Phyre2

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Description	P76543
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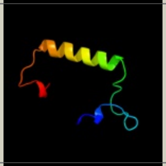
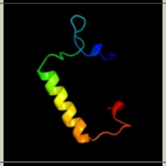
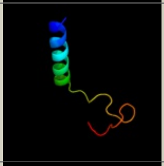
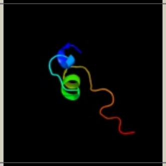
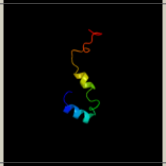
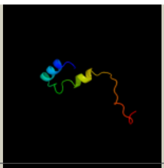
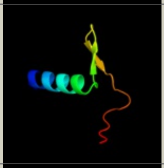
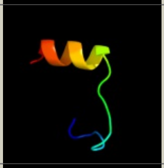
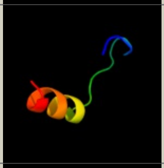
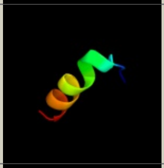
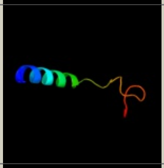
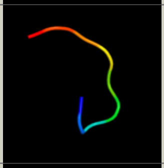
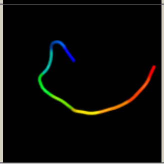
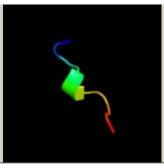
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2v79B_	Alignment		76.1	11	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**dna replication protein dnad; **PDBTitle:** crystal structure of the n-terminal domain of dnad from2 bacillus subtilis
2	c3h8dE_	Alignment		34.8	73	**PDB header:**motor protein/signaling protein **Chain:** E: **PDB Molecule:**disabled homolog 2; **PDBTitle:** crystal structure of myosin vi in complex with dab2 peptide
3	d1vjea_	Alignment		33.6	24	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
4	c2vn2B_	Alignment		32.4	20	**PDB header:**replication **Chain:** B: **PDB Molecule:**chromosome replication initiation protein; **PDBTitle:** crystal structure of the n-terminal domain of dnad protein2 from geobacillus kaustophilus hta426
5	d2r7ca2	Alignment		23.6	28	**Fold:**Rotavirus NSP2 fragment, N-terminal domain **Superfamily:**Rotavirus NSP2 fragment, N-terminal domain **Family:**Rotavirus NSP2 fragment, N-terminal domain
6	c2k5cA_	Alignment		14.4	31	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein pf0385; **PDBTitle:** nmr structure for pf0385
7	c2r7cA_	Alignment		10.2	28	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**non-structural rna-binding protein 35; **PDBTitle:** crystallographic and biochemical analysis of rotavirus nsp22 with nucleotides reveals an ndp kinase like activity
8	d1j6xa_	Alignment		8.8	19	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
9	c3zquA_	Alignment		8.7	41	**PDB header:**lyase **Chain:** A: **PDB Molecule:**probable aromatic acid decarboxylase; **PDBTitle:** structure of a probable aromatic acid decarboxylase
10	d2fmme1	Alignment		7.9	32	**Fold:**ENT-like **Superfamily:**ENT-like **Family:**Emsy N terminal (ENT) domain-like
11	c3iydE_	Alignment		7.4	38	**PDB header:**transcription/dna **Chain:** E: **PDB Molecule:**dna-directed rna polymerase subunit omega; **PDBTitle:** three-dimensional em structure of an intact activator-dependent2 transcription initiation complex

12	c2fmmE_	Alignment		7.1	32	**PDB header:**transcription **Chain:** E: **PDB Molecule:**protein emsy; **PDBTitle:** crystal structure of emsy-hp1 complex
13	d1p6ra_	Alignment		6.9	31	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Penicillinase repressor
14	c2j9wB_	Alignment		6.8	32	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**vps28-prov protein; **PDBTitle:** structural insight into the escrt-i-ii link and its role in2 mvb trafficking
15	d2j9ua1	Alignment		6.8	14	**Fold:**Four-helical up-and-down bundle **Superfamily:**VPS28 C-terminal domain-like **Family:**VPS28 C-terminal domain-like
16	c3domC_	Alignment		5.6	22	**PDB header:**transcription **Chain:** C: **PDB Molecule:**rna polymerase ii transcription factor b subunit 2; **PDBTitle:** crystal structure of the complex between tfb5 and the c-terminal2 domain of tfb2
17	d1j6wa_	Alignment		5.5	18	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
18	d9wgaa2	Alignment		5.5	56	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Plant lectins/antimicrobial peptides **Family:**Hevein-like agglutinin (lectin) domain
19	d2cwga2	Alignment		5.3	56	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Plant lectins/antimicrobial peptides **Family:**Hevein-like agglutinin (lectin) domain

20	c2gu0A_	Alignment		5.0	70	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**nonstructural protein 2; **PDBTitle:** crystal structure of human rotavirus nsp2 (group c /2 bristol strain)