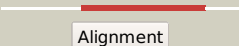

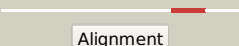

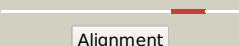

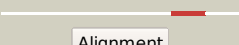

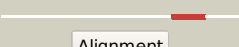

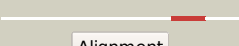











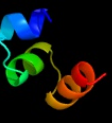
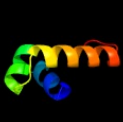


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1453_(-)_1638387_1639652
Date	Fri Aug 2 13:30:03 BST 2019
Unique Job ID	ebe3dd3cd471695a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3onqB_	 Alignment		100.0	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: regulator of polyketide synthase expression; PDBTitle: crystal structure of regulator of polyketide synthase expression2 bad_0249 from bifidobacterium adolescentis
2	d1ntca_	 Alignment		97.1	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
3	c3m1eA_	 Alignment		97.0	14	PDB header: transcription regulator Chain: A: PDB Molecule: hth-type transcriptional regulator benm; PDBTitle: crystal structure of benm_dbd
4	d1fipa_	 Alignment		97.0	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
5	c5fo5A_	 Alignment		96.9	20	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional regulator metr; PDBTitle: structure of the dna-binding domain of escherichia coli methionine2 biosynthesis regulator metr
6	d1umqa_	 Alignment		96.9	31	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
7	c1umqA_	 Alignment		96.9	31	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
8	c5z4yB_	 Alignment		96.8	13	PDB header: dna binding protein Chain: B: PDB Molecule: cys regulon transcriptional activator; PDBTitle: crystal structure of pacysb ntd domain with space group p4
9	c2esnC_	 Alignment		96.7	18	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: probable transcriptional regulator; PDBTitle: the crystal structure of probable transcriptional regulator pa04772 from pseudomonas aeruginosa
10	c1iz1B_	 Alignment		96.7	14	PDB header: dna binding protein Chain: B: PDB Molecule: lysr-type regulatory protein; PDBTitle: crystal structure of cbnr, a lysr family transcriptional2 regulator
11	c3t1bB_	 Alignment		96.6	9	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator, lysr family; PDBTitle: crystal structure of the full-length aphb n100e variant

12	d2esna1	Alignment		96.6	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: LysR-like transcriptional regulators
13	d1b9ma1	Alignment		96.6	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: N-terminal domain of molybdate-dependent transcriptional regulator ModE
14	c3ispA_	Alignment		96.6	13	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional regulator PDBTitle: crystal structure of argp from mycobacterium tuberculosis
15	c5y9sD_	Alignment		96.6	20	PDB header: transcription Chain: D: PDB Molecule: vv2_1132; PDBTitle: crystal structure of vv2_1132, a lysr family transcriptional regulator
16	c1b9nA_	Alignment		96.5	13	PDB header: transcription Chain: A: PDB Molecule: protein (mode); PDBTitle: regulator from escherichia coli
17	c2m8gX_	Alignment		96.5	26	PDB header: transcription Chain: X: PDB Molecule: transcriptional regulator; PDBTitle: structure, function, and tethering of dna-binding domains in 542 transcriptional activators
18	d1etxa_	Alignment		96.5	30	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
19	d1etob_	Alignment		96.4	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
20	c3fzjC_	Alignment		96.4	20	PDB header: transcription regulator Chain: C: PDB Molecule: lysR type regulator of tsambcd; PDBTitle: tsar low resolution crystal structure, tetragonal form
21	c3k1nB_	Alignment	not modelled	96.3	14	PDB header: transcription Chain: B: PDB Molecule: hth-type transcriptional regulator benm; PDBTitle: crystal structure of full-length benm
22	c5y2vA_	Alignment	not modelled	96.2	16	PDB header: transcription Chain: A: PDB Molecule: rubisco operon transcriptional regulator; PDBTitle: strcuture of the full-length ccmr complexed with 2-og from2 synechocystis pcc6803
23	d1ixca1	Alignment	not modelled	96.2	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: LysR-like transcriptional regulators
24	c1zljE_	Alignment	not modelled	96.1	18	PDB header: transcription Chain: E: PDB Molecule: dormancy survival regulator; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
25	c4pzjA_	Alignment	not modelled	96.1	25	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, lysr family; PDBTitle: 1.60 angstrom resolution crystal structure of a transcriptional2 regulator of the lysr family from eggerthella lenta dsm 2243
26	c1g2hA_	Alignment	not modelled	96.1	18	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein tyrr homolog; PDBTitle: solution structure of the dna-binding domain of the tyrr2 protein of haemophilus influenzae
27	d1g2ha_	Alignment	not modelled	96.1	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
28	c3fzvC_	Alignment	not modelled	96.0	11	PDB header: transcription regulator Chain: C: PDB Molecule: probable transcriptional regulator; PDBTitle: crystal structure of pa01 protein, putative lysr family2

						transcriptional regulator from pseudomonas aeruginosa PDB header: dna binding protein Chain: B: PDB Molecule: cell density-dependent motility repressor; PDBTitle: full-length structure of hypt from salmonella typhimuriuma2 (hypochlorite-specific lysr-type transcriptional regulator)
29	c5ydwB_	Alignment	not modelled	96.0	18	
30	c3hhgF_	Alignment	not modelled	95.9	18	PDB header: transcription regulator Chain: F: PDB Molecule: transcriptional regulator, lysr family; PDBTitle: structure of crga, a lysr-type transcriptional regulator from2 neisseria meningitidis.
31	c3hugA_	Alignment	not modelled	95.9	18	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
32	c4I5eA_	Alignment	not modelled	95.9	22	PDB header: protein binding Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of a. aeolicus ntrc1 dna binding domain
33	c5m7nA_	Alignment	not modelled	95.8	22	PDB header: signaling protein Chain: A: PDB Molecule: nitrogen assimilation regulatory protein; PDBTitle: crystal structure of ntrx from brucella abortus in complex with atp2 processed with the crystalDirect automated mounting and cryo-cooling3 technology
34	c6g4rE_	Alignment	not modelled	95.7	23	PDB header: transcription Chain: E: PDB Molecule: hydrogen peroxide-inducible genes activator; PDBTitle: corynebacterium glutamicum oxyr c206s mutant, h2o2-bound
35	c3e7ID_	Alignment	not modelled	95.7	10	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain
36	d1or7a1	Alignment	not modelled	95.6	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
37	d1rp3a2	Alignment	not modelled	95.5	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
38	c2ijlB_	Alignment	not modelled	95.2	9	PDB header: transcription Chain: B: PDB Molecule: molybdenum-binding transcriptional repressor; PDBTitle: the structure of a putative mode from agrobacterium tumefaciens.
39	c6c03A_	Alignment	not modelled	95.1	15	PDB header: transcription Chain: A: PDB Molecule: putative rna polymerase ecf-subfamily sigma factor; PDBTitle: the crystal structure streptomyces venezuelae rsbn-bldn complex
40	c4lfuA_	Alignment	not modelled	95.0	18	PDB header: dna binding protein Chain: A: PDB Molecule: regulatory protein sdia; PDBTitle: crystal structure of escherichia coli sdia in the space group c2
41	c3vepA_	Alignment	not modelled	94.9	15	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
42	d1a04a1	Alignment	not modelled	94.9	16	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)
43	d1p4wa_	Alignment	not modelled	94.8	15	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)
44	c1ojlD_	Alignment	not modelled	94.7	30	PDB header: response regulator Chain: D: PDB Molecule: transcriptional regulatory protein zrar; PDBTitle: crystal structure of a sigma54-activator suggests the mechanism for2 the conformational switch necessary for sigma54 binding
45	c5fgmA_	Alignment	not modelled	94.7	16	PDB header: hydrolase Chain: A: PDB Molecule: ecf rna polymerase sigma factor sigr; PDBTitle: streptomyces coelicolor sigr region 4
46	c3sztB_	Alignment	not modelled	94.6	15	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
47	c2o8xA_	Alignment	not modelled	94.4	14	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
48	c3qp5C_	Alignment	not modelled	94.3	13	PDB header: transcription Chain: C: PDB Molecule: cvir transcriptional regulator; PDBTitle: crystal structure of cvir bound to antagonist chlorolactone (cl)
49	c2rnjA_	Alignment	not modelled	94.3	13	PDB header: transcription Chain: A: PDB Molecule: response regulator protein vrar; PDBTitle: nmr structure of the s. aureus vrar dna binding domain
50	c2e1cA_	Alignment	not modelled	94.2	9	PDB header: transcription/dna Chain: A: PDB Molecule: putative hth-type transcriptional regulator ph1519; PDBTitle: structure of putative hth-type transcriptional regulator ph1519/dna2 complex
51	c2cfxD_	Alignment	not modelled	94.1	9	PDB header: transcription Chain: D: PDB Molecule: hth-type transcriptional regulator lrpc; PDBTitle: structure of b.subtilis lrpc
52	c6dvdF_	Alignment	not modelled	94.1	17	PDB header: transferase/dna Chain: F: PDB Molecule: ecf rna polymerase sigma factor sigI; PDBTitle: crystal structure of mycobacterium tuberculosis

						transcription2 initiation complex(ecf sigma factor I) with 6 nt spacer and bromine3 labelled in position "-11
53	d1l3la1	Alignment	not modelled	94.1	15	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)
54	c6jqsa	Alignment	not modelled	93.9	10	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding response regulator; PDBTitle: structure of transcription factor, gere
55	d1fsea	Alignment	not modelled	93.9	21	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)
56	c2krfB	Alignment	not modelled	93.8	13	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulatory protein coma; PDBTitle: nmr solution structure of the dna binding domain of competence protein2 a
57	d1yioa1	Alignment	not modelled	93.5	13	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)
58	c2q0oA	Alignment	not modelled	93.5	23	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional activator protein trar; PDBTitle: crystal structure of an anti-activation complex in bacterial quorum2 sensing
59	d2cg4a1	Alignment	not modelled	93.4	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
60	c1h0mD	Alignment	not modelled	93.3	15	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
61	d1i1ga1	Alignment	not modelled	93.3	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
62	c2vzbA	Alignment	not modelled	93.1	14	PDB header: dna-binding protein Chain: A: PDB Molecule: transcriptional regulatory protein; PDBTitle: feast or famine regulatory protein (rv3291c)from m.2 tuberculosis complexed with l-tryptophan
63	c3t0ya	Alignment	not modelled	93.1	18	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
64	d1s7oa	Alignment	not modelled	93.1	6	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
65	c2l4aA	Alignment	not modelled	93.0	9	PDB header: dna binding protein Chain: A: PDB Molecule: leucine responsive regulatory protein; PDBTitle: nmr structure of the dna-binding domain of e.coli lrp
66	d1xsva	Alignment	not modelled	92.9	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
67	c5zx3F	Alignment	not modelled	92.8	18	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
68	c2cg4B	Alignment	not modelled	92.7	14	PDB header: transcription Chain: B: PDB Molecule: regulatory protein asnc; PDBTitle: structure of e.coli asnc
69	c2dbbA	Alignment	not modelled	92.6	21	PDB header: transcriptional regulator Chain: A: PDB Molecule: putative hth-type transcriptional regulator ph0061; PDBTitle: crystal structure of ph0061
70	c3vdoA	Alignment	not modelled	92.5	17	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
71	d2cfxa1	Alignment	not modelled	92.5	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
72	c1x3uA	Alignment	not modelled	92.5	11	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
73	c6ideA	Alignment	not modelled	92.5	10	PDB header: transcription/dna Chain: A: PDB Molecule: transcriptional regulator luxr family; PDBTitle: crystal structure of the vibrio cholera vqma-ligand-dna complex2 provides molecular mechanisms for drug design
74	c1or7A	Alignment	not modelled	92.4	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
75	c6in7B	Alignment	not modelled	92.4	14	PDB header: transcription Chain: B: PDB Molecule: rna polymerase sigma-h factor; PDBTitle: crystal structure of algu in complex with muca(cyto)
76	c2p6tH	Alignment	not modelled	92.4	12	PDB header: transcription Chain: H: PDB Molecule: transcriptional regulator, lrp/asnc family; PDBTitle: crystal structure of transcriptional regulator nmb0573 and l-leucine2 complex from neisseria meningitidis
77	c1i1gA	Alignment	not modelled	91.9	9	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lrpa; PDBTitle: crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
						PDB header: transcription

78	c4cxfA_	Alignment	not modelled	91.6	14	Chain: A: PDB Molecule: rna polymerase sigma factor cnrh; PDBTitle: structure of cnrh in complex with the cytosolic domain of cnry
79	c2lfwA_	Alignment	not modelled	91.5	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
80	d2cyya1	Alignment	not modelled	91.5	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
81	c5o8yG_	Alignment	not modelled	91.4	15	PDB header: transcription Chain: G: PDB Molecule: transcriptional regulatory protein rcsb; PDBTitle: conformational dynamism for dna interaction in salmonella typhimurium2 rcsb response regulator.
82	c4x6gG_	Alignment	not modelled	91.0	20	PDB header: dna binding protein Chain: G: PDB Molecule: oxyr; PDBTitle: full-length oxyr c199d from pseudomonas aeruginosa
83	c2jpcA_	Alignment	not modelled	91.0	15	PDB header: dna binding protein Chain: A: PDB Molecule: ssrb; PDBTitle: ssrb dna binding protein
84	c3cloC_	Alignment	not modelled	90.7	18	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of putative transcriptional regulator containing a2 luxr dna binding domain (np_811094.1) from bacteroides3 thetaiotaomicron vpi-5482 at 2.04 a resolution
85	c4czdA_	Alignment	not modelled	90.4	15	PDB header: lyase Chain: A: PDB Molecule: putative transcriptional regulator, asnc family; PDBTitle: sirohaem decarboxylase ahba/b - an enzyme with structural homology2 to the lrp/asnc transcription factor family that is part of the3 alternative haem biosynthesis pathway.
86	c4pcqC_	Alignment	not modelled	90.1	12	PDB header: transcription Chain: C: PDB Molecule: possible transcriptional regulatory protein (probably PDBTitle: crystal structure of mtbaldr (rv2779c)
87	c2e7xA_	Alignment	not modelled	90.1	16	PDB header: transcription regulator Chain: A: PDB Molecule: 150aa long hypothetical transcriptional regulator; PDBTitle: structure of the lrp/asnc like transcriptional regulator from2 sulfolobus tokodaii 7 complexed with its cognate ligand
88	c3i4pA_	Alignment	not modelled	89.9	7	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, asnc family; PDBTitle: crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens
89	c2gqqB_	Alignment	not modelled	89.9	9	PDB header: transcription Chain: B: PDB Molecule: leucine-responsive regulatory protein; PDBTitle: crystal structure of e. coli leucine-responsive regulatory protein2 (lrp)
90	d2jn6a1	Alignment	not modelled	89.8	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Cgl2762-like
91	c4if4A_	Alignment	not modelled	89.6	13	PDB header: transcription Chain: A: PDB Molecule: response regulator protein vvar; PDBTitle: crystal structure of the magnesium and beryll fluoride-activated vvar2 from staphylococcus aureus
92	c2q1zA_	Alignment	not modelled	89.4	11	PDB header: transcription Chain: A: PDB Molecule: rpoe, ecf sige; PDBTitle: crystal structure of rhodobacter sphaeroides sige in complex with the2 anti-sigma chrr
93	c1rp3G_	Alignment	not modelled	89.0	11	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
94	c5hevC_	Alignment	not modelled	88.7	18	PDB header: transcription Chain: C: PDB Molecule: response regulator protein vvar; PDBTitle: crystal structure of the beryll fluoride-activated liar from2 enterococcus faecium
95	c5f64C_	Alignment	not modelled	88.5	12	PDB header: transcription regulator Chain: C: PDB Molecule: positive transcription regulator evga; PDBTitle: putative positive transcription regulator (sensor evgs) from shigella2 flexneri
96	c2ia0A_	Alignment	not modelled	88.1	16	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)
97	d1ttya_	Alignment	not modelled	87.9	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
98	c3mzyA_	Alignment	not modelled	87.8	13	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
99	c5wurB_	Alignment	not modelled	87.5	10	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
100	c5z7iC_	Alignment	not modelled	87.3	21	PDB header: dna binding protein/dna Chain: C: PDB Molecule: cell cycle regulatory protein gcra; PDBTitle: caulobacter crescentus gcra dna-binding domain(dbd)in complex with2 unmethylated dsdna
101	c1u78A_	Alignment	not modelled	86.8	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
102	c4czdD_	Alignment	not modelled	86.2	12	PDB header: lyase Chain: D: PDB Molecule: putative transcriptional regulator, asnc family;

102	c4c2dD	Alignment	not modelled	88.2	12	PDBTitle: sirohaem decarboxylase ahba/b - an enzyme with structural homology2 to the lrp/asnc transcription factor family that is part of the3 alternative haem biosynthesis pathway.
103	d2coba1	Alignment	not modelled	86.0	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Psq domain
104	c5uxxC	Alignment	not modelled	84.7	17	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
105	d1jhfa1	Alignment	not modelled	84.2	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: LexA repressor, N-terminal DNA-binding domain
106	d1smyf2	Alignment	not modelled	83.5	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
107	c3klnC	Alignment	not modelled	83.1	15	PDB header: transcription Chain: C: PDB Molecule: transcriptional regulator, luxr family; PDBTitle: vibrio cholerae vpst
108	c5ae5A	Alignment	not modelled	83.1	17	PDB header: transcription Chain: A: PDB Molecule: lysr-type regulatory protein; PDBTitle: structures of inactive and activated dntr provide conclusive evidence2 for the mechanism of action of lysr transcription factors
109	c5xe7A	Alignment	not modelled	82.4	13	PDB header: dna binding protein Chain: A: PDB Molecule: ecf rna polymerase sigma factor sigj; PDBTitle: crystal structure of mycobacterium tuberculosis extracytoplasmic2 function sigma factor sigj
110	c3c3wB	Alignment	not modelled	81.3	18	PDB header: transcription Chain: B: PDB Molecule: two component transcriptional regulatory protein devr; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
111	c1rnA	Alignment	not modelled	80.8	18	PDB header: signal transduction protein Chain: A: PDB Molecule: nitrate/nitrite response regulator protein narl; PDBTitle: the nitrate/nitrite response regulator protein narl from narl
112	d2auwa1	Alignment	not modelled	80.2	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE0471 C-terminal domain-like
113	c2rn7A	Alignment	not modelled	80.0	16	PDB header: unknown function Chain: A: PDB Molecule: is629 orfa; PDBTitle: nmr solution structure of tnpE protein from shigella2 flexneri. northeast structural genomics target sfr125
114	c4yn8A	Alignment	not modelled	80.0	21	PDB header: dna binding protein Chain: A: PDB Molecule: response regulator chra; PDBTitle: crystal structure of response regulator chra in heme-sensing two2 component system
115	c1zn2A	Alignment	not modelled	79.3	13	PDB header: transcription regulator Chain: A: PDB Molecule: response regulatory protein; PDBTitle: low resolution structure of response regulator styr
116	d1ku7a	Alignment	not modelled	77.2	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
117	c6amaO	Alignment	not modelled	75.3	11	PDB header: dna binding protein/dna Chain: O: PDB Molecule: putative dna-binding protein; PDBTitle: structure of s. coelicolor/s. venezuelae bldc-smea-sffa complex to2 3.09 angstrom
118	d1vz0a1	Alignment	not modelled	75.2	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
119	c4ch7A	Alignment	not modelled	74.7	17	PDB header: transcription Chain: A: PDB Molecule: nird-like protein; PDBTitle: crystal structure of the siroheme decarboxylase nirdl
120	d1i3ja	Alignment	not modelled	74.1	24	Fold: DNA-binding domain of intron-encoded endonucleases Superfamily: DNA-binding domain of intron-encoded endonucleases Family: DNA-binding domain of intron-encoded endonucleases