
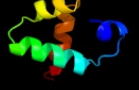








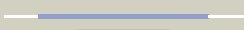










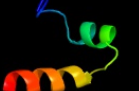

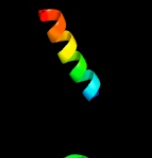

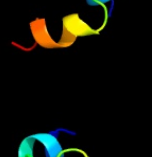
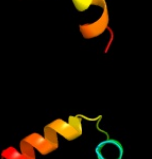



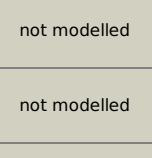


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2647 (-) _2971669_2972037
Date	Wed Aug 7 12:50:29 BST 2019
Unique Job ID	50942d887e26bf2a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1r71B_	 Alignment		48.2	25	PDB header: transcription/dna Chain: B: PDB Molecule: transcriptional repressor protein korb; PDBTitle: crystal structure of the dna binding domain of korb in complex with2 the operator dna
2	d1r71a_	 Alignment		42.8	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
3	c2vbzA_	 Alignment		34.0	16	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
4	c2cfxD_	 Alignment		30.4	10	PDB header: transcription Chain: D: PDB Molecule: hth-type transcriptional regulator lrpc; PDBTitle: structure of b.subtilis lrpc
5	c2dbaA_	 Alignment		27.6	10	PDB header: transcriptional regulator Chain: A: PDB Molecule: putative hth-type transcriptional regulator ph0061; PDBTitle: crystal structure of ph0061
6	c1vz0B_	 Alignment		23.6	20	PDB header: nuclear protein Chain: B: PDB Molecule: chromosome-partitioning protein spo0j; PDBTitle: chromosome segregation protein spo0j from thermus thermophilus
7	c1ojlD_	 Alignment		22.4	27	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
8	d1g2ha_	 Alignment		21.7	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
9	c1g2hA_	 Alignment		21.7	24	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
10	c3t72o_	 Alignment		21.5	9	PDB header: transcription/dna Chain: O: PDB Molecule: pho box dna (strand 1); PDBTitle: phob(e)-sigma70(4)-(rnap-beta-flap-tip-helix)-dna transcription2 activation sub-complex
11	c2e7xA_	 Alignment		20.2	16	PDB header: transcription regulator Chain: A: PDB Molecule: 150aa long hypothetical transcriptional regulator; PDBTitle: structure of the lrp/asnc like transcriptional regulator from2 sulfobolus tokodaii 7 complexed with its cognate ligand

12	d1b25a1	Alignment		18.3	32	Fold: Aldehyde ferredoxin oxidoreductase, C-terminal domains Superfamily: Aldehyde ferredoxin oxidoreductase, C-terminal domains Family: Aldehyde ferredoxin oxidoreductase, C-terminal domains
13	d1aora1	Alignment		18.3	47	Fold: Aldehyde ferredoxin oxidoreductase, C-terminal domains Superfamily: Aldehyde ferredoxin oxidoreductase, C-terminal domains Family: Aldehyde ferredoxin oxidoreductase, C-terminal domains
14	d2p7vb1	Alignment		17.6	5	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
15	d1umqa_	Alignment		17.5	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
16	c1umqA_	Alignment		17.5	16	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
17	c2e1cA_	Alignment		17.5	16	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
18	c2zjtB_	Alignment		16.9	64	PDB header: isomerase Chain: B: PDB Molecule: dna gyrase subunit b; PDBTitle: crystal structure of dna gyrase b' domain sheds lights on the2 mechanism for t-segment navigation
19	c2l4aA_	Alignment		16.2	19	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
20	d1ntca_	Alignment		16.1	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
21	d2cg4a1	Alignment	not modelled	15.7	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
22	c2fjrB_	Alignment	not modelled	14.5	5	PDB header: transcription regulator Chain: B: PDB Molecule: repressor protein ci; PDBTitle: crystal structure of bacteriophage 186
23	c2gm4B_	Alignment	not modelled	14.2	14	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
24	c6genS_	Alignment	not modelled	13.5	36	PDB header: nuclear protein Chain: S: PDB Molecule: vacuolar protein sorting-associated protein 71; PDBTitle: chromatin remodeller-nucleosome complex at 4.5 a resolution.
25	c4lfuA_	Alignment	not modelled	13.4	20	PDB header: dna binding protein Chain: A: PDB Molecule: regulatory protein sdia; PDBTitle: crystal structure of escherichia coli sdia in the space group c2
26	d1etxa_	Alignment	not modelled	13.1	33	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
27	c4l5eA_	Alignment	not modelled	13.1	47	PDB header: protein binding Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of a. aeolicus ntrc1 dna binding domain
28	c1l1gA_	Alignment	not modelled	12.9	38	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lrpa; PDBTitle: crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus

29	c5m7nA_	Alignment	not modelled	12.7	24	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
30	c3qp5C_	Alignment	not modelled	12.7	22	PDB header: transcription Chain: C: PDB Molecule: cvir transcriptional regulator; PDBTitle: crystal structure of cvir bound to antagonist chlorolactone (cl)
31	d1fipa_	Alignment	not modelled	12.6	33	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
32	d1ku3a_	Alignment	not modelled	12.4	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
33	d1ttya_	Alignment	not modelled	11.9	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
34	c2gqqB_	Alignment	not modelled	11.8	19	PDB header: transcription Chain: B: PDB Molecule: leucine-responsive regulatory protein; PDBTitle: crystal structure of e. coli leucine-responsive regulatory protein2 (lrp)
35	c4z3wB_	Alignment	not modelled	11.7	25	PDB header: oxidoreductase Chain: B: PDB Molecule: benzoyl-coa reductase, putative; PDBTitle: active site complex bambc of benzoyl coenzyme a reductase in complex2 with 1,5 dienoyl-coa
36	c1b4nD_	Alignment	not modelled	11.5	30	PDB header: oxidoreductase Chain: D: PDB Molecule: formaldehyde ferredoxin oxidoreductase; PDBTitle: formaldehyde ferredoxin oxidoreductase from pyrococcus furiosus,2 complexed with glutarate
37	c3i4pA_	Alignment	not modelled	11.5	16	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, asnc family; PDBTitle: crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens
38	c2ia0A_	Alignment	not modelled	11.1	21	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)
39	c1aorB_	Alignment	not modelled	10.6	47	PDB header: oxidoreductase Chain: B: PDB Molecule: aldehyde ferredoxin oxidoreductase; PDBTitle: structure of a hyperthermophilic tungstopterin enzyme,2 aldehyde ferredoxin oxidoreductase
40	c4pcqC_	Alignment	not modelled	10.1	21	PDB header: transcription Chain: C: PDB Molecule: possible transcriptional regulatory protein (probably PDBTitle: crystal structure of mtbaldr (rv2779c)
41	d1nexa1	Alignment	not modelled	10.0	36	Fold: Skp1 dimerisation domain-like Superfamily: Skp1 dimerisation domain-like Family: Skp1 dimerisation domain-like
42	c3sztB_	Alignment	not modelled	10.0	18	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
43	c3nuhB_	Alignment	not modelled	9.7	60	PDB header: isomerase Chain: B: PDB Molecule: dna gyrase subunit b; PDBTitle: a domain insertion in e. coli gyrb adopts a novel fold that plays a2 critical role in gyrase function
44	d1ku7a_	Alignment	not modelled	9.3	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
45	c2mk6A_	Alignment	not modelled	8.9	16	PDB header: gene regulation Chain: A: PDB Molecule: adapter protein meca; PDBTitle: structure determination of substrate binding domain of meca
46	c5gn0H_	Alignment	not modelled	8.7	67	PDB header: transcription Chain: H: PDB Molecule: ww domain-containing transcription regulator protein 1; PDBTitle: structure of taz-tead complex
47	c6emwg_	Alignment	not modelled	8.5	23	PDB header: chaperone Chain: G: PDB Molecule: atp-dependent clp protease atp-binding subunit clpc; PDBTitle: structure of s.aureus clpc in complex with meca
48	c2p6tH_	Alignment	not modelled	8.4	17	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
49	c2r0qF_	Alignment	not modelled	8.4	26	PDB header: recombination/dna Chain: F: PDB Molecule: putative transposon tn552 dna-invertase bin3; PDBTitle: crystal structure of a serine recombinase- dna regulatory2 complex
50	c4qccA_	Alignment	not modelled	8.4	29	PDB header: structural protein, lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxy-6-phosphogalactonate aldolase, peptidyl- PDBTitle: structure of a cube-shaped, highly porous protein cage designed by2 fusing symmetric oligomeric domains
51	c3t76A_	Alignment	not modelled	8.1	24	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator vanug; PDBTitle: crystal structure of transcriptional regulator vanug, form ii
52	c4tvxT_	Alignment	not modelled	7.8	28	PDB header: PDB COMPND:
53	c3fofD_	Alignment	not modelled	7.7	55	PDB header: isomerase/dna Chain: D: PDB Molecule: dna topoisomerase 4 subunit b; PDBTitle: structural insight into the quinolone-dna cleavage complex2 of type iia topoisomerases

54	c4gdoF_	Alignment	not modelled	7.6	57	PDB header: structural protein Chain: F; PDB Molecule: plectin; PDBTitle: structure of a fragment of the rod domain of plectin
55	c3t0yA_	Alignment	not modelled	7.3	29	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
56	c4tmaH_	Alignment	not modelled	7.1	70	PDB header: isomerase/isomerase inhibitor Chain: H; PDB Molecule: dna gyrase subunit b; PDBTitle: crystal structure of gyrase bound to its inhibitor yacg
57	d2cyya1	Alignment	not modelled	7.0	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
58	d2o7ta2	Alignment	not modelled	7.0	15	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
59	d1etob_	Alignment	not modelled	6.5	37	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
60	c4uf2A_	Alignment	not modelled	6.0	43	PDB header: viral protein Chain: A; PDB Molecule: antiapoptotic membrane protein; PDBTitle: deerpox virus dpv022 in complex with bax bh3
61	d2htja1	Alignment	not modelled	5.9	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: FaeA-like
62	c4dhxC_	Alignment	not modelled	5.8	38	PDB header: transport protein/dna binding protein Chain: C; PDB Molecule: enhancer of yellow 2 transcription factor homolog; PDBTitle: eny2:ganp complex
63	c2cg4B_	Alignment	not modelled	5.8	17	PDB header: transcription Chain: B; PDB Molecule: regulatory protein asnc; PDBTitle: structure of e.coli asnc
64	c4umkA_	Alignment	not modelled	5.7	15	PDB header: dna binding protein/dna Chain: A; PDB Molecule: probable chromosome-partitioning protein parb; PDBTitle: the complex of spo0j and pars dna in chromosomal partition system
65	c2m8gX_	Alignment	not modelled	5.7	19	PDB header: transcription Chain: X; PDB Molecule: transcriptional regulator; PDBTitle: structure, function, and tethering of dna-binding domains in 542 transcriptional activators
66	c3e7lD_	Alignment	not modelled	5.6	22	PDB header: transcription regulator Chain: D; PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain
67	c4gdoC_	Alignment	not modelled	5.5	57	PDB header: structural protein Chain: C; PDB Molecule: plectin; PDBTitle: structure of a fragment of the rod domain of plectin
68	d1l1ga1	Alignment	not modelled	5.3	35	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
69	c5zwoZ_	Alignment	not modelled	5.3	75	PDB header: splicing Chain: Z; PDB Molecule: pre-mrna leakage protein 1; PDBTitle: cryo-em structure of the yeast b complex at average resolution of 3.92 angstrom
70	c1ynmA_	Alignment	not modelled	5.1	78	PDB header: hydrolase Chain: A; PDB Molecule: r.hinp1i restriction endonuclease; PDBTitle: crystal structure of restriction endonuclease hinp1i
71	c6fkqC_	Alignment	not modelled	5.1	10	PDB header: toxin Chain: C; PDB Molecule: rv1990c (mbca); PDBTitle: crystal structure of the m.tuberculosis mbct-mbca toxin-antitoxin2 complex.