Phyre^{2}

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Description	P33920
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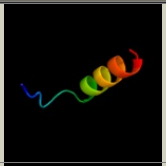
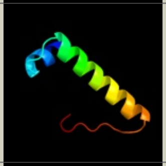
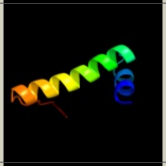
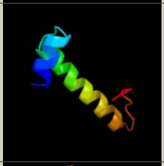
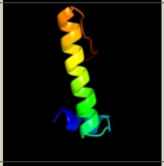
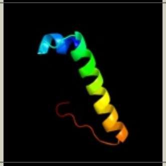
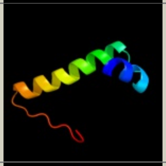
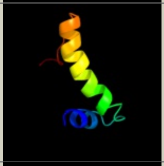
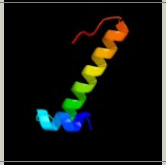
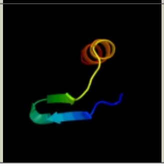
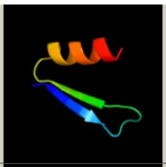
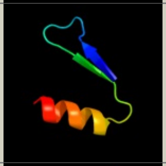
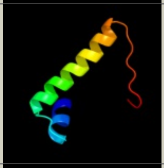
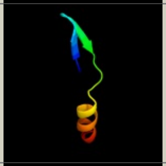
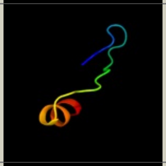
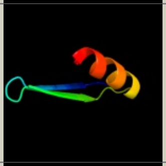
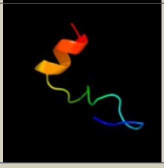
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2bsqe1	Alignment		63.6	9	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Trafficking protein A-like
2	d1mula_	Alignment		46.0	21	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
3	d1huua_	Alignment		36.5	16	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
4	c3c4iA_	Alignment		34.9	12	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna-binding protein hu homolog; **PDBTitle:** crystal structure analysis of n terminal region containing the2 dimerization domain and dna binding domain of hu protein(histone like3 protein-dna binding) from mycobacterium tuberculosis [h37rv]
5	d1p71a_	Alignment		34.3	19	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
6	d1owfa_	Alignment		33.9	14	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
7	c2iifA_	Alignment		33.2	16	**PDB header:**recombination/dna **Chain:** A: **PDB Molecule:**integration host factor; **PDBTitle:** single chain integration host factor mutant protein (scihf2-2 k45ae) in complex with dna
8	d1exea_	Alignment		28.9	9	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
9	d1b8za_	Alignment		28.3	18	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
10	c2k42A_	Alignment		19.4	29	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**wiskott-aldrich syndrome protein; **PDBTitle:** solution structure of the gtpase binding domain of wasp in2 complex with espfu, an ehec effector
11	c2kl8A_	Alignment		19.0	19	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**or15; **PDBTitle:** solution nmr structure of de novo designed ferredoxin-like2 fold protein, northeast structural genomics consortium3 target or15

