Phyre^2

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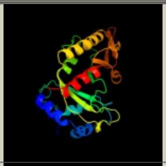
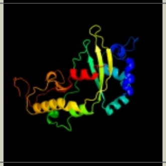
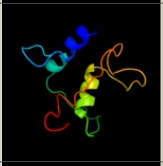
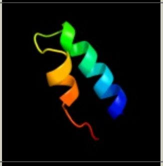
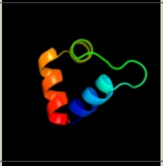
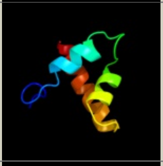
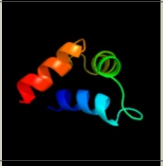
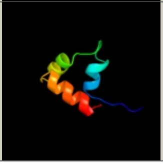
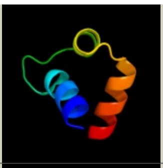
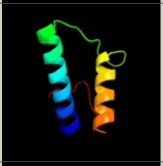
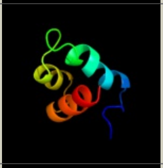
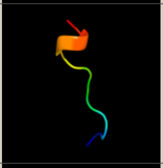
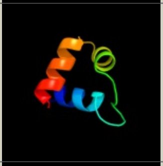
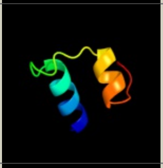
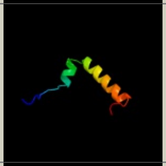
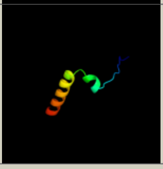
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1azoa_	Alignment		100.0	99	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**DNA mismatch repair protein MutH from
2	c2aorB_	Alignment		100.0	60	**PDB header:**hydrolase/dna **Chain:** B: **PDB Molecule:**dna mismatch repair protein muth; **PDBTitle:** crystal structure of muth-hemimethylated dna complex
3	c2reuA_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**type ii restriction enzyme sau3ai; **PDBTitle:** crystal structure of the c-terminal of sau3ai fragment
4	c2odiA_	Alignment		97.9	22	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**r.bcni; **PDBTitle:** restriction endonuclease bcni-cognate dna substrate complex
5	c2oa9B_	Alignment		94.3	32	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**r.mvai; **PDBTitle:** restriction endonuclease mvai in the absence of dna
6	d1ku3a_	Alignment		35.7	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
7	c6paxA_	Alignment		28.9	29	**PDB header:**gene regulation/dna **Chain:** A: **PDB Molecule:**homeobox protein pax-6; **PDBTitle:** crystal structure of the human pax-6 paired domain-dna2 complex reveals a general model for pax protein-dna3 interactions
8	d1pdnc_	Alignment		24.8	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
9	c1q0wA_	Alignment		23.6	50	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**vacuolar protein sorting-associated protein **PDBTitle:** solution structure of vps27 amino-terminal uim-ubiquitin2 complex
10	d1ttya_	Alignment		22.6	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
11	d1ku7a_	Alignment		22.3	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain

12	d2p7vb1	Alignment		21.6	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
13	c3gcgB_	Alignment		15.2	17	**PDB header:**signaling protein/transcription **Chain:** B: **PDB Molecule:**l0028 (mitochondria associated protein); **PDBTitle:** crystal structure of map and cdc42 complex
14	d1k78a1	Alignment		13.8	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
15	c3abdY_	Alignment		12.1	54	**PDB header:**cell cycle/replication **Chain:** Y: **PDB Molecule:**dna polymerase zeta catalytic subunit; **PDBTitle:** structure of human rev7 in complex with a human rev3 fragment in a2 monoclinic crystal
16	c1rp3G_	Alignment		11.9	15	**PDB header:**transcription **Chain:** G: **PDB Molecule:**rna polymerase sigma factor sigma-28 (flia); **PDBTitle:** cocrystal structure of the flagellar sigma/anti-sigma2 complex, sigma-28/flgm
17	d1rp3a2	Alignment		11.7	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
18	d1or7a1	Alignment		11.4	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
19	d1pqwa_	Alignment		10.7	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
20	d1gu7a2	Alignment		10.7	3	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
21	d2jn6a1	Alignment	not modelled	10.6	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Cgl2762-like
22	d1ngra_	Alignment	not modelled	10.3	26	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
23	c2l4aA_	Alignment	not modelled	9.1	26	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**leucine responsive regulatory protein; **PDBTitle:** nmr structure of the dna-binding domain of e.coli lrp
24	d2hfha_	Alignment	not modelled	9.0	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
25	d1bkba2	Alignment	not modelled	8.7	24	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
26	c3mzyA_	Alignment	not modelled	8.3	21	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**rna polymerase sigma-h factor; **PDBTitle:** the crystal structure of the rna polymerase sigma-h factor from2 fusobacterium nucleatum to 2.5a
27	c2pbxB_	Alignment	not modelled	7.9	24	**PDB header:**transcription **Chain:** B: **PDB Molecule:**hemagglutinin/protease regulatory protein; **PDBTitle:** vibrio cholerae hapr
28	c2g7lA_	Alignment	not modelled	7.9	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**tetr-family transcriptional regulator; **PDBTitle:** crystal structure of putative transcription regulator sco7704 from2 streptomyces coelicor
						PDB header:transcription regulator

29	c2fjrB_	Alignment	not modelled	7.6	12	**Chain:** B: **PDB Molecule:**repressor protein ci; **PDBTitle:** crystal structure of bacteriophage 186
30	c2e5zA_	Alignment	not modelled	7.2	8	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**splicing factor, arginine/serine-rich 8; **PDBTitle:** solution structure of the surp2 domain in splicing factor,2 arginine/serine-rich 8
31	c2k27A_	Alignment	not modelled	6.7	28	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**paired box protein pax-8; **PDBTitle:** solution structure of human pax8 paired box domain
32	d1iz6a2	Alignment	not modelled	6.3	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
33	c2iv1J_	Alignment	not modelled	6.0	15	**PDB header:**lyase **Chain:** J: **PDB Molecule:**cyanate hydratase; **PDBTitle:** site directed mutagenesis of key residues involved in the2 catalytic mechanism of cyanase
34	d1d5va_	Alignment	not modelled	5.8	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain