Phyre2

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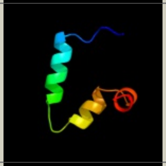
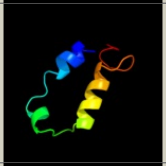
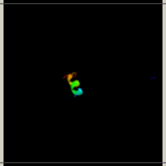
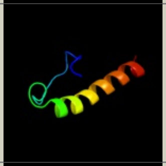
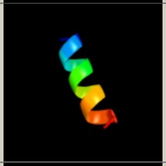
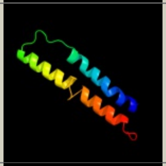
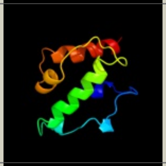
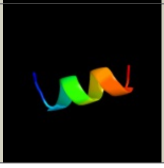
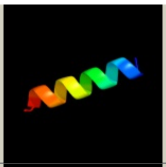
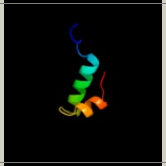
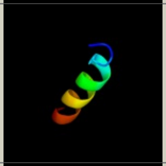
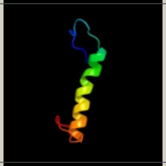
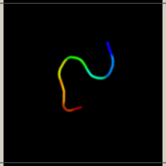
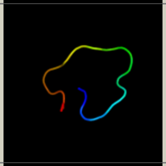
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3k64A_	Alignment		39.0	33	**PDB header:**rna/rna binding protein **Chain:** A: **PDB Molecule:**fem-3 mrna-binding factor 2; **PDBTitle:** crystal structure of fbf-2/fem-3 pme complex
2	c3gebC_	Alignment		17.4	33	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**eyes absent homolog 2; **PDBTitle:** crystal structure of edeya2
3	d1trra_	Alignment		17.3	36	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**Trp repressor, TrpR
4	d1f44a1	Alignment		17.1	19	**Fold:**SAM domain-like **Superfamily:**lambda integrase-like, N-terminal domain **Family:**lambda integrase-like, N-terminal domain
5	c3v71A_	Alignment		14.0	27	**PDB header:**rna binding protein/rna **Chain:** A: **PDB Molecule:**puf (pumilio/fbf) domain-containing protein 7, confirmed by **PDBTitle:** crystal structure of puf-6 in complex with 5be13 rna
6	c2r4gA_	Alignment		12.8	5	**PDB header:**transferase **Chain:** A: **PDB Molecule:**telomerase reverse transcriptase; **PDBTitle:** the high resolution structure of the rna-binding domain of telomerase
7	c1a2xB_	Alignment		12.3	43	**PDB header:**complex (skeletal muscle/muscle protein) **Chain:** B: **PDB Molecule:**troponin i; **PDBTitle:** complex of troponin c with a 47 residue (1-47) fragment of2 troponin i
8	d2az0a1	Alignment		12.1	29	**Fold:**ROP-like **Superfamily:**FHV B2 protein-like **Family:**FHV B2 protein-like
9	c3k49C_	Alignment		11.4	40	**PDB header:**rna binding protein / rna **Chain:** C: **PDB Molecule:**mrna-binding protein puf3; **PDBTitle:** puf3 rna binding domain bound to cox17 rna 3' utr recognition sequence2 site b
10	d1wjoa_	Alignment		10.0	12	**Fold:**CH domain-like **Superfamily:**Calponin-homology domain, CH-domain **Family:**Calponin-homology domain, CH-domain
11	d1u0ja_	Alignment		9.0	33	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain

12	c1jrjA_	Alignment		9.0	41	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**exendin-4; **PDBTitle:** solution structure of exendin-4 in 30-vol% trifluoroethanol
13	d1itya_	Alignment		8.9	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**DNA-binding domain of telomeric protein
14	d3vuba_	Alignment		8.6	31	**Fold:**SH3-like barrel **Superfamily:**Cell growth inhibitor/plasmid maintenance toxic component **Family:**CcdB
15	d2enda_	Alignment		8.3	32	**Fold:**T4 endonuclease V **Superfamily:**T4 endonuclease V **Family:**T4 endonuclease V
16	d1mxaa2	Alignment		7.4	63	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase
17	d1a8da2	Alignment		6.9	25	**Fold:**beta-Trefoil **Superfamily:**STI-like **Family:**Clostridium neurotoxins, C-terminal domain
18	c3jrzA_	Alignment		6.8	50	**PDB header:**toxin **Chain:** A: **PDB Molecule:**ccdb; **PDBTitle:** ccdbvfi-formii-ph5.6
19	d1jhga_	Alignment		6.8	40	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**Trp repressor, TrpR
20	c1d0rA_	Alignment		6.7	29	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**glucagon-like peptide-1-(7-36)-amide; **PDBTitle:** solution structure of glucagon-like peptide-1-(7-36)-amide2 in trifluoroethanol/water
21	d1v92a_	Alignment	not modelled	6.7	10	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TAP-C domain-like
22	d2p02a2	Alignment	not modelled	6.7	50	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase
23	d1qm4a2	Alignment	not modelled	6.6	50	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase
24	c3sviA_	Alignment	not modelled	6.4	30	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**type iii effector hopab2; **PDBTitle:** structure of the pto-binding domain of hoppmal generated by limited2 thermolysin digestion
25	c2rmrA_	Alignment	not modelled	6.0	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**paired amphipathic helix protein sin3a; **PDBTitle:** solution structure of msin3a pah1 domain
26	d1eyea_	Alignment	not modelled	6.0	38	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
27	c2dhyA_	Alignment	not modelled	5.4	11	**PDB header:**immune system **Chain:** A: **PDB Molecule:**cue domain-containing protein 1; **PDBTitle:** solution structure of the cue domain in the human cue2 domain containing protein 1 (cuedc1)