Phyre^2

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Description	Q46866
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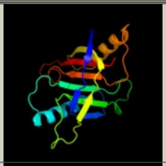
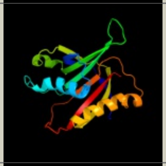
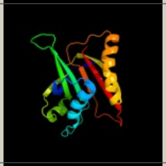
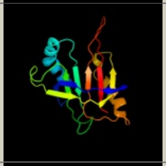
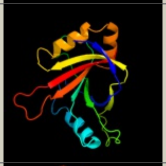
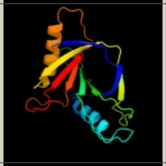
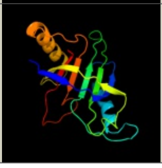
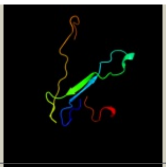
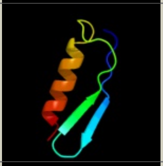
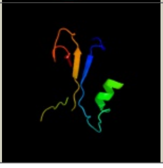
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1jyha_	Alignment		100.0	26	**Fold:**Probable bacterial effector-binding domain **Superfamily:**Probable bacterial effector-binding domain **Family:**Gyrase inhibitory protein GyrI (SbmC, YeeB)
2	c2kcuA_	Alignment		100.0	13	**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
3	c3lurB_	Alignment		100.0	10	**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
4	c1d5yD_	Alignment		100.0	14	**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	d1d5ya3	Alignment		100.0	14	**Fold:**Probable bacterial effector-binding domain **Superfamily:**Probable bacterial effector-binding domain **Family:**Rob transcription factor, C-terminal domain
6	c3b49A_	Alignment		99.9	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin2189 protein; **PDBTitle:** crystal structure of an uncharacterized conserved protein from2 listeria innocua
7	c3gk6A_	Alignment		99.9	15	**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.
8	d1r8ea2	Alignment		99.9	12	**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	9	**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	d2gova1	Alignment		97.3	10	**Fold:**Probable bacterial effector-binding domain **Superfamily:**Probable bacterial effector-binding domain **Family:**SOUL heme-binding protein
11	c3r8kB_	Alignment		97.0	10	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**heme-binding protein 2; **PDBTitle:** crystal structure of human soul protein (hexagonal form)

12	d2df7a1	Alignment		26.8	21	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Birnaviridae-like VP
13	d1vc1a_	Alignment		11.4	7	**Fold:**SpoIIaa-like **Superfamily:**SpoIIaa-like **Family:**Anti-sigma factor antagonist SpoIIaa
14	c1yfsB_	Alignment		7.4	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**alanyl-trna synthetase; **PDBTitle:** the crystal structure of alanyl-trna synthetase in complex2 with l-alanine

15	d1riqa2	Alignment		6.9	15	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain