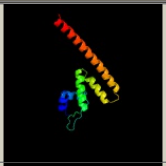
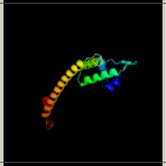
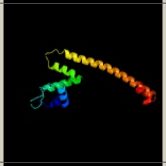
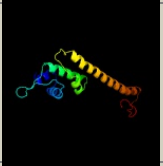
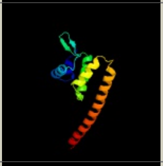
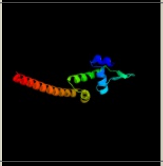
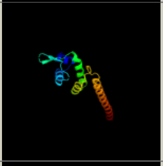
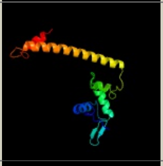
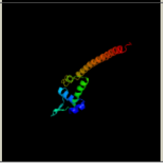
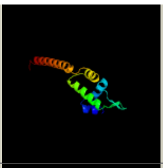
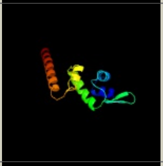
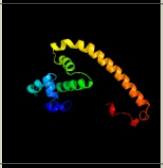
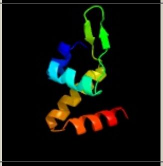
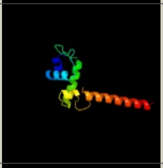
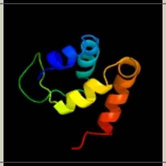
Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3334_(-)_3721428_3721868
Date	Thu Aug 8 16:20:54 BST 2019
Unique Job ID	0cca1a8c2b874d97

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3gp4B_	Alignment		100.0	27	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, merr family; **PDBTitle:** crystal structure of putative merr family transcriptional regulator2 from listeria monocytogenes
2	d1q06a_	Alignment		100.0	30	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**DNA-binding N-terminal domain of transcription activators
3	c5gpeB_	Alignment		100.0	39	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator, merr-family; **PDBTitle:** crystal structure of the transcription regulator pbrr691 from2 ralstonia metallidurans ch34 in complex with lead(ii)
4	c2zhhA_	Alignment		99.9	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**redox-sensitive transcriptional activator soxr; **PDBTitle:** crystal structure of soxr
5	c3gpvA_	Alignment		99.9	21	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, merr family; **PDBTitle:** crystal structure of a transcriptional regulator, merr2 family from bacillus thuringiensis
6	c3d6zA_	Alignment		99.9	24	**PDB header:**transcription regulator/dna **Chain:** A: **PDB Molecule:**multidrug-efflux transporter 1 regulator; **PDBTitle:** crystal structure of r275e mutant of bmrr bound to dna and rhodamine
7	c5xqlA_	Alignment		99.9	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**multidrug-efflux transporter 1 regulator; **PDBTitle:** crystal structure of a pseudomonas aeruginosa transcriptional2 regulator
8	c3hh0C_	Alignment		99.9	18	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcriptional regulator, merr family; **PDBTitle:** crystal structure of a transcriptional regulator, merr family from2 bacillus cereus
9	c3qaoA_	Alignment		99.9	25	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**merr-like transcriptional regulator; **PDBTitle:** the crystal structure of the n-terminal domain of a merr-like2 transcriptional regulator from listeria monocytogenes egd-e
10	c5crlA_	Alignment		99.9	30	**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)
11	d1r8ea1	Alignment		99.9	22	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**DNA-binding N-terminal domain of transcription activators

12	d1r8da_	Alignment		99.9	24	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**DNA-binding N-terminal domain of transcription activators
13	c2vz4A_	Alignment		99.9	29	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hth-type transcriptional activator tipa; **PDBTitle:** the n-terminal domain of merr-like protein tipal bound to promoter dna
14	c4ua2B_	Alignment		99.9	33	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**regulatory protein; **PDBTitle:** crystal structure of dual function transcriptional regulator merr from2 bacillus megaterium mb1
15	c4r24B_	Alignment		99.8	39	**PDB header:**transcrption/dna **Chain:** B: **PDB Molecule:**hth-type transcriptional regulator tnra; **PDBTitle:** complete dissection of b. subtilis nitrogen homeostatic circuitry
16	c4r4eA_	Alignment		99.8	34	**PDB header:**transcription regulator/dna **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator glnr; **PDBTitle:** structure of glnr-dna complex
17	c5i44E_	Alignment		99.8	25	**PDB header:**dna binding protein/dna **Chain:** E: **PDB Molecule:**chromosome-anchoring protein raca; **PDBTitle:** structure of raca-dna complex; p21 form
