

Table 13.1

| TABLE 13.1 Some <i>E. coli</i> global regulatory systems |                                                                          |                                        |                                     |                                                                                                                                                                                             |
|----------------------------------------------------------|--------------------------------------------------------------------------|----------------------------------------|-------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| System                                                   | Response                                                                 | Regulatory gene(s)<br>(protein[s])     | Category of<br>mechanism            | Some genes and<br>operons regulated                                                                                                                                                         |
| A. Nutrient limitation                                   |                                                                          |                                        |                                     |                                                                                                                                                                                             |
| Carbon                                                   | Catabolite repression                                                    | <i>crp</i> (CAP, also called CRP)      | DNA-binding activator or repressor  | <i>lac</i> , <i>ara</i> , <i>gal</i> , <i>mal</i> , and numerous other C source operons                                                                                                     |
|                                                          | Control of fermentative vs oxidative metabolism                          | <i>cra</i> ( <i>fruR</i> ) (CRA)       | DNA-binding activator or repressor  | Enzymes of glycolysis, Krebs cycle                                                                                                                                                          |
| Nitrogen                                                 | Response to ammonia limitation                                           | <i>rpoN</i> (NtrA)                     | Sigma factor ( $\sigma^{54}$ )      | <i>glnA</i> (GS) and operons for amino acid degradation                                                                                                                                     |
| Phosphorus                                               | Starvation for inorganic orthophosphate (P <sub>i</sub> )                | <i>ntrBC</i> (NtrBC)                   | Two-component system                | >38 genes, including <i>phoA</i> (bacterial alkaline phosphatase) and <i>pst</i> operon (P <sub>i</sub> uptake)                                                                             |
|                                                          |                                                                          | <i>phoBR</i> (PhoBR)                   | Two-component system                |                                                                                                                                                                                             |
| B. Growth limitation                                     |                                                                          |                                        |                                     |                                                                                                                                                                                             |
| Stringent response                                       | Response to lack of sufficient aminoacylated-tRNAs for protein synthesis | <i>relA</i> (RelA), <i>spoT</i> (SpoT) | (p)ppGpp metabolism                 | rRNA, tRNA                                                                                                                                                                                  |
| Stationary phase                                         | Switch to maintenance metabolism and stress protection                   | <i>rpoS</i> (RpoS)                     | Sigma factor ( $\sigma^s$ )         | >40 genes, including <i>otsBA</i> (trehalose synthesis) and <i>dps</i> (DNA-binding protein)                                                                                                |
| Oxygen                                                   | Response to anaerobic environment                                        | <i>fnr</i> (Fnr)                       | CAP family of DNA-binding protein   | >31 transcripts, including <i>narGHJ</i> (nitrate reductase)                                                                                                                                |
|                                                          |                                                                          | <i>arcAB</i> (ArcAB)                   | Two-component system                | >20 genes, including <i>cob</i> (cobalamin synthesis)                                                                                                                                       |
| C. Stress                                                |                                                                          |                                        |                                     |                                                                                                                                                                                             |
| Osmoregulation                                           | Response to abrupt osmotic upshift                                       | <i>kdpDE</i> (KdpD, KdpE)              | Two-component system                | <i>kdpFABC</i> (K <sup>+</sup> uptake system)                                                                                                                                               |
|                                                          | Adjustment to osmotic environment                                        | <i>rpoS</i> (RpoS)                     | Sigma factor ( $\sigma^s$ )         | >16 genes, including <i>osmB</i> (an outer membrane lipoprotein)                                                                                                                            |
|                                                          |                                                                          | <i>envZ/ompR</i> (EnvZ/OmpR)           | Two-component system                | OmpC and OmpF outer membrane porins                                                                                                                                                         |
| Oxygen stress                                            | Protection against reactive oxygen species                               | <i>micF</i>                            | Antisense RNA                       | <i>ompF</i> (porin)                                                                                                                                                                         |
|                                                          |                                                                          | <i>soxS</i> (SoxS)                     | AraC family of DNA-binding proteins | >10 genes, including <i>sodA</i> (superoxide dismutase) and <i>micF</i> (antisense RNA regulator of <i>ompF</i> )                                                                           |
| Heat shock                                               | Tolerance to abrupt temperature increase                                 | <i>oxyR</i> (OxyR)                     | LysR family of DNA-binding proteins | >10 genes, including <i>katG</i> (catalase)                                                                                                                                                 |
|                                                          |                                                                          | <i>rpoH</i> (RpoH)                     | Sigma factor ( $\sigma^{32}$ )      | >20 genes encoding Hsps (heat shock proteins), including <i>dnaK</i> , <i>dnaJ</i> , and <i>grpE</i> (chaperones), and <i>lon</i> , <i>clpP</i> , <i>clpX</i> , and <i>hflB</i> (proteases) |
|                                                          |                                                                          | <i>rpoE</i> (RpoE)                     | Sigma factor ( $\sigma^{24}$ )      | >10 genes, including <i>rpoH</i> ( $\sigma^{32}$ ) and <i>degP</i> (a periplasmic protease)                                                                                                 |
| pH shock                                                 | Tolerance of acidic environment                                          | <i>cadC</i> (CadC)                     | ToxR-related DNA-binding protein    | Many genes, including <i>cadBA</i> (amino acid decarboxylase)                                                                                                                               |

