Phyre^2

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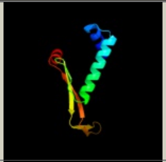
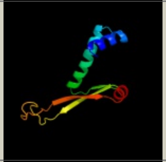
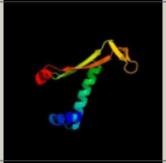
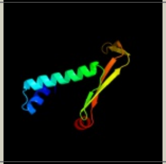
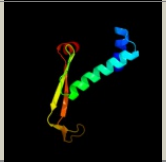
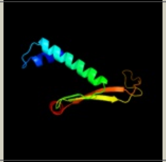
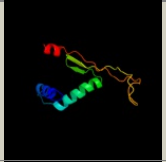
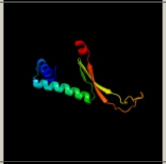
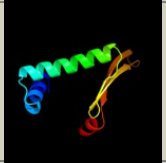
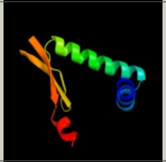
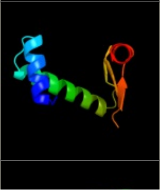
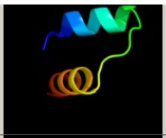
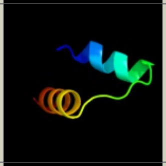
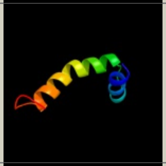
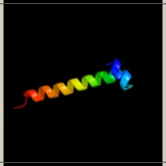
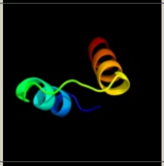
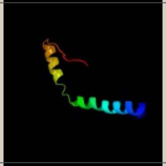
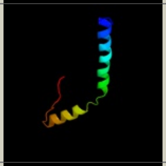
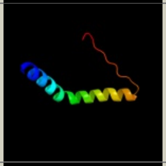
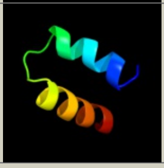
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1p71a_	Alignment		99.9	43	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
2	c2iifA_	Alignment		99.9	32	**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	c3c4iA_	Alignment		99.9	34	**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]
4	d1owfb_	Alignment		99.9	37	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
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	33	**PDB header:**dna binding protein/dna **Chain:** B: **PDB Molecule:**hbb; **PDBTitle:** hbb-dna complex
7	d1exea_	Alignment		99.9	34	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
8	d1huua_	Alignment		99.8	57	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
9	d1mula_	Alignment		99.7	61	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
10	d2o97b1	Alignment		99.7	100	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
11	d1b8za_	Alignment		99.6	48	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein

12	d1o17a1	Alignment		52.3	27	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
13	d1brwa1	Alignment		51.2	20	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
14	d1z67a1	Alignment		50.5	10	**Fold:**YidB-like **Superfamily:**YidB-like **Family:**YidB-like
15	c3mzyA_	Alignment		46.6	16	**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
16	c1o17A_	Alignment		45.7	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**anthranilate phosphoribosyltransferase; **PDBTitle:** anthranilate phosphoribosyl-transferase (trpd)
17	d1nria_	Alignment		41.0	12	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
18	c1nriA_	Alignment		41.0	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein hi0754; **PDBTitle:** crystal structure of putative phosphosugar isomerase hi0754 from2 haemophilus influenzae
19	c3cvjB_	Alignment		38.7	13	**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
20	d1i27a_	Alignment		36.7	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal domain of the rap74 subunit of TFIIF
21	c2yskA_	Alignment	not modelled	35.5	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ttha1432; **PDBTitle:** crystal structure of a hypothetical protein ttha1432 from thermus2 thermophilus
22	d1hq1a_	Alignment	not modelled	33.7	24	**Fold:**Signal peptide-binding domain **Superfamily:**Signal peptide-binding domain **Family:**Signal peptide-binding domain
23	d1nh2d1	Alignment	not modelled	32.3	26	**Fold:**Transcription factor IIA (TFIIA), alpha-helical domain **Superfamily:**Transcription factor IIA (TFIIA), alpha-helical domain **Family:**Transcription factor IIA (TFIIA), alpha-helical domain
24	d1vola2	Alignment	not modelled	32.1	12	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Transcription factor IIB (TFIIB), core domain
25	d1dula_	Alignment	not modelled	31.5	24	**Fold:**Signal peptide-binding domain **Superfamily:**Signal peptide-binding domain **Family:**Signal peptide-binding domain
26	d1khda1	Alignment	not modelled	31.4	10	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
27	c2jqeA_	Alignment	not modelled	29.1	24	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** soution structure of af54 m-domain
28	d1qb2a_	Alignment	not modelled	29.0	20	**Fold:**Signal peptide-binding domain **Superfamily:**Signal peptide-binding domain **Family:**Signal peptide-binding domain
29	d2ffha2	Alignment	not modelled	29.0	24	**Fold:**Signal peptide-binding domain **Superfamily:**Signal peptide-binding domain

						Family: Signal peptide-binding domain
30	c2v79B_	Alignment	not modelled	28.8	21	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**dna replication protein dnad; **PDBTitle:** crystal structure of the n-terminal domain of dnad from2 bacillus subtilis
31	c2vn2B_	Alignment	not modelled	27.5	13	**PDB header:**replication **Chain:** B: **PDB Molecule:**chromosome replication initiation protein; **PDBTitle:** crystal structure of the n-terminal domain of dnad protein2 from geobacillus kaustophilus hta426
32	d2tpta1	Alignment	not modelled	26.5	17	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
33	d1z6ra1	Alignment	not modelled	24.9	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ROK associated domain
34	d2cp9a1	Alignment	not modelled	24.2	14	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain
35	d1qzxa2	Alignment	not modelled	23.9	16	**Fold:**Signal peptide-binding domain **Superfamily:**Signal peptide-binding domain **Family:**Signal peptide-binding domain
36	d2o4ta1	Alignment	not modelled	22.7	13	**Fold:**Left-handed superhelix **Superfamily:**BH3980-like **Family:**BH3980-like
37	d1aipc1	Alignment	not modelled	22.4	23	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain
38	d1aisb2	Alignment	not modelled	22.4	18	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Transcription factor IIB (TFIIB), core domain
39	c1l0oC_	Alignment	not modelled	22.3	29	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**sigma factor; **PDBTitle:** crystal structure of the bacillus stearothermophilus anti-2 sigma factor spoiiab with the sporulation sigma factor3 sigmaf
40	d1l0oc_	Alignment	not modelled	22.3	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
41	d1uoua1	Alignment	not modelled	21.6	22	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
42	c2krcA_	Alignment	not modelled	21.1	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna-directed rna polymerase subunit delta; **PDBTitle:** solution structure of the n-terminal domain of bacillus2 subtilis delta subunit of rna polymerase
43	c1tr8A_	Alignment	not modelled	20.9	21	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**conserved protein (mth177); **PDBTitle:** crystal structure of archaeal nascent polypeptide-associated complex2 (aenac)
44	c1otpA_	Alignment	not modelled	19.8	17	**PDB header:**phosphorylase **Chain:** A: **PDB Molecule:**thymidine phosphorylase; **PDBTitle:** structural and theoretical studies suggest domain movement produces an2 active conformation of thymidine phosphorylase
45	d1nvpd1	Alignment	not modelled	19.6	14	**Fold:**Transcription factor IIA (TFIIA), alpha-helical domain **Superfamily:**Transcription factor IIA (TFIIA), alpha-helical domain **Family:**Transcription factor IIA (TFIIA), alpha-helical domain
46	d1xb2b1	Alignment	not modelled	19.5	15	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain
47	d1ussa_	Alignment	not modelled	18.4	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Linker histone H1/H5
48	c1brwB_	Alignment	not modelled	17.7	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein (pyrimidine nucleoside phosphorylase); **PDBTitle:** the crystal structure of pyrimidine nucleoside2 phosphorylase in a closed conformation
49	c3g2bA_	Alignment	not modelled	17.1	12	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**coenzyme pqq synthesis protein d; **PDBTitle:** crystal structure of pqqd from xanthomonas campestris
50	d1njra_	Alignment	not modelled	17.0	21	**Fold:**Macro domain-like **Superfamily:**Macro domain-like **Family:**Macro domain
51	c1khdD_	Alignment	not modelled	16.9	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)
52	d1g8ia_	Alignment	not modelled	16.8	7	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
53	d1vr3a1	Alignment	not modelled	14.8	25	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Acireductone dioxygenase
54	d1uxda_	Alignment	not modelled	14.7	30	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains

						Family: GalR/LacI-like bacterial regulator
55	d1uxca_	Alignment	not modelled	14.7	30	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
56	c3bwgA_	Alignment	not modelled	14.0	22	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**uncharacterized hth-type transcriptional regulator yydk; **PDBTitle:** the crystal structure of possible transcriptional regulator yydk from2 bacillus subtilis subsp. subtilis str. 168
57	d1tdza1	Alignment	not modelled	14.0	18	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
58	d1ee8a1	Alignment	not modelled	13.9	18	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
59	d1smyf2	Alignment	not modelled	13.7	3	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
60	c1dpuA_	Alignment	not modelled	13.5	12	**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)
61	d1dpua_	Alignment	not modelled	13.5	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal domain of RPA32
62	d2bjca1	Alignment	not modelled	13.3	26	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
63	c1vquB_	Alignment	not modelled	13.3	14	**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
64	d1tk9a_	Alignment	not modelled	13.3	18	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
65	c2dsjA_	Alignment	not modelled	13.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyrimidine-nucleoside (thymidine) phosphorylase; **PDBTitle:** crystal structure of project id tt0128 from thermus thermophilus hb8
66	d1v8ga1	Alignment	not modelled	13.0	19	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
67	d1z05a1	Alignment	not modelled	12.2	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ROK associated domain
68	d1k82a1	Alignment	not modelled	12.1	21	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
69	d1qpza1	Alignment	not modelled	12.1	20	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
70	c2k4jA_	Alignment	not modelled	12.0	8	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** arsr dna binding domain
71	c2kwpA_	Alignment	not modelled	12.0	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation protein nusa; **PDBTitle:** solution structure of the aminoterminal domain of e. coli nusa
72	d1ay7b_	Alignment	not modelled	11.7	18	**Fold:**Barstar-like **Superfamily:**Barstar-related **Family:**Barstar-related
73	c3tsuA_	Alignment	not modelled	11.6	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcriptional regulatory protein; **PDBTitle:** crystal structure of e. coli hypf with amp-pnp and carbamoyl phosphate
74	c2l8nA_	Alignment	not modelled	11.5	37	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional repressor cytr; **PDBTitle:** nmr structure of the cytidine repressor dna binding domain in presence2 of operator half-site dna
75	d2elca1	Alignment	not modelled	11.1	19	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
76	c2vfyA_	Alignment	not modelled	11.0	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**akap18 delta; **PDBTitle:** akap18 delta central domain
77	c1rp3G_	Alignment	not modelled	11.0	12	**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
78	d1r2za1	Alignment	not modelled	10.9	21	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
						Fold: Colicin D/E5 nuclease domain

79	d1v74a_	Alignment	not modelled	10.8	21	**Superfamily:**Colicin D/E5 nuclease domain **Family:**Colicin D nuclease domain
80	d1efub3	Alignment	not modelled	10.7	13	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain
81	d1k3xa1	Alignment	not modelled	10.6	15	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
82	d2hsga1	Alignment	not modelled	10.5	32	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
83	c1v8gB_	Alignment	not modelled	10.3	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**anthranilate phosphoribosyltransferase; **PDBTitle:** crystal structure of anthranilate phosphoribosyltransferase2 (trpd) from thermus thermophilus hb8
84	d1lcda_	Alignment	not modelled	10.2	21	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
85	d1x92a_	Alignment	not modelled	9.9	11	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
86	d1mkma1	Alignment	not modelled	9.9	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcriptional regulator IclR, N-terminal domain
87	c3hugA_	Alignment	not modelled	9.8	19	**PDB header:**transcription/membrane protein **Chain:** A: **PDB Molecule:**rna polymerase sigma factor; **PDBTitle:** crystal structure of mycobacterium tuberculosis anti-sigma factor rsla2 in complex with -35 promoter binding domain of sigl
88	c2bpqB_	Alignment	not modelled	9.7	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**anthranilate phosphoribosyltransferase; **PDBTitle:** anthranilate phosphoribosyltransferase (trpd) from2 mycobacterium tuberculosis (apo structure)
89	c1u5tA_	Alignment	not modelled	9.5	7	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**appears to be functionally related to snf7; **PDBTitle:** structure of the escrt-ii endosomal trafficking complex
90	c2lcvA_	Alignment	not modelled	9.3	37	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**hth-type transcriptional repressor cytr; **PDBTitle:** structure of the cytidine repressor dna-binding domain; an alternate2 calculation
91	d2i10a1	Alignment	not modelled	9.1	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
92	d1ku7a_	Alignment	not modelled	9.1	3	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
93	c3kfoA_	Alignment	not modelled	9.0	20	**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
94	d2fq4a1	Alignment	not modelled	8.9	31	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
95	c3edpB_	Alignment	not modelled	8.6	25	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**lin2111 protein; **PDBTitle:** the crystal structure of the protein lin2111 (functionally unknown)2 from listeria innocua clip11262
96	c3e21A_	Alignment	not modelled	8.5	13	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**fas-associated factor 1; **PDBTitle:** crystal structure of faf-1 uba domain
97	d1u5ta1	Alignment	not modelled	8.5	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
98	c2yvaB_	Alignment	not modelled	8.5	16	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dnaa initiator-associating protein diaa; **PDBTitle:** crystal structure of escherichia coli diaa
99	d1rp3a2	Alignment	not modelled	8.5	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain