

Figure 8.8

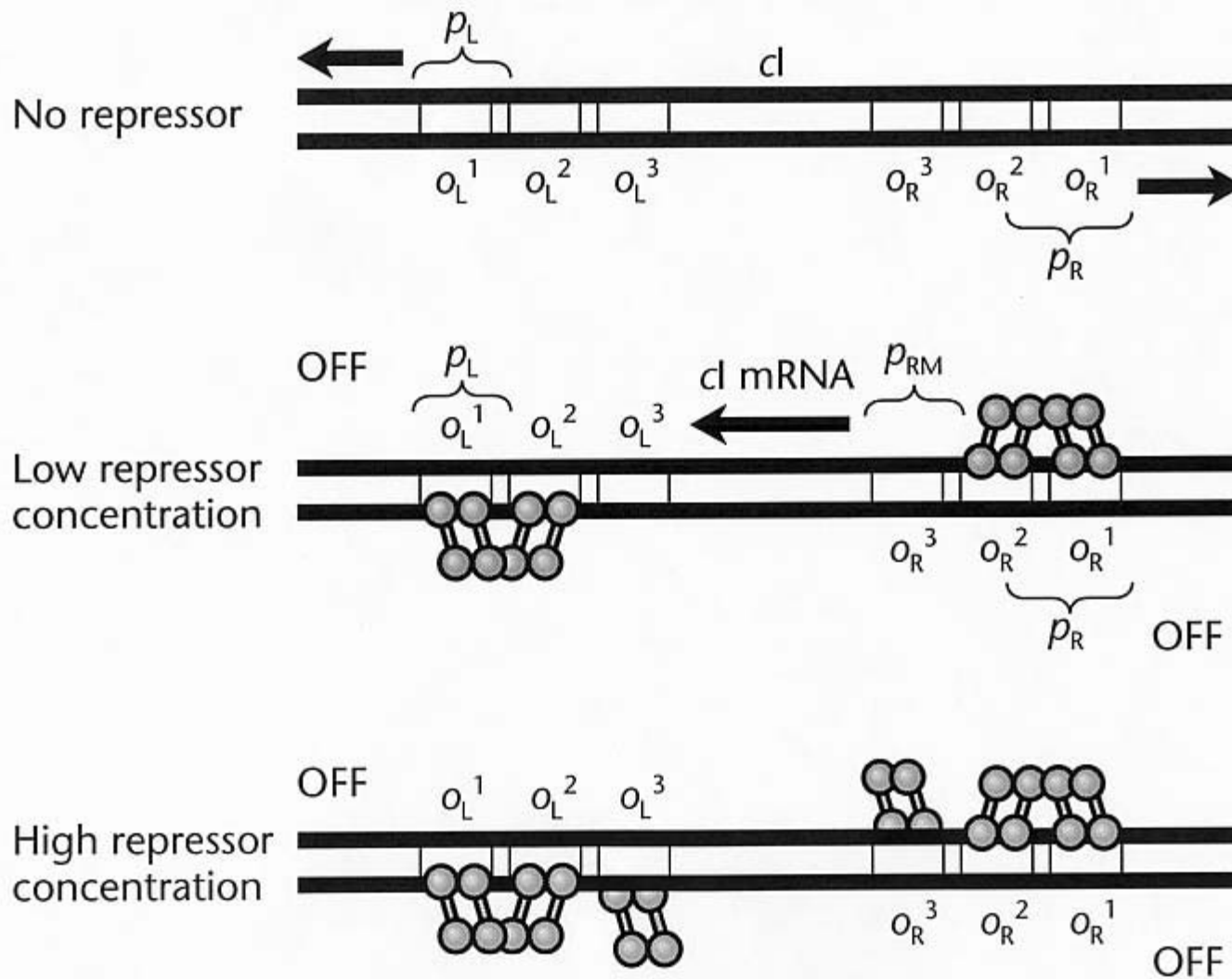


Figure 8.9

