Phyre^2

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Description	P0A6Y1
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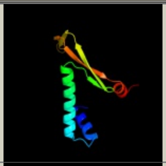
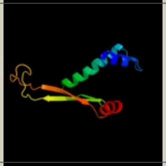
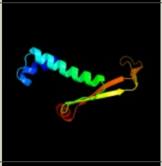
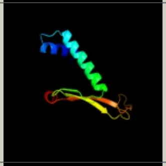
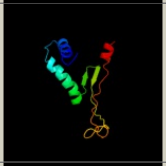
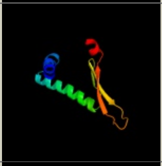
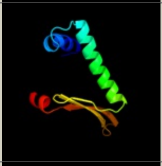
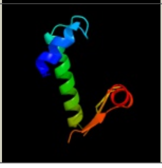
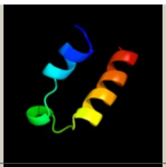
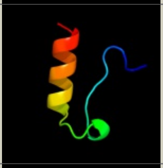
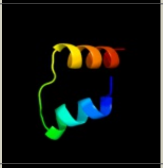
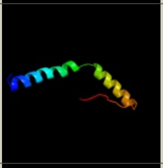
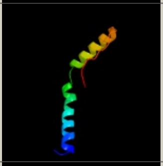
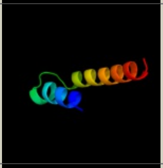
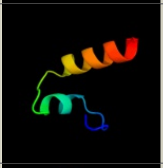
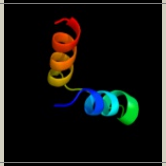
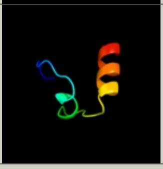
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1owfb_	Alignment		99.9	99	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
2	c2iifA_	Alignment		99.9	33	**PDB header:**recombination/dna **Chain:** A: **PDB Molecule:**integration host factor; **PDBTitle:** single chain integration host factor mutant protein (scihf2-2 k45ae) in complex with dna
3	d1p71a_	Alignment		99.9	33	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
4	c3c4iA_	Alignment		99.9	33	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna-binding protein hu homolog; **PDBTitle:** crystal structure analysis of n terminal region containing the2 dimerization domain and dna binding domain of hu protein(histone like3 protein-dna binding) from mycobacterium tuberculosis [h37rv]
5	d1owfa_	Alignment		99.9	32	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
6	c2np2B_	Alignment		99.9	32	**PDB header:**dna binding protein/dna **Chain:** B: **PDB Molecule:**hbb; **PDBTitle:** hbb-dna complex
7	d1exea_	Alignment		99.9	28	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
8	d1huua_	Alignment		99.8	38	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
9	d1mula_	Alignment		99.7	29	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
10	d2o97b1	Alignment		99.7	32	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
11	d1b8za_	Alignment		99.6	45	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein

12	d1i27a_	Alignment		43.3	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal domain of the rap74 subunit of TFIIF
13	d1dula_	Alignment		35.6	23	**Fold:**Signal peptide-binding domain **Superfamily:**Signal peptide-binding domain **Family:**Signal peptide-binding domain
14	d1o17a1	Alignment		33.3	20	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
15	c1nriA_	Alignment		31.5	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein hi0754; **PDBTitle:** crystal structure of putative phosphosugar isomerase hi0754 from2 haemophilus influenzae
16	d1nria_	Alignment		31.5	16	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
17	d1nh2d1	Alignment		29.9	16	**Fold:**Transcription factor IIA (TFIIA), alpha-helical domain **Superfamily:**Transcription factor IIA (TFIIA), alpha-helical domain **Family:**Transcription factor IIA (TFIIA), alpha-helical domain
18	d1hq1a_	Alignment		29.7	26	**Fold:**Signal peptide-binding domain **Superfamily:**Signal peptide-binding domain **Family:**Signal peptide-binding domain
19	d1brwa1	Alignment		28.5	17	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
20	d1qzxa2	Alignment		28.1	29	**Fold:**Signal peptide-binding domain **Superfamily:**Signal peptide-binding domain **Family:**Signal peptide-binding domain
21	c3cvjB_	Alignment	not modelled	27.4	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative phosphoheptose isomerase; **PDBTitle:** crystal structure of a putative phosphoheptose isomerase (bh3325) from2 bacillus halodurans c-125 at 2.00 a resolution
22	c2jqeA_	Alignment	not modelled	25.2	32	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** soution structure of af54 m-domain
23	d2ffha2	Alignment	not modelled	21.3	32	**Fold:**Signal peptide-binding domain **Superfamily:**Signal peptide-binding domain **Family:**Signal peptide-binding domain
24	c1o17A_	Alignment	not modelled	19.3	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**anthranilate phosphoribosyltransferase; **PDBTitle:** anthranilate phosphoribosyl-transferase (trpd)
25	d1khda1	Alignment	not modelled	18.1	10	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
26	c3tsuA_	Alignment	not modelled	17.3	30	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcriptional regulatory protein; **PDBTitle:** crystal structure of e. coli hypf with amp-pnp and carbamoyl phosphate
27	d1nvpd1	Alignment	not modelled	16.8	18	**Fold:**Transcription factor IIA (TFIIA), alpha-helical domain **Superfamily:**Transcription factor IIA (TFIIA), alpha-helical domain **Family:**Transcription factor IIA (TFIIA), alpha-helical domain
28	c2k6sB_	Alignment	not modelled	13.9	16	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**rab11fip2 protein; **PDBTitle:** structure of rab11-fip2 c-terminal coiled-coil domain
						Fold: Methionine synthase domain-like

29	d2tpta1	Alignment	not modelled	12.9	7	**Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
30	d1njra_	Alignment	not modelled	12.3	11	**Fold:**Macro domain-like **Superfamily:**Macro domain-like **Family:**Macro domain
31	d2o4ta1	Alignment	not modelled	12.2	15	**Fold:**Left-handed superhelix **Superfamily:**BH3980-like **Family:**BH3980-like
32	d1vola2	Alignment	not modelled	11.9	15	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Transcription factor IIB (TFIIB), core domain
33	d1ussa_	Alignment	not modelled	11.3	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Linker histone H1/H5
34	c3kfoA_	Alignment	not modelled	10.9	9	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**nucleoporin nup133; **PDBTitle:** crystal structure of the c-terminal domain from the nuclear pore2 complex component nup133 from saccharomyces cerevisiae
35	d1ee8a1	Alignment	not modelled	10.7	11	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
36	c3thgA_	Alignment	not modelled	10.3	11	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ribulose bisphosphate carboxylase/oxygenase activase 1, **PDBTitle:** crystal structure of the creosote rubisco activase c-domain
37	d1uoua1	Alignment	not modelled	10.2	15	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
38	c2yskA_	Alignment	not modelled	10.1	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ttha1432; **PDBTitle:** crystal structure of a hypothetical protein ttha1432 from thermus2 thermophilus
39	d1tdza1	Alignment	not modelled	9.7	7	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
40	d1dpua_	Alignment	not modelled	9.3	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal domain of RPA32
41	c1dpuA_	Alignment	not modelled	9.3	20	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**replication protein a (rpa32) c-terminal domain; **PDBTitle:** solution structure of the c-terminal domain of human rpa322 complexed with ung2(73-88)
42	d1soua_	Alignment	not modelled	9.1	16	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**Methenyltetrahydrofolate synthetase
43	d1k82a1	Alignment	not modelled	9.0	14	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
44	d1z67a1	Alignment	not modelled	8.9	13	**Fold:**YidB-like **Superfamily:**YidB-like **Family:**YidB-like
45	c2v3cC_	Alignment	not modelled	8.9	29	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** crystal structure of the srp54-srp19-7s.s srp rna complex2 of m. jannaschii
46	c2vfyA_	Alignment	not modelled	8.6	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**akap18 delta; **PDBTitle:** akap18 delta central domain
47	d1qb2a_	Alignment	not modelled	8.5	20	**Fold:**Signal peptide-binding domain **Superfamily:**Signal peptide-binding domain **Family:**Signal peptide-binding domain
48	d1r2za1	Alignment	not modelled	8.2	19	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
49	d1x94a_	Alignment	not modelled	8.2	21	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
50	c2kloA_	Alignment	not modelled	8.1	14	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**dna replication factor cdt1; **PDBTitle:** structure of the cdt1 c-terminal domain
51	d1tk9a_	Alignment	not modelled	8.0	28	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
52	c1khdD_	Alignment	not modelled	7.8	10	**PDB header:**transferase **Chain:** D: **PDB Molecule:**anthranilate phosphoribosyltransferase; **PDBTitle:** crystal structure analysis of the anthranilate2 phosphoribosyltransferase from erwinia carotovora at 1.93 resolution (current name, pectobacterium carotovorum)
53	c3g2bA_	Alignment	not modelled	7.8	18	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**coenzyme pqq synthesis protein d; **PDBTitle:** crystal structure of pqqd from xanthomonas campestris
54	d1k3xa1	Alignment	not modelled	7.6	15	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins

55	c1nvpD_	Alignment	not modelled	7.5	18	**PDB header:**transcription/dna **Chain:** D: **PDB Molecule:**transcription initiation factor iia gamma chain; **PDBTitle:** human tfiia/tbp/dna complex
56	d2fqla1	Alignment	not modelled	7.5	22	**Fold:**N domain of copper amine oxidase-like **Superfamily:**Frataxin/Nqo15-like **Family:**Frataxin-like
57	c1otpA_	Alignment	not modelled	7.4	7	**PDB header:**phosphorylase **Chain:** A: **PDB Molecule:**thymidine phosphorylase; **PDBTitle:** structural and theoretical studies suggest domain movement produces an2 active conformation of thymidine phosphorylase
58	c1tr8A_	Alignment	not modelled	7.2	21	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**conserved protein (mth177); **PDBTitle:** crystal structure of archaeal nascent polypeptide-associated complex2 (aenac)
59	c2i2aA_	Alignment	not modelled	7.1	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable inorganic polyphosphate/atp-nad kinase 1; **PDBTitle:** crystal structure of lmnadk1 from listeria monocytogenes
60	c3dm5A_	Alignment	not modelled	6.8	35	**PDB header:**rna binding protein, transport protein **Chain:** A: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** structures of srp54 and srp19, the two proteins assembling2 the ribonucleic core of the signal recognition particle3 from the archaeon pyrococcus furiosus.
61	d1aipc1	Alignment	not modelled	6.5	17	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain
62	d1hh2p4	Alignment	not modelled	6.5	19	**Fold:**Transcription factor NusA, N-terminal domain **Superfamily:**Transcription factor NusA, N-terminal domain **Family:**Transcription factor NusA, N-terminal domain
63	d1mzba_	Alignment	not modelled	6.4	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**FUR-like
64	d1aisb2	Alignment	not modelled	6.2	16	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Transcription factor IIB (TFIIB), core domain
65	d2cp9a1	Alignment	not modelled	6.2	11	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain
66	c3eyyA_	Alignment	not modelled	6.1	19	**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
67	d1z6ra1	Alignment	not modelled	6.0	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ROK associated domain
68	c3jx9B_	Alignment	not modelled	5.9	19	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative phosphoheptose isomerase; **PDBTitle:** crystal structure of putative phosphoheptose isomerase2 (yp_001815198.1) from exiguobacterium sp. 255-15 at 1.95 a resolution
69	c2az1B_	Alignment	not modelled	5.8	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**nucleoside diphosphate kinase; **PDBTitle:** structure of a halophilic nucleoside diphosphate kinase2 from halobacterium salinarum
70	c3a4cA_	Alignment	not modelled	5.8	14	**PDB header:**cell cycle, replication **Chain:** A: **PDB Molecule:**dna replication factor cdt1; **PDBTitle:** crystal structure of cdt1 c terminal domain
71	c2d4gA_	Alignment	not modelled	5.7	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein bsu11850; **PDBTitle:** structure of yjcg protein, a putative 2'-5' rna ligase from2 bacillus subtilis
72	c2o03A_	Alignment	not modelled	5.7	23	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**probable zinc uptake regulation protein furb; **PDBTitle:** crystal structure of furb from m. tuberculosis- a zinc uptake2 regulator
73	c2dsjA_	Alignment	not modelled	5.6	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyrimidine-nucleoside (thymidine) phosphorylase; **PDBTitle:** crystal structure of project id tt0128 from thermus thermophilus hb8
74	c2fu4B_	Alignment	not modelled	5.5	19	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**ferric uptake regulation protein; **PDBTitle:** crystal structure of the dna binding domain of e.coli fur (ferric2 uptake regulator)
75	c1brwB_	Alignment	not modelled	5.4	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein (pyrimidine nucleoside phosphorylase); **PDBTitle:** the crystal structure of pyrimidine nucleoside2 phosphorylase in a closed conformation
76	d1krha1	Alignment	not modelled	5.4	35	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
77	c3mwmA_	Alignment	not modelled	5.3	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative metal uptake regulation protein; **PDBTitle:** graded expression of zinc-responsive genes through two regulatory2 zinc-binding sites in zur
78	d2elca1	Alignment	not modelled	5.3	0	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
79	c2xigA_	Alignment	not modelled	5.3	6	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ferric uptake regulation protein; **PDBTitle:** the structure of the helicobacter pylori ferric uptake2

						regulator fur reveals three functional metal binding sites
80	d1v8ga1	 Alignment	not modelled	5.3	0	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
81	c1vquB_	 Alignment	not modelled	5.3	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**anthranilate phosphoribosyltransferase 2; **PDBTitle:** crystal structure of anthranilate phosphoribosyltransferase 22 (17130499) from nostoc sp. at 1.85 a resolution
82	c3mzyA_	 Alignment	not modelled	5.2	11	**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
83	c2w2mP_	 Alignment	not modelled	5.2	33	**PDB header:**hydrolase/receptor **Chain:** P: **PDB Molecule:**proprotein convertase subtilisin/kexin type 9; **PDBTitle:** wt pcsk9-deltac bound to wt egf-a of ldlr
84	c2pmwA_	 Alignment	not modelled	5.2	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**proprotein convertase subtilisin/kexin type 9; **PDBTitle:** the crystal structure of proprotein convertase subtilisin2 kexin type 9 (pcsk9)
85	c2p4eP_	 Alignment	not modelled	5.2	33	**PDB header:**hydrolase **Chain:** P: **PDB Molecule:**proprotein convertase subtilisin/kexin type 9; **PDBTitle:** crystal structure of pcsk9
86	c2q3vB_	 Alignment	not modelled	5.1	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein at2g34160; **PDBTitle:** ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at2g34160