporter 1 regulator; PDBTitle: crystal structure of r275e mutant of bmrr bound to dna and rhodamine
10	c3r8kB_	 Alignment		97.8	15	PDB header: apoptosis Chain: B: PDB Molecule: heme-binding protein 2; PDBTitle: crystal structure of human soul protein (hexagonal form)
11	d2gova1	 Alignment		97.7	14	Fold: Probable bacterial effector-binding domain Superfamily: Probable bacterial effector-binding domain Family: SOUL heme-binding protein

12 [c2z51A](#)

Alignment



10.8

11

PDB header:metal transport
Chain: A: **PDB Molecule:**nifu-like protein 2, chloroplast;
PDBTitle: crystal structure of arabidopsis cnfu involved in iron-2 sulfur cluster biosynthesis