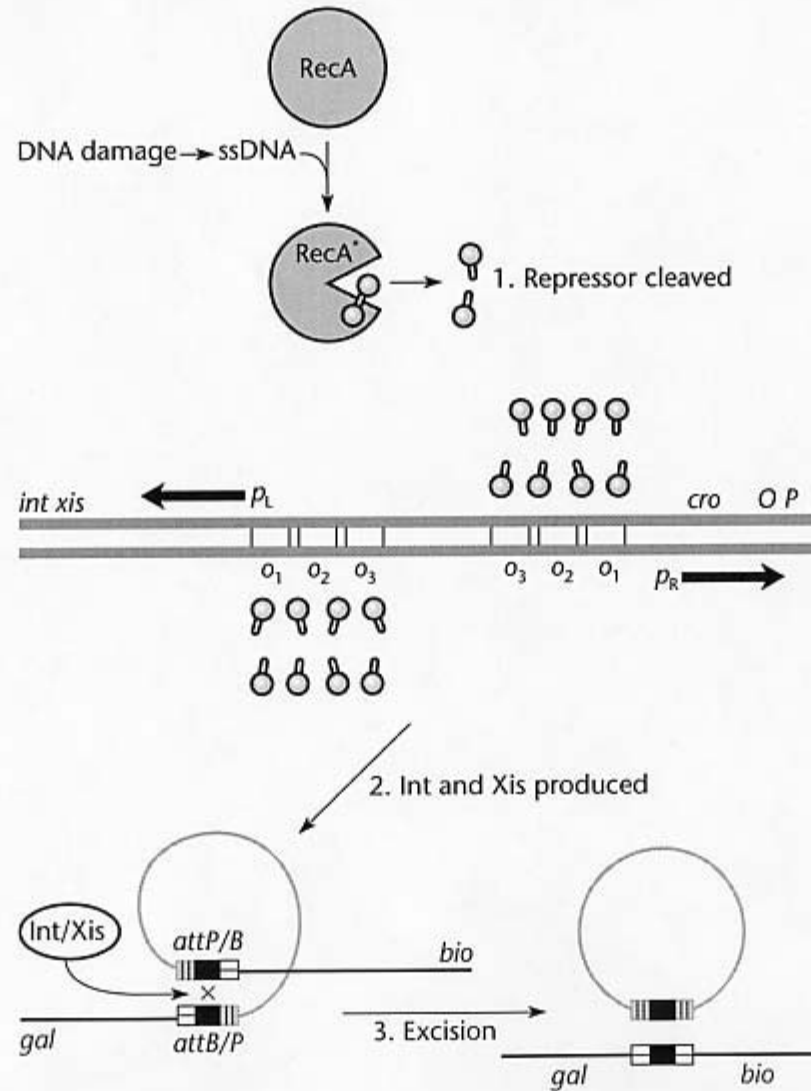
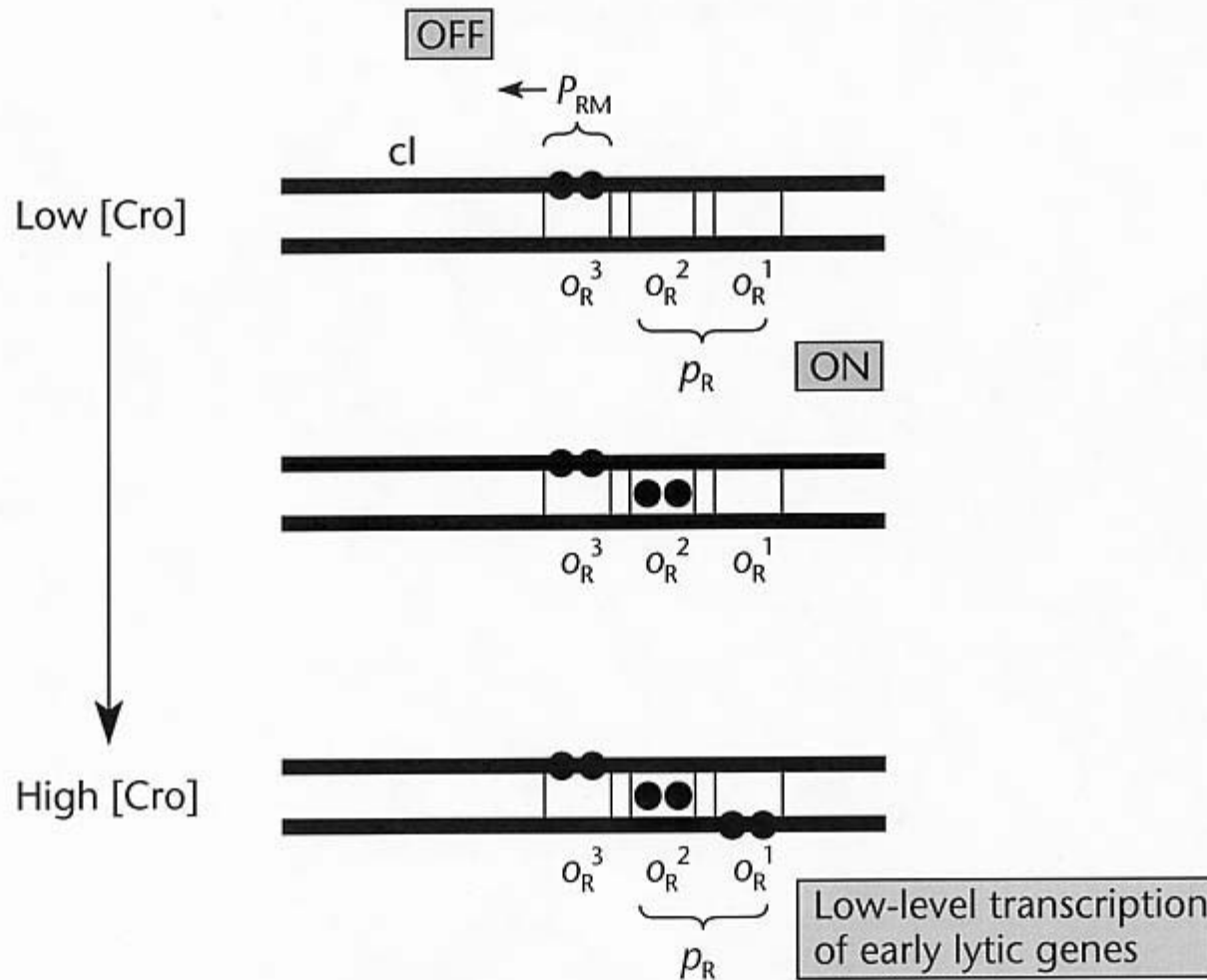


