Phyre^2

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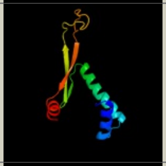
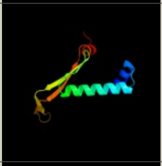
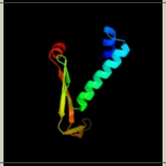
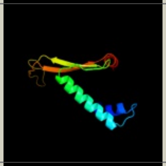
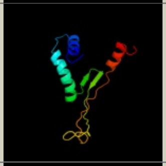
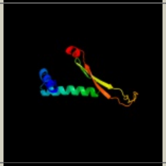
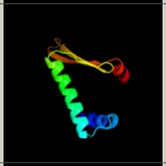
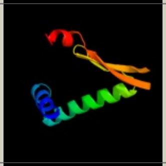
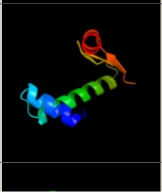
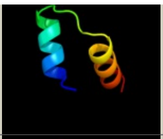
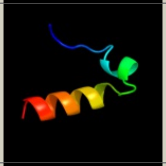
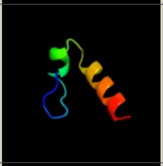
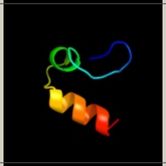
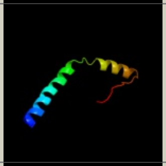
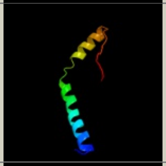
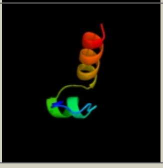
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1owfa_	Alignment		99.9	100	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
2	c2iifA_	Alignment		99.9	98	**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	37	**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	d1p71a_	Alignment		99.9	33	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
5	d1owfb_	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	27	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
8	d1huua_	Alignment		99.8	41	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
9	d1mula_	Alignment		99.8	32	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
10	d2o97b1	Alignment		99.7	28	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
11	d1b8za_	Alignment		99.6	37	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein

12	d1o17a1	Alignment		47.7	23	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
13	d1z67a1	Alignment		47.3	26	**Fold:**YidB-like **Superfamily:**YidB-like **Family:**YidB-like
14	d1dula_	Alignment		46.8	19	**Fold:**Signal peptide-binding domain **Superfamily:**Signal peptide-binding domain **Family:**Signal peptide-binding domain
15	d1brwa1	Alignment		46.2	13	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
16	d1hq1a_	Alignment		45.9	23	**Fold:**Signal peptide-binding domain **Superfamily:**Signal peptide-binding domain **Family:**Signal peptide-binding domain
17	d1qzxa2	Alignment		44.7	24	**Fold:**Signal peptide-binding domain **Superfamily:**Signal peptide-binding domain **Family:**Signal peptide-binding domain
18	d1nria_	Alignment		44.3	18	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
19	c1nriA_	Alignment		44.3	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein hi0754; **PDBTitle:** crystal structure of putative phosphosugar isomerase hi0754 from2 haemophilus influenzae
20	d1qb2a_	Alignment		42.0	23	**Fold:**Signal peptide-binding domain **Superfamily:**Signal peptide-binding domain **Family:**Signal peptide-binding domain
21	d1nh2d1	Alignment	not modelled	36.7	13	**Fold:**Transcription factor IIA (TFIIA), alpha-helical domain **Superfamily:**Transcription factor IIA (TFIIA), alpha-helical domain **Family:**Transcription factor IIA (TFIIA), alpha-helical domain
22	c2yskA_	Alignment	not modelled	34.8	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ttha1432; **PDBTitle:** crystal structure of a hypothetical protein ttha1432 from thermus2 thermophilus
23	c1o17A_	Alignment	not modelled	34.7	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**anthranilate phosphoribosyltransferase; **PDBTitle:** anthranilate phosphoribosyl-transferase (trpd)
24	c2krcA_	Alignment	not modelled	30.6	15	**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
25	d1khda1	Alignment	not modelled	30.5	17	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
26	d2tpta1	Alignment	not modelled	29.8	13	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
27	d2ffha2	Alignment	not modelled	29.2	23	**Fold:**Signal peptide-binding domain **Superfamily:**Signal peptide-binding domain **Family:**Signal peptide-binding domain
28	d1ussa_	Alignment	not modelled	26.7	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Linker histone H1/H5

29	d1vola2	Alignment	not modelled	26.5	15	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Transcription factor IIB (TFIIB), core domain
30	d2cp9a1	Alignment	not modelled	26.4	22	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain
31	c3mzyA_	Alignment	not modelled	25.2	8	**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
32	c1tr8A_	Alignment	not modelled	24.9	18	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**conserved protein (mth177); **PDBTitle:** crystal structure of archaeal nascent polypeptide-associated complex2 (aenac)
33	d1aipc1	Alignment	not modelled	23.2	19	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain
34	d1uoua1	Alignment	not modelled	22.5	22	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
35	d1nvpd1	Alignment	not modelled	22.1	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
36	c1nvpD_	Alignment	not modelled	21.8	20	**PDB header:**transcription/dna **Chain:** D: **PDB Molecule:**transcription initiation factor iia gamma chain; **PDBTitle:** human tfiia/tbp/dna complex
37	c3g2bA_	Alignment	not modelled	20.7	9	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**coenzyme pqq synthesis protein d; **PDBTitle:** crystal structure of pqqd from xanthomonas campestris
38	c3cvjB_	Alignment	not modelled	20.7	12	**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
39	d1z6ra1	Alignment	not modelled	20.5	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ROK associated domain
40	d1xb2b1	Alignment	not modelled	20.4	24	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain
41	c1khdD_	Alignment	not modelled	20.2	17	**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)
42	c3tsuA_	Alignment	not modelled	19.8	30	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcriptional regulatory protein; **PDBTitle:** crystal structure of e. coli hypf with amp-pnp and carbamoyl phosphate
43	c1zvvA_	Alignment	not modelled	19.6	17	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**glucose-resistance amylase regulator; **PDBTitle:** crystal structure of a ccpa-crh-dna complex
44	d2o4ta1	Alignment	not modelled	19.0	18	**Fold:**Left-handed superhelix **Superfamily:**BH3980-like **Family:**BH3980-like
45	c2v79B_	Alignment	not modelled	18.6	13	**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
46	d1i27a_	Alignment	not modelled	17.6	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal domain of the rap74 subunit of TFIIF
47	c2vn2B_	Alignment	not modelled	17.4	17	**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
48	c1otpA_	Alignment	not modelled	17.3	13	**PDB header:**phosphorylase **Chain:** A: **PDB Molecule:**thymidine phosphorylase; **PDBTitle:** structural and theoretical studies suggest domain movement produces an2 active conformation of thymidine phosphorylase
49	c3bwgA_	Alignment	not modelled	16.8	28	**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
50	d1q1va_	Alignment	not modelled	14.9	8	**Fold:**Another 3-helical bundle **Superfamily:**DEK C-terminal domain **Family:**DEK C-terminal domain
51	c2kloA_	Alignment	not modelled	14.3	24	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**dna replication factor cdt1; **PDBTitle:** structure of the cdt1 c-terminal domain
52	d1l0oc_	Alignment	not modelled	14.3	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
53	c1l0oC_	Alignment	not modelled	14.3	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
						PDB header:signaling protein

54	c2jqeA_	Alignment	not modelled	14.2	21	**Chain:** A: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** soution structure of af54 m-domain
55	d1aisb2	Alignment	not modelled	13.9	26	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Transcription factor IIB (TFIIB), core domain
56	c1nh2D_	Alignment	not modelled	13.7	15	**PDB header:**transcription/dna **Chain:** D: **PDB Molecule:**transcription initiation factor iia small chain; **PDBTitle:** crystal structure of a yeast tfiia/tbp/dna complex
57	c1vquB_	Alignment	not modelled	13.7	24	**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
58	c3edpB_	Alignment	not modelled	13.5	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
59	c3a4cA_	Alignment	not modelled	13.3	24	**PDB header:**cell cycle, replication **Chain:** A: **PDB Molecule:**dna replication factor cdt1; **PDBTitle:** crystal structure of cdt1 c terminal domain
60	d1ee8a1	Alignment	not modelled	12.6	25	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
61	c2v3cC_	Alignment	not modelled	12.4	19	**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
62	d1v8ga1	Alignment	not modelled	12.2	12	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
63	d1tdza1	Alignment	not modelled	12.0	18	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
64	d1efub3	Alignment	not modelled	11.9	24	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain
65	d1k82a1	Alignment	not modelled	11.7	21	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
66	d1njra_	Alignment	not modelled	11.3	4	**Fold:**Macro domain-like **Superfamily:**Macro domain-like **Family:**Macro domain
67	d2elca1	Alignment	not modelled	11.3	12	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
68	c1brwB_	Alignment	not modelled	11.0	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein (pyrimidine nucleoside phosphorylase); **PDBTitle:** the crystal structure of pyrimidine nucleoside2 phosphorylase in a closed conformation
69	c2dsjA_	Alignment	not modelled	10.6	3	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyrimidine-nucleoside (thymidine) phosphorylase; **PDBTitle:** crystal structure of project id tt0128 from thermus thermophilus hb8
70	c3dm5A_	Alignment	not modelled	10.6	29	**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.
71	d1dpua_	Alignment	not modelled	10.5	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal domain of RPA32
72	c1dpuA_	Alignment	not modelled	10.5	21	**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)
73	d1g8ia_	Alignment	not modelled	10.2	21	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
74	d1r2za1	Alignment	not modelled	10.0	25	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
75	d1z05a1	Alignment	not modelled	9.6	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ROK associated domain
76	c2vfyA_	Alignment	not modelled	9.4	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**akap18 delta; **PDBTitle:** akap18 delta central domain
77	d1x92a_	Alignment	not modelled	9.3	13	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
78	d1k3xa1	Alignment	not modelled	8.8	15	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
						PDB header:isomerase

79	c3jx9B_	Alignment	not modelled	8.4	19	**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
80	c1aipG_	Alignment	not modelled	8.2	19	**PDB header:**complex of two elongation factors **Chain:** G: **PDB Molecule:**elongation factor ts; **PDBTitle:** ef-tu ef-ts complex from thermus thermophilus
81	d1uxda_	Alignment	not modelled	8.2	15	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
82	d1v92a_	Alignment	not modelled	8.2	17	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TAP-C domain-like
83	d1uxca_	Alignment	not modelled	8.2	15	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
84	d1un2a_	Alignment	not modelled	7.9	11	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbA-like
85	c3kfoA_	Alignment	not modelled	7.7	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
86	d1pvga1	Alignment	not modelled	7.6	7	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**DNA gyrase/MutL, second domain
87	c2j37W_	Alignment	not modelled	7.6	29	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**signal recognition particle 54 kda protein **PDBTitle:** model of mammalian srp bound to 80s rncs
88	c2yvaB_	Alignment	not modelled	7.6	11	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dnaa initiator-associating protein diaa; **PDBTitle:** crystal structure of escherichia coli diaa
89	c2bpqB_	Alignment	not modelled	7.6	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**anthranilate phosphoribosyltransferase; **PDBTitle:** anthranilate phosphoribosyltransferase (trpd) from2 mycobacterium tuberculosis (apo structure)
90	c3thgA_	Alignment	not modelled	7.6	19	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ribulose bisphosphate carboxylase/oxygenase activase 1, **PDBTitle:** crystal structure of the creosote rubisco activase c-domain
91	d2bjca1	Alignment	not modelled	7.5	15	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
92	d1mkma1	Alignment	not modelled	7.5	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcriptional regulator IclR, N-terminal domain
93	d1ay7b_	Alignment	not modelled	7.4	13	**Fold:**Barstar-like **Superfamily:**Barstar-related **Family:**Barstar-related
94	c2l8nA_	Alignment	not modelled	7.4	10	**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
95	c1rp3G_	Alignment	not modelled	7.3	21	**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
96	c1v8gB_	Alignment	not modelled	7.2	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**anthranilate phosphoribosyltransferase; **PDBTitle:** crystal structure of anthranilate phosphoribosyltransferase2 (trpd) from thermus thermophilus hb8
97	d1lcda_	Alignment	not modelled	7.1	15	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
98	d1qpza1	Alignment	not modelled	6.8	5	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
99	c2lcvA_	Alignment	not modelled	6.8	10	**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