Phyre2

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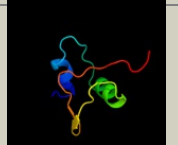
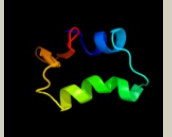
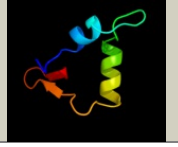
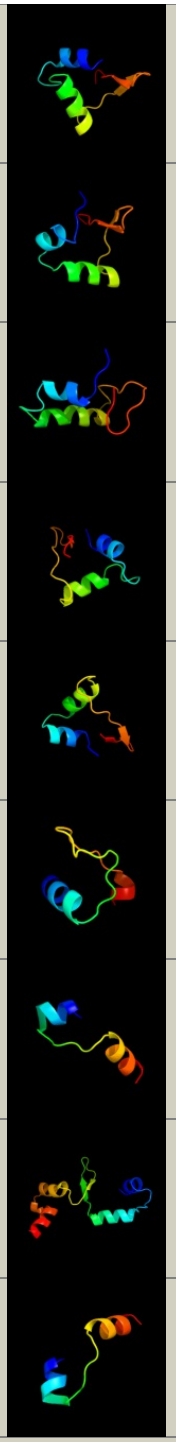
Description	P75970
Date	Thu Jan 5 12:16:37 GMT 2012
Unique Job ID	13b9ebd88e1d54e4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1pm6a_	Alignment		100.0	38	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Excisionase-like
2	d1rh6a_	Alignment		99.9	39	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Excisionase-like
3	c1z4hA_	Alignment		90.8	15	**PDB header:**protein binding, dna binding protein **Chain:** A: **PDB Molecule:**tor inhibition protein; **PDBTitle:** the response regulator tori belongs to a new family of2 atypical excisionase
4	d1r8ea1	Alignment		88.6	21	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**DNA-binding N-terminal domain of transcription activators
5	c2zhhA_	Alignment		86.2	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**redox-sensitive transcriptional activator soxr; **PDBTitle:** crystal structure of soxr
6	c3hh0C_	Alignment		83.9	30	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcriptional regulator, merr family; **PDBTitle:** crystal strucure of a transcriptional regulator, merr family2 from bacillus cereus
7	c3d6zA_	Alignment		81.9	25	**PDB header:**transcription regulator/dna **Chain:** A: **PDB Molecule:**multidrug-efflux transporter 1 regulator; **PDBTitle:** crystal structure of r275e mutant of bmrr bound to dna and rhodamine
8	d1q06a_	Alignment		70.1	14	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**DNA-binding N-terminal domain of transcription activators
9	c3gpvA_	Alignment		68.2	26	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, merr family; **PDBTitle:** crystal structure of a transcriptional regulator, merr2 family from bacillus thuringiensis
10	c1y6uA_	Alignment		68.0	25	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**excisionase from transposon tn916; **PDBTitle:** the structure of the excisionase (xis) protein from2 conjugative transposon tn916 provides insights into the3 regulation of heterobivalent tyrosine recombinases
11	c3qaoA_	Alignment		67.5	27	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**merr-like transcriptional regulator; **PDBTitle:** the crystal structure of the n-terminal domain of a merr-like2 transcriptional regulator from listeria monocytogenes egd-e

12	c2vz4A_	Alignment		65.0	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hth-type transcriptional activator tipa; **PDBTitle:** the n-terminal domain of merr-like protein tipal bound to2 promoter dna
13	d1r8da_	Alignment		61.6	18	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**DNA-binding N-terminal domain of transcription activators
14	c2jmlA_	Alignment		56.9	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna binding domain/transcriptional regulator; **PDBTitle:** solution structure of the n-terminal domain of cara repressor
15	c3gp4B_	Alignment		50.0	19	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, merr family; **PDBTitle:** crystal structure of putative merr family transcriptional regulator2 from listeria monocytogenes
16	c2kfsA_	Alignment		41.0	13	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**conserved hypothetical regulatory protein; **PDBTitle:** nmr structure of rv2175c
17	d1j9ia_	Alignment		35.1	15	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Terminase gpNU1 subunit domain
18	d2ezha_	Alignment		26.0	38	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
19	c1b4aA_	Alignment		25.3	22	**PDB header:**repressor **Chain:** A: **PDB Molecule:**arginine repressor; **PDBTitle:** structure of the arginine repressor from bacillus stearothermophilus
20	d2ezia_	Alignment		24.1	38	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
21	d1aoya_	Alignment	not modelled	23.5	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Arginine repressor (ArgR), N-terminal DNA-binding domain
22	c3hosA_	Alignment	not modelled	11.6	25	**PDB header:**transferase, dna binding protein/dna **Chain:** A: **PDB Molecule:**transposable element mariner, complete cds; **PDBTitle:** crystal structure of the mariner mos1 paired end complex with mg
23	c3v4gA_	Alignment	not modelled	10.2	9	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**arginine repressor; **PDBTitle:** 1.60 angstrom resolution crystal structure of an arginine repressor2 from vibrio vulnificus cmcp6
24	d1pqwa_	Alignment	not modelled	9.9	3	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
25	d1tvxb_	Alignment	not modelled	9.9	38	**Fold:**IL8-like **Superfamily:**Interleukin 8-like chemokines **Family:**Interleukin 8-like chemokines
26	c3l4hA_	Alignment	not modelled	9.8	16	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase hecw1; **PDBTitle:** helical box domain and second ww domain of the human e3 ubiquitin-2 protein ligase hecw1
27	c1t6zB_	Alignment	not modelled	9.7	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**riboflavin kinase/fmn adenylyltransferase; **PDBTitle:** crystal structure of riboflavin bound tm379
28	d1juqa_	Alignment	not modelled	8.8	10	**Fold:**alpha-alpha superhelix **Superfamily:**ENTH/VHS domain **Family:**VHS domain

