(a) Strong *E. coli* promoters

| | | −35 | | −10 | +1 |
|---|---|---|---|---|---|

```
tyr tRNA     TCTCAACGTAACAC TTTACA GCGGCG • • CGTCATTTGA TATGATGC • GCCCC GCTTCCCGATAAGGG
rrn D1       GATCAAAAAAATAC TTGTGC AAAAAA • • TTGGGATCCC TATAAT GCGCCTCC GTTGAGACGACAACG
rrn X1       ATGCATTTTTCCGC TTGTCTT CCTGA • • GCCGACTCCC TATAAT GCGCCTCCA TCGACACGGCGGAT
rrn (DXE)₂   CCTGAAATTCAGGG TTGACT CTGAAA • • GAGGAAAGCG TAATATAC • GCCACC TCGCGACAGTGAGC
rrn E1       CTGCAATTTTTCTA TTGCGG CCTGCG • • GAGAACTCCC TATAAT GCGCCTCCA TCGACACGGCGGAT
rrn A1       TTTTAAATTTCCTC TTGTCA GGCCGG • • AATAACTCCC TATAAT GCGCCACCA CTGACACGGAACAA
rrn A2       GCAAAAATAAATGC TTGACT CTGTAG • • CGGGAAGGCG TATTATGC • ACACCC CGCGCCGCTGAGAA
λ PR         TAACACCGTGCGTG TTGACT ATTTTA • CCTCTGGCGGTGATAATGG • • TTGCA TGTACTAAGGAGGT
λ PL         TATCTCTGGCGGTG TTGACAT AAATA • CCACTGGCGGTGATACTGA • • GCACA TCAGCAGGACGCAC
T7 A3        GTGAAACAAAACGG TTGACA ACATGA • AGTAAACACGGTACGATGT • ACCACA TGAAACGACAGTGA
T7 A1        TATCAAAAAGAGTA TTGACTT AAAGT • CTAACCTATAGGATACTTA • CAGCCA TCGAGAGGGACACG
T7 A2        ACGAAAAACAGGTA TTGACA ACATGAAGTAACATGCAGTAAGATAC • AAAT CGCTAGGTAACACTAG
fd VIII      GATACAAATCTCCG TTGTACT TTGTT • • TCGCGCTTGG TATAAT CG • CTGGGGGTCAAAGATGAGTG
```
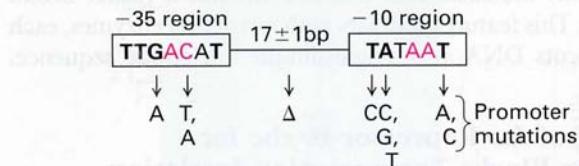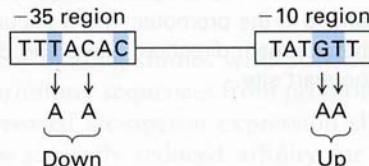
(b) Consensus sequences of σ⁷⁰ promoters



(c) *Lac* promoter sequence



▲ **FIGURE 10-11 Promoters recognized by *E. coli* RNA polymerase containing σ⁷⁰.** (a) Sequences of some strong promoters with spaces (dots) introduced to maximize homology in the −35 region and −10 region. These sequences correspond to the top strand of the promoter with transcription proceeding to the right (see Figure 10-9). Bases that match the −35 and −10 consensus sequences are highlighted in yellow. The six rrn sequences control genes encoding rRNA. The λ, T7, and fd sequences, which are on viral genomes, direct transcription by the host-cell RNA polymerase. (b) Consensus sequences of −35 and −10 regions, which are separated by 15–17 base pairs. Mutations known to significantly decrease the frequency of transcription from a number of different promoters are indicated.

In the consensus sequences, the frequency with which the indicated base occurs at each position in different σ⁷⁰ promoters is indicated as follows: red letters, >75 percent; boldface black letters, 50–75 percent; black letters, 40–50 percent. (c) Sequences of the −35 and −10 regions of *lac* promoter, which deviates from the consensus sequences in four positions (blue highlight). Down mutations cause a decrease in *lac*-operon expression. The two up mutations, which increase the match to the −10 consensus sequence, increase expression. [Part (a) see W. Siebenlist, R. B. Simpson, and W. Gilbert, 1980, *Cell* **20**:269. Part (b) see W. R. McClure, 1985, *Ann. Rev. Biochem.* **54**:171. Part (c) see R. C. Dickson et al., 1975, *Science* **187**:27.]