Figure 8.10



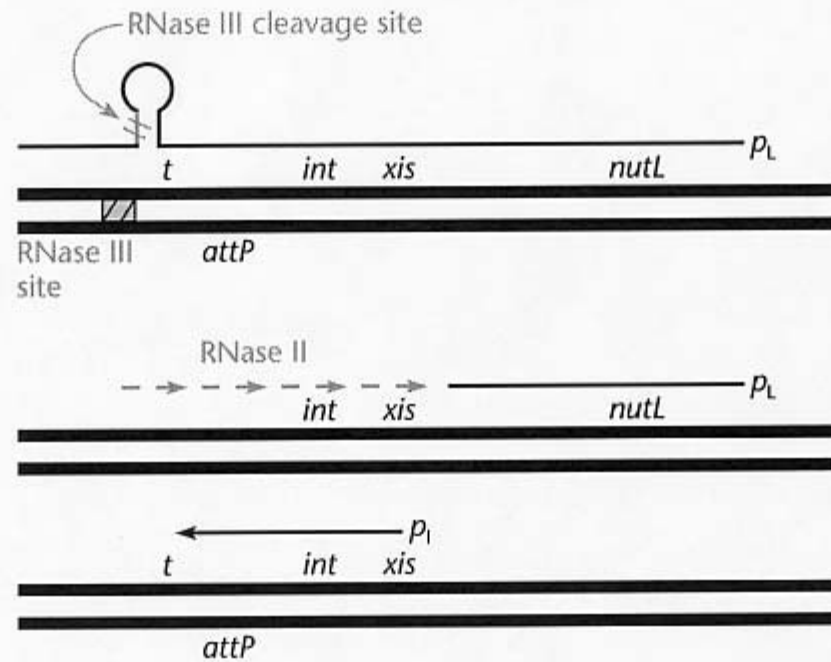
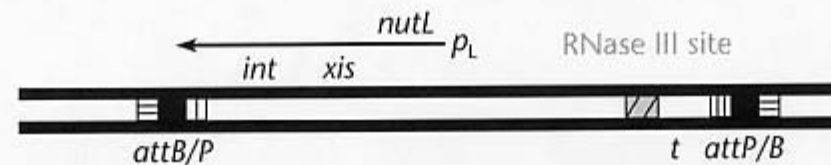
Affinity of  $o_R$  for Cro:  $o_R^1 > o_R^2 = o_R^3$



### Table 8.3

TABLE 8.3 Steps leading to lytic growth and lysogeny	
Steps leading to lytic growth	Steps leading to lysogeny
1. Transcription from $p_L$ and $p_R$	1. Same as for lytic growth
2. N and Cro are made	2. Same as for lytic growth
3. N allows CII expression	3. Same as for lytic growth
4. <b>CII degraded</b>	4. <b>CII stable</b>
5. Low CII concentration means that little CI is made	5a. High CII concentration activates $p_I$ , and so Int is made and $\lambda$ DNA integrates
	5b. High CII concentration activates $p_{RE}$ , and so CI is made
6. Cro binds at $o_R^3$ and $o_L^3$ , blocking binding by any low level of CI that is made	6. CI outcompetes Cro, and so CI binding at $o_R$ and $o_L$ both represses $p_L$ and $p_R$ and positively autoregulates at $p_{RM}$ , maintaining lysogeny
7. Meanwhile, N allows O and P replication gene transcription	
8. A second antiterminator, Q, allows late-gene transcription, and so $\lambda$ phage particles are made	

## Box 8.2

A After  $\lambda$  infection, *int* expressed from  $p_i$ B After induction, *int* and *xis* expressed from  $p_L$ 

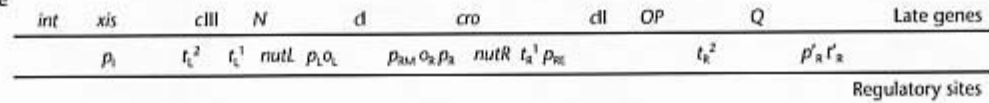
# 8 Phage $\lambda$ and Lysogeny

FIND

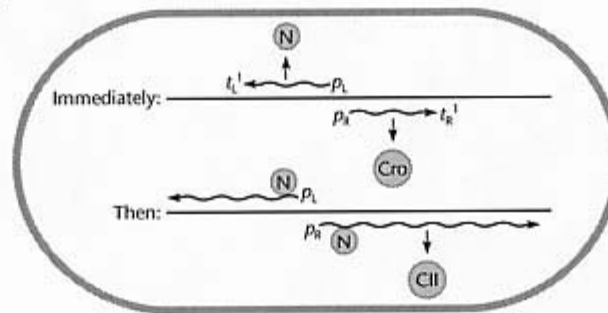
CHAP TOC

Figure 8.11

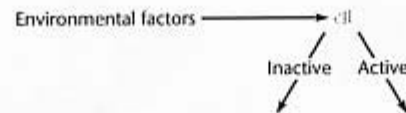
A  $\lambda$  genome



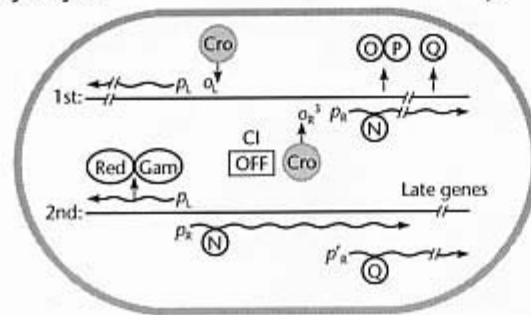
B Early after infection



C Decision

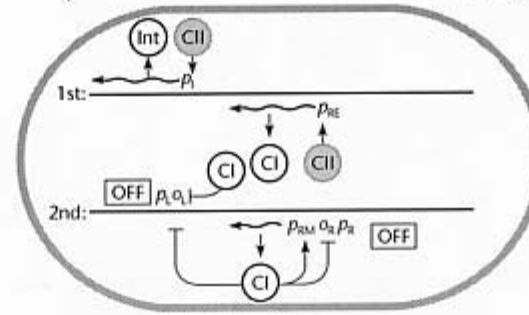


D Lytic cycle



Replication  
Phage production and lysis

E Lysogeny



Phage DNA integration  
Maintenance of lysogen



**Figure 8.12**

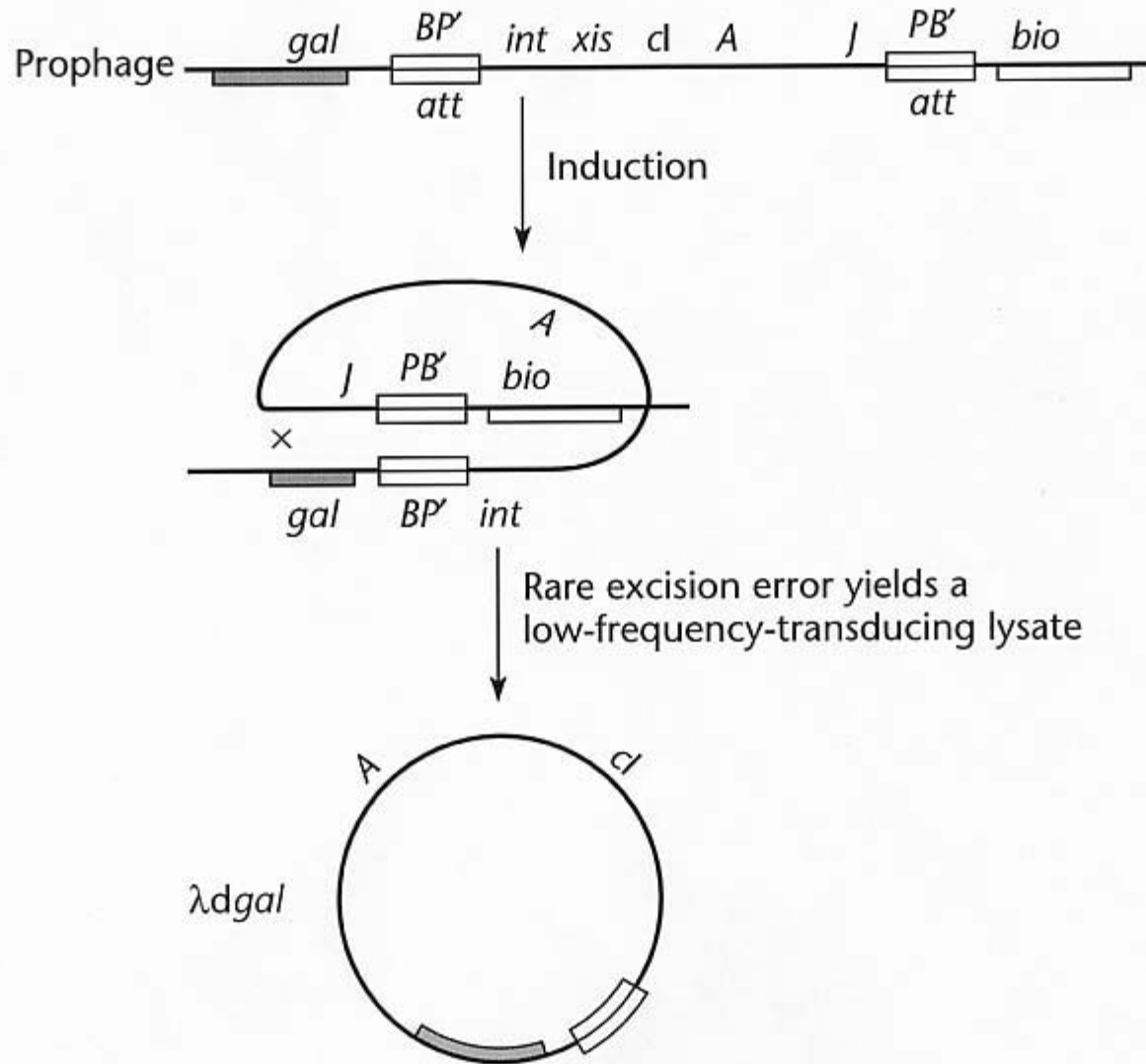
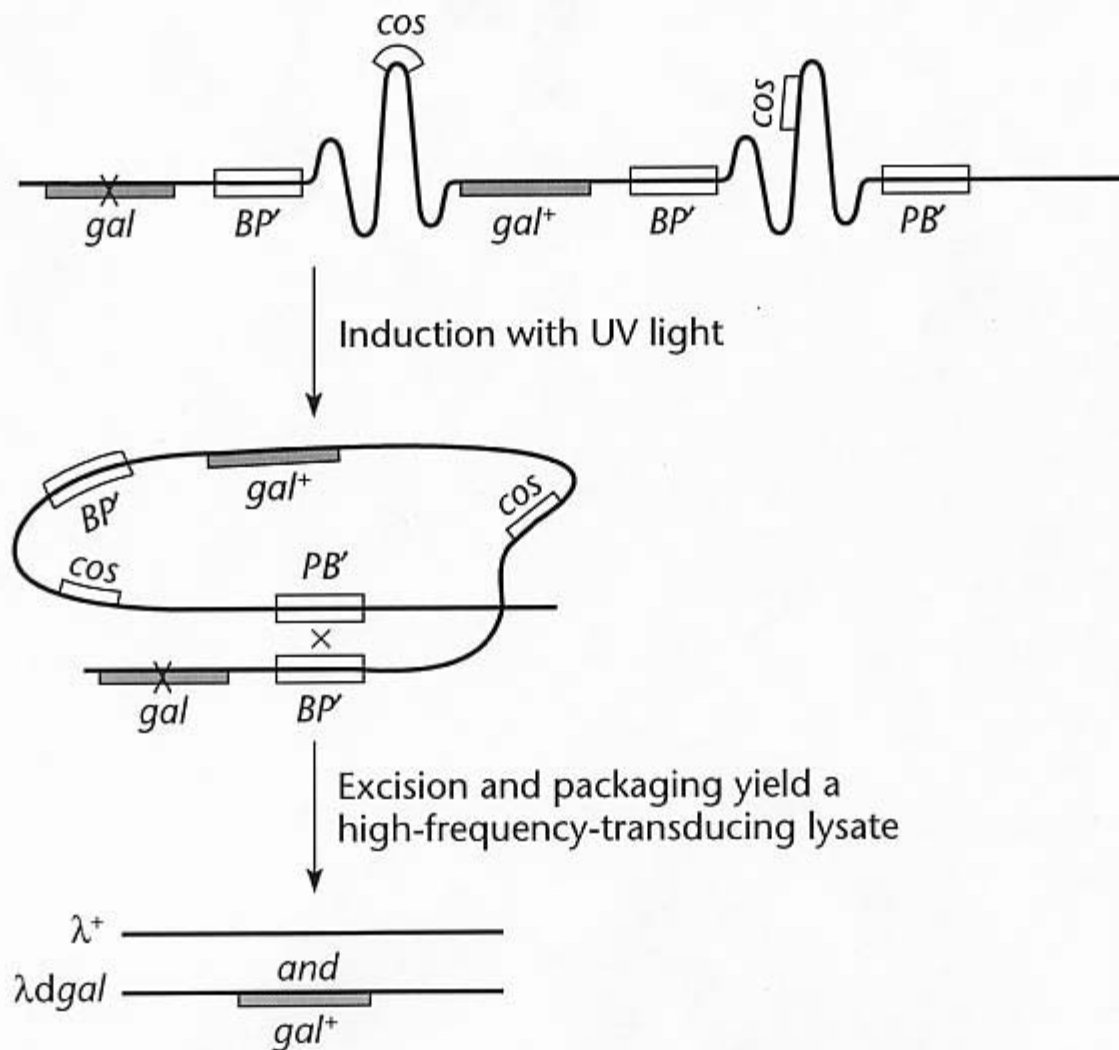


Figure 8.13





Name: \_\_\_\_\_

EXTRA CREDIT (10 pts)

The cotransduction frequencies of 6 *E. coli* markers are listed in the table below. From this data, deduce the order of these markers. Present your answer in such a way that I can follow your reasoning.

Selected Donor Marker	Inheritance of unselected donor marker (no. inheriting marker/total colonies scored).				
	dsdA	purC	aroC	ptsI	supN
supN			20/212	183/212	
ptsI	15/128	10/228	0/304		88/108
purC				54/967	33/976
dsdA			50/240	22/240	
guaB		72/227	0/227	0/277	