12	c3gr5A_	Alignment		18.5	7	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**escc; **PDBTitle:** periplasmic domain of the outer membrane secretin escc from2 enteropathogenic e.coli (epec)
13	c2y9kG_	Alignment		18.2	18	**PDB header:**protein transport **Chain:** G: **PDB Molecule:**protein invg; **PDBTitle:** three-dimensional model of salmonella's needle complex at2 subnanometer resolution
14	d1owfb_	Alignment		17.5	9	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
15	d1mnta_	Alignment		16.4	24	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Arc/Mnt-like phage repressors
16	c1f3mB_	Alignment		16.2	30	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine/threonine-protein kinase pak-alpha; **PDBTitle:** crystal structure of human serine/threonine kinase pak1
17	c2xflB_	Alignment		16.1	26	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dyne7; **PDBTitle:** induced-fit and allosteric effects upon polyene binding2 revealed by crystal structures of the dynemicin3 thioesterase
18	c1ceeB_	Alignment		15.0	29	**PDB header:**structural protein regulation **Chain:** B: **PDB Molecule:**wiskott-aldrich syndrome protein wasp; **PDBTitle:** solution structure of cdc42 in complex with the gtpase2 binding domain of wasp
19	c2y3mA_	Alignment		14.6	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**protein transport protein hofq; **PDBTitle:** structure of the extra-membranous domain of the secretin2 hofq from actinobacillus actinomycetemcomitans
20	d1ej5a_	Alignment		14.5	32	**Fold:**Wiscott-Aldrich syndrome protein, WASP, C-terminal domain **Superfamily:**Wiscott-Aldrich syndrome protein, WASP, C-terminal domain **Family:**Wiscott-Aldrich syndrome protein, WASP, C-terminal domain
21	c3fwcO_	Alignment	not modelled	14.3	7	**PDB header:**cell cycle, transcription **Chain:** O: **PDB Molecule:**protein sus1; **PDBTitle:** sac3:sus1:cdc31 complex
22	d1ucra_	Alignment	not modelled	13.2	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Dissimilatory sulfite reductase DsvD
23	c1u9pA_	Alignment	not modelled	12.3	12	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**parc; **PDBTitle:** permuted single-chain arc
24	d2o97b1	Alignment	not modelled	11.1	25	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
25	c3eudE_	Alignment	not modelled	9.5	23	**PDB header:**nuclear protein **Chain:** E: **PDB Molecule:**protein shq1; **PDBTitle:** structure of the cs domain of the essential h/aca rnp2 assembly protein shq1p
26	d1d5ya1	Alignment	not modelled	8.4	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
27	c2ptvA_	Alignment	not modelled	8.1	12	**PDB header:**immune system **Chain:** A: **PDB Molecule:**cd48 antigen; **PDBTitle:** structure of nk cell receptor ligand cd48
28	c3ossD_	Alignment	not modelled	7.8	7	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**type 2 secretion system, secretin gspd; **PDBTitle:** the crystal structure of enterotoxigenic escherichia coli gspc-gspd2 complex from the type ii secretion system
29	d2o4ta1	Alignment	not modelled	7.8	14	**Fold:**Left-handed superhelix **Superfamily:**BH3980-like

						Family:BH3980-like
30	d1d6za4	Alignment	not modelled	7.4	20	**Fold:**N domain of copper amine oxidase-like **Superfamily:**Copper amine oxidase, domain N **Family:**Copper amine oxidase, domain N
31	d1d8ja_	Alignment	not modelled	6.6	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**The central core domain of TFIIE beta
32	d2qi2a1	Alignment	not modelled	6.6	31	**Fold:**Sm-like fold **Superfamily:**Dom34/Pelota N-terminal domain-like **Family:**Dom34/Pelota N-terminal domain-like
33	d2b0ga1	Alignment	not modelled	6.6	13	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
34	c3kf8D_	Alignment	not modelled	6.4	25	**PDB header:**structural protein **Chain:** D: **PDB Molecule:**protein ten1; **PDBTitle:** crystal structure of c. tropicalis stn1-ten1 complex
35	c2edoA_	Alignment	not modelled	6.0	26	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**cd48 antigen; **PDBTitle:** solution structure of the first ig-like domain from human2 cd48 antigen
36	c1e0aB_	Alignment	not modelled	5.8	24	**PDB header:**signalling protein **Chain:** B: **PDB Molecule:**serine/threonine-protein kinase pak-alpha; **PDBTitle:** cdc42 complexed with the gtpase binding domain of p212 activated kinase
37	c2np2B_	Alignment	not modelled	5.6	21	**PDB header:**dna binding protein/dna **Chain:** B: **PDB Molecule:**hbb; **PDBTitle:** hbb-dna complex
38	d1rxta1	Alignment	not modelled	5.6	31	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-myristoyl transferase, NMT
39	c3aqjQ_	Alignment	not modelled	5.6	38	**PDB header:**metal binding protein **Chain:** Q: **PDB Molecule:**baseplate assembly protein v; **PDBTitle:** crystal structure of a c-terminal domain of the bacteriophage p2 tail2 spike protein, gpv
40	d1qa9b_	Alignment	not modelled	5.3	26	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**V set domains (antibody variable domain-like)
41	c2o37A_	Alignment	not modelled	5.1	18	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**protein sis1; **PDBTitle:** j-domain of sis1 protein, hsp40 co-chaperone from2 saccharomyces cerevisiae.