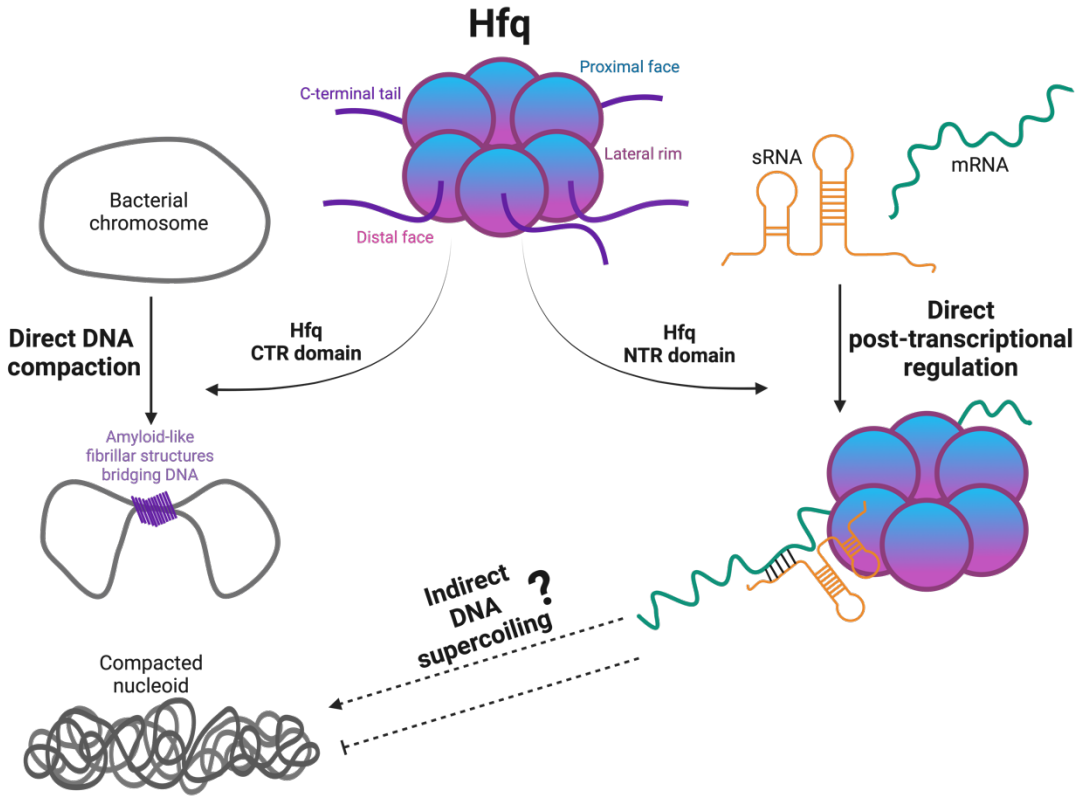


Figure 1. Hfq: a dual-function protein. Hfq is a homohexameric protein. Each monomer is composed of two domains named the N-terminal region (NTR) and the C-terminal region (CTR). The six NTRs forming the toroidal structure can be divided into three parts: the proximal face (in blue), the distal face (in pink) and the lateral rim. Hfq is an RNA chaperone that facilitates base pairing between sRNAs (in orange) and their mRNA target (in green): the U-rich 3'-end of sRNA binds to the proximal face, whereas A-rich sequences of mRNA bind to the distal face of Hfq (right panel). Hfq binds DNA *via* the CTR domain (C-terminal tail in purple), inducing the formation of long amyloid-like fibrillar structures that bridge the chromosome and lead to DNA compaction (left panel). Figure created using BioRender.com.

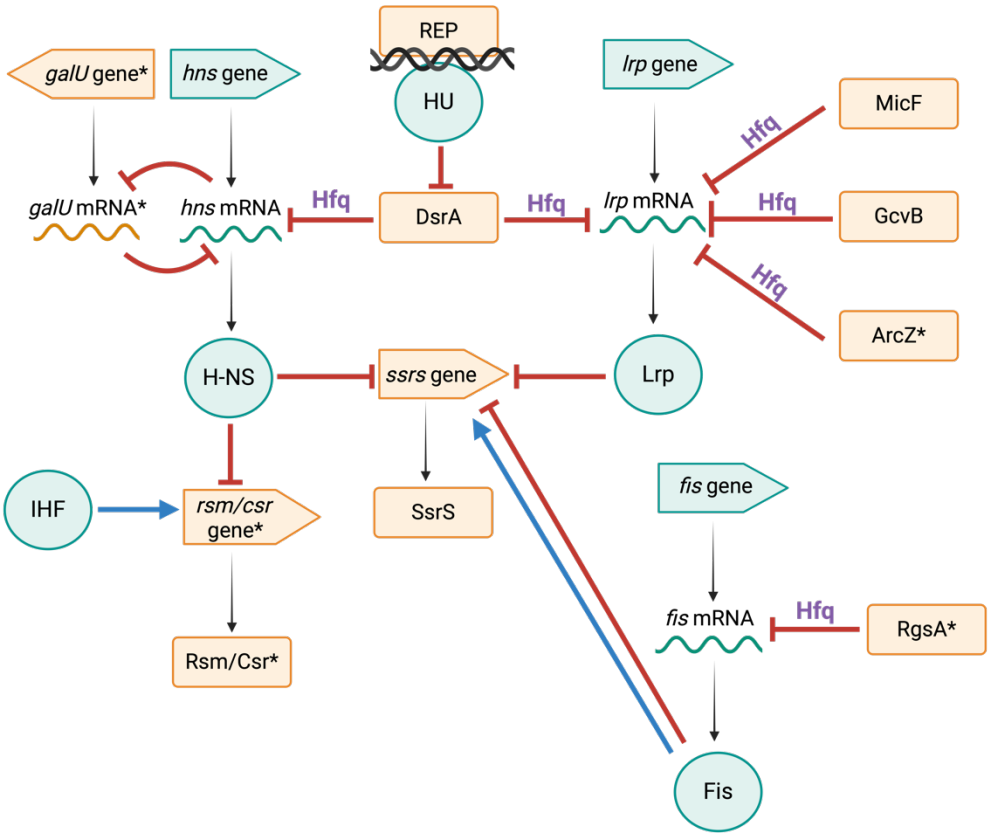


Figure 2. Regulatory network involving NAPs and sRNAs in Gram-negative bacteria. The regulation by NAPs occurs at the transcriptional level while the regulation by sRNAs occurs at the post-transcriptional level. NAPs are shown in green; regulatory RNAs in orange; Hfq acting as a RNA chaperon in purple; positive regulation is indicated by a blue arrow and negative regulation by a red bar. Asterisks indicate interactions that have not been demonstrated in *E. coli*. In particular, *rsm/csr* genes are inhibited by H-NS homologues in *P. aeruginosa* and activated by IHF in *P. fluorescens*, *S. enterica* and *E. amylovora.* RgsA repression of Fis is specific to *P. aeruginosa,* ArcZ repression of *lrp* is specific to *E. amylovora,* and mutual repression of the bifunctional RNAs *galU* mRNA and *hns* mRNA has only been demonstrated in *S. enterica*. Figure created using BioRender.com.

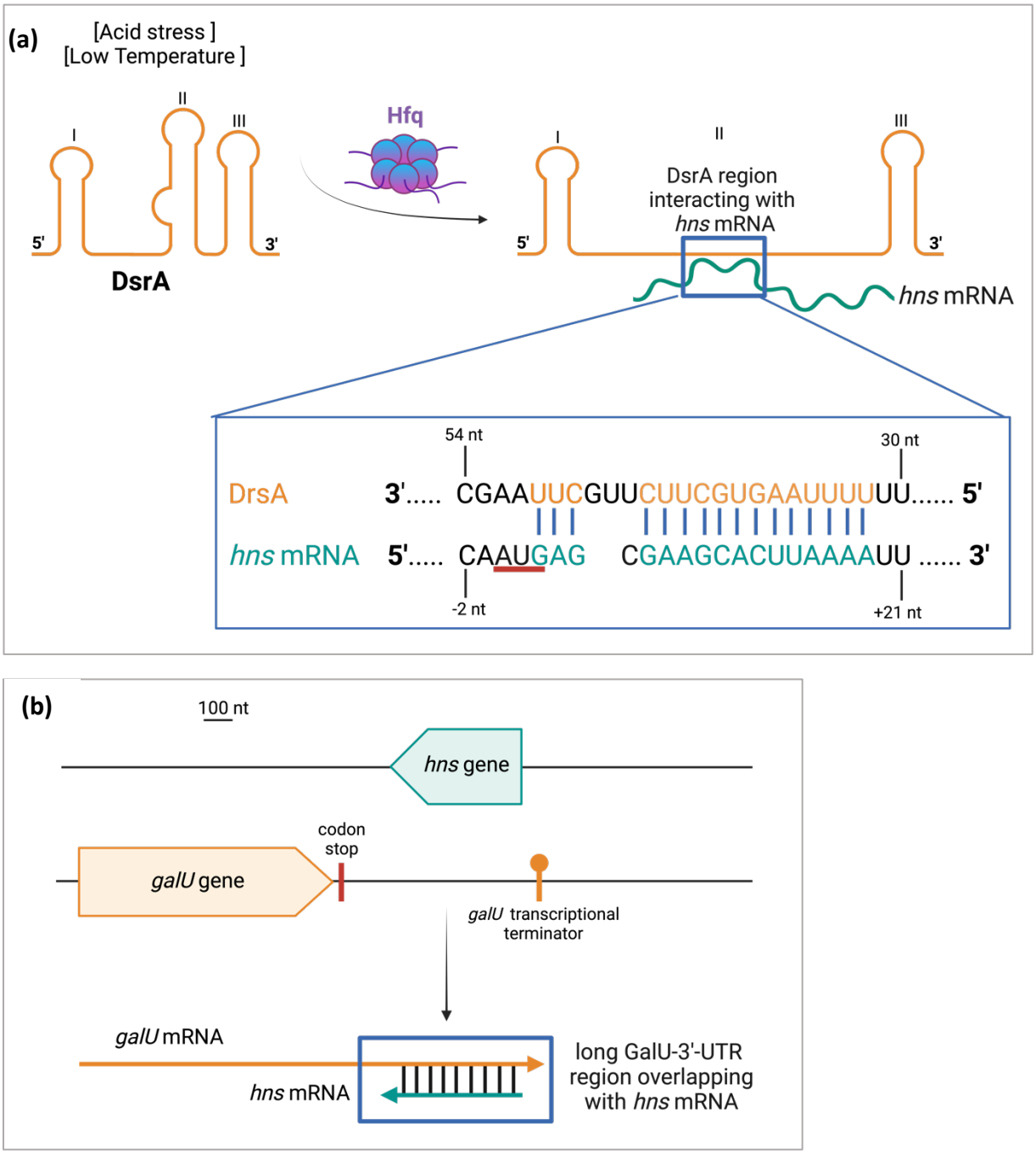
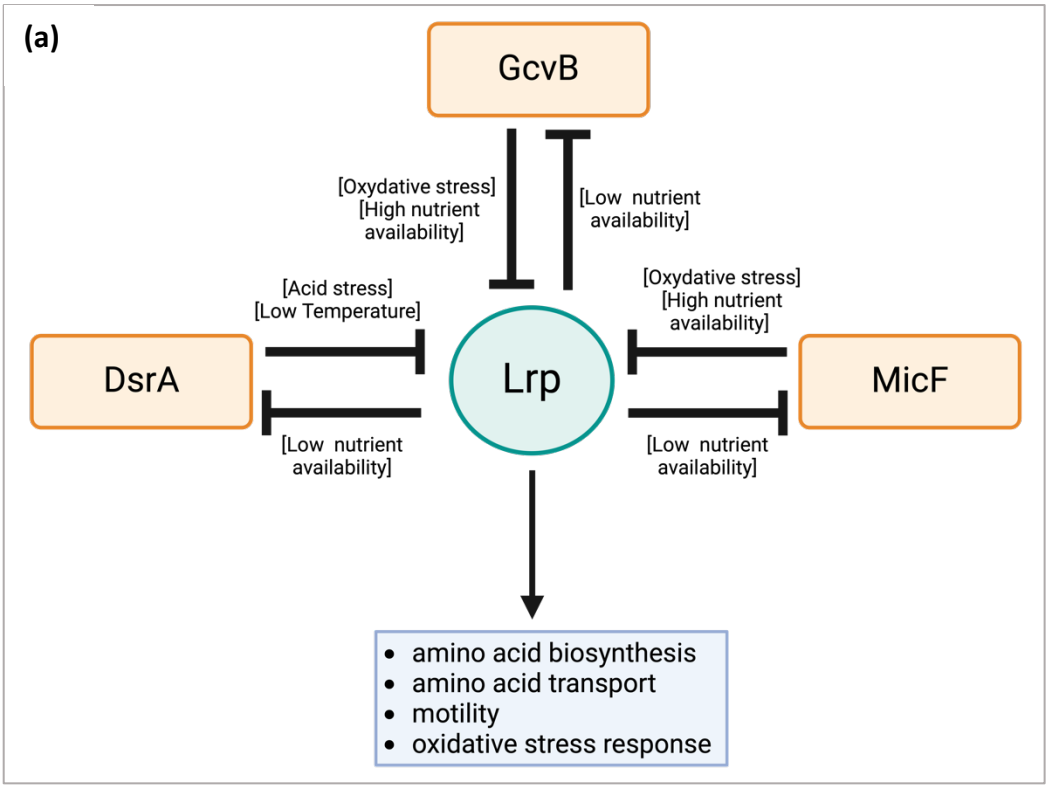
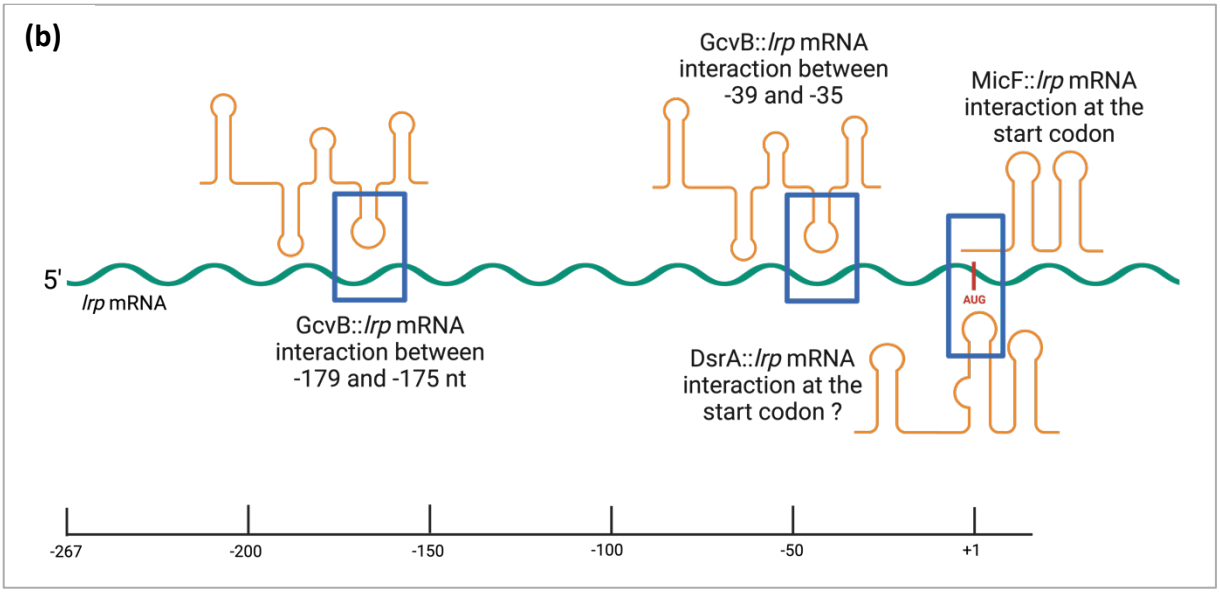
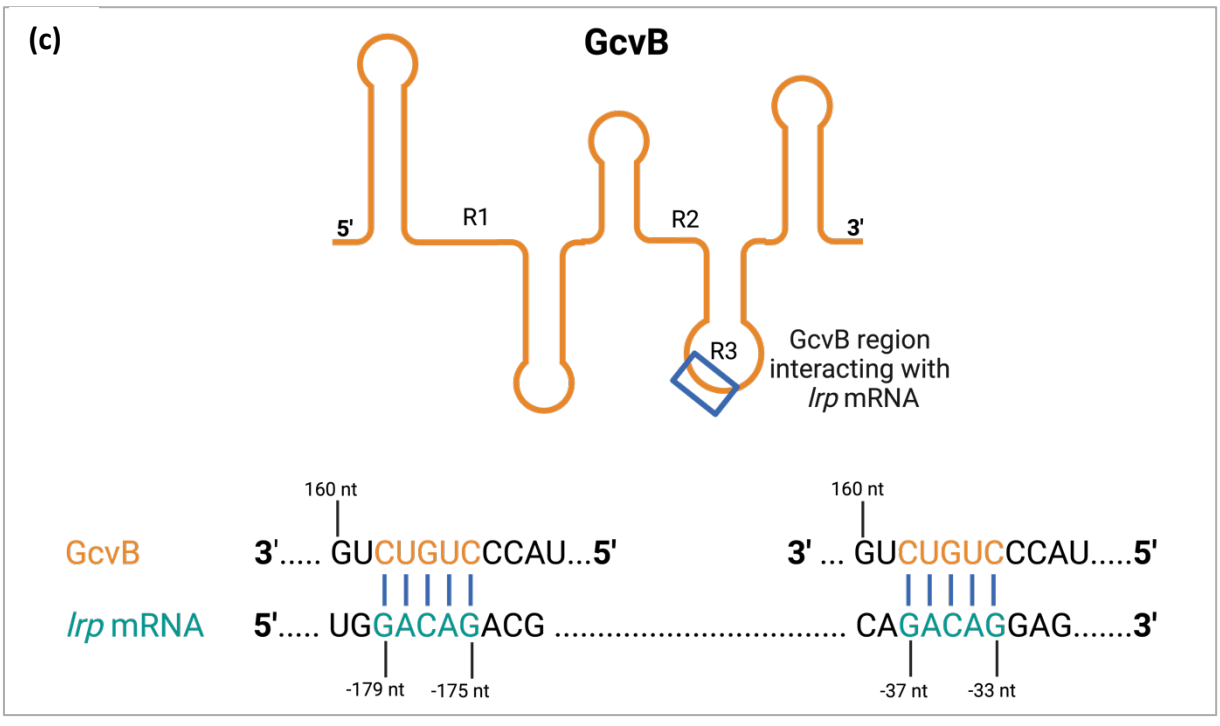


Figure 3. Post-transcriptional regulation of *hns* mRNA. (a) The DsrA sRNA, which is structured in three stem-loops (in orange), alters the stability of the *hns* mRNA and reduces the synthesis of the H-NS protein. Hfq alters the structure of the DsrA stem-loop II, allowing base pairing with *hns* mRNA at the translation initiation region (TIR). The interaction sequences between DsrA and *hns* mRNA are shown in the frame. The sequences are numbered according to the start codon for *hns* (in red). **(b)** The *hns* and *galU* genes are organized in a convergence on the chromosomal double-stranded DNA. The long 3'UTR region of *galU* overlaps with the *hns* mRNA. The transcriptional termination site of *galU* is estimated to be between 584 and 701 nucleotides downstream of the *galU* termination codon, represented by a horizontal red line. Figure created using BioRender.com.


(a)
GcvB
[Oxydative stress]
[High nutrient availability]
[Low nutrient availability]
[Acid stress]
[Low Temperature]
[Oxydative stress]
[High nutrient availability]
DsrA
Lrp
MicF
[Low nutrient availability]
[Low nutrient availability]
amino acid biosynthesis
amino acid transport
motility
oxidative stress response


(b)
GcvB::lrp mRNA interaction between -39 and -35
MicF::lrp mRNA interaction at the start codon
5'
lrp mRNA
AUG
GcvB::lrp mRNA interaction between -179 and -175 nt
DsrA::lrp mRNA interaction at the start codon ?
-267
-200
-150
-100
-50
+1


(c)
GcvB
5'
R1
R2
3'
R3
GcvB region interacting with lrp mRNA
160 nt
160 nt
GcvB
3'..... GUCUGUCCCAU...5'
3' ... GUCUGUCCCAU.....5'
lrp mRNA
5'..... UGGACAGACG ..... CAGACAGGAG.....3'
-179 nt
-175 nt
-37 nt
-33 nt

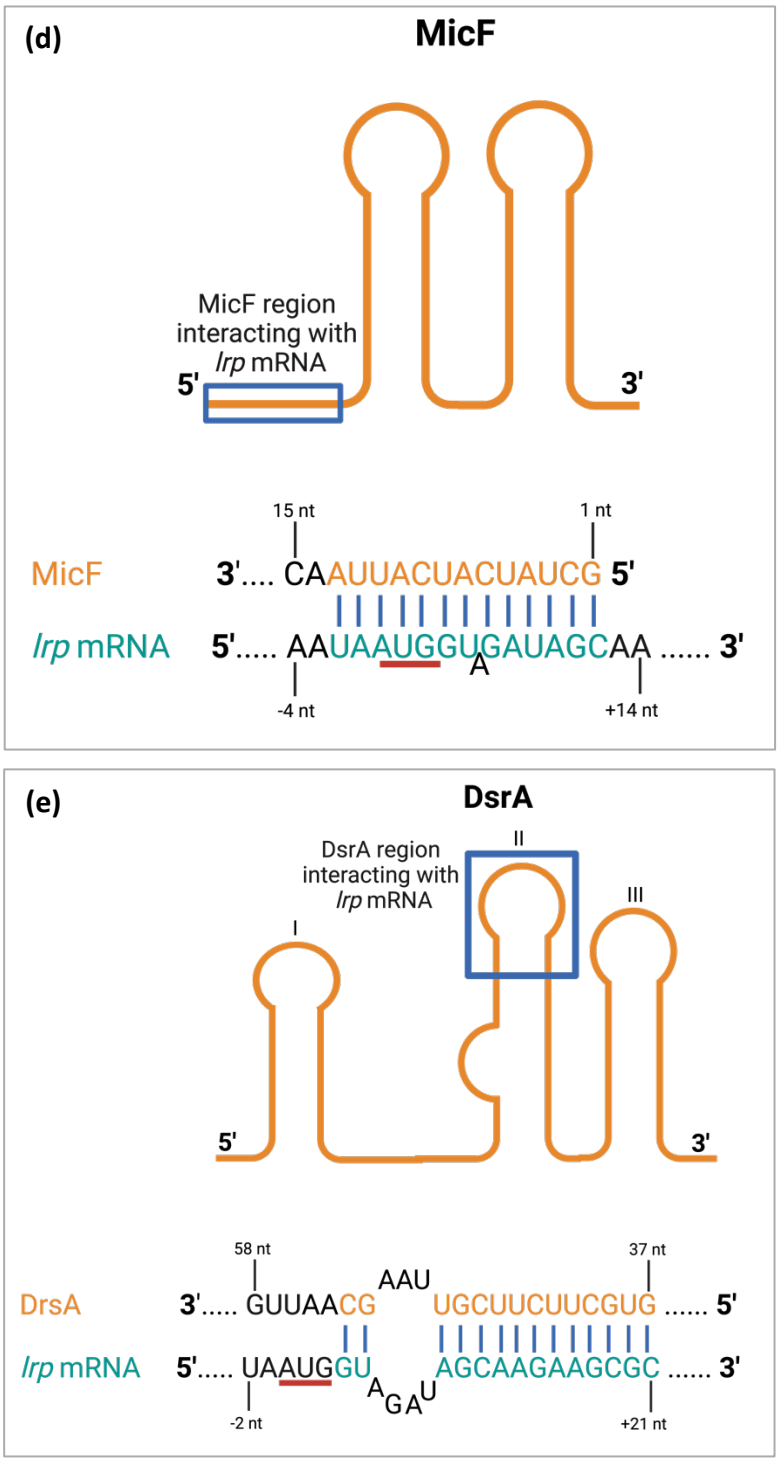


Figure 4. Regulation of Lrp by several sRNAs in *E. coli*. (a) The mutual regulation of Lrp and the sRNAs DrsA, GcvB and MicF. The physiological state that induces the regulation is shown between square brackets, negative regulation is shown by black bars and the Lrp regulon is summarized in the light blue box. **(b)** The three sRNAs (DsrA, GcvB and MicF) bind to the long 5'-untranslated leader region (5'UTR) of *lrp* and repress the *lrp* mRNA translation. **(c-d-e)** The binding sites of sRNAs and *lrp* mRNA, together with the positions of these binding sites within the structures of the sRNAs. Regions R1, R2 and R3 for GcvB and domains I, II and III for DsrA are indicated. sRNAs are shown in orange, mRNA in green. The numbering of *lrp* mRNA is relative to the AUG, which is underlined in red. Figure created using BioRender.com.

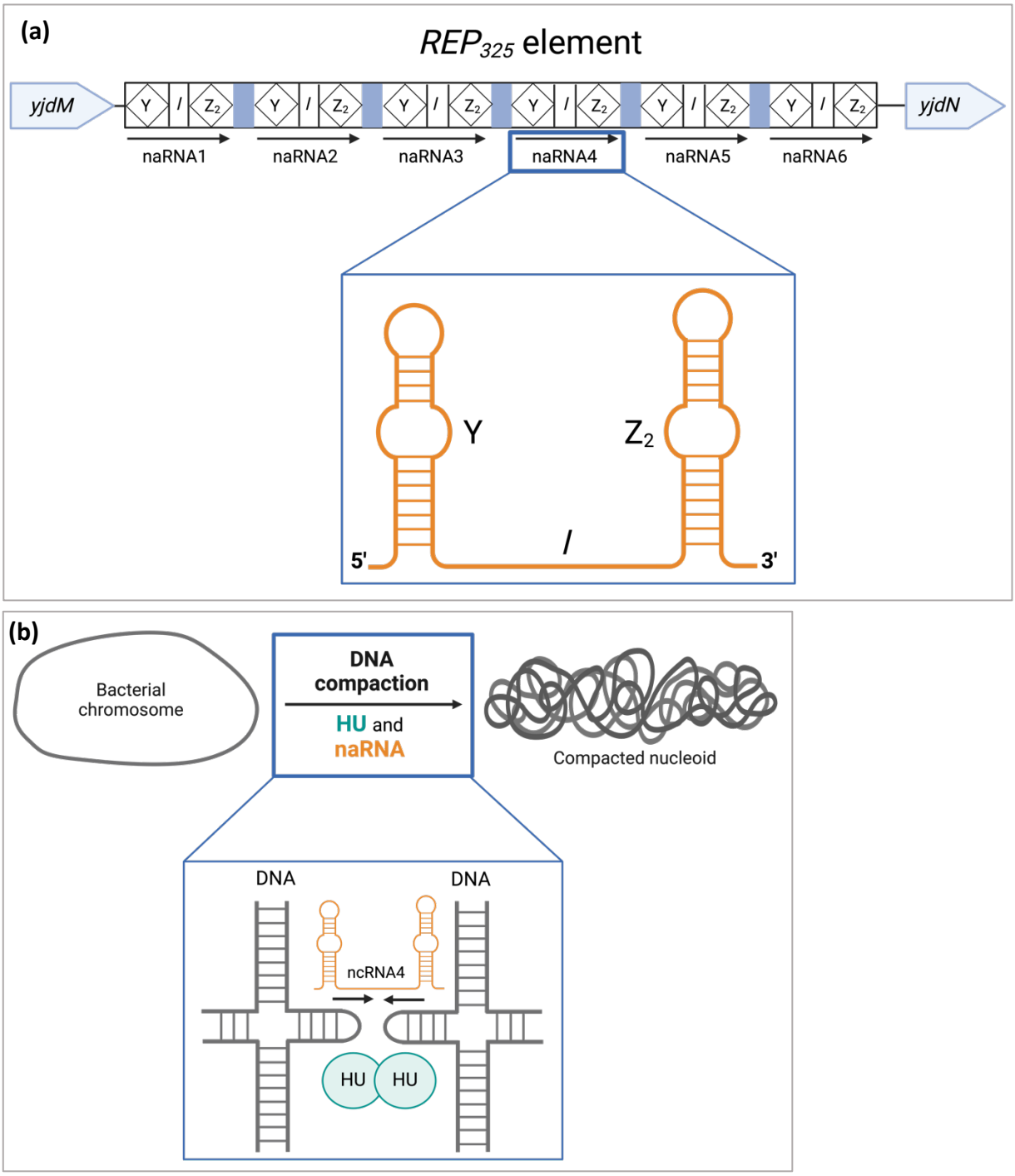


Figure 5. Schematic representation of HU- and naRNA-mediated DNA condensation. (a) The *REP*$_{325}$ element is located in the intergenic region between the *yjdM* and *yjdN*. The element consists of 6 homologous repeats separated by 5 unknown spacers with exactly the same DNA sequence (in blue). The transcripts of the 6 repeats are named naRNA1 to naRNA6. Each unit contains the palindrome Y and the palindrome Z_2, which are separated by a constant linker (*I*). The predicted secondary structure of naRNA4 contains a Y motif and a Z_2 motif, connected by a linker (*I*) (Qian et al., 2017). **(b)** Cruciform DNA structures may be bridged together by the ncRNA4 encoded by the *REP*$_{325}$ element. This interaction is facilitated by an HU dimer and leads to DNA condensation. Figure created using BioRender.com.