Phyre2

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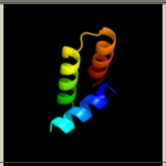
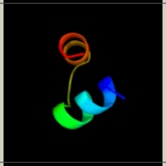
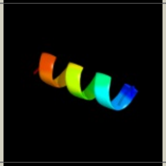
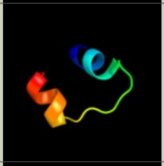
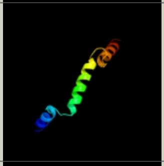
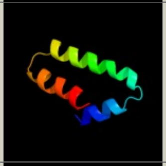
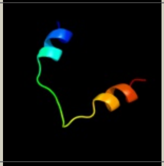
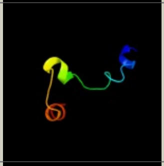
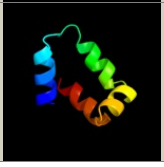
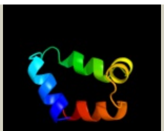
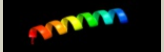
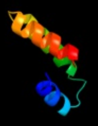
Description	P75992
Date	Thu Jan 5 12:17:05 GMT 2012
Unique Job ID	70bc9700fcfceeb5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2oxlA_	Alignment		42.6	20	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**hypothetical protein ymgb; **PDBTitle:** structure and function of the e. coli protein ymgb: a protein critical2 for biofilm formation and acid resistance
2	d1z05a1	Alignment		31.6	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ROK associated domain
3	c3a7oB_	Alignment		29.8	29	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**autophagy protein 16; **PDBTitle:** the crystal structure of the coiled-coil domain of2 saccharomyces cerevisiae atg16
4	d1biaa1	Alignment		25.3	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
5	d1z6ra1	Alignment		23.6	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ROK associated domain
6	d2acva1	Alignment		23.1	6	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDPGT-like
7	c2kztB_	Alignment		23.1	11	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**programmed cell death protein 4; **PDBTitle:** structure of the tandem ma-3 region of pdcd4
8	c3hbjA_	Alignment		20.5	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**flavonoid 3-o-glucosyltransferase; **PDBTitle:** structure of ugt78g1 complexed with udp
9	c2yudA_	Alignment		20.0	12	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**yth domain-containing protein 1; **PDBTitle:** solution structure of the yth domain in yth domain-2 containing protein 1 (putative splicing factor yt521)
10	d1ub9a_	Alignment		19.5	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
11	c2iolB_	Alignment		18.4	9	**PDB header:**antitumor protein **Chain:** B: **PDB Molecule:**programmed cell death 4, pdcd4; **PDBTitle:** crystal structure of the c-terminal ma3 domain of pdcd4 (mouse); form2 1

12	c2iolA_	Alignment		18.4	9	**PDB header:**antitumor protein **Chain:** A: **PDB Molecule:**programmed cell death 4, pdcd4; **PDBTitle:** crystal structure of the c-terminal ma3 domain of pdcd4 (mouse); form2 1
13	d1xmka1	Alignment		15.8	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Z-DNA binding domain
14	d2nsza1	Alignment		15.6	11	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**MIF4G domain-like
15	c2nszA_	Alignment		15.6	11	**PDB header:**antitumor protein **Chain:** A: **PDB Molecule:**programmed cell death protein 4; **PDBTitle:** 1.15 angstrom crystal structure of the ma3 domain of pdcd4
16	c2ionA_	Alignment		15.6	11	**PDB header:**antitumor protein **Chain:** A: **PDB Molecule:**programmed cell death 4, pdcd4; **PDBTitle:** crystal structure of the c-terminal ma3 domain of pdcd4 (mouse); form2
17	c1usdA_	Alignment		14.5	24	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**vasodilator-stimulated phosphoprotein; **PDBTitle:** human vasp tetramerisation domain l352m
18	c2hm8A_	Alignment		14.2	11	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**pdcd4 c-terminal ma-3 domain; **PDBTitle:** solution structure of the c-terminal ma-3 domain of pdcd4
19	c3eitB_	Alignment		14.0	29	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**putative atp/gtp binding protein; **PDBTitle:** the 2.6 angstrom crystal structure of chbp, the cif homologue from2 burkholderia pseudomallei
20	c3eyyA_	Alignment		13.9	13	**PDB header:**transport **Chain:** A: **PDB Molecule:**putative iron uptake regulatory protein; **PDBTitle:** structural basis for the specialization of nur, a nickel-2 specific fur homologue, in metal sensing and dna3 recognition
21	d2pq6a1	Alignment	not modelled	13.4	10	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDPGT-like
22	d1i1ga1	Alignment	not modelled	13.2	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
23	c3nj2B_	Alignment	not modelled	13.1	26	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**duf269-containing protein; **PDBTitle:** crystal structure of cce_0566 from the cyanobacterium cyanothece2 51142, a protein associated with nitrogen fixation from the duf2693 family
24	c3gqjA_	Alignment	not modelled	11.8	31	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**cell inhibiting factor (cif); **PDBTitle:** crystal structure of cell inhibiting factor (cif) from photorhabdus2 luminescens
25	c1qeyD_	Alignment	not modelled	10.4	40	**PDB header:**gene regulation **Chain:** D: **PDB Molecule:**protein (regulatory protein mnt); **PDBTitle:** nmr structure determination of the tetramerization domain2 of the mnt repressor: an asymmetric a-helical assembly in3 slow exchange
26	c1qeyA_	Alignment	not modelled	10.4	40	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**protein (regulatory protein mnt); **PDBTitle:** nmr structure determination of the tetramerization domain2 of the mnt repressor: an asymmetric a-helical assembly in3 slow exchange
27	c1qeyC_	Alignment	not modelled	10.4	40	**PDB header:**gene regulation **Chain:** C: **PDB Molecule:**protein (regulatory protein mnt); **PDBTitle:** nmr structure determination of the tetramerization domain2 of the mnt repressor: an asymmetric a-helical assembly in3 slow exchange
						PDB header:gene regulation