18	c3ucsB_	Alignment		99.8	15	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**chaperone-modulator protein cbpm; **PDBTitle:** crystal structure of the complex between cbpa j-domain and cbpm
19	c2jmlA_	Alignment		99.7	28	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna binding domain/transcriptional regulator; **PDBTitle:** solution structure of the n-terminal domain of cara repressor
20	c2dg6A_	Alignment		99.7	24	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of the putative transcriptional regulator sco55502 from streptomyces coelicolor a3(2)
21	c5c8eC_	Alignment	not modelled	99.7	22	**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
22	c5af3A_	Alignment	not modelled	99.7	12	**PDB header:**dna binding **Chain:** A: **PDB Molecule:**vapbc49; **PDBTitle:** x-ray crystal structure of rv2018 from mycobacterium tuberculosis
23	d1q08a_	Alignment	not modelled	99.4	29	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**DNA-binding N-terminal domain of transcription activators
24	c6amaO_	Alignment	not modelled	99.3	30	**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
25	c4j2nB_	Alignment	not modelled	97.9	28	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**gp37; **PDBTitle:** crystal structure of mycobacteriophage pukovnik xis
26	c4j2nA_	Alignment	not modelled	97.7	28	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**gp37; **PDBTitle:** crystal structure of mycobacteriophage pukovnik xis
27	c5ydcA_	Alignment	not modelled	96.9	12	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**uncharacterized hth-type transcriptional regulator rv1828; **PDBTitle:** crystal structure of mercury soaked c-terminal domain of rv1828 from2 mycobacterium tuberculosis
28	c2ev2B_	Alignment	not modelled	96.5	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**hypothetical protein rv1264/mt1302; **PDBTitle:** structure of rv1264n, the regulatory domain of the

						mycobacterial2 adenylyl cylcase rv1264, at ph 8.5
29	c1z4hA_	Alignment	not modelled	95.6	13	**PDB header:**protein binding, dna binding protein **Chain:** A: **PDB Molecule:**tor inhibition protein; **PDBTitle:** the response regulator tori belongs to a new family of2 atypical excisionase
30	c3ezfA_	Alignment	not modelled	95.5	15	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**para; **PDBTitle:** partition protein
31	c1hlvA_	Alignment	not modelled	94.9	20	**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
32	c2wusR_	Alignment	not modelled	93.3	12	**PDB header:**structural protein **Chain:** R: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** bacterial actin mreb assembles in complex with cell shape protein rodz
33	d1j9ia_	Alignment	not modelled	92.9	17	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Terminase gpNU1 subunit domain
34	c1u78A_	Alignment	not modelled	91.9	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
35	c5dukA_	Alignment	not modelled	91.3	21	**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
36	d1j5ya1	Alignment	not modelled	91.3	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
37	c6j05B_	Alignment	not modelled	91.2	11	**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
38	d1stza1	Alignment	not modelled	90.7	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Heat-inducible transcription repressor HrcA, N-terminal domain
39	c3b7hA_	Alignment	not modelled	90.3	17	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**prophage lp1 protein 11; **PDBTitle:** crystal structure of the prophage lp1 protein 11
40	c3cuoB_	Alignment	not modelled	90.1	13	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**uncharacterized hth-type transcriptional regulator ygav; **PDBTitle:** crystal structure of the predicted dna-binding transcriptional2 regulator from e. coli
41	c5j9iH_	Alignment	not modelled	90.0	36	**PDB header:**antitoxin **Chain:** H: **PDB Molecule:**antitoxin iga-2; **PDBTitle:** crystal structure of the higa2 antitoxin c-terminal domain
42	c3clcC_	Alignment	not modelled	89.7	15	**PDB header:**transcription regulator/dna **Chain:** C: **PDB Molecule:**regulatory protein; **PDBTitle:** crystal structure of the restriction-modification controller protein2 c.esp1396i tetramer in complex with its natural 35 base-pair operator
43	d2ppxa1	Alignment	not modelled	88.7	27	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
44	c2ppxA_	Alignment	not modelled	88.7	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu1735; **PDBTitle:** crystal structure of a hth xre-family like protein from agrobacterium2 tumefaciens
45	c2kfsA_	Alignment	not modelled	88.3	22	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**conserved hypothetical regulatory protein; **PDBTitle:** nmr structure of rv2175c
46	d2jn6a1	Alignment	not modelled	88.3	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Cgl2762-like
47	d1utxa_	Alignment	not modelled	88.1	24	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
48	c3fmyA_	Alignment	not modelled	88.0	14	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator mqsa **PDBTitle:** structure of the c-terminal domain of the e. coli protein2 mqsa (ygit/b3021)
49	c3fymA_	Alignment	not modelled	87.7	11	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** the 1a structure of ymfm, a putative dna-binding membrane2 protein from staphylococcus aureus
50	c3jthA_	Alignment	not modelled	87.6	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription activator hlyu; **PDBTitle:** crystal structure of a transcriptional regulator hlyu from2 vibrio vulnificus cmcp6
51	c3op9A_	Alignment	not modelled	87.5	24	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**pli0006 protein; **PDBTitle:** crystal structure of transcriptional regulator from listeria innocua
52	c5jaaB_	Alignment	not modelled	87.2	32	**PDB header:**toxin **Chain:** B: **PDB Molecule:**antitoxin iga-2; **PDBTitle:** crystal structure of the higba2 toxin-antitoxin complex
53	d2b5aa1	Alignment	not modelled	87.1	17	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
54	c2ebyA_	Alignment	not modelled	86.4	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ybaq;

						PDBTitle: crystal structure of a hypothetical protein from e. coli
55	c5lcwN_	Alignment	not modelled	86.4	14	**PDB header:**cell cycle **Chain:** N: **PDB Molecule:**anaphase-promoting complex subunit 2; **PDBTitle:** cryo-em structure of the anaphase-promoting complex/cyclosome, in2 complex with the mitotic checkpoint complex (apc/c-mcc) at 4.23 angstrom resolution
56	d2coba1	Alignment	not modelled	86.3	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Psq domain
57	c2kpjA_	Alignment	not modelled	86.2	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
58	c1r22B_	Alignment	not modelled	85.3	11	**PDB header:**transcription repressor **Chain:** B: **PDB Molecule:**transcriptional repressor smtb; **PDBTitle:** crystal structure of the cyanobacterial metallothionein2 repressor smtb (c14s/c61s/c121s mutant) in the zn2alpha5-3 form
59	c3by6C_	Alignment	not modelled	85.0	20	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**predicted transcriptional regulator; **PDBTitle:** crystal structure of a transcriptional regulator from oenococcus oeni
60	c6j0eB_	Alignment	not modelled	85.0	20	**PDB header:**transcription **Chain:** B: **PDB Molecule:**arsenic responsive repressor arsr; **PDBTitle:** structures of two arsr as(iii)-responsive repressors: implications for2 the mechanism of derepression
61	d1pdnc_	Alignment	not modelled	84.7	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
62	c3bs3A_	Alignment	not modelled	84.6	14	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative dna-binding protein; **PDBTitle:** crystal structure of a putative dna-binding protein from bacteroides2 fragilis
63	c3neuA_	Alignment	not modelled	84.6	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin1836 protein; **PDBTitle:** the crystal structure of a functionally-unknown protein lin1836 from2 listeria innocua clip11262
64	c1stzB_	Alignment	not modelled	84.6	24	**PDB header:**transcription **Chain:** B: **PDB Molecule:**heat-inducible transcription repressor hrca homolog; **PDBTitle:** crystal structure of a hypothetical protein at 2.2 a resolution
65	d1uxca_	Alignment	not modelled	84.3	35	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
66	d1y7ya1	Alignment	not modelled	84.1	13	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
67	c3kxaD_	Alignment	not modelled	83.9	25	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of ngo0477 from neisseria gonorrhoeae
68	c2lkpB_	Alignment	not modelled	83.8	11	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, arsr family; **PDBTitle:** solution structure of apo-nmtr
69	c5d50I_	Alignment	not modelled	83.8	16	**PDB header:**dna binding protein **Chain:** I: **PDB Molecule:**repressor; **PDBTitle:** crystal structure of rep-ant complex from salmonella-temperate phage
70	c1lbgB_	Alignment	not modelled	83.6	9	**PDB header:** **PDB COMPND:**
71	d1r1ta_	Alignment	not modelled	83.4	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ArsR-like transcriptional regulators
72	d1pm6a_	Alignment	not modelled	83.2	21	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Excisionase-like
73	c5chhA_	Alignment	not modelled	83.2	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**arac family transcriptional regulator; **PDBTitle:** crystal structure of transcriptional regulator cdpr from pseudomonas2 aeruginosa
74	c2oqgA_	Alignment	not modelled	83.1	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**possible transcriptional regulator, arsr family protein; **PDBTitle:** arsr-like transcriptional regulator from rhodococcus sp. rha1
75	d2d1ha1	Alignment	not modelled	83.0	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**TrmB-like
76	c5woqA_	Alignment	not modelled	82.8	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator clgr; **PDBTitle:** crystal structure of an xre family protein transcriptional regulator2 from mycobacterium smegmatis
77	d2hsga1	Alignment	not modelled	82.8	25	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
78	c3omtA_	Alignment	not modelled	82.7	5	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** putative antitoxin component, chu_2935 protein, from xre family from2 prevotella buccae.
79	c4omzG_	Alignment	not modelled	82.7	13	**PDB header:**transcription **Chain:** G: **PDB Molecule:**nolr; **PDBTitle:** crystal structure of nolr from sinorhizobium fredii

80	d1r69a_	Alignment	not modelled	82.2	23	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
81	c5yszA_	Alignment	not modelled	82.0	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** transcriptional regulator celr-cellobiose complex
82	c5xxuZ_	Alignment	not modelled	81.9	13	**PDB header:**ribosome **Chain:** Z: **PDB Molecule:**ribosomal protein es25; **PDBTitle:** small subunit of toxoplasma gondii ribosome
83	c5tmxA_	Alignment	not modelled	81.7	15	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**protein sini; **PDBTitle:** solution structure of sini, antagonist to the master biofilm-regulator2 sinr in bacillus subtilis
84	d1x57a1	Alignment	not modelled	81.6	18	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**EDF1-like
85	d1adra_	Alignment	not modelled	81.6	9	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
86	d1uxda_	Alignment	not modelled	81.6	35	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
87	d1mkma1	Alignment	not modelled	81.4	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcriptional regulator IclR, N-terminal domain
88	c1efaA_	Alignment	not modelled	81.1	9	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**lac repressor; **PDBTitle:** crystal structure of the lac repressor dimer bound to operator and the2 anti-inducer onpf
89	c3vk0B_	Alignment	not modelled	80.9	14	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of hypothetical transcription factor nhtf from2 neisseria
90	c2kkoB_	Alignment	not modelled	80.8	20	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**possible transcriptional regulatory protein **PDBTitle:** solution nmr structure of the homodimeric winged helix-turn-2 helix dna-binding domain (fragment 1-100) mb0332 from3 mycobacterium bovis, a possible arsr-family transcriptional4 regulator. northeast structural genomics consortium target5 mbr242e.
91	c4gqmA_	Alignment	not modelled	80.6	12	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**ct009; **PDBTitle:** crystal structure of a helix-turn-helix containing hypothetical2 protein (ct009) from chlamydia trachomatis in a sub-domain swap3 conformation
92	c6paxA_	Alignment	not modelled	80.6	18	**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
93	d1sq8a_	Alignment	not modelled	80.6	18	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
94	c3h5tA_	Alignment	not modelled	80.3	16	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of a transcriptional regulator, lacl2 family protein from corynebacterium glutamicum
95	c1b0nA_	Alignment	not modelled	80.1	23	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**protein (sinr protein); **PDBTitle:** sinr protein/sini protein complex
96	d1ku9a_	Alignment	not modelled	79.9	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**DNA-binding protein Mj223
97	d1jt6a1	Alignment	not modelled	79.8	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
98	c5wayB_	Alignment	not modelled	79.8	22	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional activator; **PDBTitle:** mgaspn protein, mga regulator from streptococcus pneumoniae
99	c3f52A_	Alignment	not modelled	79.6	23	**PDB header:**transcription activator **Chain:** A: **PDB Molecule:**clp gene regulator (clgr); **PDBTitle:** crystal structure of the clp gene regulator clgr from c. glutamicum
100	d2ofya1	Alignment	not modelled	79.6	32	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
101	c4ghjA_	Alignment	not modelled	79.4	32	**PDB header:**transcription **Chain:** A: **PDB Molecule:**probable transcriptional regulator; **PDBTitle:** 1.75 angstrom crystal structure of transcriptional regulator ftom2 vibrio vulnificus.
102	d1r1ua_	Alignment	not modelled	79.4	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ArsR-like transcriptional regulators
103	c3kjxD_	Alignment	not modelled	79.4	16	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of a transcriptional regulator, lacl2 family protein from silicibacter pomeroyi
104	c3dnvB_	Alignment	not modelled	79.3	27	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**hth-type transcriptional regulator hipb; **PDBTitle:** mdt protein
105	d2r1jl1	Alignment	not modelled	79.0	9	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors

106	c1zljE_	Alignment	not modelled	78.8	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
107	d1b0na2	Alignment	not modelled	78.8	23	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
108	d2o7ta1	Alignment	not modelled	78.8	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
109	c3t76A_	Alignment	not modelled	78.6	18	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator vanug; **PDBTitle:** crystal structure of transcriptional regulator vanug, form ii
110	d1t56a1	Alignment	not modelled	78.5	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
111	c4ivnB_	Alignment	not modelled	78.5	32	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator; **PDBTitle:** the vibrio vulnificus nanr protein complexed with mannac-6p
112	c3mlfC_	Alignment	not modelled	78.4	23	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcriptional regulator; **PDBTitle:** putative transcriptional regulator from staphylococcus aureus.
113	d1lcda_	Alignment	not modelled	78.3	20	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
114	c3f6vA_	Alignment	not modelled	78.3	19	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**possible transcriptional regulator, arsr family protein; **PDBTitle:** crystal structure of possible transcriptional regulator for arsenical2 resistance
115	c3trbA_	Alignment	not modelled	78.1	14	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**virulence-associated protein i; **PDBTitle:** structure of an addiction module antidote protein of a higa (higa)2 family from coxiella burnetii
116	c2rn7A_	Alignment	not modelled	78.0	23	**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
117	c4ybaA_	Alignment	not modelled	78.0	23	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**regulatory protein c; **PDBTitle:** the structure of the c.kpn2i controller protein
118	c2jvlA_	Alignment	not modelled	77.8	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**trmbf1; **PDBTitle:** nmr structure of the c-terminal domain of mbf1 of trichoderma reesei
119	d2icta1	Alignment	not modelled	77.8	14	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
120	c2ef8A_	Alignment	not modelled	77.4	23	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**putative transcription factor; **PDBTitle:** crystal structure of c.ecot38is