Figure 13.1

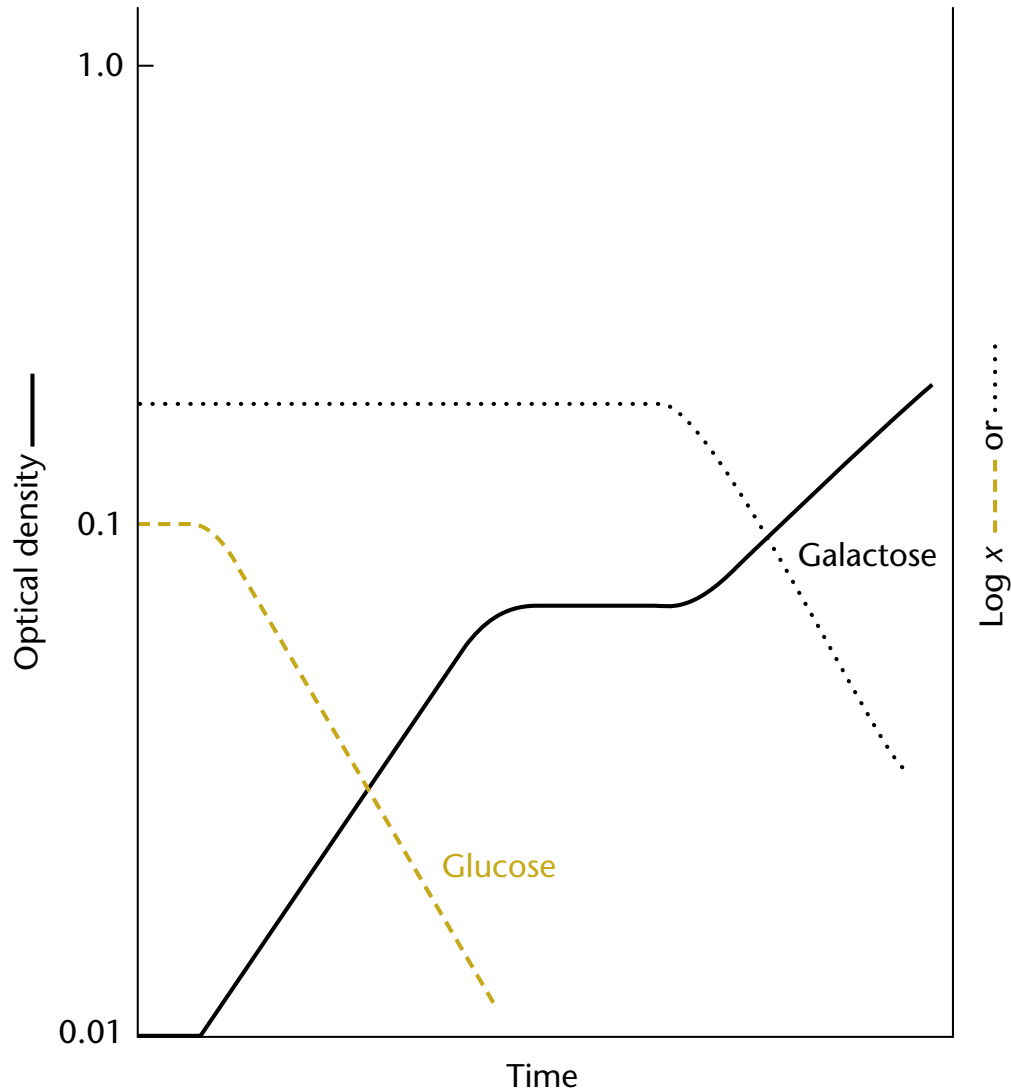
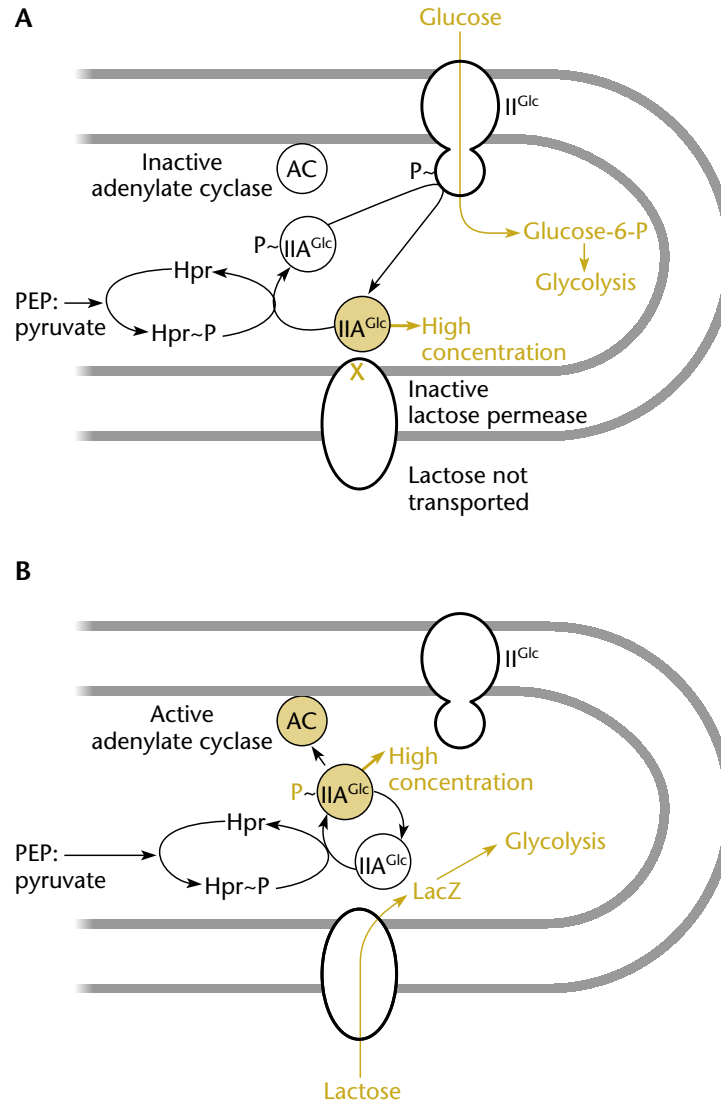
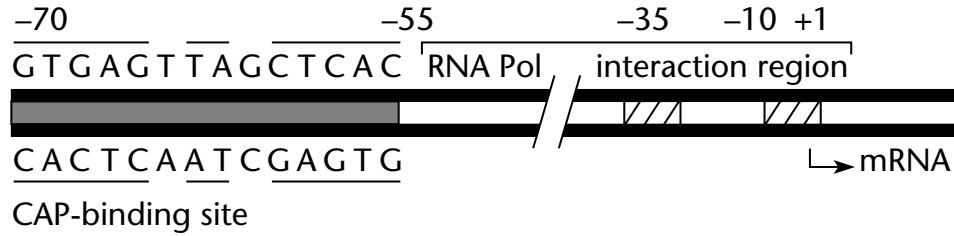
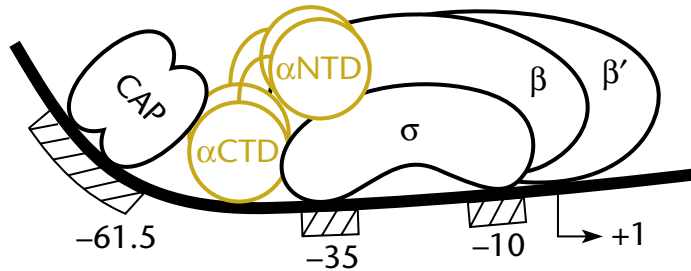


Figure 13.2

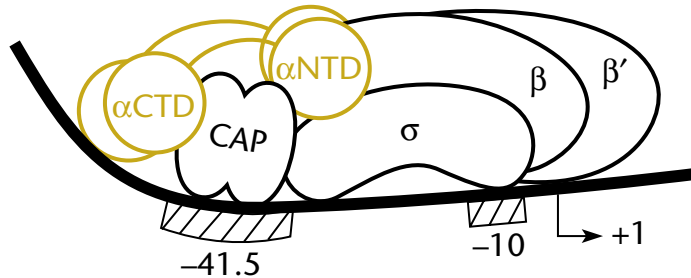


**Figure 13.3****A****B**

Class I promoter



Class II promoter



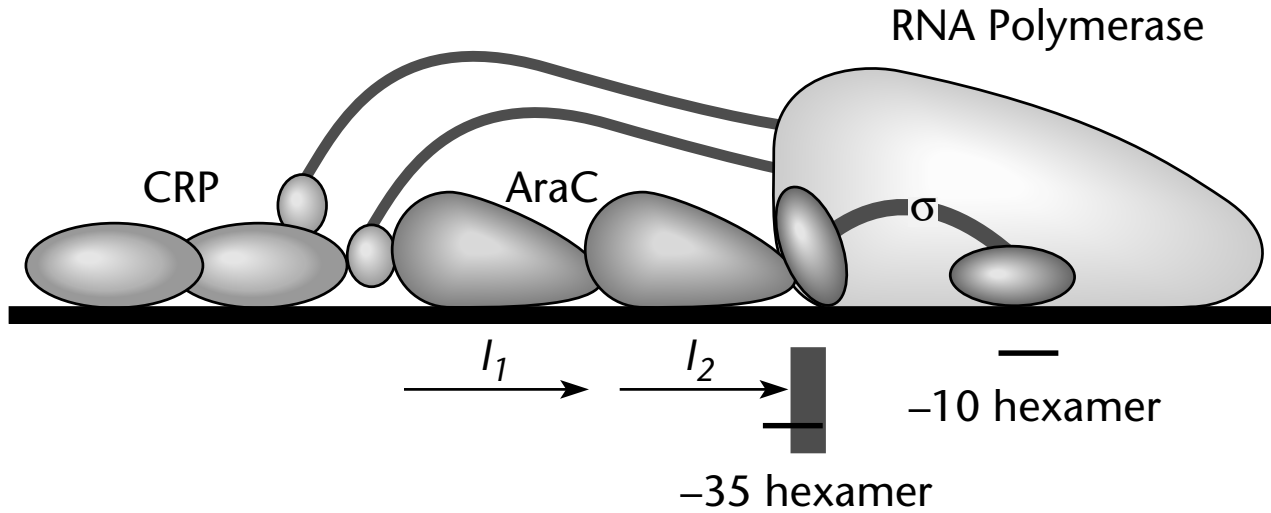
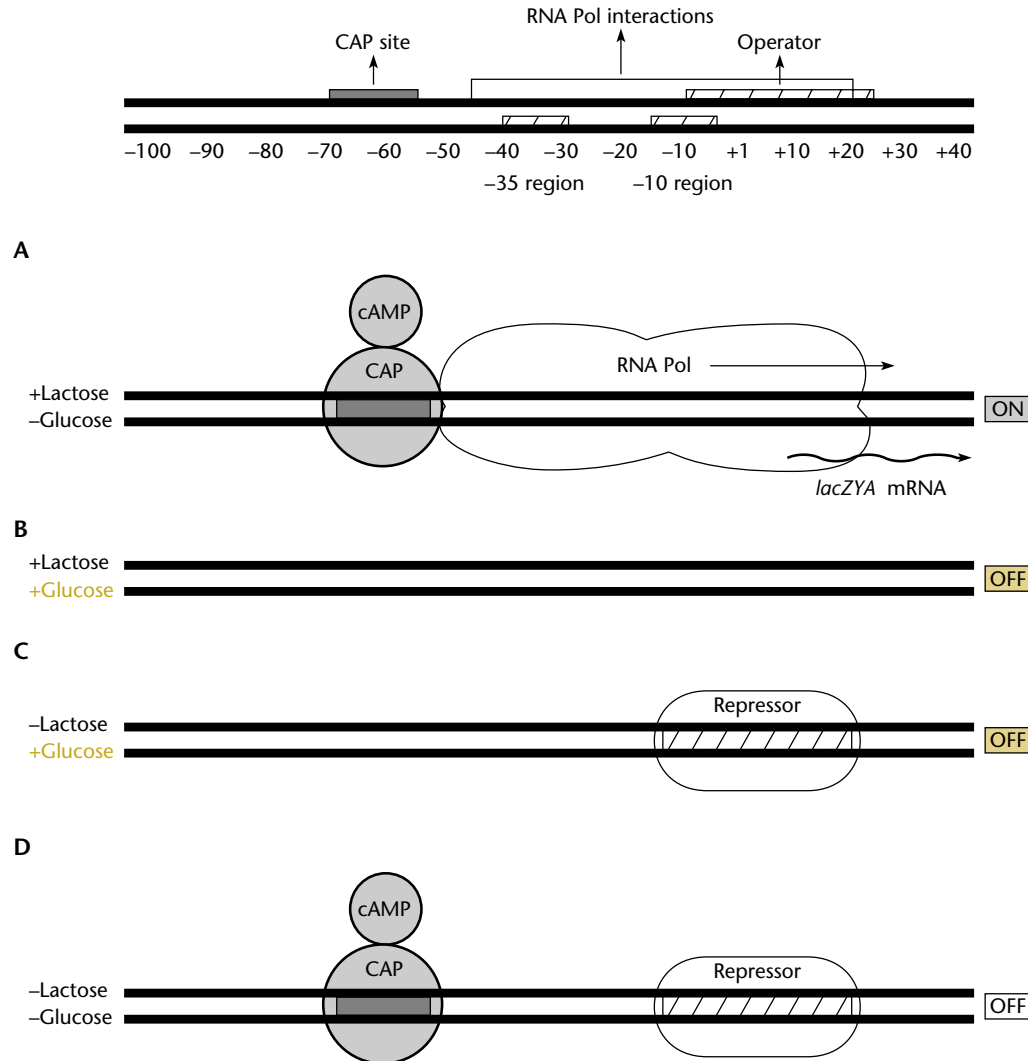
**Figure 13.4**

Figure 13.5



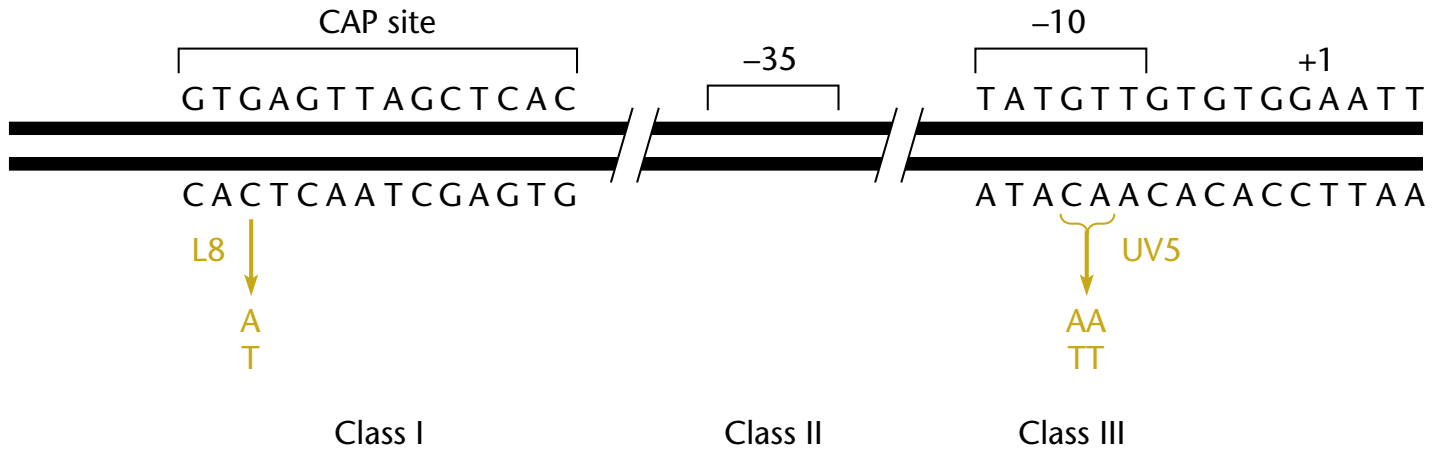
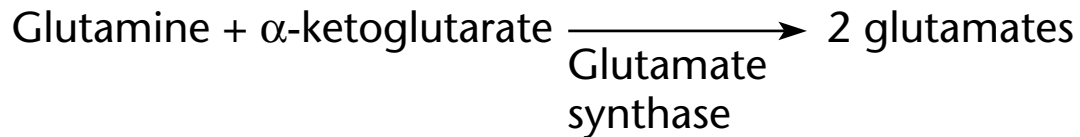
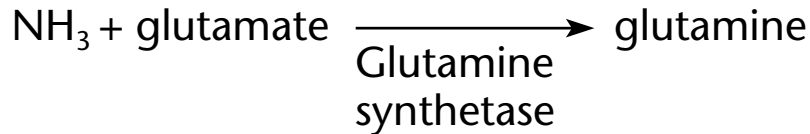
**Figure 13.6**

Figure 13.7

Low  $\text{NH}_3$



High  $\text{NH}_3$

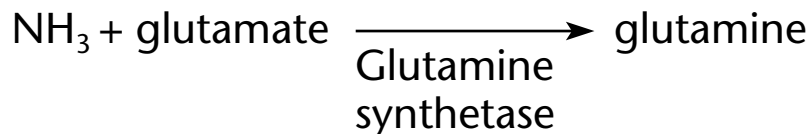
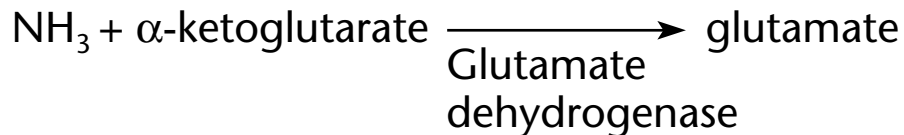
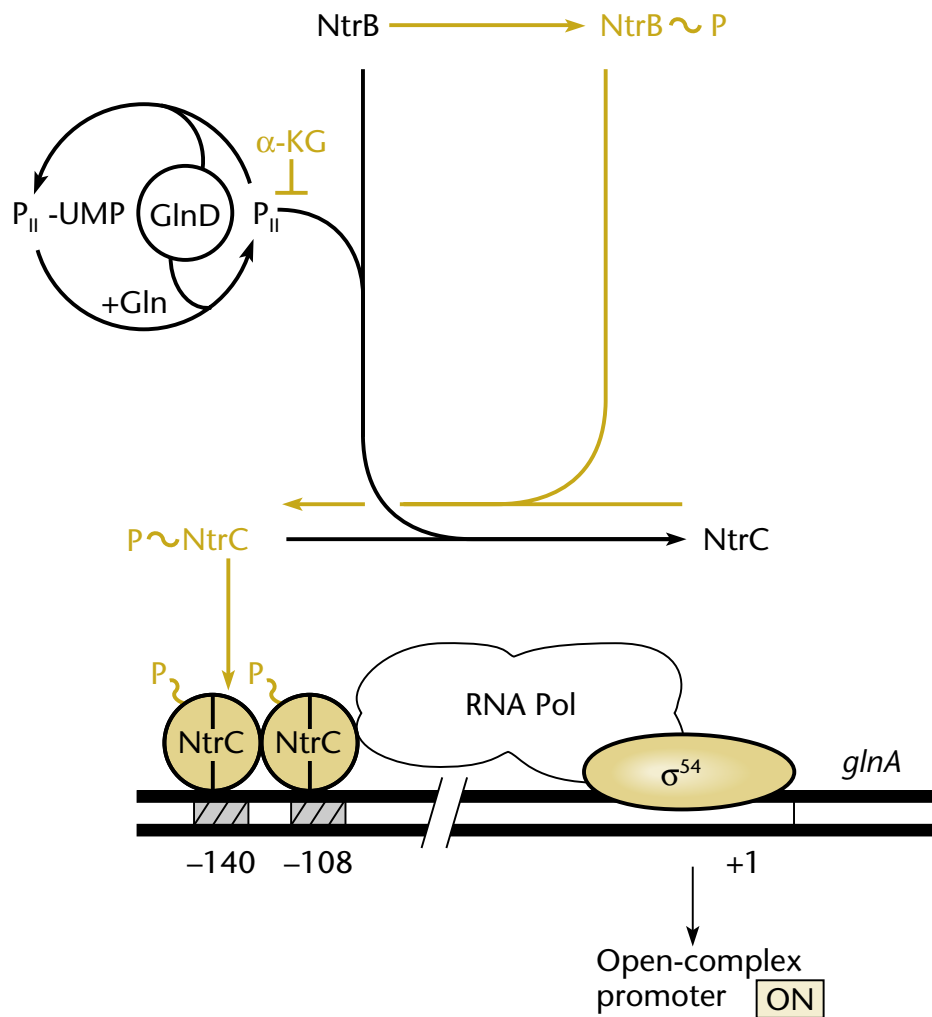
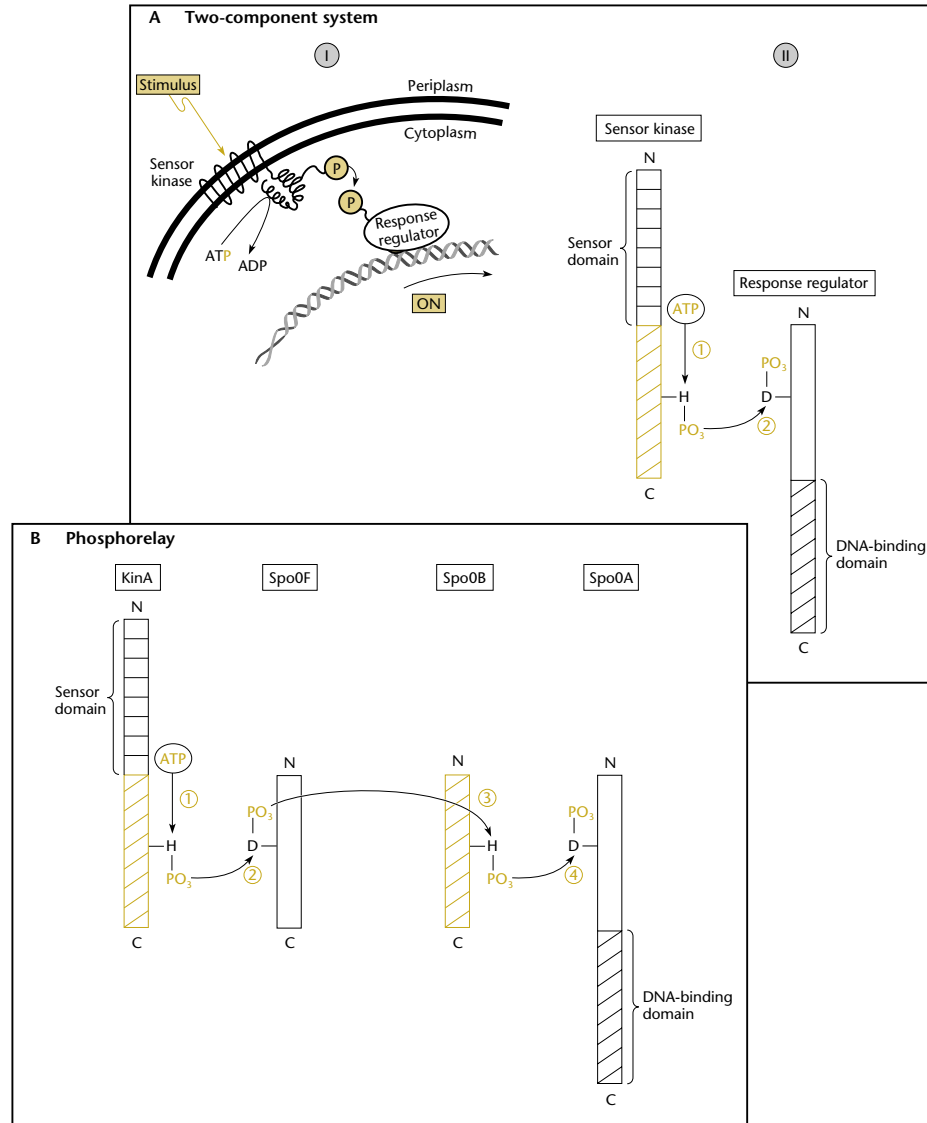


Figure 13.8

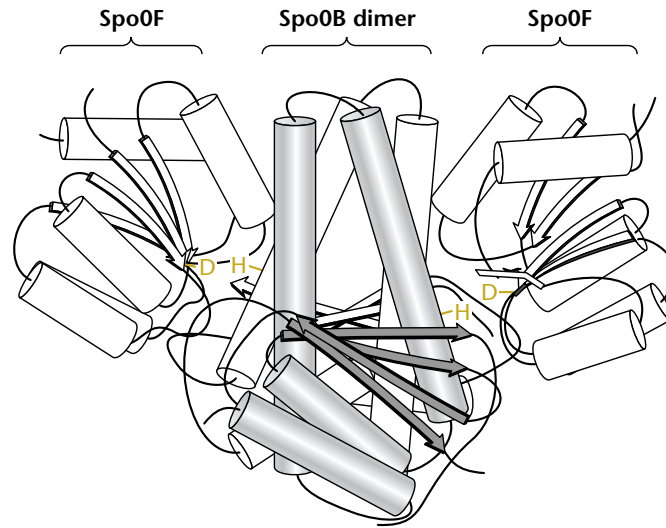


## Box 13.3



## Box 13.3 cont.

## C Spo0B-Spo0F cocrystal structure



## D Spo0A (C-terminal domain)-DNA cocrystal structure

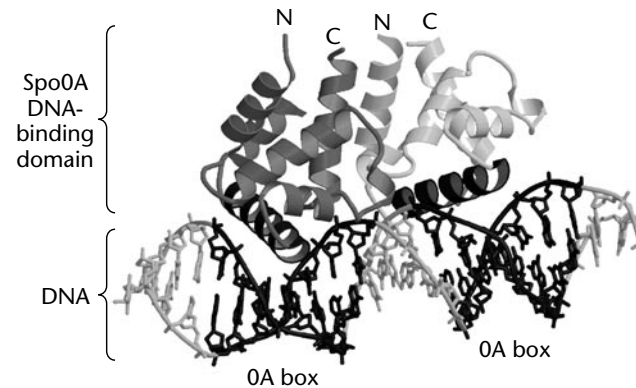


Figure 13.9

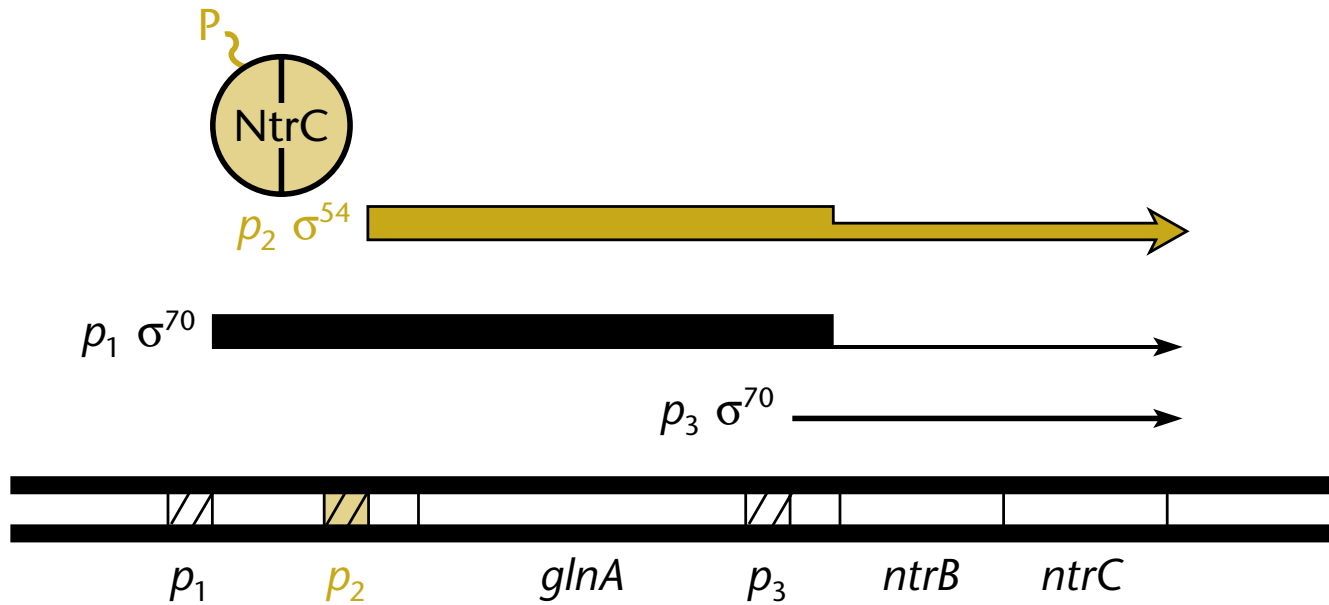
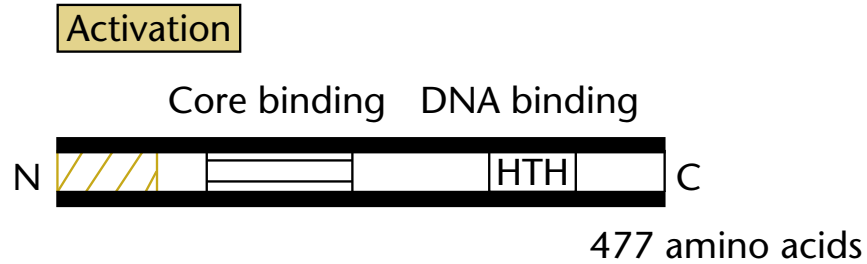


Figure 13.10

 $\sigma^{70}$  promoter $\sigma^{54}$  promoter $\sigma^{32}$  promoter

## Box 13.4

A



B

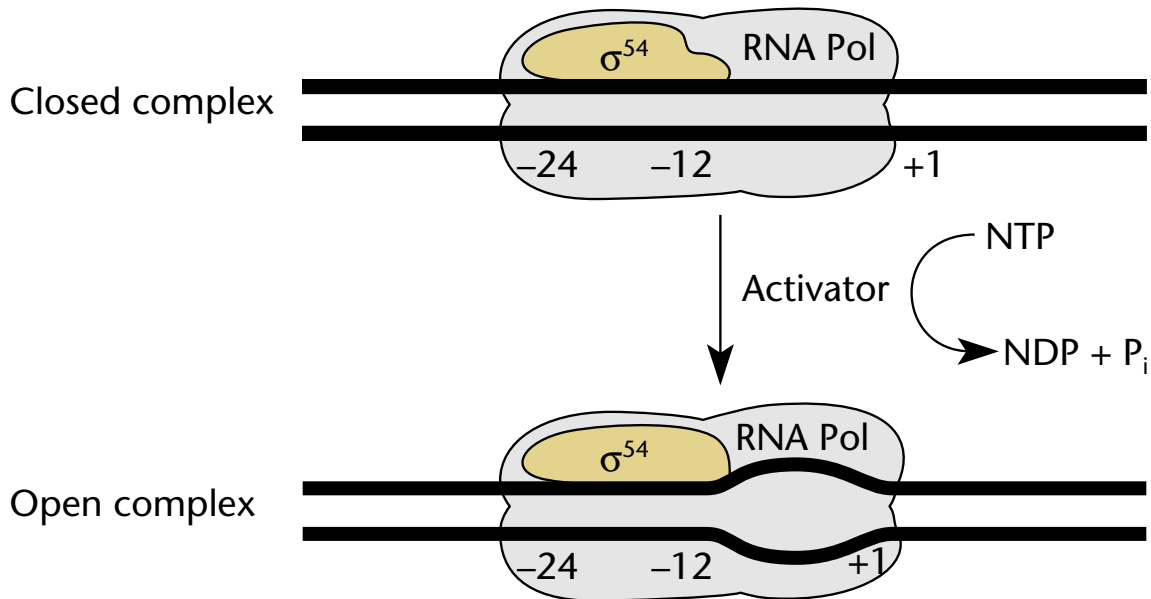
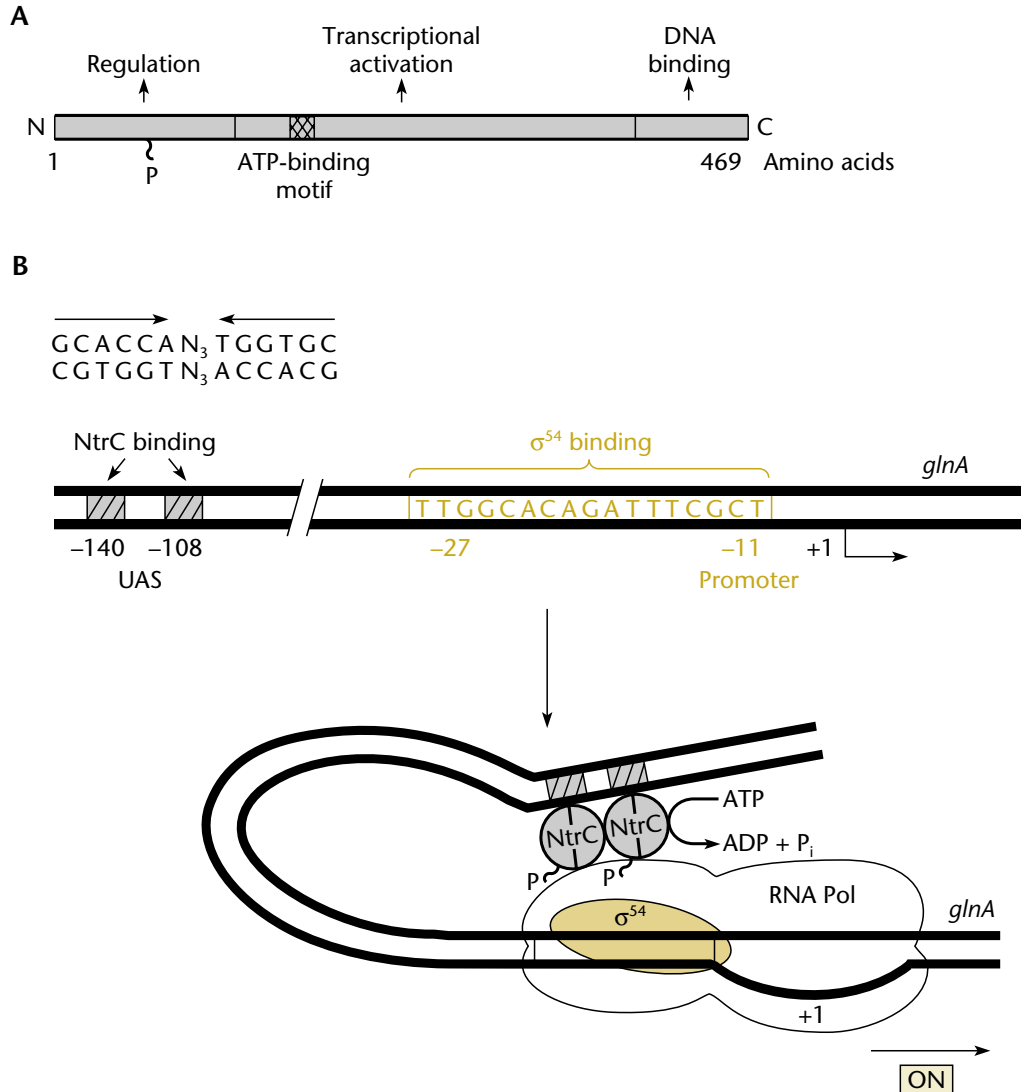


Table 13.2

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

Figure 13.11



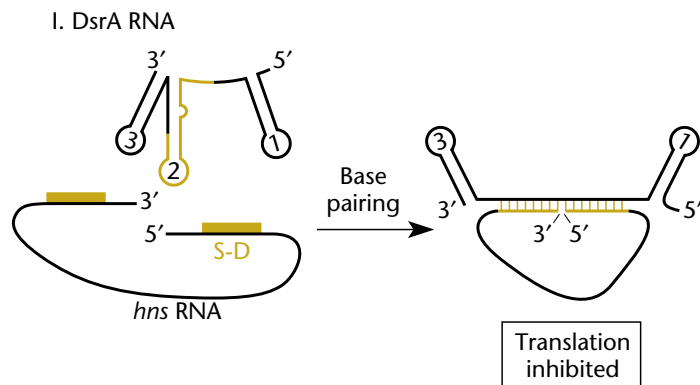
**Table 13.3**

| <b>TABLE 13.3    Phenotypes of <i>envZ</i> and <i>ompR</i> mutations</b>                       |                                                       |
|------------------------------------------------------------------------------------------------|-------------------------------------------------------|
| <b>Genotype</b>                                                                                | <b>Phenotype</b>                                      |
| <i>envZ</i> <sup>+</sup> <i>ompR</i> <sup>+</sup>                                              | OmpC <sup>+</sup> OmpF <sup>+</sup>                   |
| <i>envZ</i> <sup>+</sup> <i>ompR1</i>                                                          | OmpC <sup>-</sup> OmpF <sup>-</sup>                   |
| <i>envZ</i> (null) <i>ompR</i> <sup>+</sup>                                                    | OmpC <sup>-</sup> OmpF <sup>+-a</sup>                 |
| <i>envZ</i> <sup>+</sup> <i>ompR2</i> (Con)                                                    | OmpC <sup>-</sup> OmpF <sup>+</sup> (low osmolarity)  |
|                                                                                                | OmpC <sup>-</sup> OmpF <sup>+</sup> (high osmolarity) |
| <i>envZ</i> (null) <i>ompR2</i> (Con)                                                          | OmpC <sup>-</sup> OmpF <sup>+</sup> (low osmolarity)  |
|                                                                                                | OmpC <sup>-</sup> OmpF <sup>+</sup> (high osmolarity) |
| <i>envZ</i> <sup>+</sup> <i>ompR3</i> (Con)                                                    | OmpC <sup>+</sup> OmpF <sup>-</sup> (low osmolarity)  |
|                                                                                                | OmpC <sup>+</sup> OmpF <sup>-</sup> (high osmolarity) |
| <i>envZ</i> <sup>+</sup> <i>ompR3</i> (Con)/ <i>envZ</i> <sup>+</sup> <i>ompR</i> <sup>+</sup> | OmpC <sup>+</sup> OmpF <sup>-</sup> (low osmolarity)  |
|                                                                                                | OmpC <sup>+</sup> OmpF <sup>-</sup> (high osmolarity) |

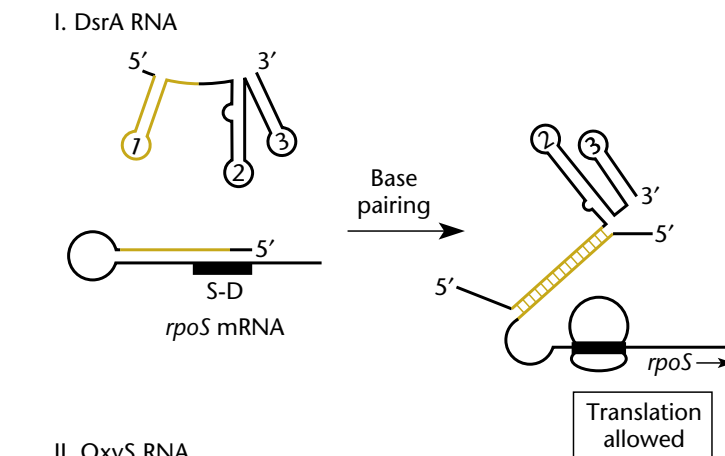
<sup>a</sup>+ – indicates that OmpF levels are reduced but not eliminated.

## Box 13.5

## A Negative regulation



## B Positive regulation



## II. OxyS RNA

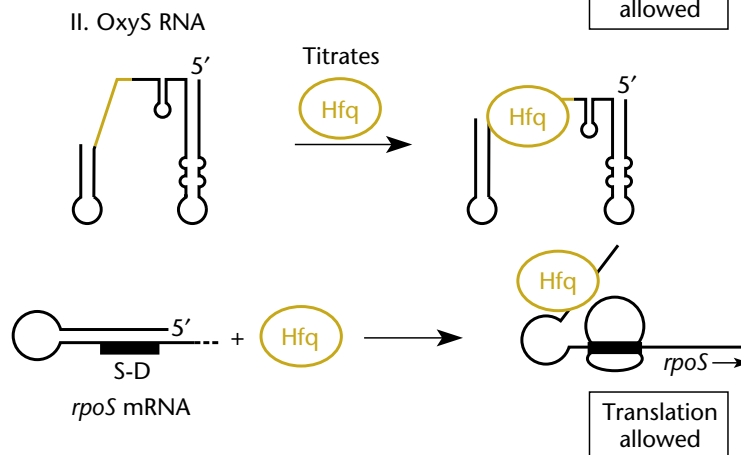
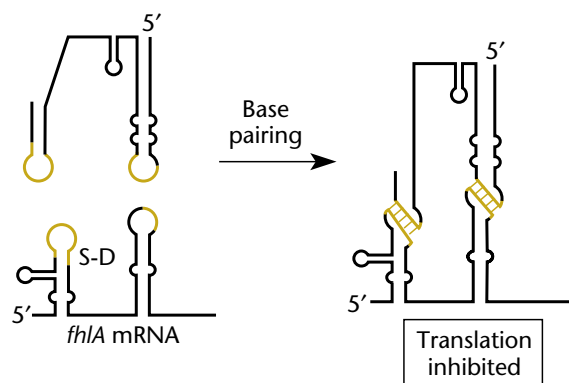


Figure 13.12

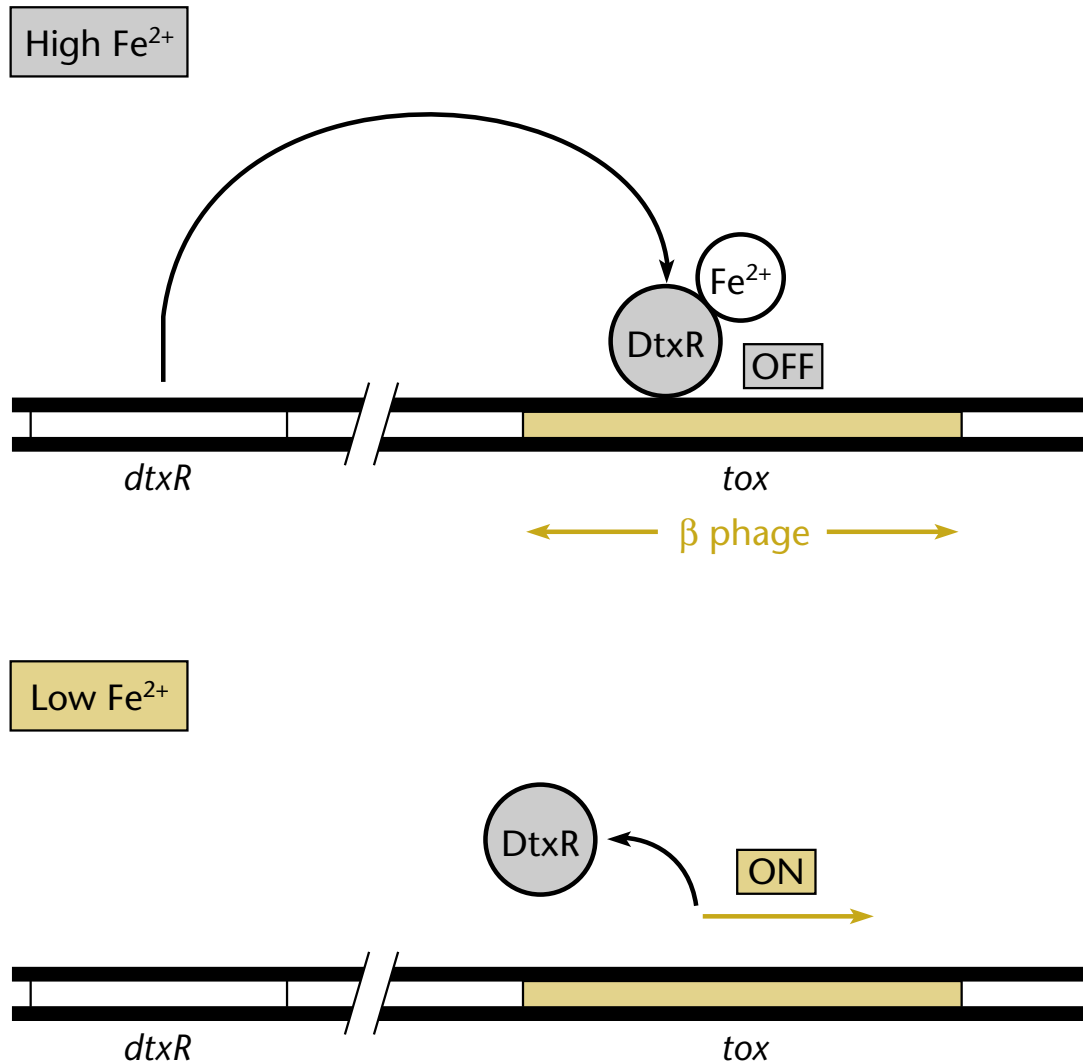


Figure 13.13

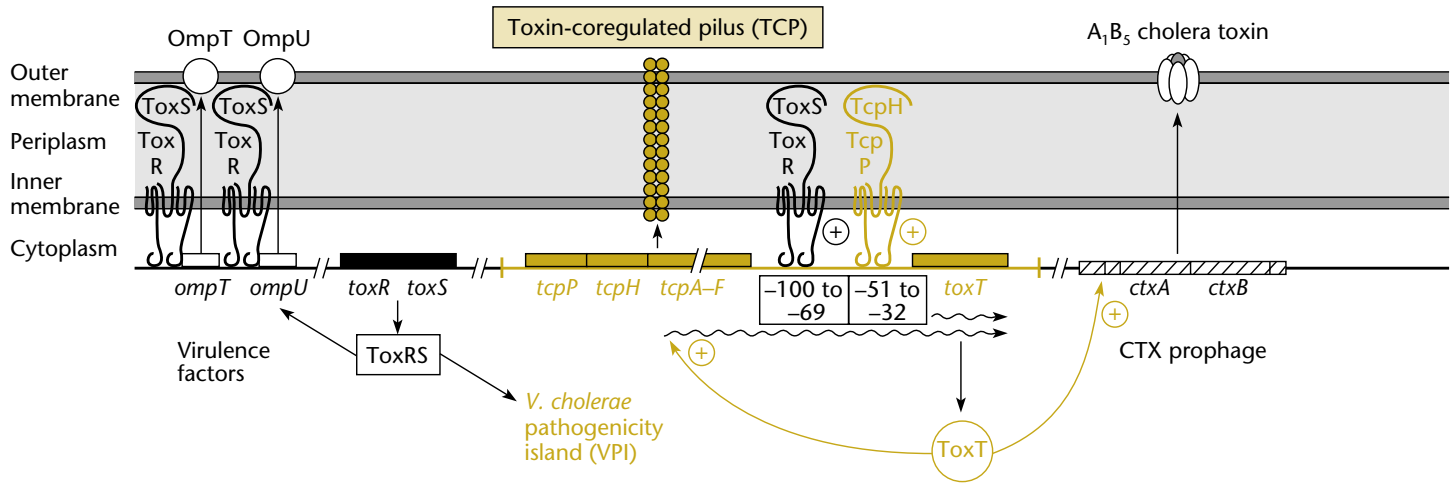


Figure 13.14

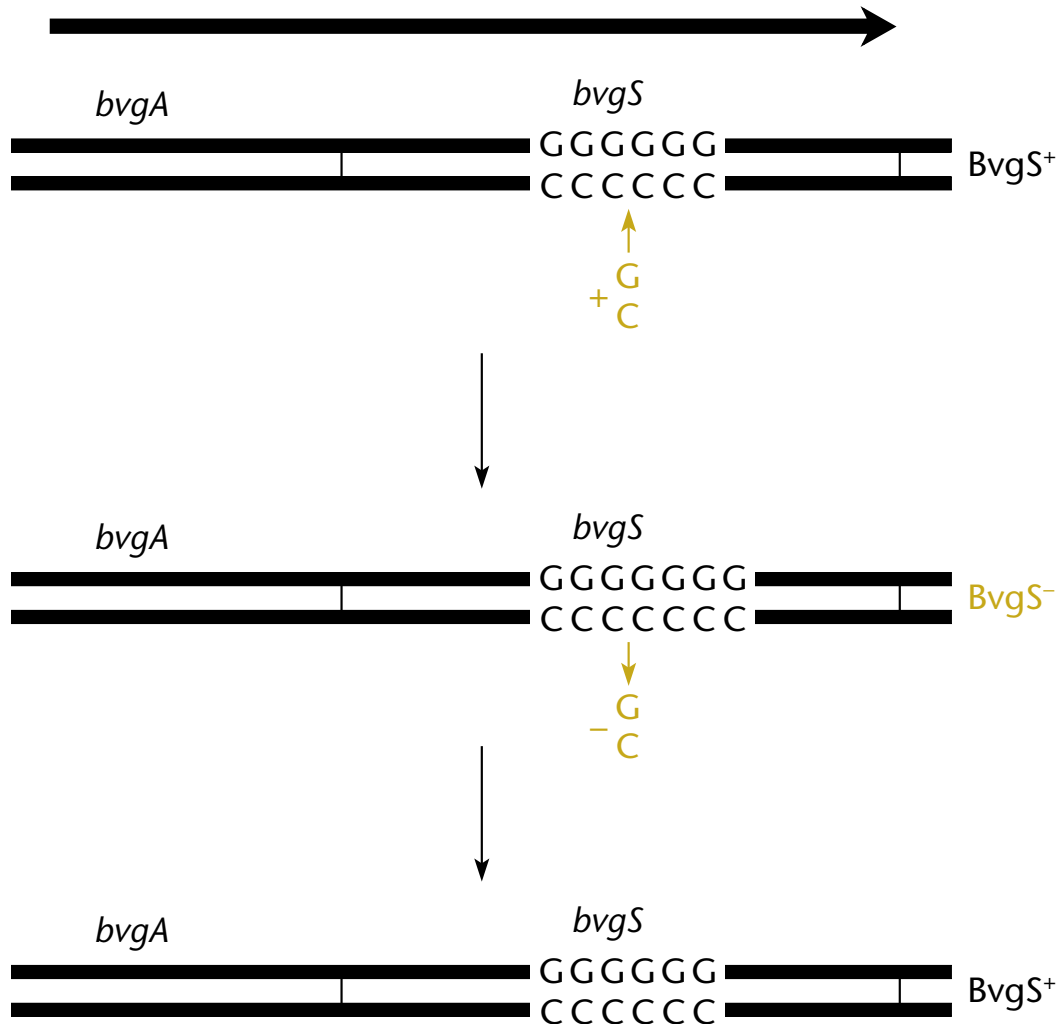
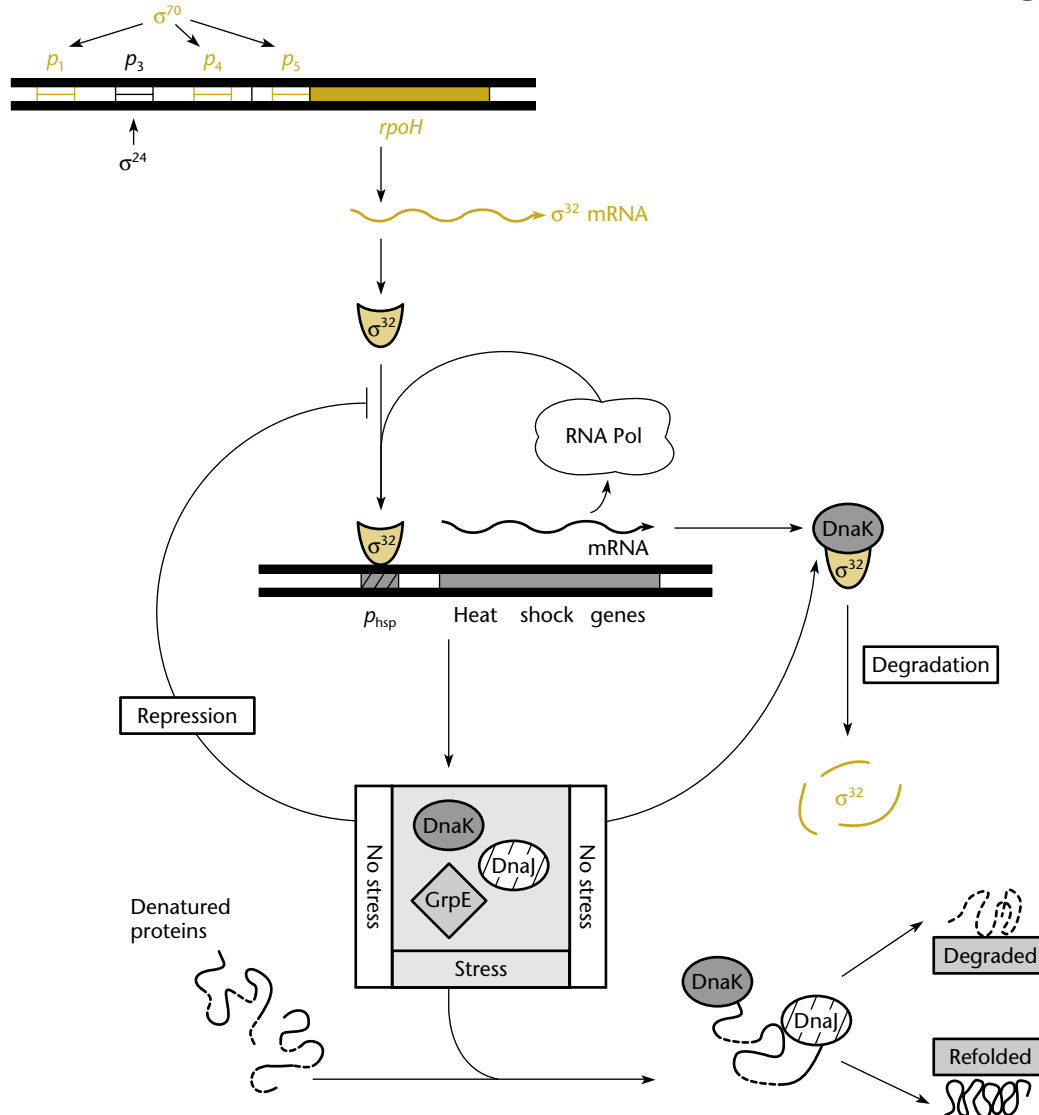
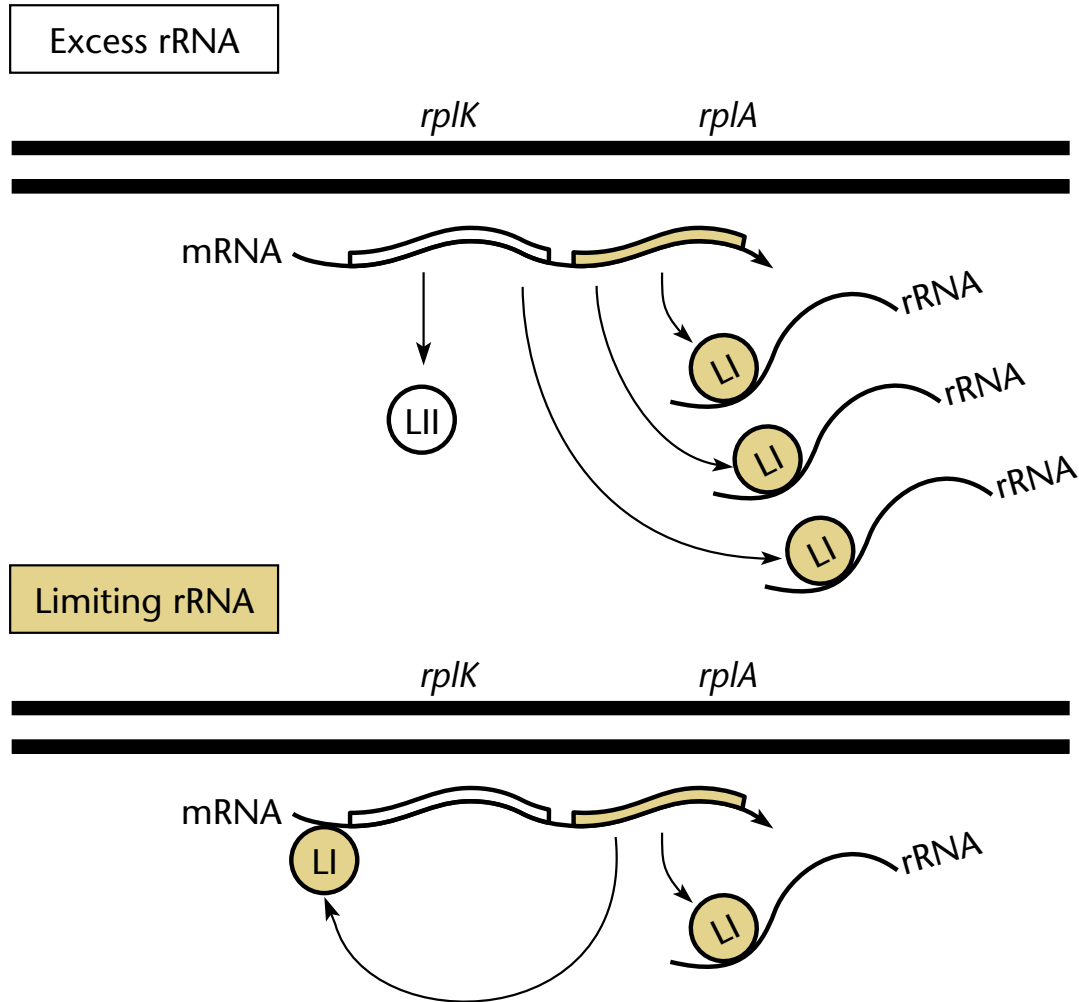


Figure 13.15



**Figure 13.16**

Figure 13.17



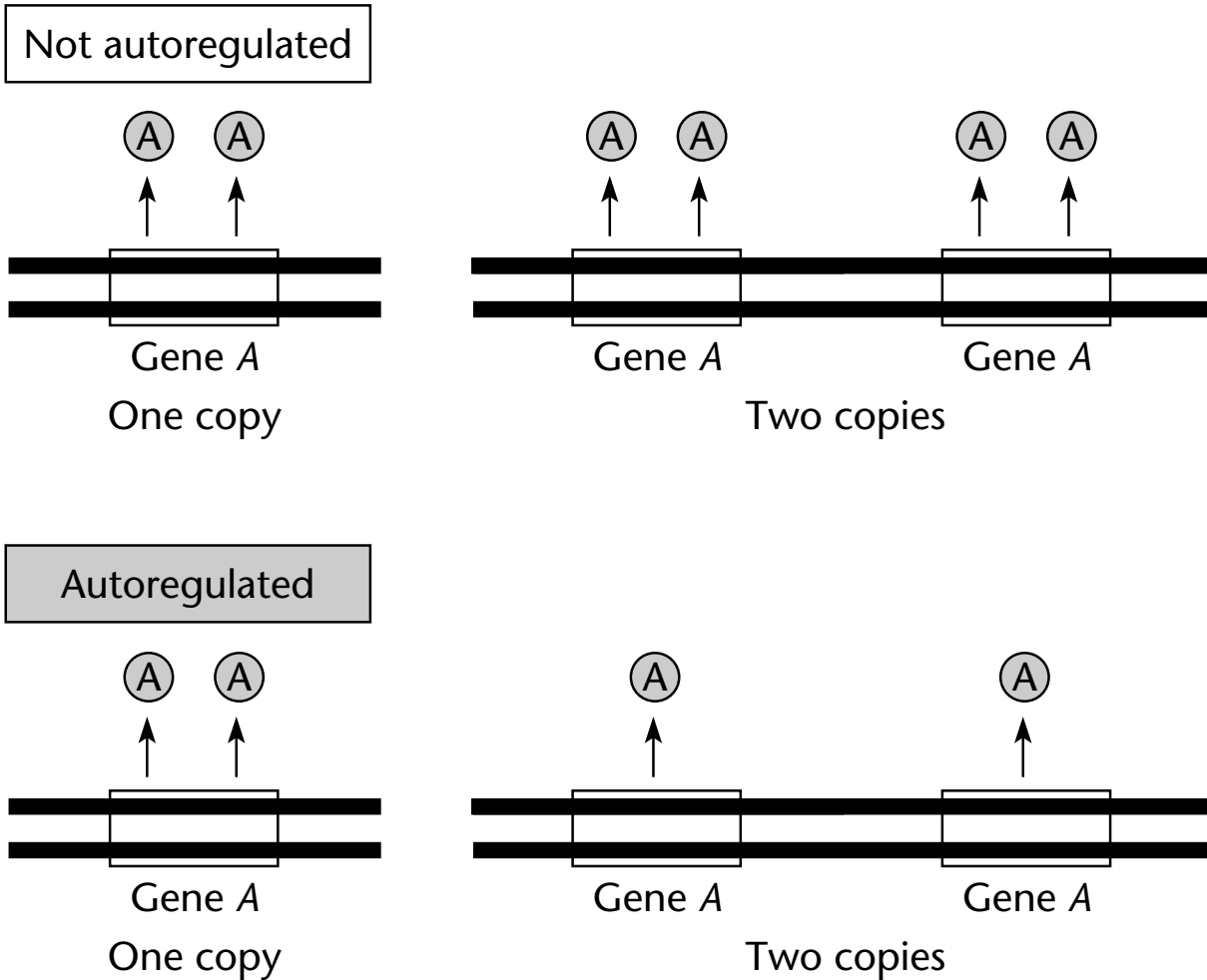
**Figure 13.18**

Figure 13.19

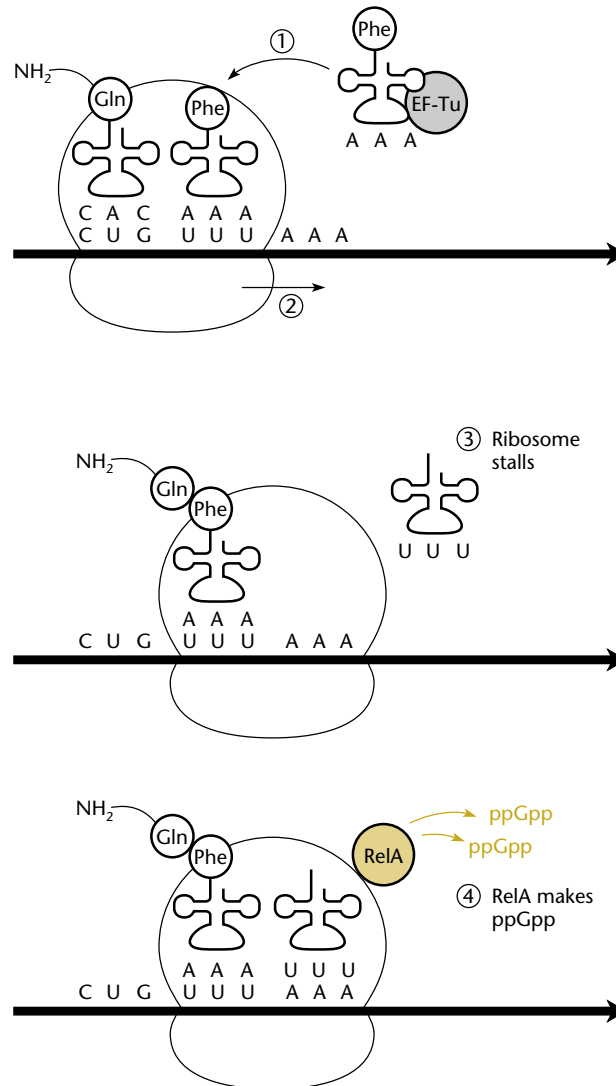


Figure 13.20

