
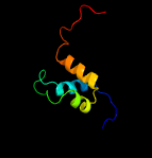
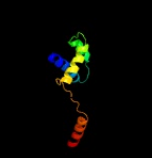





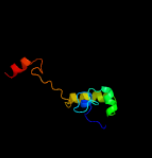


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1763_(-)_1996159_1996485
Date	Fri Aug 2 13:30:37 BST 2019
Unique Job ID	641d24d459f43358

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2rn7A_	Alignment		99.9	43	PDB header: unknown function Chain: A; PDB Molecule: is629 orfa; PDBTitle: nmr solution structure of tnpε protein from shigella2 flexneri. northeast structural genomics target sfr125
2	d2jn6a1	Alignment		99.7	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Cgl2762-like
3	c1hlvA_	Alignment		97.8	19	PDB header: dna binding protein/dna Chain: A; PDB Molecule: major centromere autoantigen b; PDBTitle: crystal structure of cenp-b(1-129) complexed with the cenp-2 b box dna
4	c2elhA_	Alignment		97.5	18	PDB header: dna binding protein Chain: A; PDB Molecule: cg11849-pa; PDBTitle: solution structure of the cenp-b n-terminal dna-binding2 domain of fruit fly distal antenna cg11849-pa
5	d1hlva1	Alignment		97.2	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
6	d1bw6a_	Alignment		97.1	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
7	c1u78A_	Alignment		97.0	10	PDB header: dna binding protein/dna Chain: A; PDB Molecule: transposable element tc3 transposase; PDBTitle: structure of the bipartite dna-binding domain of tc32 transposase bound to transposon dna
8	c6paxA_	Alignment		97.0	19	PDB header: gene regulation/dna Chain: A; PDB Molecule: homeobox protein pax-6; PDBTitle: crystal structure of the human pax-6 paired domain-dna2 complex reveals a general model for pax protein-dna3 interactions
9	d6paxa1	Alignment		96.9	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
10	d1pdnc_	Alignment		96.8	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
11	d1k78a1	Alignment		96.7	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain

12	c2gloA	Alignment		96.3	14	PDB header: transcription/dna Chain: A: PDB Molecule: brinker cg9653-pa; PDBTitle: solution structure of the brinker dna binding domain in2 complex with the omb enhancer
13	d2coba1	Alignment		95.7	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Psq domain
14	c2w48D	Alignment		94.7	14	PDB header: transcription Chain: D: PDB Molecule: sorbitol operon regulator; PDBTitle: crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
15	c3hefB	Alignment		94.5	18	PDB header: viral protein Chain: B: PDB Molecule: gene 1 protein; PDBTitle: crystal structure of the bacteriophage sf6 terminase small subunit
16	c2pbxB	Alignment		94.2	16	PDB header: transcription Chain: B: PDB Molecule: hemagglutinin/protease regulatory protein; PDBTitle: vibrio cholerae hapr
17	c1iufA	Alignment		93.5	6	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
18	c2k27A	Alignment		93.1	19	PDB header: transcription regulator Chain: A: PDB Molecule: paired box protein pax-8; PDBTitle: solution structure of human pax8 paired box domain
19	c2mqkA	Alignment		92.8	13	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent target dna activator b; PDBTitle: solution structure of n terminal domain of the mub aaa+ atpase
20	c4go1A	Alignment		92.6	15	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lsrr; PDBTitle: crystal structure of full length transcription repressor lsrr from e.2 coli.
21	c2m8eA	Alignment	not modelled	91.6	13	PDB header: dna binding protein Chain: A: PDB Molecule: sleeping beauty transposase; PDBTitle: nmr structure of the pai subdomain of sleeping beauty transposase
22	c4lfuA	Alignment	not modelled	90.3	14	PDB header: dna binding protein Chain: A: PDB Molecule: regulatory protein sdia; PDBTitle: crystal structure of escherichia coli sdia in the space group c2
23	c3sztB	Alignment	not modelled	90.2	10	PDB header: transcription Chain: B: PDB Molecule: quorum-sensing control repressor; PDBTitle: quorum sensing control repressor, qscr, bound to n-3-oxo-dodecanoyl-l-2 homoserine lactone
24	d1or7a1	Alignment	not modelled	89.9	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
25	c2lvsA	Alignment	not modelled	89.4	20	PDB header: dna binding protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: nmr solution structure of a crispr repeat binding protein
26	c3e7qB	Alignment	not modelled	89.4	16	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: the crystal structure of the putative transcriptional regulator from2 pseudomonas aeruginosa pao1
27	c1zljE	Alignment	not modelled	88.6	12	PDB header: transcription Chain: E: PDB Molecule: dormancy survival regulator; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
28	d1a04a1	Alignment	not modelled	88.5	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)

29	d2ezla_	Alignment	not modelled	88.3	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
30	c2q0aA_	Alignment	not modelled	88.3	12	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional activator protein trar; PDBTitle: crystal structure of an anti-activation complex in bacterial quorum2 sensing
31	c6jqsA_	Alignment	not modelled	88.2	5	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding response regulator; PDBTitle: structure of transcription factor, gere
32	c4cxfA_	Alignment	not modelled	87.9	21	PDB header: transcription Chain: A: PDB Molecule: rna polymerase sigma factor cnrh; PDBTitle: structure of cnrh in complex with the cytosolic domain of cnry
33	c3mzyA_	Alignment	not modelled	87.9	12	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
34	d1rp3a2	Alignment	not modelled	87.5	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
35	c1h0mD_	Alignment	not modelled	87.3	17	PDB header: transcription/dna Chain: D: PDB Molecule: transcriptional activator protein trar; PDBTitle: three-dimensional structure of the quorum sensing protein trar bound2 to its autoinducer and to its target dna
36	c2krfB_	Alignment	not modelled	87.0	12	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulatory protein coma; PDBTitle: nmr solution structure of the dna binding domain of competence protein2 a
37	c4j2nB_	Alignment	not modelled	86.9	20	PDB header: viral protein Chain: B: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
38	d1ijwc_	Alignment	not modelled	86.8	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
39	c1dipA_	Alignment	not modelled	86.5	32	PDB header: acetylation Chain: A: PDB Molecule: delta-sleep-inducing peptide immunoreactive PDBTitle: the solution structure of porcine delta-sleep-inducing2 peptide immunoreactive peptide, nmr, 10 structures
40	c2jpcA_	Alignment	not modelled	86.3	7	PDB header: dna binding protein Chain: A: PDB Molecule: ssrb; PDBTitle: ssrb dna binding protein
41	c3vdoA_	Alignment	not modelled	85.9	12	PDB header: dna binding protein/protein binding Chain: A: PDB Molecule: rna polymerase sigma factor sigk; PDBTitle: structure of extra-cytoplasmic function(ecf) sigma factor sigk in2 complex with its negative regulator rskA from mycobacterium3 tuberculosis
42	c3qp5C_	Alignment	not modelled	85.8	10	PDB header: transcription Chain: C: PDB Molecule: cvir transcriptional regulator; PDBTitle: crystal structure of cvir bound to antagonist chlorolactone (cl)
43	c3frwF_	Alignment	not modelled	85.7	10	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: putative trp repressor protein; PDBTitle: crystal structure of putative trpr protein from ruminococcus obeum
44	c1or7A_	Alignment	not modelled	85.6	14	PDB header: transcription Chain: A: PDB Molecule: rna polymerase sigma-e factor; PDBTitle: crystal structure of escherichia coli sigmae with the cytoplasmic2 domain of its anti-sigma rsea
45	d1l3la1	Alignment	not modelled	85.5	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
46	c3hugA_	Alignment	not modelled	85.5	7	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 sigI
47	d1hcra_	Alignment	not modelled	85.2	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
48	c3vepA_	Alignment	not modelled	85.1	21	PDB header: membrane protein/transcription Chain: A: PDB Molecule: probable rna polymerase sigma-d factor; PDBTitle: crystal structure of sigd4 in complex with its negative regulator rsda
49	c3t0yA_	Alignment	not modelled	85.0	21	PDB header: transcription regulator/protein binding Chain: A: PDB Molecule: response regulator; PDBTitle: structure of the phyr anti-anti-sigma domain bound to the anti-sigma2 factor, nepr
50	c4j2nA_	Alignment	not modelled	85.0	20	PDB header: viral protein Chain: A: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
51	d1p4wa_	Alignment	not modelled	84.8	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
52	c2o8xA_	Alignment	not modelled	84.8	10	PDB header: transcription Chain: A: PDB Molecule: probable rna polymerase sigma-c factor; PDBTitle: crystal structure of the "-35 element" promoter recognition domain of2 mycobacterium tuberculosis sigc
53	c5uxxC_	Alignment	not modelled	84.8	14	PDB header: dna binding protein/unknown function Chain: C: PDB Molecule: rna polymerase sigma factor; PDBTitle: co-crystal structure of the sigma factor rpoe in complex with the2 anti-sigma factor nepr from bartonella quintana
						Fold: DNA/RNA-binding 3-helical bundle

54	d1fsea_	Alignment	not modelled	84.3	10	Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
55	d2fq4a1	Alignment	not modelled	84.2	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
56	c2r0qF_	Alignment	not modelled	84.0	29	PDB header: recombination/dna Chain: F: PDB Molecule: putative transposon tn552 dna-invertase bin3; PDBTitle: crystal structure of a serine recombinase- dna regulatory2 complex
57	c6amaO_	Alignment	not modelled	83.9	20	PDB header: dna binding protein/dna Chain: O: PDB Molecule: putative dna-binding protein; PDBTitle: structure of s. coelicolor/s. venezuelae bldc-smea-ssfa complex to2 3.09 angstrom
58	d1yioa1	Alignment	not modelled	83.9	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
59	c1x3uA_	Alignment	not modelled	83.9	7	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein fixj; PDBTitle: solution structure of the c-terminal transcriptional2 activator domain of fixj from sinorhizobium melilot
60	c3korD_	Alignment	not modelled	83.8	13	PDB header: transcription Chain: D: PDB Molecule: possible trp repressor; PDBTitle: crystal structure of a putative trp repressor from staphylococcus2 aureus
61	c5fgmA_	Alignment	not modelled	83.8	24	PDB header: hydrolase Chain: A: PDB Molecule: ecf rna polymerase sigma factor sigr; PDBTitle: streptomyces coelicolor sigr region 4
62	c5c8eC_	Alignment	not modelled	83.6	18	PDB header: transcription regulator/dna Chain: C: PDB Molecule: light-dependent transcriptional regulator carh; PDBTitle: crystal structure of thermus thermophilus carh bound to2 adenosylcobalamin and a 26-bp dna segment
63	c2rnjA_	Alignment	not modelled	83.4	7	PDB header: transcription Chain: A: PDB Molecule: response regulator protein vvar; PDBTitle: nmr structure of the s. aureus vvar dna binding domain
64	d1fup_	Alignment	not modelled	83.3	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
65	c5scr1A_	Alignment	not modelled	82.8	24	PDB header: metal binding protein Chain: A: PDB Molecule: mercuric resistance operon regulatory protein; PDBTitle: crystal structure of the transcription activator tn501 merr in complex2 with mercury (ii)
66	d1trra_	Alignment	not modelled	82.2	32	Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: Trp repressor, TrpR
67	d2ao9a1	Alignment	not modelled	82.1	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Nanomeric phage protein-like
68	c5zx3F_	Alignment	not modelled	82.0	17	PDB header: transcription Chain: F: PDB Molecule: ecf rna polymerase sigma factor sigh; PDBTitle: mycobacterium tuberculosis rna polymerase holoenzyme with ecf sigma2 factor sigma h
69	c6j05B_	Alignment	not modelled	81.6	14	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator arsr; PDBTitle: structures of two arsr as(iii)-responsive repressors: implications for2 the mechanism of derepression
70	c3c3wB_	Alignment	not modelled	81.3	16	PDB header: transcription Chain: B: PDB Molecule: two component transcriptional regulatory protein devr; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
71	d1jhga_	Alignment	not modelled	81.3	29	Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: Trp repressor, TrpR
72	c2dg7A_	Alignment	not modelled	80.8	20	PDB header: gene regulation Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of the putative transcriptional regulator sco03372 from streptomyces coelicolor a3(2)
73	c6in7B_	Alignment	not modelled	80.6	14	PDB header: transcription Chain: B: PDB Molecule: rna polymerase sigma-h factor; PDBTitle: crystal structure of algu in complex with muca(cyto)
74	c6dvdF_	Alignment	not modelled	80.6	14	PDB header: transferase/dna Chain: F: PDB Molecule: ecf rna polymerase sigma factor sigl; PDBTitle: crystal structure of mycobacterium tuberculosis transcription2 initiation complex(ecf sigma factor I) with 6 nt spacer and bromine3 labelled in position "-11
75	c3gpvA_	Alignment	not modelled	80.4	7	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal structure of a transcriptional regulator, merr2 family from bacillus thuringiensis
76	c5dukA_	Alignment	not modelled	80.4	14	PDB header: transcription Chain: A: PDB Molecule: putative dna binding protein; PDBTitle: n-terminal structure of putative dna binding transcription factor from2 thermoplasmatales archaeon scgc ab-539-n05
77	d2oi8a1	Alignment	not modelled	80.3	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
78	c5wurB_	Alignment	not modelled	80.1	17	PDB header: metal binding protein Chain: B: PDB Molecule: ecf rna polymerase sigma factor sigw; PDBTitle: crystal structure of sigw in complex with its anti-sigma rsiw, an2 oxidized form
						PDB header: dna binding protein

79	c2l4aA	Alignment	not modelled	79.9	12	Chain: A: PDB Molecule: leucine responsive regulatory protein; PDBTitle: nmr structure of the dna-binding domain of e.coli lrp
80	c2kpiA	Alignment	not modelled	79.0	18	PDB header: transcription regulator Chain: A: PDB Molecule: sos-response transcriptional repressor, lexa; PDBTitle: solution structure of protein sos-response transcriptional2 repressor, lexa from eubacterium rectale. northeast3 structural genomics consortium target err9a
81	c6c03A	Alignment	not modelled	78.5	17	PDB header: transcription Chain: A: PDB Molecule: putative rna polymerase ecf-subfamily sigma factor; PDBTitle: the crystal structure streptomyces venezuelae rsbn-bldn complex
82	c2lfwA	Alignment	not modelled	78.3	17	PDB header: signaling protein Chain: A: PDB Molecule: phyr sigma-like domain; PDBTitle: nmr structure of the phyrsl-nepr complex from sphingomonas sp. fr1
83	c2f07A	Alignment	not modelled	78.3	17	PDB header: transcription Chain: A: PDB Molecule: yvdt; PDBTitle: crystal structure of yvdt from bacillus subtilis
84	c2ao9H	Alignment	not modelled	78.2	17	PDB header: structural genomics, unknown function Chain: H: PDB Molecule: phage protein; PDBTitle: structural genomics, the crystal structure of a phage protein2 (phbc6a51) from bacillus cereus atcc 14579
85	c4r4eA	Alignment	not modelled	77.9	10	PDB header: transcription regulator/dna Chain: A: PDB Molecule: hth-type transcriptional regulator glnr; PDBTitle: structure of glnr-dna complex
86	d1xsva	Alignment	not modelled	77.4	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
87	c3ivpD	Alignment	not modelled	77.3	7	PDB header: dna binding protein Chain: D: PDB Molecule: putative transposon-related dna-binding protein; PDBTitle: the structure of a possible transposon-related dna-binding protein2 from clostridium difficile 630.
88	c2gd7B	Alignment	not modelled	77.1	26	PDB header: transcription Chain: B: PDB Molecule: hexim1 protein; PDBTitle: the structure of the cyclin t-binding domain of hexim12 reveals the molecular basis for regulation of3 transcription elongation
89	c2gm4B	Alignment	not modelled	76.8	9	PDB header: recombination, dna Chain: B: PDB Molecule: transposon gamma-delta resolvase; PDBTitle: an activated, tetrameric gamma-delta resolvase: hin chimaera bound to2 cleaved dna
90	c2l0kA	Alignment	not modelled	76.6	15	PDB header: transcription Chain: A: PDB Molecule: stage iii sporulation protein d; PDBTitle: nmr solution structure of a transcription factor spoiii in complex2 with dna
91	c5m9eA	Alignment	not modelled	76.4	17	PDB header: cell cycle Chain: A: PDB Molecule: microtubule integrity protein mal3; PDBTitle: interactions between the mal3 eb1-like domain and dis1
92	c5i44E	Alignment	not modelled	76.4	16	PDB header: dna binding protein/dna Chain: E: PDB Molecule: chromosome-anchoring protein raca; PDBTitle: structure of raca-dna complex; p21 form
93	d1ntca	Alignment	not modelled	76.0	33	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
94	c5jvmA	Alignment	not modelled	75.9	16	PDB header: motor protein Chain: A: PDB Molecule: chimera protein of kinesin-like protein kif3c and PDBTitle: the neck-linker and alpha 7 helix of mus musculus kif3c
95	d1t33a1	Alignment	not modelled	75.8	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
96	c2d6yA	Alignment	not modelled	75.4	20	PDB header: gene regulation Chain: A: PDB Molecule: putative tetr family regulatory protein; PDBTitle: crystal structure of transcriptional factor sco4008 from streptomyces2 coelicolor a3(2)
97	c3gziA	Alignment	not modelled	75.1	14	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: crystal structure of a transcriptional regulator of the tetr family2 (shew_3567) from shewanella loihica pv-4 at 2.05 a resolution
98	d1rioA	Alignment	not modelled	75.1	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
99	c2guhA	Alignment	not modelled	74.8	17	PDB header: transcription Chain: A: PDB Molecule: putative tetr-family transcriptional regulator; PDBTitle: crystal structure of the putative tetr-family transcriptional2 regulator from rhodococcus sp. rha1
100	d2g7sa1	Alignment	not modelled	74.6	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
101	c3gp4B	Alignment	not modelled	74.3	16	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal structure of putative merr family transcriptional regulator2 from listeria monocytogenes
102	d1lui5a1	Alignment	not modelled	74.2	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
103	d1pb6a1	Alignment	not modelled	74.1	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain

104	c4fcyA_	Alignment	not modelled	73.1	24	PDB header: dna binding protein/dna Chain: A: PDB Molecule: transposase; PDBTitle: crystal structure of the bacteriophage mu transpososome
105	d1jt6a1	Alignment	not modelled	73.1	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
106	d1r1ua_	Alignment	not modelled	72.6	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ArsR-like transcriptional regulators
107	d1llib_	Alignment	not modelled	72.5	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
108	d2cg4a1	Alignment	not modelled	72.4	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
109	c4r24B_	Alignment	not modelled	72.3	16	PDB header: transcription/dna Chain: B: PDB Molecule: hth-type transcriptional regulator tnra; PDBTitle: complete dissection of b. subtilis nitrogen homeostatic circuitry
110	c2k9qB_	Alignment	not modelled	71.8	19	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of hth_xre family transcriptional2 regulator bt_p548217 from bacteroides thetaiotaomicron.3 northeast structural genomics consortium target btr244.
111	d2vkv1	Alignment	not modelled	71.8	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
112	c4dzmB_	Alignment	not modelled	71.5	36	PDB header: de novo protein Chain: B: PDB Molecule: coiled-coil peptide cc-di; PDBTitle: a de novo designed coiled coil cc-di
113	c4dzmA_	Alignment	not modelled	71.5	36	PDB header: de novo protein Chain: A: PDB Molecule: coiled-coil peptide cc-di; PDBTitle: a de novo designed coiled coil cc-di
114	c2m8gX_	Alignment	not modelled	71.4	18	PDB header: transcription Chain: X: PDB Molecule: transcriptional regulator; PDBTitle: structure, function, and tethering of dna-binding domains in 542 transcriptional activators
115	c1rp3G_	Alignment	not modelled	71.4	13	PDB header: transcription Chain: G: PDB Molecule: rna polymerase sigma factor sigma-28 (flia); PDBTitle: cocrystal structure of the flagellar sigma/anti-sigma complex, sigma-2 28/flgm
116	c1ui6B_	Alignment	not modelled	71.1	17	PDB header: antibiotic Chain: B: PDB Molecule: a-factor receptor homolog; PDBTitle: crystal structure of gamma-butyrolactone receptor (arpa-like protein)
117	c1umqA_	Alignment	not modelled	71.1	21	PDB header: dna-binding protein Chain: A: PDB Molecule: photosynthetic apparatus regulatory protein; PDBTitle: solution structure and dna binding of the effector domain2 from the global regulator prra(rega) from r. sphaeroides:3 insights into dna binding specificity
118	d1umqa_	Alignment	not modelled	71.1	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
119	c2ia0A_	Alignment	not modelled	70.8	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative hth-type transcriptional regulator pf0864; PDBTitle: transcriptional regulatory protein pf0864 from pyrococcus furiosus a2 member of the asnc family (pf0864)
120	d1v7ba1	Alignment	not modelled	70.5	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain