

Box 13.3

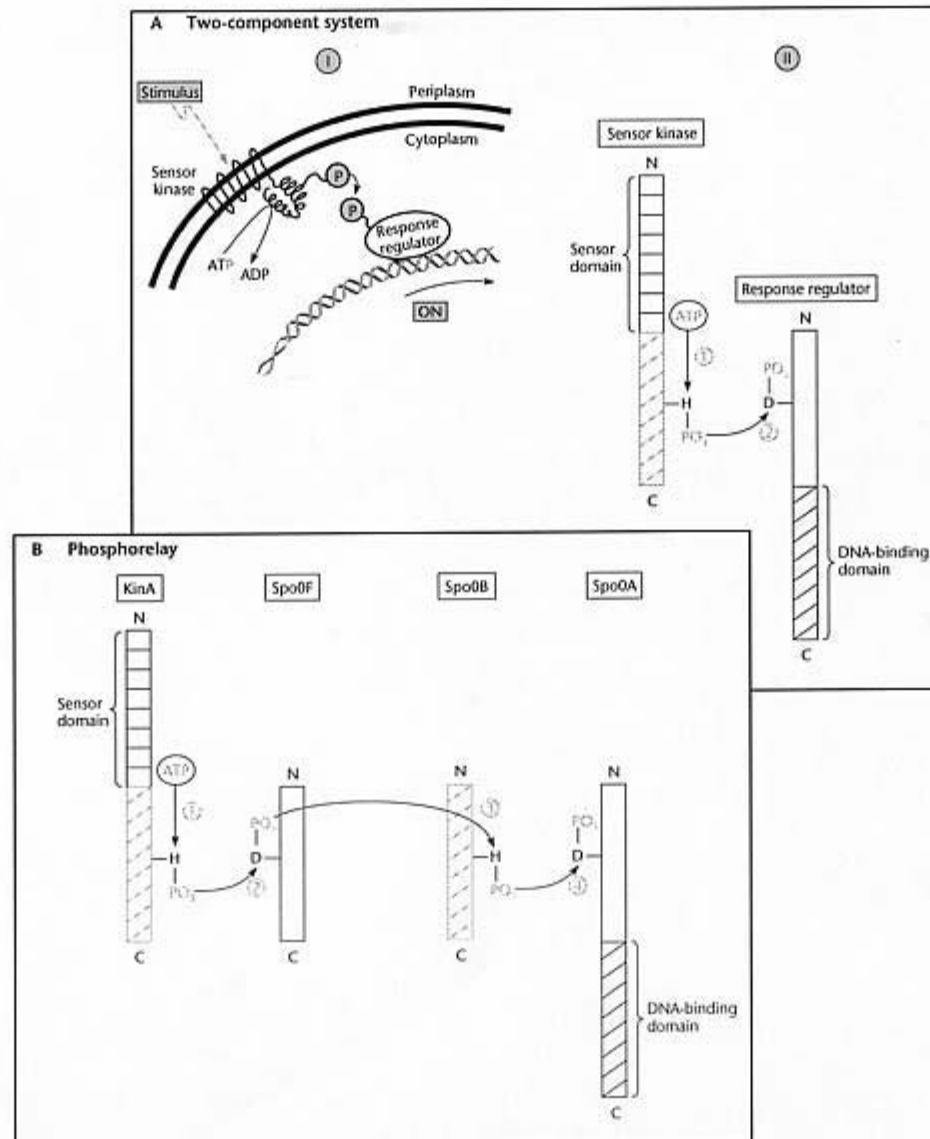


Figure 13.11

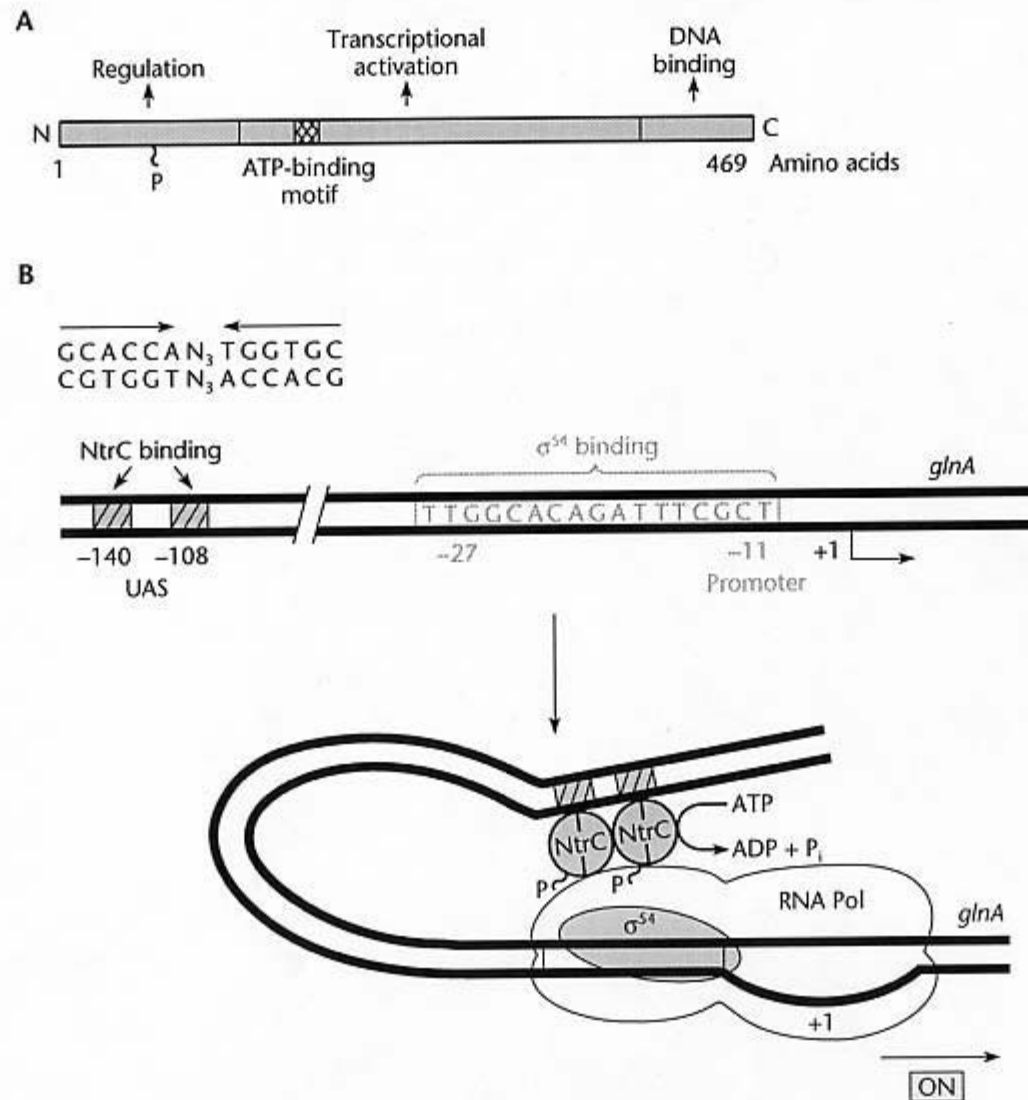
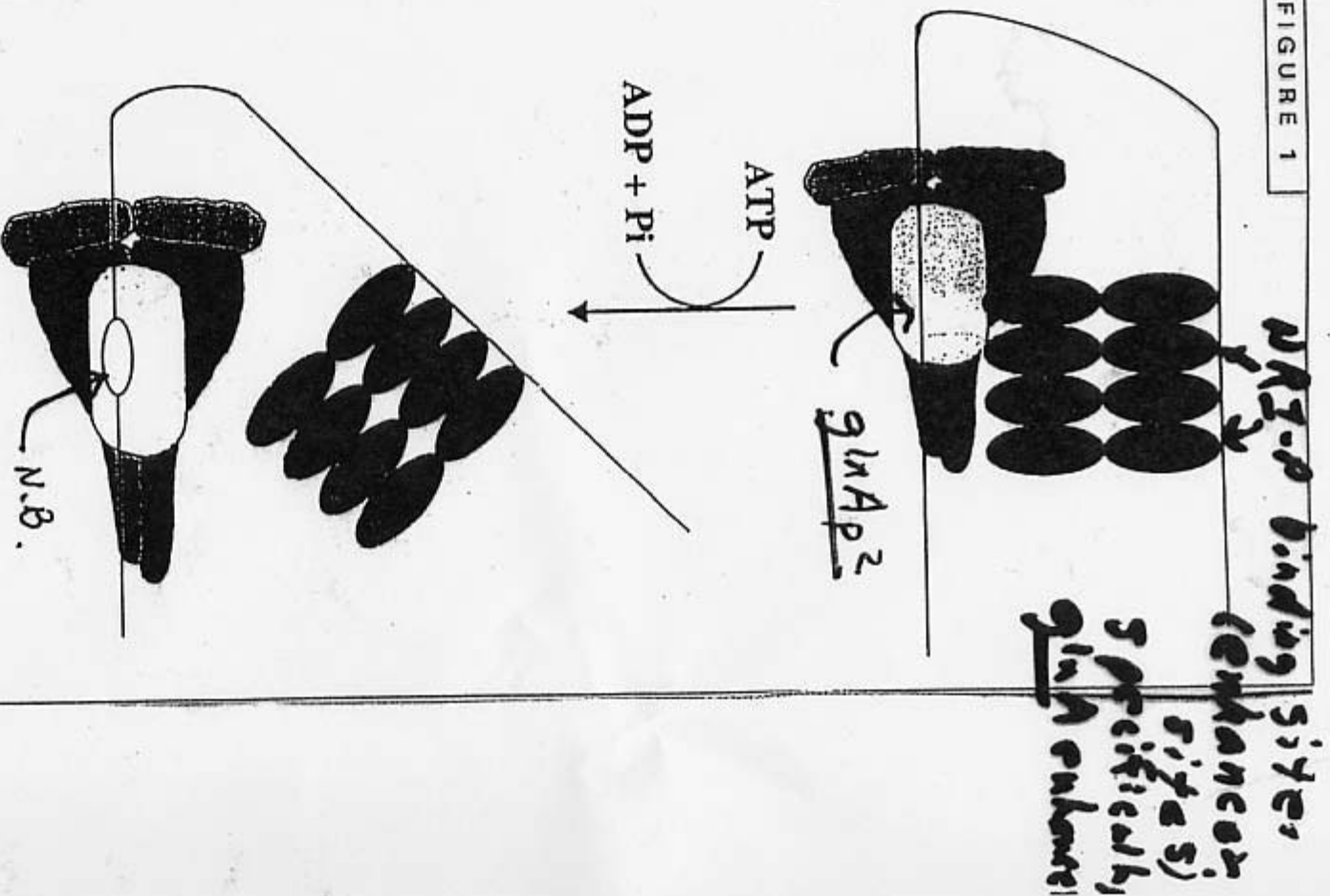


FIGURE 1



Mechanism of transcriptional activation by σ^{54} -holoenzyme. Activators of σ^{54} -holoenzyme (magenta) bind cooperatively to sites upstream of the promoter to form an oligomeric complex. The complex contacts σ^{54} -holoenzyme through DNA looping and catalyzes the isomerization of the closed complex between σ^{54} -holoenzyme and the promoter to an open complex. This isomerization requires ATP hydrolysis by the activator. The activator is believed to contact σ^{54} (yellow) and the β subunit of RNA polymerase (green) to activate transcription. The α and β' subunits of RNA polymerase are indicated in blue and red, respectively.

glnAp2 enhancer

N.R.T.-P = bacterial enhancer binding protein
 Activates σ^{54} holoenzyme

Figure 13.9

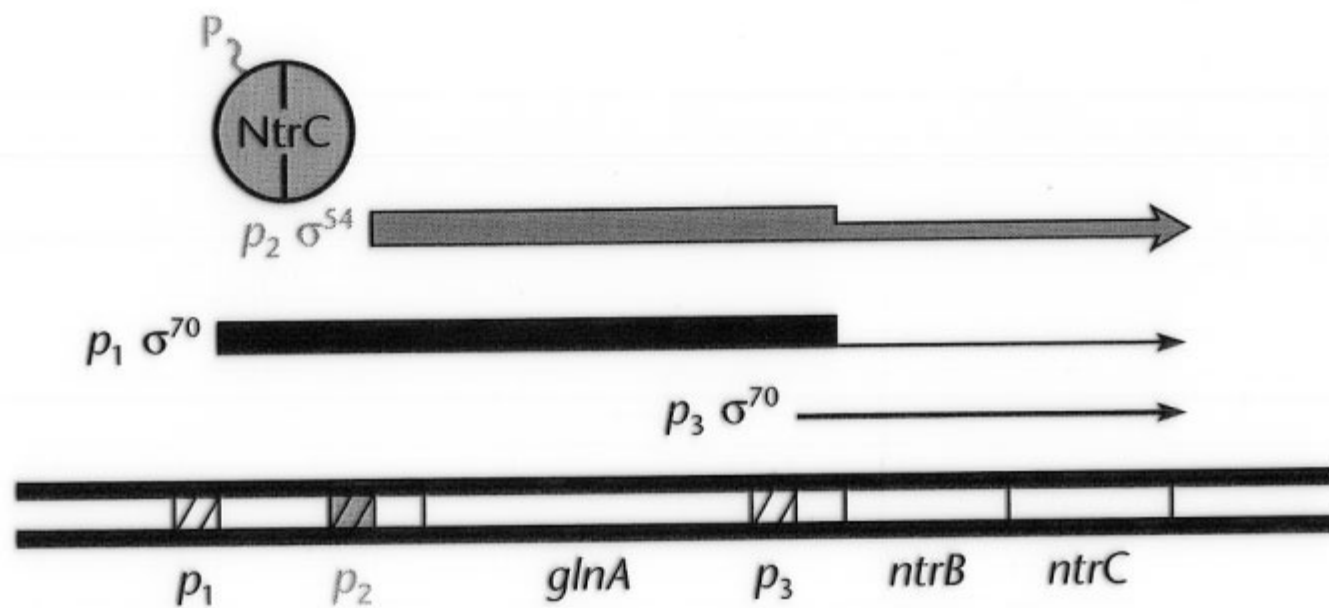


Table 13.2

TABLE 13.2 Genes for nitrogen regulation			
Gene	Alternate name	Product	Function
<i>glnA</i>		Glutamine synthetase	Synthesize glutamine
<i>glnB</i>		P _{II} , P _{II} -UMP —	Inhibit phosphatase of NtrB, activate adenylyltransferase
<i>glnD</i>		Uridyltransferase (UTase)/Uridyl-removing enzyme (UR)	Transfer UMP to and from P _{II}
<i>glnE</i>		Adenylyltransferase (ATase)	Transfer AMP to glutamine synthetase
<i>glnF</i>	<i>rpoN</i>	σ^{54}	RNA polymerase recognition of promoters of Ntr operons
<i>ntrC</i>	<i>glnG</i>	NtrC, NtrC-PO ₄	Activator of promoters of Ntr operons
<i>ntrB</i>	<i>glnL</i>	NtrB, NtrB-PO ₄	Autokinase, phosphatase; phosphate transferred to NtrC

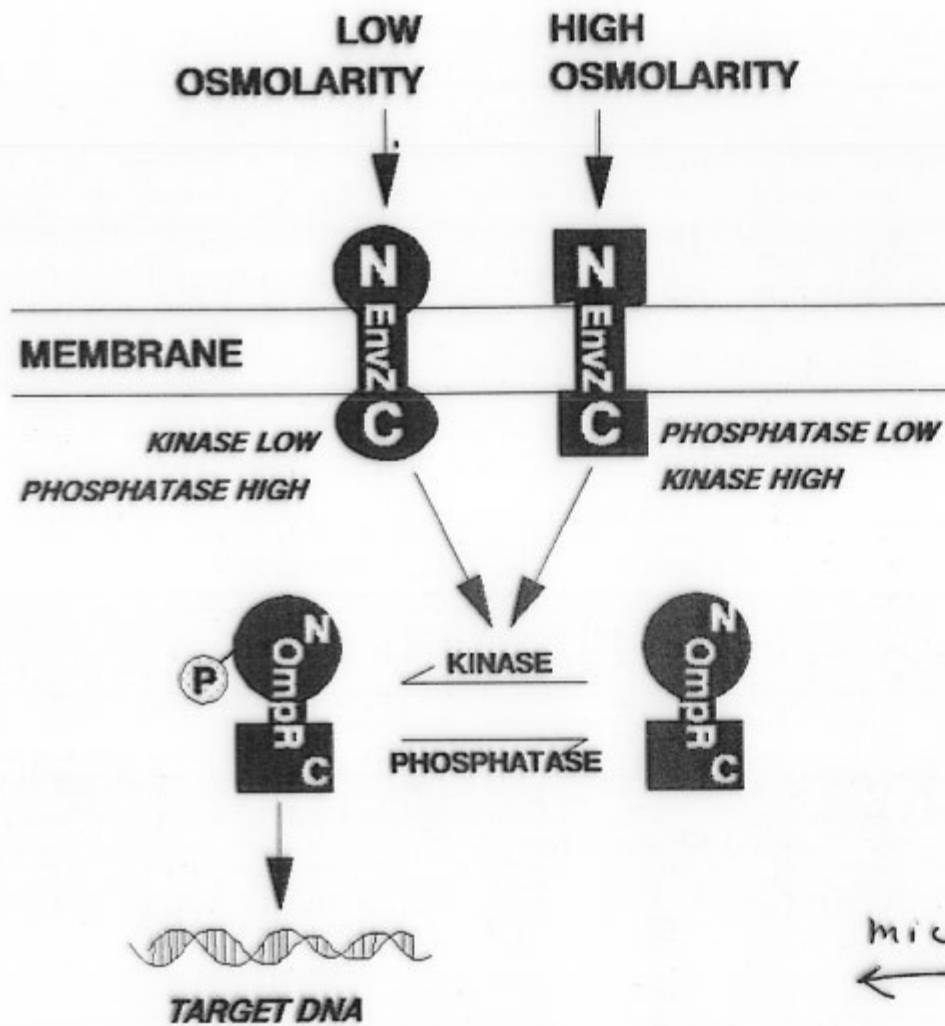
Table 13.3

TABLE 13.3 Phenotypes of <i>envZ</i> and <i>ompR</i> mutations	
Genotype	Phenotype
<i>envZ</i> ⁺ <i>ompR</i> ⁺	OmpC ⁺ OmpF ⁺
<i>envZ</i> ⁺ <i>ompR1</i>	OmpC ⁻ OmpF ⁻
! <i>envZ</i> (null) <i>ompR</i> ⁺	OmpC ⁻ OmpF ^{+a}
<i>envZ</i> ⁺ <i>ompR2</i> (Con)	OmpC ⁻ OmpF ⁺ (low osmolarity) OmpC ⁻ OmpF ⁺ (high osmolarity)
<i>envZ</i> (null) <i>ompR2</i> (Con)	OmpC ⁻ OmpF ⁺ (low osmolarity) OmpC ⁻ OmpF ⁺ (high osmolarity)
<i>envZ</i> ⁺ <i>ompR3</i> (Con)	OmpC ⁺ OmpF ⁻ (low osmolarity) OmpC ⁺ OmpF ⁻ (high osmolarity)
! <i>envZ</i> ⁺ <i>ompR3</i> (Con)/ <i>envZ</i> ⁺ <i>ompR</i> ⁺	OmpC ⁺ OmpF ⁻ (low osmolarity) OmpC ⁺ OmpF ⁻ (high osmolarity)

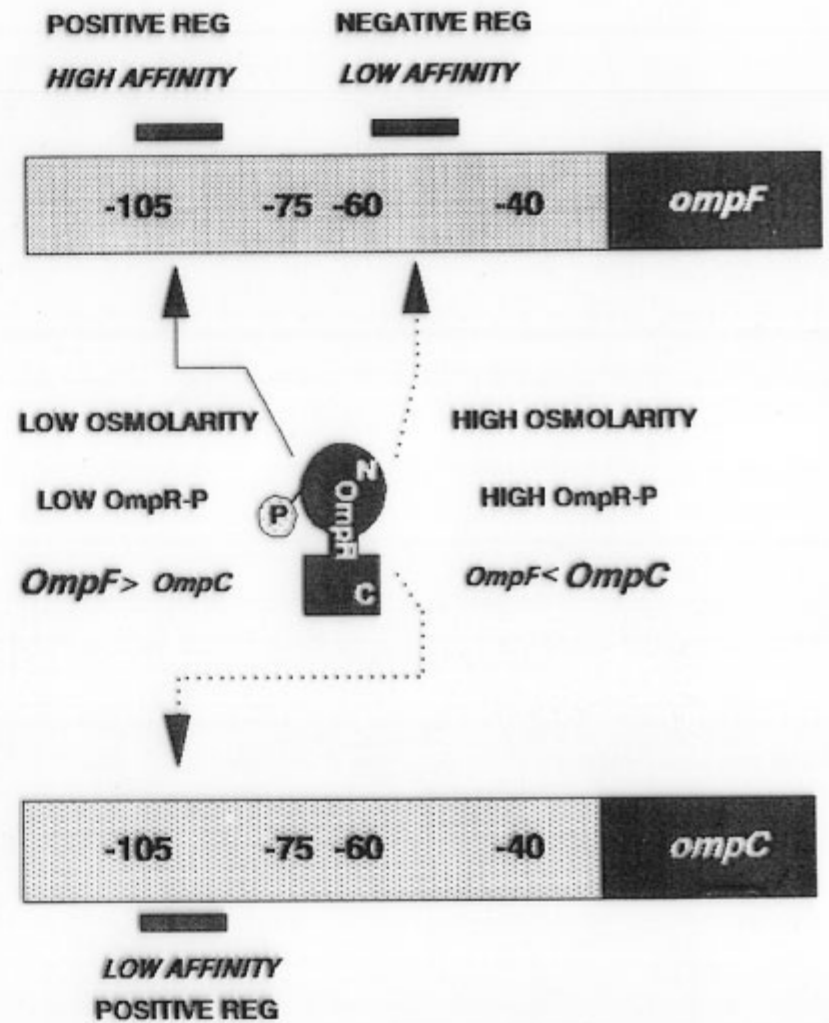
^a+ - indicates that OmpF levels are reduced but not eliminated.

OmpC pores are smaller than OmpF pores
OmpC predominates in high
osmolarity environments (& at
higher temps)

EnvZ: sensor/transmitter; modulator; protein kinase; HK
 OmpR: receiver/regulator; effector; phosphorylated response; RR



(a)

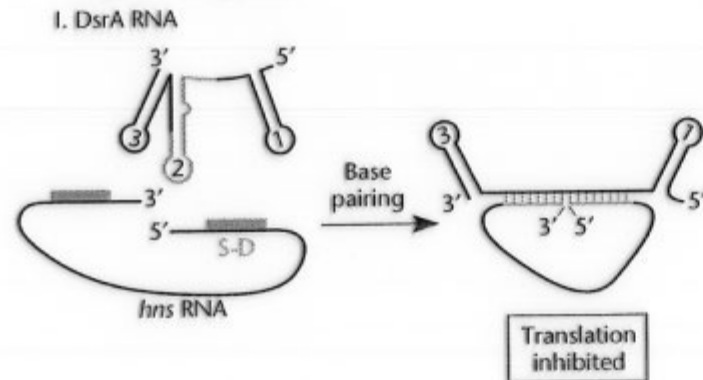


(b)

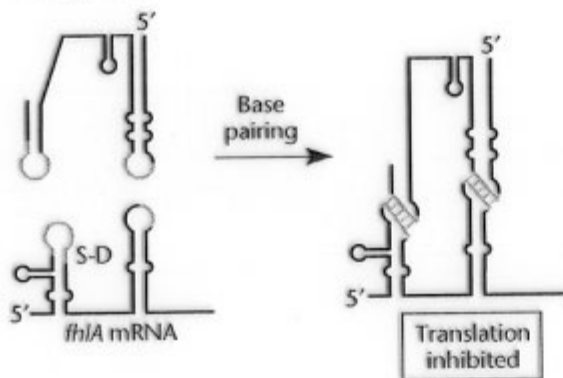
Fig. 4-21. Osmoregulation of major outer-membrane proteins OmpF and OmpC (see text for details).

Box 13.5

A Negative regulation

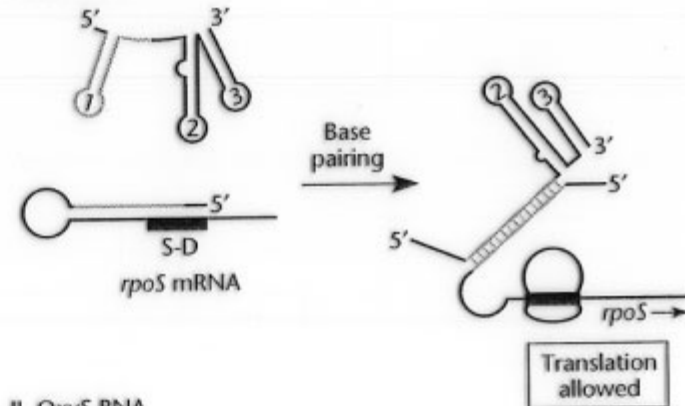


II. OxyS RNA

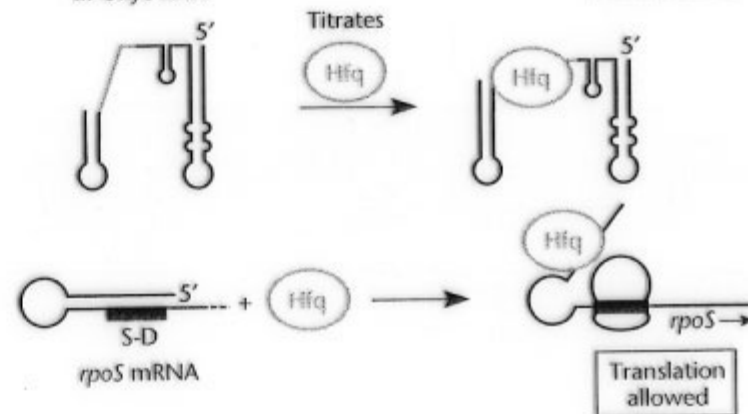


B Positive regulation

I. DsrA RNA



II. OxyS RNA



Hfq = RNA chaperone (promotes annealing)
 (Mol. Mic 50(4) 1111 (03))