Phyre^2

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Description	P0A8W8
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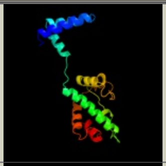
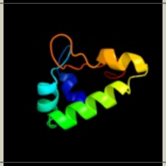
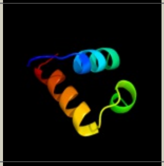
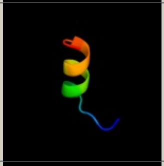
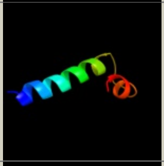
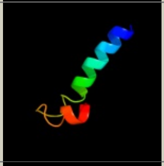
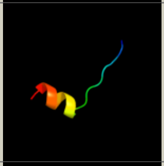
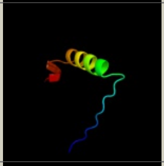
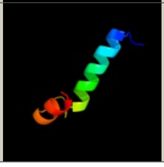
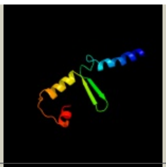
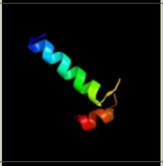
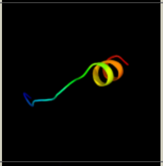
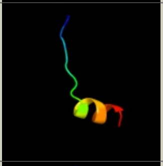
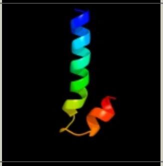
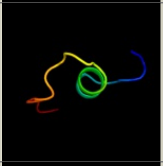
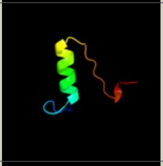
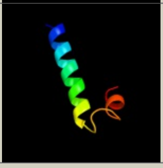
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1wpba_	Alignment		100.0	100	**Fold:**YfbU-like **Superfamily:**YfbU-like **Family:**YfbU-like
2	d1zara1	Alignment		32.5	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Rio2 serine protein kinase N-terminal domain
3	d2bcgg2	Alignment		32.4	17	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**GDI-like N domain
4	d2cfxa1	Alignment		22.3	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
5	c3ayhA_	Alignment		20.6	36	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna-directed rna polymerase iii subunit rpc9; **PDBTitle:** crystal structure of the c17/25 subcomplex from s. pombe rna2 polymerase iii
6	c2ckzC_	Alignment		20.2	27	**PDB header:**transferase **Chain:** C: **PDB Molecule:**dna-directed rna polymerase iii 18 kd **PDBTitle:** x-ray structure of rna polymerase iii subcomplex c17-c25.
7	d1ksoa_	Alignment		16.4	9	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**S100 proteins
8	d3c1va1	Alignment		15.6	16	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**S100 proteins
9	d1vq0a2	Alignment		15.4	24	**Fold:**HSP33 redox switch-like **Superfamily:**HSP33 redox switch-like **Family:**HSP33 redox switch-like
10	d2op5a1	Alignment		14.3	24	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Marine metagenome family DABB1
11	d1psra_	Alignment		14.0	12	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**S100 proteins

12	c3mk4A_	Alignment		12.9	15	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**peroxisomal biogenesis factor 3; **PDBTitle:** x-ray structure of human pex3 in complex with a pex19 derived peptide
13	d1nsha_	Alignment		12.3	18	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**S100 proteins
14	d1xjha_	Alignment		11.9	35	**Fold:**HSP33 redox switch-like **Superfamily:**HSP33 redox switch-like **Family:**HSP33 redox switch-like
15	d1vzya2	Alignment		10.8	18	**Fold:**HSP33 redox switch-like **Superfamily:**HSP33 redox switch-like **Family:**HSP33 redox switch-like
16	d1xk4c1	Alignment		8.8	16	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**S100 proteins
17	c2l4wA_	Alignment		8.7	36	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** nmr structure of the xanthomonas virb7
18	d1gsaa1	Alignment		8.1	18	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**Prokaryotic glutathione synthetase, N-terminal domain
19	d2foka2	Alignment		7.5	42	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Restriction endonuclease FokI, N-terminal (recognition) domain
20	c1irjG_	Alignment		7.3	16	**PDB header:**metal binding protein **Chain:** G: **PDB Molecule:**migration inhibitory factor-related protein 14; **PDBTitle:** crystal structure of the mrp14 complexed with chaps
21	d1qlsa_	Alignment	not modelled	7.3	12	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**S100 proteins
22	d1rr7a_	Alignment	not modelled	7.1	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Middle operon regulator, Mor
23	c1rr7A_	Alignment	not modelled	7.1	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**middle operon regulator; **PDBTitle:** crystal structure of the middle operon regulator protein of2 bacteriophage mu
24	d2aq0a1	Alignment	not modelled	7.0	15	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
25	c2kaxA_	Alignment	not modelled	6.7	25	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**protein s100-a5; **PDBTitle:** solution structure and dynamics of s100a5 in the apo and2 ca2+ -bound states
26	d1hmca_	Alignment	not modelled	6.3	17	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Short-chain cytokines
27	c1ontA_	Alignment	not modelled	6.2	31	**PDB header:**antagonist **Chain:** A: **PDB Molecule:**conantokin-t; **PDBTitle:** nmda receptor antagonist, conantokin-t, nmr, 17 structures
28	c2i6hA_	Alignment	not modelled	6.2	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein atu0120; **PDBTitle:** structure of protein of unknown function atu0120 from agrobacterium2 tumefaciens
						Fold:alpha-alpha superhelix

29	d2i6ha1	Alignment	not modelled	6.2	21	**Superfamily:**TPR-like **Family:**Atu0120-like
30	c1vzyA_	Alignment	not modelled	6.0	18	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**33 kda chaperonin; **PDBTitle:** crystal structure of the bacillus subtilis hsp33
31	c2rgiA_	Alignment	not modelled	5.9	16	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**protein s100-a2; **PDBTitle:** crystal structure of ca2+-free s100a2 at 1.6 a resolution
32	d1k8ua_	Alignment	not modelled	5.9	22	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**S100 proteins
33	d1dqna_	Alignment	not modelled	5.8	23	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
34	d1mxsa_	Alignment	not modelled	5.5	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
35	d1e8aa_	Alignment	not modelled	5.2	28	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**S100 proteins