28	c1qeyB_	Alignment	not modelled	10.4	40	**Chain:** B: **PDB Molecule:**protein (regulatory protein mnt); **PDBTitle:** nmr structure determination of the tetramerization domain2 of the mnt repressor: an asymmetric a-helical assembly in3 slow exchange
29	d2cfxa1	Alignment	not modelled	10.2	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
30	d1b79a_	Alignment	not modelled	10.0	13	**Fold:**N-terminal domain of DnaB helicase **Superfamily:**N-terminal domain of DnaB helicase **Family:**N-terminal domain of DnaB helicase
31	c2veeC_	Alignment	not modelled	9.6	18	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**protoglobin; **PDBTitle:** structure of protoglobin from methanosarcina acetivorans2 c2a
32	c2l4aA_	Alignment	not modelled	8.6	21	**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
33	c4a1qB_	Alignment	not modelled	8.6	38	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**orf e73; **PDBTitle:** solution structure of e73 protein from sulfolobus spindle-2 shaped virus ragged hills, a hyperthermophilic3 crenarchaeal virus from yellowstone national park
34	d1q1va_	Alignment	not modelled	8.3	12	**Fold:**Another 3-helical bundle **Superfamily:**DEK C-terminal domain **Family:**DEK C-terminal domain
35	c2ggfA_	Alignment	not modelled	7.6	9	**PDB header:**translation **Chain:** A: **PDB Molecule:**programmed cell death 4, isoform 1; **PDBTitle:** solution structure of the ma3 domain of human programmed2 cell death 4
36	d2gxba1	Alignment	not modelled	7.5	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Z-DNA binding domain
37	d1qo0d_	Alignment	not modelled	7.4	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**Positive regulator of the amidase operon AmiR
38	d2g7ga1	Alignment	not modelled	7.3	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
39	c1zrwA_	Alignment	not modelled	7.3	50	**PDB header:**antimicrobial protein, antibiotic **Chain:** A: **PDB Molecule:**spinigerin; **PDBTitle:** solution structure of spinigerin in h20/tfe 10%
40	c1zrvA_	Alignment	not modelled	7.3	50	**PDB header:**antimicrobial protein, antibiotic **Chain:** A: **PDB Molecule:**spinigerin; **PDBTitle:** solution structure of spinigerin in h20/tfe 50%
41	c2ewnA_	Alignment	not modelled	7.1	20	**PDB header:**ligase, transcription **Chain:** A: **PDB Molecule:**bira bifunctional protein; **PDBTitle:** ecoli biotin repressor with co-repressor analog
42	d2ev0a1	Alignment	not modelled	6.9	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Iron-dependent repressor protein
43	d2iu5a1	Alignment	not modelled	6.4	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
44	d2cg4a1	Alignment	not modelled	6.4	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
45	d1ixsa_	Alignment	not modelled	6.1	35	**Fold:**RuvA C-terminal domain-like **Superfamily:**DNA helicase RuvA subunit, C-terminal domain **Family:**DNA helicase RuvA subunit, C-terminal domain
46	c2l5yA_	Alignment	not modelled	5.8	29	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**stromal interaction molecule 2; **PDBTitle:** nmr structure of calcium-loaded stim2 ef-sam.
47	d2cyya1	Alignment	not modelled	5.7	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
48	d1zoqc1	Alignment	not modelled	5.3	40	**Fold:**Nuclear receptor coactivator interlocking domain **Superfamily:**Nuclear receptor coactivator interlocking domain **Family:**Nuclear receptor coactivator interlocking domain