Phyre2

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Description	P0ACV8
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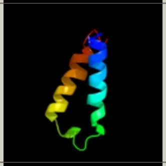
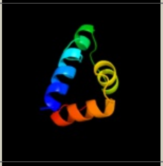
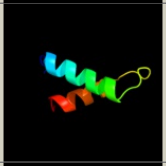
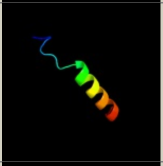
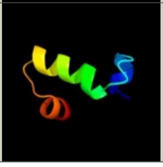
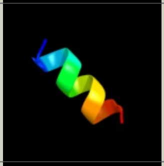
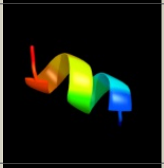
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2fug21	Alignment		63.7	31	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**NQO2-like
2	c1oxjA_	Alignment		61.4	21	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**rna-binding protein smaug; **PDBTitle:** crystal structure of the smaug rna binding domain
3	c3fdqB_	Alignment		51.8	26	**PDB header:**dna binding protein/dna **Chain:** B: **PDB Molecule:**motility gene repressor mogr; **PDBTitle:** recognition of at-rich dna binding sites by the mogr2 repressor
4	d2dt5a1	Alignment		47.3	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcriptional repressor Rex, N-terminal domain
5	c2dt5A_	Alignment		43.8	17	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**at-rich dna-binding protein; **PDBTitle:** crystal structure of ttha1657 (at-rich dna-binding protein) from2 thermus thermophilus hb8
6	c2vt2A_	Alignment		35.2	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**redox-sensing transcriptional repressor rex; **PDBTitle:** structure and functional properties of the bacillus2 subtilis transcriptional repressor rex
7	c3ol4B_	Alignment		30.5	28	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a putative uncharacterized protein from2 mycobacterium smegmatis, an ortholog of rv0543c
8	c2k89A_	Alignment		24.3	18	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**phospholipase a-2-activating protein; **PDBTitle:** solution structure of a novel ubiquitin-binding domain from2 human plaa (pfuc, gly76-pro77 cis isomer)
9	c3n2lA_	Alignment		24.2	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** 2.1 angstrom resolution crystal structure of an orotate2 phosphoribosyltransferase (pyre) from vibrio cholerae o1 biovar eltor3 str. n16961
10	c3ketA_	Alignment		19.5	17	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**redox-sensing transcriptional repressor rex; **PDBTitle:** crystal structure of a rex-family transcriptional regulatory protein2 from streptococcus agalactiae bound to a palindromic operator
11	d1xg7a_	Alignment		19.2	22	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**AgoG-like

12	c2dceA_	Alignment		17.5	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**kiaa1915 protein; **PDBTitle:** solution structure of the swirm domain of human kiaa19152 protein
13	d2fq3a1	Alignment		16.8	33	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**SWIRM domain
14	d2dw4a1	Alignment		16.6	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**SWIRM domain
15	d2qgsa1	Alignment		16.1	24	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
16	c3p8cE_	Alignment		16.1	50	**PDB header:**protein binding **Chain:** E: **PDB Molecule:**probable protein brick1; **PDBTitle:** structure and control of the actin regulatory wave complex
17	d2a4ha1	Alignment		15.9	30	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Selenoprotein W-related
18	c2kfdA_	Alignment		14.6	70	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**pre-mrna-processing protein prp40; **PDBTitle:** prp40 ff4 domain
19	c3pp5A_	Alignment		14.1	55	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**brk1; **PDBTitle:** high-resolution structure of the trimeric scar/wave complex precursor2 brk1
20	d1m47a_	Alignment		12.4	75	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Short-chain cytokines
21	d1jsxa_	Alignment	not modelled	11.7	10	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Glucose-inhibited division protein B (GidB)
22	c3godA_	Alignment	not modelled	11.2	27	**PDB header:**immune system **Chain:** A: **PDB Molecule:**cas1; **PDBTitle:** structural basis for dnase activity of a conserved protein2 implicated in crispr-mediated antiviral defense
23	c1xfzA_	Alignment	not modelled	10.8	52	**PDB header:**lyase/metal binding protein **Chain:** A: **PDB Molecule:**calmodulin-sensitive adenylate cyclase; **PDBTitle:** crystal structure of anthrax edema factor (ef) in complex2 with calmodulin in the presence of 1 millimolar3 exogenously added calcium chloride
24	c1xfuE_	Alignment	not modelled	10.8	52	**PDB header:**lyase/metal binding protein **Chain:** E: **PDB Molecule:**calmodulin-sensitive adenylate cyclase; **PDBTitle:** crystal structure of anthrax edema factor (ef) truncation2 mutant, ef-delta 64 in complex with calmodulin
25	d2hqya1	Alignment	not modelled	9.6	38	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**FemXAB nonribosomal peptidyltransferases
26	d1regx_	Alignment	not modelled	9.0	57	**Fold:**Ferredoxin-like **Superfamily:**Translational regulator protein regA **Family:**Translational regulator protein regA
27	c3gr1A_	Alignment	not modelled	8.6	18	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**protein prgh; **PDBTitle:** periplamic domain of the t3ss inner membrane protein prgh2 from s.typhimurium (fragment 170-392)
28	d1khda1	Alignment	not modelled	8.1	20	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-

						terminal domain
29	c2zooA_	Alignment	not modelled	7.7	38	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable nitrite reductase; **PDBTitle:** crystal structure of nitrite reductase from pseudoalteromonas2 haloplanktis tac125
30	c3s83A_	Alignment	not modelled	7.1	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ggdef family protein; **PDBTitle:** crystal structure of eal domain from caulobacter crescentus cb15
31	c2przB_	Alignment	not modelled	7.0	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**orotate phosphoribosyltransferase 1; **PDBTitle:** s. cerevisiae orotate phosphoribosyltransferase complexed2 with omp
32	c3if8B_	Alignment	not modelled	7.0	18	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**protein zwilch homolog; **PDBTitle:** crystal structure of zwilch, a member of the rzz kinetochore complex
33	c3k6zA_	Alignment	not modelled	6.9	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**possible membrane-associated serine protease; **PDBTitle:** crystal structure of rv3671c protease, inactive form
34	d1lnsa1	Alignment	not modelled	6.6	28	**Fold:**CH domain-like **Superfamily:**X-Prolyl dipeptidyl aminopeptidase PepX, N-terminal domain **Family:**X-Prolyl dipeptidyl aminopeptidase PepX, N-terminal domain
35	c2hwyB_	Alignment	not modelled	6.5	30	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**protein smg5; **PDBTitle:** structure of pin domain of human smg5.
36	d1kfta_	Alignment	not modelled	6.0	22	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Excinuclease UvrC C-terminal domain
37	c1kftA_	Alignment	not modelled	6.0	22	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**excinuclease abc subunit c; **PDBTitle:** solution structure of the c-terminal domain of uvrc from e-2 coli
38	c3frwF_	Alignment	not modelled	5.9	22	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**putative trp repressor protein; **PDBTitle:** crystal structure of putative trpr protein from ruminococcus obeum
39	d1huua_	Alignment	not modelled	5.7	10	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
40	d1xqoa_	Alignment	not modelled	5.6	29	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**AgoG-like
41	d1w53a_	Alignment	not modelled	5.4	26	**Fold:**KaiA/RbsU domain **Superfamily:**KaiA/RbsU domain **Family:**Phosphoserine phosphatase RsbU, N-terminal domain
42	c3nkeA_	Alignment	not modelled	5.4	23	**PDB header:**immune system **Chain:** A: **PDB Molecule:**protein ygbt; **PDBTitle:** high resolution structure of the c-terminal domain crisp-associated2 protein cas1 from escherichia coli str. k-12