29	d1r6ra_	Alignment	not modelled	8.5	22	**Fold:**Flavivirus capsid protein C **Superfamily:**Flavivirus capsid protein C **Family:**Flavivirus capsid protein C
30	c1r6rA_	Alignment	not modelled	8.5	22	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**genome polyprotein; **PDBTitle:** solution structure of dengue virus capsid protein reveals a2 new fold
31	c2dn4A_	Alignment	not modelled	7.9	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general transcription factor ii-i; **PDBTitle:** solution structure of rsgi ruh-060, a gtf2i domain in human2 cdna
32	c3hefB_	Alignment	not modelled	7.8	31	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**gene 1 protein; **PDBTitle:** crystal structure of the bacteriophage sf6 terminase small2 subunit
33	c3eusB_	Alignment	not modelled	7.8	9	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dna-binding protein; **PDBTitle:** the crystal structure of the dna binding protein from silicibacter2 pomeroyi
34	d1sfka_	Alignment	not modelled	7.7	22	**Fold:**Flavivirus capsid protein C **Superfamily:**Flavivirus capsid protein C **Family:**Flavivirus capsid protein C
35	c2d99A_	Alignment	not modelled	7.7	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general transcription factor ii-i repeat domain- **PDBTitle:** solution structure of rsgi ruh-048, a gtf2i domain in human2 cdna
36	d1b4aa1	Alignment	not modelled	7.4	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Arginine repressor (ArgR), N-terminal DNA-binding domain
37	d1q60a_	Alignment	not modelled	7.4	22	**Fold:**GTF2I-like repeat **Superfamily:**GTF2I-like repeat **Family:**GTF2I-like repeat
38	c2ed2A_	Alignment	not modelled	7.1	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general transcription factor ii-i; **PDBTitle:** solution structure of rsgi ruh-069, a gtf2i domain in human2 cdna
39	d1tvxa_	Alignment	not modelled	7.0	38	**Fold:**IL8-like **Superfamily:**Interleukin 8-like chemokines **Family:**Interleukin 8-like chemokines
40	c2dn5A_	Alignment	not modelled	7.0	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general transcription factor ii-i repeat domain- **PDBTitle:** solution structure of rsgi ruh-057, a gtf2i domain in human2 cdna
41	c2dg6A_	Alignment	not modelled	7.0	22	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of the putative transcriptional regulator sco55502 from streptomyces coelicolor a3(2)
42	d1te7a_	Alignment	not modelled	6.9	4	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**yqfB-like
43	c2dzqA_	Alignment	not modelled	6.8	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general transcription factor ii-i repeat domain- **PDBTitle:** solution structure of rsgi ruh-066, a gtf2i domain in human2 cdna
44	c2e3lA_	Alignment	not modelled	6.7	31	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor gtf2ird2 beta; **PDBTitle:** solution structure of rsgi ruh-068, a gtf2i domain in human2 cdna
45	c1iufA_	Alignment	not modelled	6.6	25	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**centromere abp1 protein; **PDBTitle:** low resolution solution structure of the two dna-binding2 domains in schizosaccharomyces pombe abp1 protein
46	d1f9na1	Alignment	not modelled	6.4	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Arginine repressor (ArgR), N-terminal DNA-binding domain
47	d1f9pa_	Alignment	not modelled	6.3	38	**Fold:**IL8-like **Superfamily:**Interleukin 8-like chemokines **Family:**Interleukin 8-like chemokines
48	c2x0kB_	Alignment	not modelled	6.0	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**riboflavin biosynthesis protein ribf; **PDBTitle:** crystal structure of modular fad synthetase from2 corynebacterium ammoniagenes
49	c2ejeA_	Alignment	not modelled	5.4	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general transcription factor ii-i; **PDBTitle:** solution structure of rsgi ruh-071, a gtf2i domain in human2 cdna
50	c2djyA_	Alignment	not modelled	5.4	22	**PDB header:**ligase/signaling protein **Chain:** A: **PDB Molecule:**smad ubiquitination regulatory factor 2; **PDBTitle:** solution structure of smurf2 ww3 domain-smad7 py peptide2 complex
51	c2rn7A_	Alignment	not modelled	5.1	36	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**is629 orfa; **PDBTitle:** nmr solution structure of tnpe protein from shigella2 flexneri. northeast structural genomics target sfr125