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Fig. 25-4. Comparison of the promoter regions of the late operons in phages P2, 186 and P4. The transcriptional start sites are indicated by the arrows. The common sequences are indicated in bold, and their consensus sequences are indicated below the promoter sequences and compared to conserved -10 and -35 regions of the σ^{70} promoter.

P2 P _P	CGGA TGGCTTATCACTGACACA ACAGCACCT TAGCGA ATCGCGGGCGCGACTCA GTAGCC TTGCCGTGTA	9	18	→
186 P ₁₂	CGAC TGGACAACCGCCCACACA ACAGCACCT TAGCGA ATCACTGACGCCATTAA GTAGCCT TGCCCTGAA	9	18	→
P2 P _O	CTGT TGTGTCAGTGATAAGCCA TCCGGGACTGA TGGCGG AGGATGCGCATCGTCG GGAAACT GATGCCGAC	11	16	→
186 P _V	CTGT TGTGTGGCGGTTGTCCA GTCGTCATTGG TGGTCT GGCGTGTCTGAGTCT GGAAACT GGCGTGACC	11	16	→
P2 P _V	TGT TGTCTGGTAGTTCTACAA ATGAATCCAGA TAGCAT AACTTTATATATTGT GCAATCT CACATGCATG	11	16	→
186 P _J	GT TGTGCCAGACATCATCCA GCCCTGACAAA TAGCCC CTCAAAGACCAGCCAG GACAATAA CACTCGCCCA	11	16	→
P2 P _F	GGT TGTGCTGTCGATTAGCCA ACCGGGACAAA TAGCCT GACATCTCCGGCGCAACT GAAAATA CCACTCAC	11	17	→
P4 P _{Sid}	TCC TGTGTCAGGGCTGGCACA TCTGCAATGCG TCGTGT TGTTGTCCGGTGTACGT CACAATT TTCTTAACC	9	17	→
P4 P _{LL}	GCCAT TGTAAGACAGCCTGAACA AATCCCCC TGTTGCG TCTGCGTAAAATATTC ACAAAAT AAAGCGCTA	9	17	→
Consensus	TGtgt-a-cGct-a-CA	-55	T-Gcg-	-35
σ^{70}			TTGaca	
				TAtaaTG

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