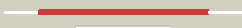





















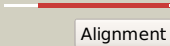

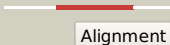

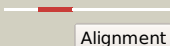
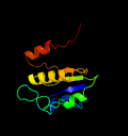










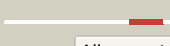


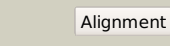
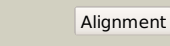


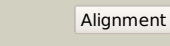
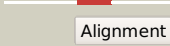
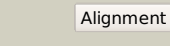


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3646c_(topA)_4084632_4087436
Date	Fri Aug 9 18:20:33 BST 2019
Unique Job ID	f5ebdd7b24ffefa6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4ru1A_	 Alignment		100.0	38	PDB header: isomerase/dna Chain: A; PDB Molecule: dna topoisomerase 1; PDBTitle: crystal structure of full-length e.coli topoisomerase i in complex2 with ssdna
2	c5d5hA_	 Alignment		100.0	100	PDB header: isomerase Chain: A; PDB Molecule: dna topoisomerase 1; PDBTitle: crystal structure of mycobacterium tuberculosis topoisomerase i
3	c2o59B_	 Alignment		100.0	23	PDB header: isomerase/dna Chain: B; PDB Molecule: dna topoisomerase 3; PDBTitle: structure of e. coli topoisomerase iii in complex with an 8-base2 single stranded oligonucleotide. frozen in glycerol ph 8.0
4	c2gajA_	 Alignment		100.0	39	PDB header: isomerase Chain: A; PDB Molecule: dna topoisomerase i; PDBTitle: structure of full length topoisomerase i from thermotoga maritima in2 monoclinic crystal form
5	d1mw9x_	 Alignment		100.0	45	Fold: Prokaryotic type I DNA topoisomerase Superfamily: Prokaryotic type I DNA topoisomerase Family: Prokaryotic type I DNA topoisomerase
6	d1i7da_	 Alignment		100.0	23	Fold: Prokaryotic type I DNA topoisomerase Superfamily: Prokaryotic type I DNA topoisomerase Family: Prokaryotic type I DNA topoisomerase
7	c4chtA_	 Alignment		100.0	24	PDB header: cell cycle Chain: A; PDB Molecule: dna topoisomerase 3-alpha; PDBTitle: crystal structure of the human topoisomerase iii alpha-rm1 complex2 with bound calcium ion
8	c6ozwA_	 Alignment		100.0	41	PDB header: isomerase,dna binding protein Chain: A; PDB Molecule: dna topoisomerase 1; PDBTitle: crystal structure of the 65-kilodalton amino-terminal fragment of dna2 topoisomerase i from streptococcus mutans
9	c5gveA_	 Alignment		100.0	25	PDB header: isomerase/protein binding Chain: A; PDB Molecule: dna topoisomerase 3-beta-1; PDBTitle: human top3b-tddr3 complex
10	c4ddvA_	 Alignment		100.0	32	PDB header: hydrolase Chain: A; PDB Molecule: reverse gyrase; PDBTitle: thermotoga maritima reverse gyrase, triclinic form
11	c1ql9B_	 Alignment		100.0	33	PDB header: topoisomerase Chain: B; PDB Molecule: reverse gyrase; PDBTitle: archaeoglobus fulgidus reverse gyrase complexed with adpnp

12	d1gkub3	 Alignment		100.0	32	Fold: Prokaryotic type I DNA topoisomerase Superfamily: Prokaryotic type I DNA topoisomerase Family: Prokaryotic type I DNA topoisomerase
13	d1cy9a_	 Alignment		100.0	38	Fold: Prokaryotic type I DNA topoisomerase Superfamily: Prokaryotic type I DNA topoisomerase Family: Prokaryotic type I DNA topoisomerase
14	d1vdda_	 Alignment		99.2	27	Fold: Recombination protein RecR Superfamily: Recombination protein RecR Family: Recombination protein RecR
15	c1vddC_	 Alignment		98.9	27	PDB header: recombination Chain: C: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recombinational repair protein recr
16	c5zvqA_	 Alignment		98.9	33	PDB header: recombination Chain: A: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recombination mediator protein recr
17	c5z2vB_	 Alignment		97.1	26	PDB header: dna binding protein Chain: B: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recr from pseudomonas aeruginosa pao1
18	d2fcja1	 Alignment		96.0	27	Fold: Toprim domain Superfamily: Toprim domain Family: Toprim domain
19	c3ve5D_	 Alignment		95.8	33	PDB header: recombination Chain: D: PDB Molecule: recombination protein recr; PDBTitle: structure of recombination mediator protein recr16-196 deletion mutant
20	c4q77B_	 Alignment		95.8	12	PDB header: dna binding protein Chain: B: PDB Molecule: hth-type transcriptional regulator rot; PDBTitle: crystal structure of rot, a global regulator of virulence genes in2 staphylococcus aureus
21	d1nuia1	 Alignment	not modelled	94.9	15	Fold: DNA primase core Superfamily: DNA primase core Family: Primase fragment of primase-helicase protein
22	c1nuia_	 Alignment	not modelled	94.4	18	PDB header: replication Chain: A: PDB Molecule: dna primase/helicase; PDBTitle: crystal structure of the primase fragment of bacteriophage t7 primase-2 helicase protein
23	c5zc2B_	 Alignment	not modelled	92.4	11	PDB header: flavoprotein Chain: B: PDB Molecule: p-hydroxyphenylacetate 3-hydroxylase, reductase component; PDBTitle: acinetobacter baumannii p-hydroxyphenylacetate 3-hydroxylase (hpah),2 reductase component (c1)
24	c1f5tA_	 Alignment	not modelled	92.2	13	PDB header: transcription/dna Chain: A: PDB Molecule: diphtheria toxin repressor; PDBTitle: diphtheria tox repressor (c102d mutant) complexed with2 nickel and dtxr consensus binding sequence
25	c3hruA_	 Alignment	not modelled	92.1	9	PDB header: transcription Chain: A: PDB Molecule: metalloregulator scar; PDBTitle: crystal structure of scar with bound zn2+
26	c5cviB_	 Alignment	not modelled	92.1	13	PDB header: transcription regulator Chain: B: PDB Molecule: slor; PDBTitle: structure of the manganese regulator slor
27	c4o6jA_	 Alignment	not modelled	92.0	15	PDB header: metal binding protein Chain: A: PDB Molecule: iron-dependent transcription repressor related protein; PDBTitle: crystal structure of t. acidophilum ider
28	c1g3wA_	 Alignment	not modelled	91.8	13	PDB header: gene regulation Chain: A: PDB Molecule: diphtheria toxin repressor; PDBTitle: cd-cys102ser dtxr

29	c5foeA_	Alignment	not modelled	91.8	27	PDB header: transferase Chain: A: PDB Molecule: gdp-fucose protein o-fucosyltransferase 2,thrombospondin-1; PDBTitle: crystal structure of the c. elegans protein o-fucosyltransferase 22 (cepofut2) double mutant (r298k-r299k) in complex with gdp and the3 human tsr1 from thrombospondin 1
30	c1q57G_	Alignment	not modelled	91.5	20	PDB header: transferase Chain: G: PDB Molecule: dna primase/helicase; PDBTitle: the crystal structure of the bifunctional primase-helicase of2 bacteriophage t7
31	c3nrvC_	Alignment	not modelled	91.3	13	PDB header: transcription regulator Chain: C: PDB Molecule: putative transcriptional regulator (marr/emrr family); PDBTitle: crystal structure of marr/emrr family transcriptional regulator from2 acinetobacter sp. adp1
32	c1fx7C_	Alignment	not modelled	90.5	15	PDB header: signaling protein Chain: C: PDB Molecule: iron-dependent repressor ider; PDBTitle: crystal structure of the iron-dependent regulator (ider) from2 mycobacterium tuberculosis
33	c4mnuA_	Alignment	not modelled	90.2	19	PDB header: transcription regulator Chain: A: PDB Molecule: slya-like transcription regulator; PDBTitle: crystal structure of uncharacterized slya-like transcription regulator2 from listeria monocytogenes
34	c2h09A_	Alignment	not modelled	89.9	17	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator mntr; PDBTitle: crystal structure of diphtheria toxin repressor like protein2 from e. coli
35	c2x4hA_	Alignment	not modelled	89.6	16	PDB header: transcription Chain: A: PDB Molecule: hypothetical protein sso2273; PDBTitle: crystal structure of the hypothetical protein sso2273 from2 sulfolobus solfataricus
36	c3e6mD_	Alignment	not modelled	89.3	21	PDB header: transcription regulator Chain: D: PDB Molecule: marr family transcriptional regulator; PDBTitle: the crystal structure of a marr family transcriptional2 regulator from silicibacter pomeroyi dss.
37	c5eriA_	Alignment	not modelled	89.3	24	PDB header: transcription Chain: A: PDB Molecule: marr family transcriptional regulator; PDBTitle: marr protein from peptoclostridium difficile da00132
38	c6jbxB_	Alignment	not modelled	88.6	14	PDB header: transcription/dna Chain: B: PDB Molecule: fatty acid biosynthesis transcriptional regulator; PDBTitle: crystal structure of streptococcus pneumoniae fabt in complex with dna
39	d3broa1	Alignment	not modelled	88.6	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
40	d2fbia1	Alignment	not modelled	88.3	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
41	c3f3xA_	Alignment	not modelled	88.1	13	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, marr family, putative; PDBTitle: crystal structure of the transcriptional regulator bldr from2 sulfolobus solfataricus
42	c2it0A_	Alignment	not modelled	88.0	15	PDB header: transcription/dna Chain: A: PDB Molecule: iron-dependent repressor ider; PDBTitle: crystal structure of a two-domain ider-dna complex crystal2 form ii
43	d2fxaa1	Alignment	not modelled	87.9	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
44	c3s2wB_	Alignment	not modelled	87.8	14	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, marr family; PDBTitle: the crystal structure of a marr transcriptional regulator from2 methanosarcina mazei g01
45	d1s3ja_	Alignment	not modelled	87.7	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
46	c2fxaB_	Alignment	not modelled	87.5	14	PDB header: transcription Chain: B: PDB Molecule: protease production regulatory protein hpr; PDBTitle: structure of the protease production regulatory protein hpr from2 bacillus subtilis.
47	d2a61a1	Alignment	not modelled	87.5	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
48	c5jlsA_	Alignment	not modelled	87.4	10	PDB header: transcription Chain: A: PDB Molecule: adhesin competence repressor; PDBTitle: crystal structure of adhesin competence repressor (adcr) from2 streptococcus pyogenes (c-terminally his tagged)
49	c3boqB_	Alignment	not modelled	87.4	17	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of marr family transcriptional regulator from2 silicibacter pomeroyi
50	d1t6t1_	Alignment	not modelled	87.1	26	Fold: Toprim domain Superfamily: Toprim domain Family: Toprim domain
51	c3nqoB_	Alignment	not modelled	87.0	16	PDB header: transcription Chain: B: PDB Molecule: marr-family transcriptional regulator; PDBTitle: crystal structure of a marr family transcriptional regulator (cd1569)2 from clostridium difficile 630 at 2.20 a resolution
52	d1jgsa_	Alignment	not modelled	86.7	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
53	c2pexA_	Alignment	not modelled	86.5	14	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator ohrr; PDBTitle: structure of reduced c22s ohrr from xanthamonas

						campestris
54	d1r7ja_	Alignment	not modelled	86.3	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Archaeal DNA-binding protein
55	d1lnwa_	Alignment	not modelled	85.4	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
56	c2fa5B_	Alignment	not modelled	85.3	18	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator marr/emrr family; PDBTitle: the crystal structure of an unliganded multiple antibiotic-2 resistance repressor (marr) from xanthomonas campestris
57	c5yhxB_	Alignment	not modelled	85.3	9	PDB header: metal binding protein Chain: H: PDB Molecule: zinc transport transcriptional regulator; PDBTitle: structure of lactococcus lactis zittr, wild type
58	c3g3zA_	Alignment	not modelled	84.9	15	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, marr family; PDBTitle: the structure of nmb1585, a marr family regulator from neisseria2 meningitidis
59	d3ctaa1	Alignment	not modelled	84.7	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
60	c3kp3B_	Alignment	not modelled	84.7	9	PDB header: transcription regulator/antibiotic Chain: B: PDB Molecule: transcriptional regulator tcar; PDBTitle: staphylococcus epidermidis in complex with ampicillin
61	c4yifE_	Alignment	not modelled	84.5	13	PDB header: dna binding protein Chain: E: PDB Molecule: marr family protein rv0880; PDBTitle: crystal structure of rv0880
62	c2rdpA_	Alignment	not modelled	84.4	14	PDB header: transcription Chain: A: PDB Molecule: putative transcriptional regulator marr; PDBTitle: the structure of a marr family protein from bacillus2 stearothermophilus
63	d2hr3a1	Alignment	not modelled	84.2	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
64	d2fbha1	Alignment	not modelled	84.1	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
65	c3bj6B_	Alignment	not modelled	84.1	12	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of marr family transcription regulator sp03579
66	c4hblA_	Alignment	not modelled	84.0	12	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of abfr of staphylococcus epidermidis
67	d1p4xa1	Alignment	not modelled	84.0	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
68	c4xrfA_	Alignment	not modelled	83.4	11	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of mepr like protein complexed with pseudoligands
69	c3fm5D_	Alignment	not modelled	82.8	15	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator; PDBTitle: x-ray crystal structure of transcriptional regulator (marr family)2 from rhodococcus sp. rha1
70	d1lj9a_	Alignment	not modelled	79.9	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
71	d2fbka1	Alignment	not modelled	79.4	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
72	d2bv6a1	Alignment	not modelled	79.2	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
73	c2qxB_	Alignment	not modelled	79.0	9	PDB header: transcription Chain: A: PDB Molecule: 146aa long hypothetical transcriptional regulator; PDBTitle: crystal structure of emrr homolog from hyperthermophilic archaea2 sulfobolus tokodaii strain7
74	c2nyxB_	Alignment	not modelled	78.8	8	PDB header: transcription Chain: B: PDB Molecule: probable transcriptional regulatory protein, rv1404; PDBTitle: crystal structure of rv1404 from mycobacterium tuberculosis
75	c3jw4C_	Alignment	not modelled	78.7	11	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator, marr/emrr family; PDBTitle: the structure of a putative marr family transcriptional regulator from2 clostridium acetobutylicum
76	c4hw0B_	Alignment	not modelled	78.0	7	PDB header: dna binding protein Chain: B: PDB Molecule: dna-binding protein sso10a-2; PDBTitle: crystal structure of sso10a-2, a dna-binding protein from sulfobolus2 solfataricus
77	c3hrmA_	Alignment	not modelled	77.6	13	PDB header: transcription regulator Chain: A: PDB Molecule: hth-type transcriptional regulator sarz; PDBTitle: crystal structure of staphylococcus aureus protein sarz in sulfenic2 acid form
78	c5fo5A_	Alignment	not modelled	77.4	13	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
79	c3deuB_	Alignment	not modelled	77.2	7	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator slya; PDBTitle: crystal structure of transcription regulatory protein slya

						from2 salmonella typhimurium in complex with salicylate ligands
80	d2etha1	Alignment	not modelled	77.2	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
81	c3bjaA	Alignment	not modelled	76.5	17	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, marr family, putative; PDBTitle: crystal structure of putative marr-like transcription regulator2 (np_978771.1) from bacillus cereus atcc 10987 at 2.38 a resolution
82	c2ev5B	Alignment	not modelled	76.0	12	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator mntr; PDBTitle: bacillus subtilis manganese transport regulator (mntr)2 bound to calcium
83	c1p4xA	Alignment	not modelled	75.9	17	PDB header: transcription Chain: A: PDB Molecule: staphylococcal accessory regulator a homologue; PDBTitle: crystal structure of sars protein from staphylococcus aureus
84	c4fx0A	Alignment	not modelled	75.7	9	PDB header: transcription regulator Chain: A: PDB Molecule: probable transcriptional repressor protein; PDBTitle: crystal structure of m. tuberculosis transcriptional regulator mosr
85	c3zplE	Alignment	not modelled	75.5	16	PDB header: transcription/dna Chain: E: PDB Molecule: putative marr-family transcriptional repressor; PDBTitle: crystal structure of sco3205, a marr family transcriptional regulator2 from streptomyces coelicolor, in complex with dna
86	d1stza1	Alignment	not modelled	74.9	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Heat-inducible transcription repressor HrcA, N-terminal domain
87	c2nnnB	Alignment	not modelled	74.8	11	PDB header: transcription Chain: B: PDB Molecule: probable transcriptional regulator; PDBTitle: crystal structure of probable transcriptional regulator from2 pseudomonas aeruginosa
88	c6o5cB	Alignment	not modelled	74.7	12	PDB header: dna binding protein Chain: B: PDB Molecule: putative metal-dependent transcriptional regulator; PDBTitle: x-ray crystal structure of metal-dependent transcriptional regulator2 mtrsr
89	d1ub9a	Alignment	not modelled	74.1	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
90	c3bpxB	Alignment	not modelled	73.8	14	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of marr
91	c4z2cD	Alignment	not modelled	73.0	22	PDB header: isomerase Chain: D: PDB Molecule: dna gyrase subunit b; PDBTitle: quinolone(moxifloxacin)-dna cleavage complex of gyrase from s.2 pneumoniae
92	c3zmdD	Alignment	not modelled	72.7	19	PDB header: transcription Chain: D: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of absc, a marr family transcriptional2 regulator from streptomyces coelicolor
93	d1p4xa2	Alignment	not modelled	72.2	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
94	d1olta	Alignment	not modelled	71.9	8	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: Oxygen-independent coproporphyrinogen III oxidase HemN
95	c5hsmA	Alignment	not modelled	71.7	13	PDB header: transcription Chain: A: PDB Molecule: uncharacterized hth-type transcriptional regulator rv2887; PDBTitle: crystal structure of mycobacterium tuberculosis marr family protein2 rv2887
96	c4b8xB	Alignment	not modelled	71.3	10	PDB header: transcription Chain: B: PDB Molecule: possible marr-transcriptional regulator; PDBTitle: near atomic resolution crystal structure of sco5413, a marr family2 transcriptional regulator from streptomyces coelicolor
97	d1z91a1	Alignment	not modelled	70.8	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
98	c3k0IA	Alignment	not modelled	70.6	16	PDB header: transcription regulator Chain: A: PDB Molecule: repressor protein; PDBTitle: crystal structure of putative marr family transcriptional2 regulator from acinetobacter sp. adp
99	c4nb5D	Alignment	not modelled	70.6	10	PDB header: dna binding protein Chain: D: PDB Molecule: dna binding protein; PDBTitle: crystal structure of a transcriptional regulator
100	c5aiqD	Alignment	not modelled	70.5	13	PDB header: transcription Chain: D: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of ligand-free nadr
101	c6c28C	Alignment	not modelled	70.3	14	PDB header: dna binding protein Chain: C: PDB Molecule: transcriptional regulator, marr family; PDBTitle: transcriptional repressor, cour, bound to p-coumaroyl-coa
102	c2yqpA	Alignment	not modelled	70.2	23	PDB header: gene regulation, hydrolase Chain: A: PDB Molecule: probable atp-dependent rna helicase ddx59; PDBTitle: solution structure of the zf-hit domain in dead (asp-glu-2 ala-asp) box polypeptide 59
103	c4fhtA	Alignment	not modelled	69.6	23	PDB header: transcription Chain: A: PDB Molecule: pcav transcriptional regulator; PDBTitle: crystal structure of the pcav transcriptional regulator from2 streptomyces coelicolor in complex with its natural ligand
						Fold: DNA/RNA-binding 3-helical bundle

104	d2isya1	Alignment	not modelled	69.0	13	Superfamily: "Winged helix" DNA-binding domain Family: Iron-dependent repressor protein
105	c4omzG_	Alignment	not modelled	67.8	13	PDB header: transcription Chain: G; PDB Molecule: nolr; PDBTitle: crystal structure of nolr from sinorhizobium fredii
106	d2cg4a1	Alignment	not modelled	67.7	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
107	d2esna1	Alignment	not modelled	67.4	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: LysR-like transcriptional regulators
108	c5fywW_	Alignment	not modelled	67.2	13	PDB header: transcription Chain: W; PDB Molecule: transcription initiation factor iie subunit alpha; PDBTitle: transcription initiation complex structures elucidate dna opening (oc)
109	c2k4bA_	Alignment	not modelled	67.0	9	PDB header: dna binding protein Chain: A; PDB Molecule: transcriptional regulator; PDBTitle: copr repressor structure
110	c5fmfR_	Alignment	not modelled	67.0	13	PDB header: transcription Chain: R; PDB Molecule: transcription initiation factor iie subunit alpha, tfa1; PDBTitle: the p-lobe of rna polymerase ii pre-initiation complex
111	c5w34A_	Alignment	not modelled	65.6	24	PDB header: transferase Chain: A; PDB Molecule: dna primase; PDBTitle: crystal structure of the rna polymerase domain (rpd) of mycobacterium2 tuberculosis primase dnag in complex with double-stranded dna3 gaccggaagtgg
112	c2wteB_	Alignment	not modelled	65.5	18	PDB header: antiviral protein Chain: B; PDB Molecule: csa3; PDBTitle: the structure of the crispr-associated protein, csa3, from2 sulfobolus solfataricus at 1.8 angstrom resolution.
113	d1g3wa1	Alignment	not modelled	65.5	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Iron-dependent repressor protein
114	d2ev0a1	Alignment	not modelled	64.8	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Iron-dependent repressor protein
115	d1p6ra_	Alignment	not modelled	62.8	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Penicillinase repressor
116	c2qwwB_	Alignment	not modelled	62.2	12	PDB header: transcription Chain: B; PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of multiple antibiotic-resistance repressor (marr)2 (yp_013417.1) from listeria monocytogenes 4b f2365 at 2.07 a3 resolution
117	c3nuhB_	Alignment	not modelled	61.6	19	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
118	c1zreB_	Alignment	not modelled	60.8	22	PDB header: gene regulation/dna Chain: B; PDB Molecule: catabolite gene activator; PDBTitle: 4 crystal structures of cap-dna with all base-pair substitutions at2 position 6, cap-[6g;17c]icap38 dna
119	c3ecoB_	Alignment	not modelled	59.4	12	PDB header: transcription Chain: B; PDB Molecule: meprr; PDBTitle: crystal structure of meprr, a transcription regulator of the2 staphylococcus aureus multidrug efflux pump mepa
120	d1ilga1	Alignment	not modelled	59.0	30	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain