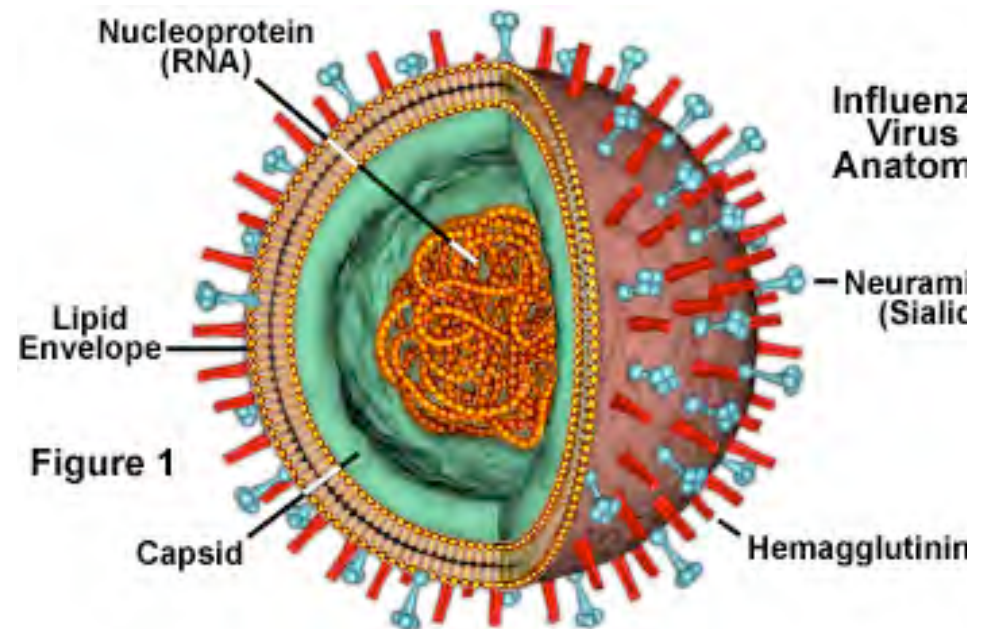
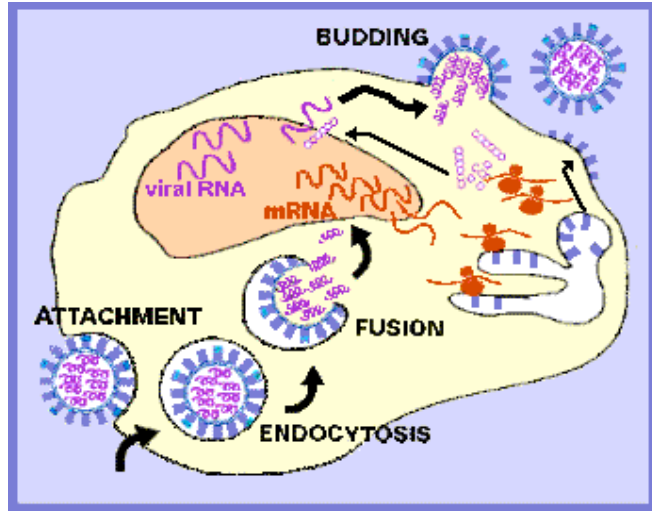


# Homework 2 comments

<http://web.uct.ac.za/depts/mmi/jmoodie/flu2life.gif>



<http://micro.magnet.fsu.edu/cells/viruses/influenzavirus>

# Homework 2 comments

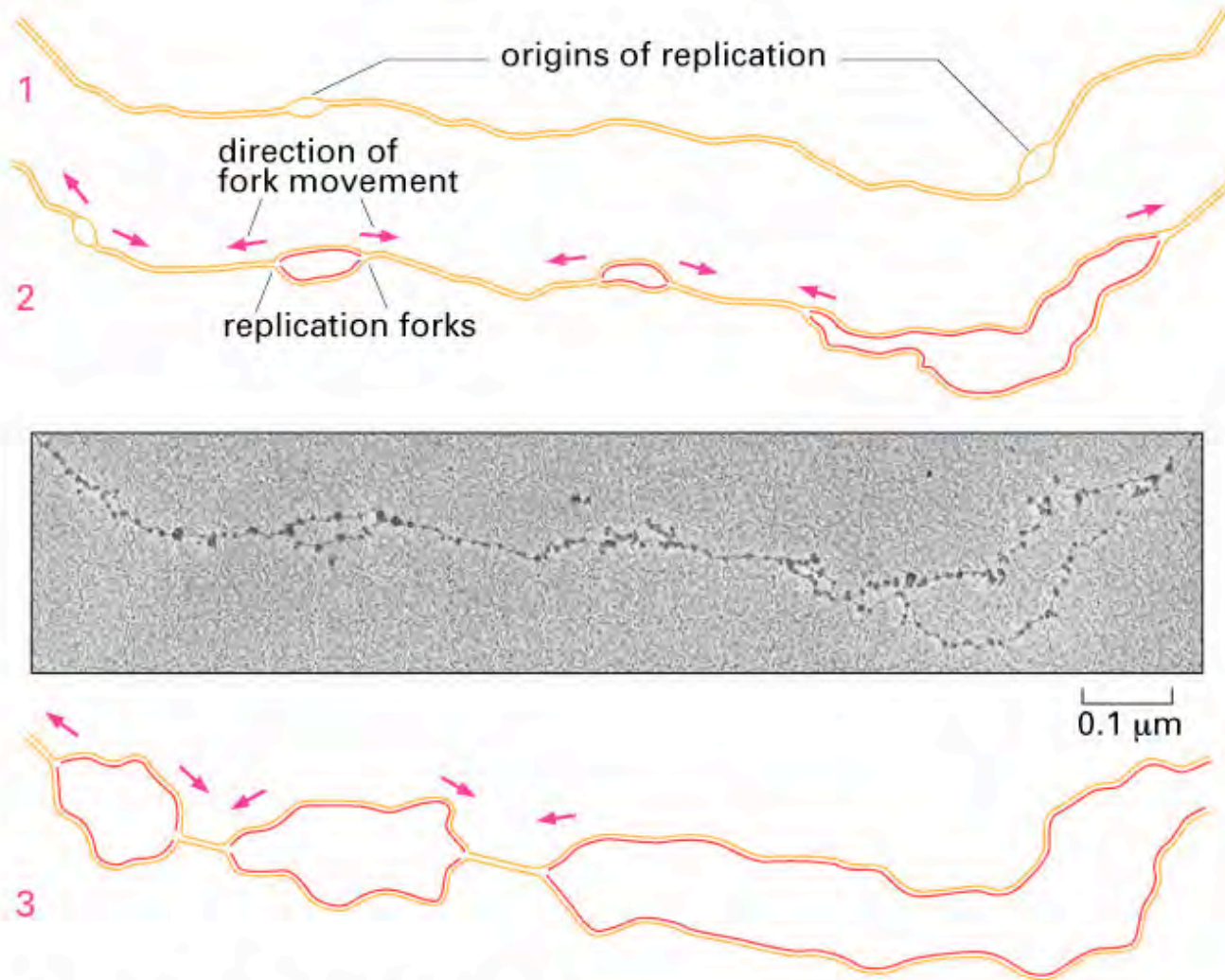
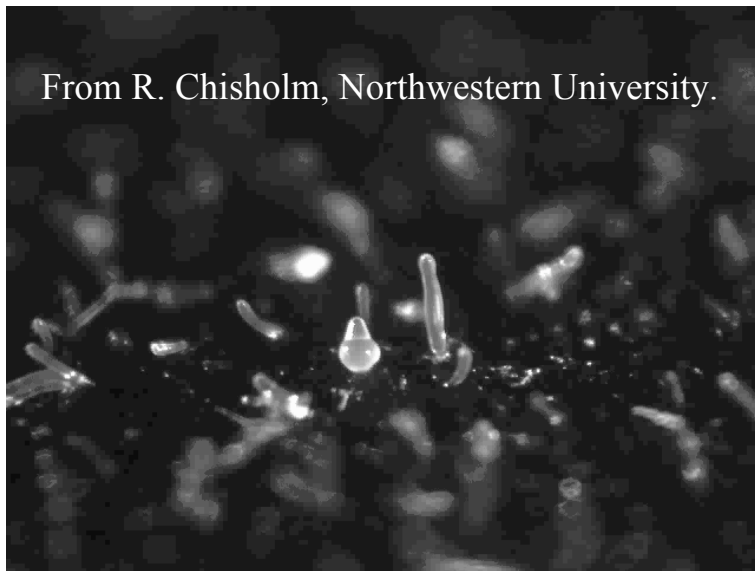
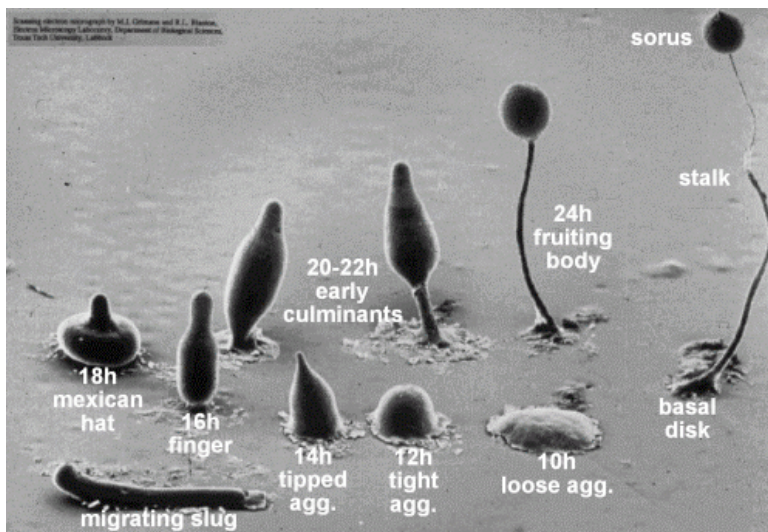
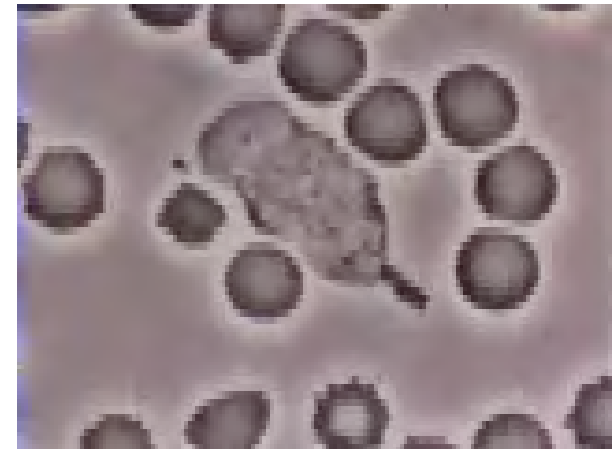


Figure 6-9 Essential Cell Biology, 2/e. (© 2004 Garland Science)

# How Cells Decide Where to Go, What to Eat and What to Become: The Physics of Signaling and Regulation



David Rogers



## Neutrophils: life as a hunter

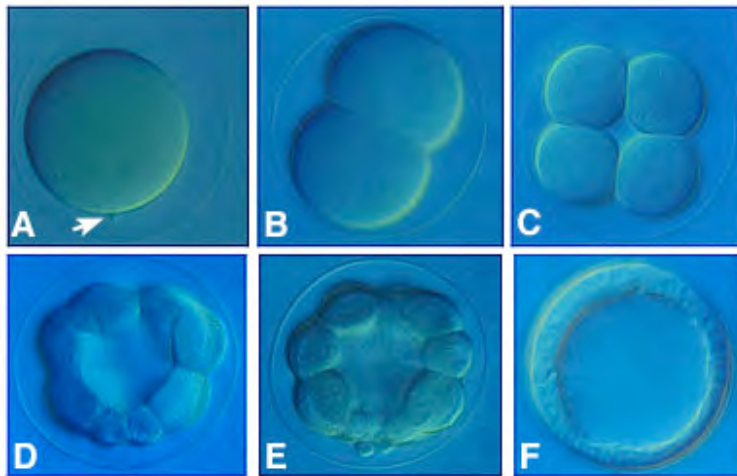
- Neutrophils cruise around looking for unwelcome invaders which they hunt and kill.
- When starved, amoeba can undertake program to form a collective in which some of the cells are sacrificed.
- The bottom line: signaling, detection and decision making are central to cellular

For the greater good: Dictyostelium



# How Cells Decide What to Become

## Becoming a Sea Urchin

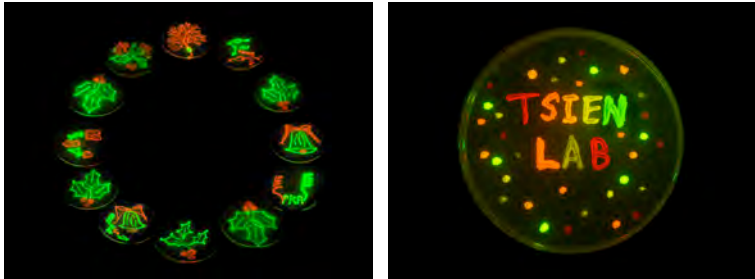


- *After fertilization, sea urchin embryo undergoes a series of synchronized decisions and differentiation.*
- *Exquisite control in both space and time.*
- *The list of examples is virtually endless.*

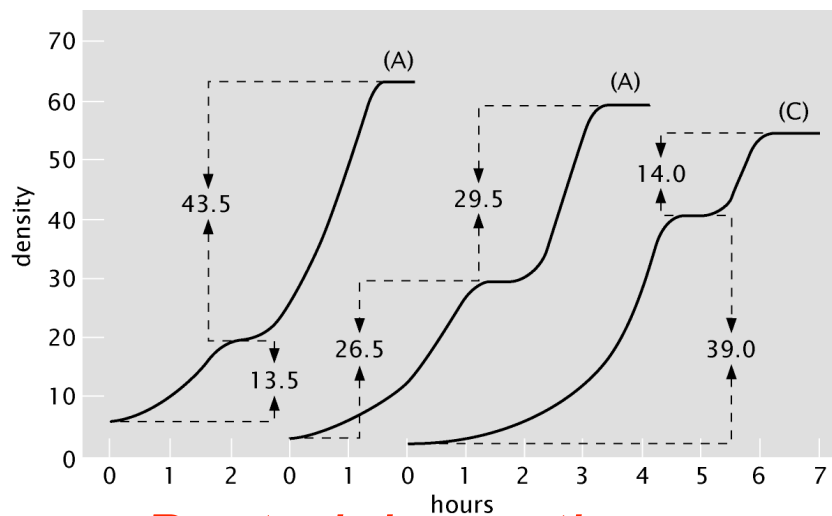
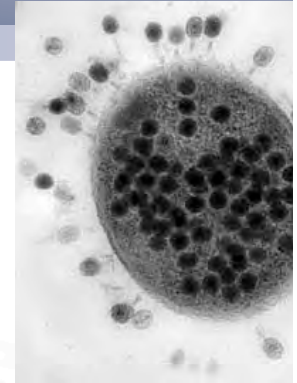


## Forming the Gut

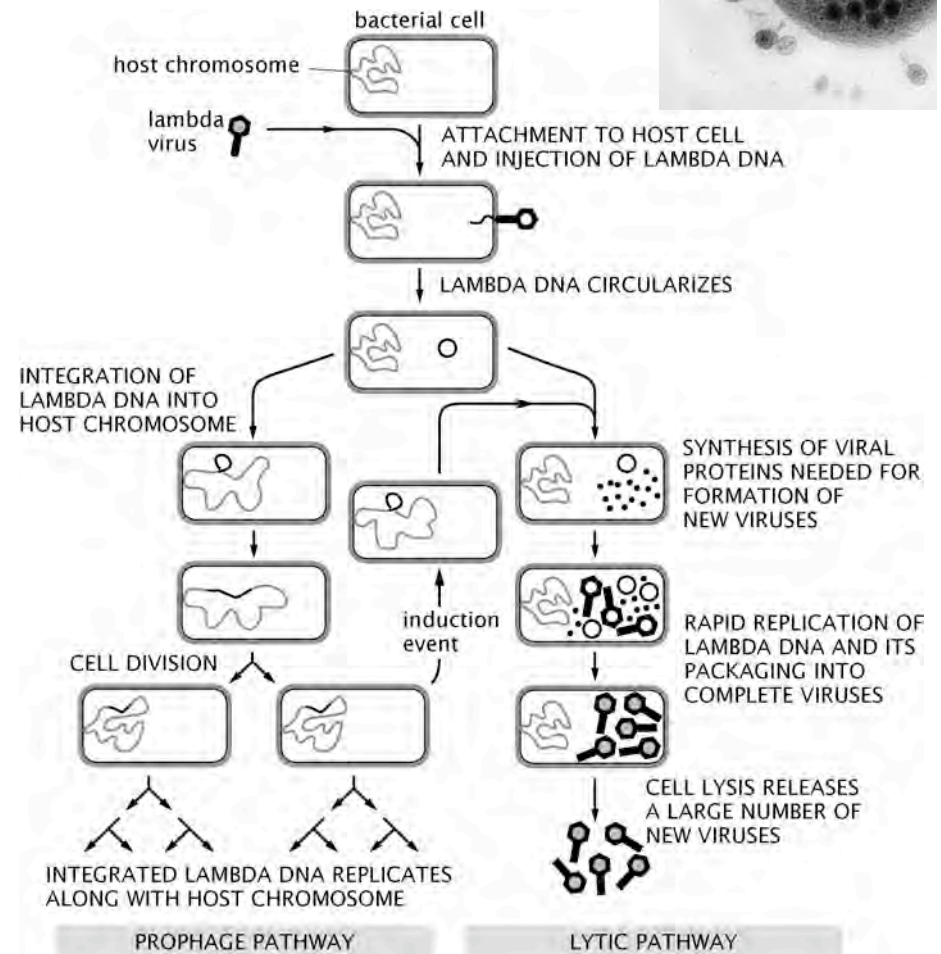
# The Development of the Operon Concept: What Cells Eat and When They Die



• **The big idea: there are genes that control other genes!**



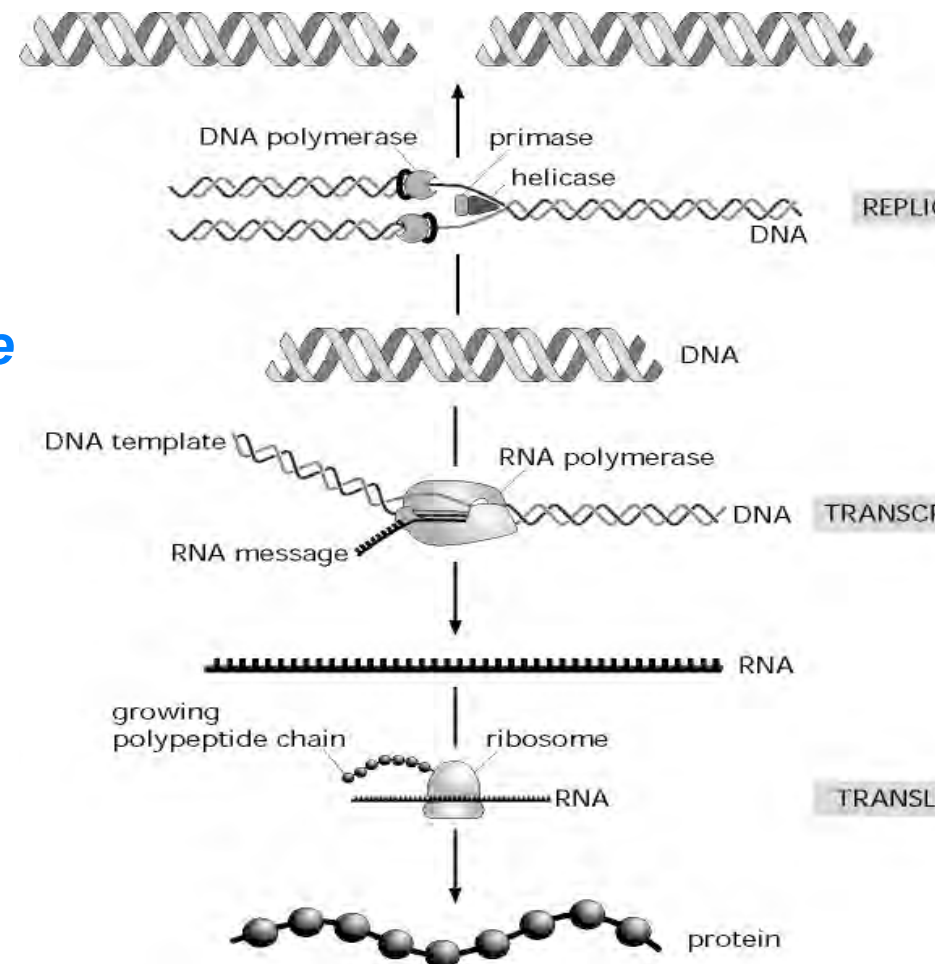
**Bacterial growth curves**



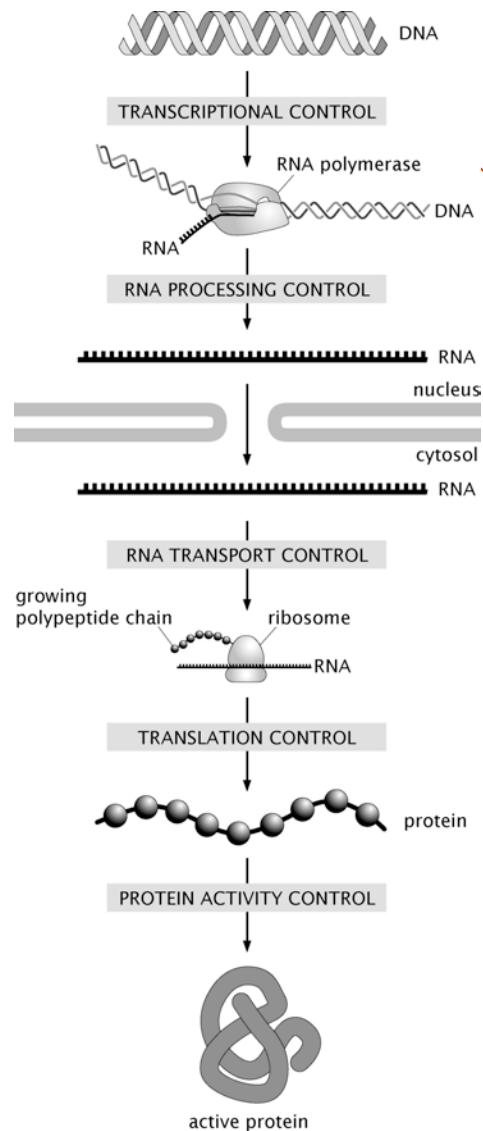
# Gene Expression and the Central Dogma

## Managing the Great Polymer Languages

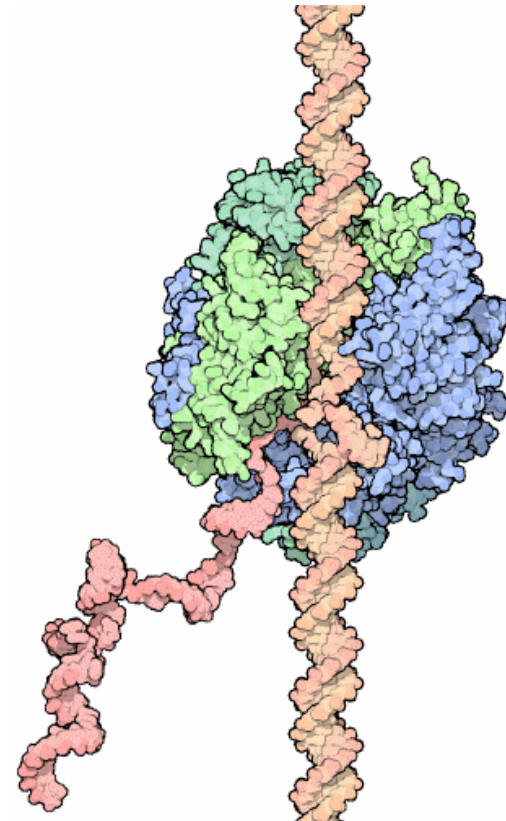
- ◆ The central dogma tells us about the connection between what Crick dubbed “the two great polymer languages”.
- ◆ Gene expression refers to the chain of processes that relate the informational content of DNA to the protein consequences of that DNA.



# But, Genes Are Precisely Controlled: Transcriptional Regulation



- ◆ **Regulation takes place very far upstream**  
**In particular, the “decision” is made**  
**whether or not to produce mRNA.**
- ◆ **Question: What are the molecules that**  
**mediate this control?**





# Repressors: The Cartoon

- **Repressor molecules inhibit action of RNA polymerase.**
- **Repressors can be under the control of other molecules (i.e. inducers) that dictate when repressor is bound and not.**

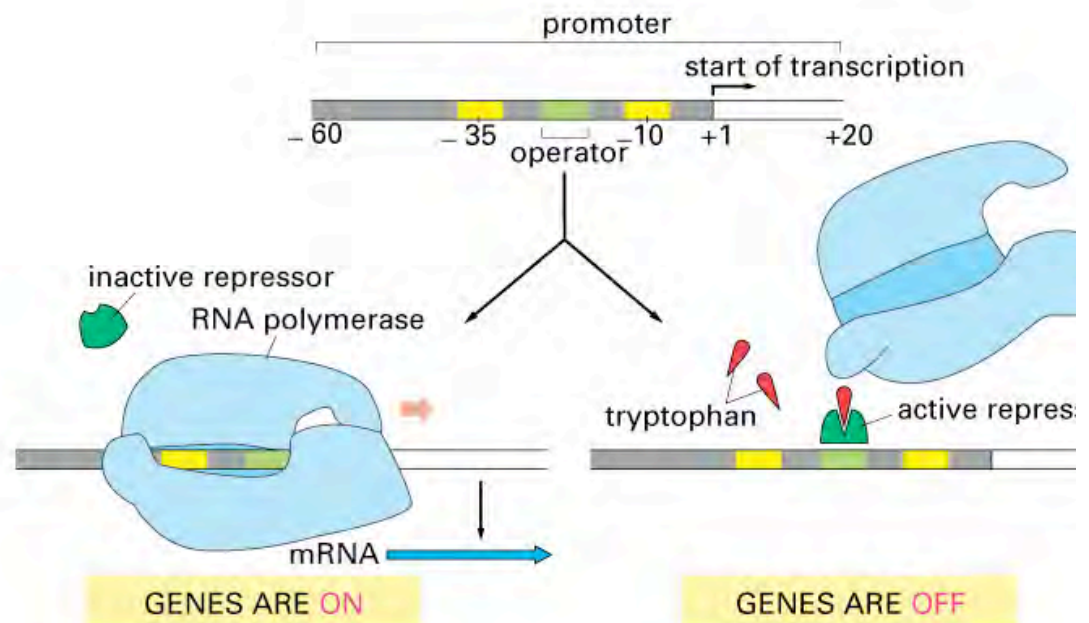
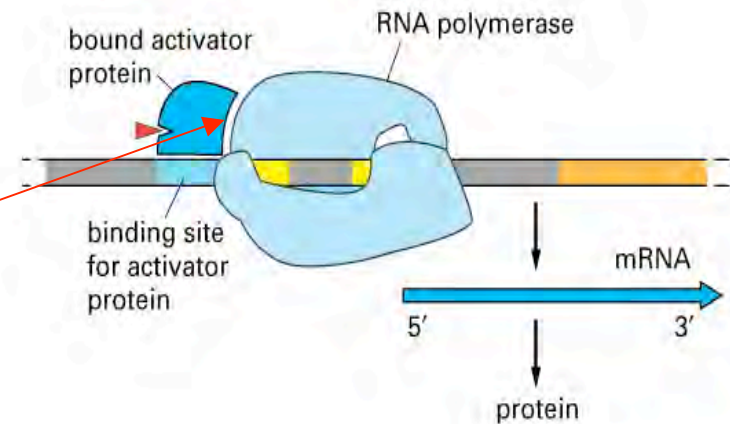


Figure 8-7 Essential Cell Biology, 2/e. (© 2004 Garland Science)



# Activators: The Cartoon

- ▶ **Activator molecules enhance the action of RNA polymerase.**
- ▶ **Activators can be under the control of other molecules (i.e. inducers) that dictate when activator is bound and not.**
- ▶ **Activators *“RECRUIT”* the polymerase.**



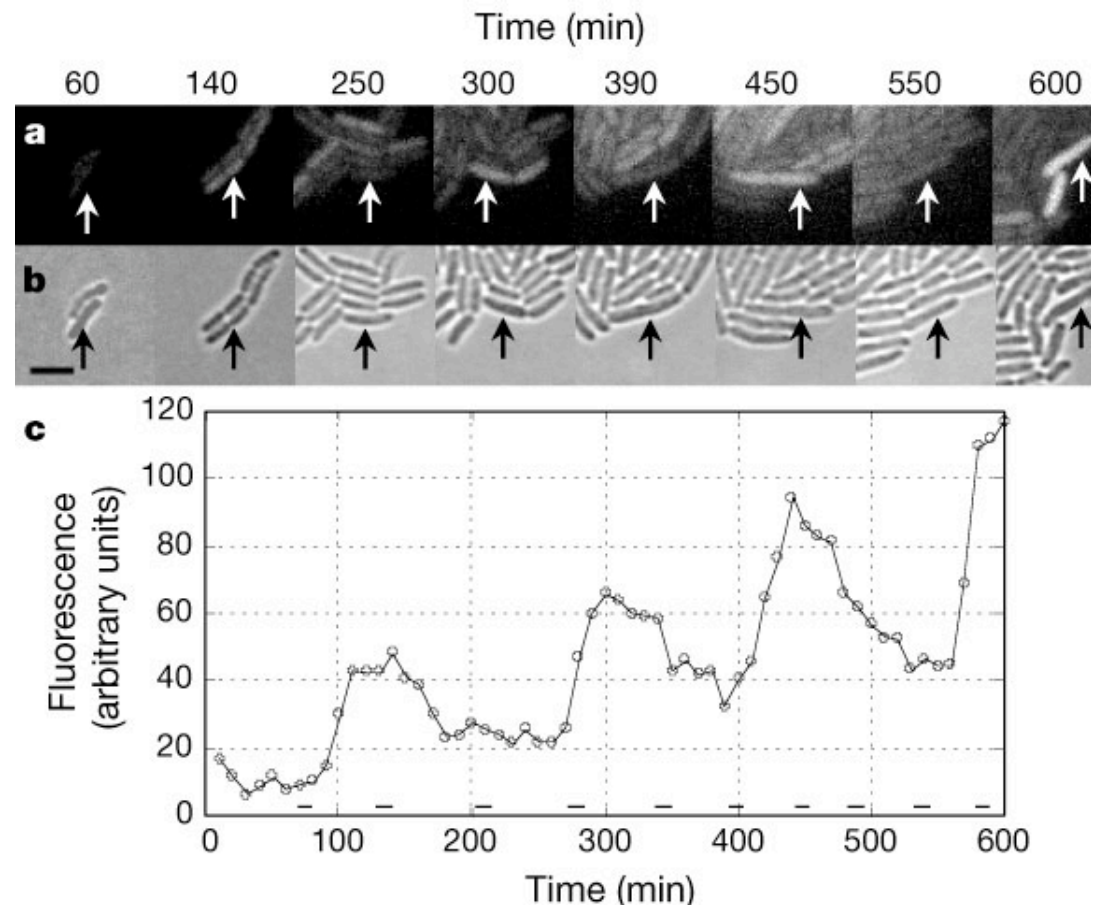
**Adhesive interaction between RNAP and activator**

**But quantitative data demands more than cartoons!**

# Quantitative Measurement of Gene Expression: When?

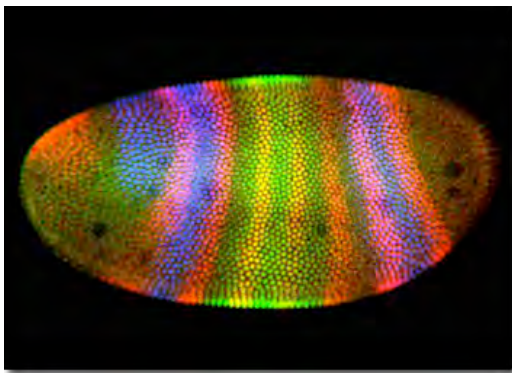
(Elowitz and Leibler)

- *Measurement of when genes are expressed.*
- *An example: the repressilator, a transcriptional regulatory network which leads to a time varying concentration of various gene products.*
- *The idea: stick an engineered set of genes into the cell and then turn them on.*

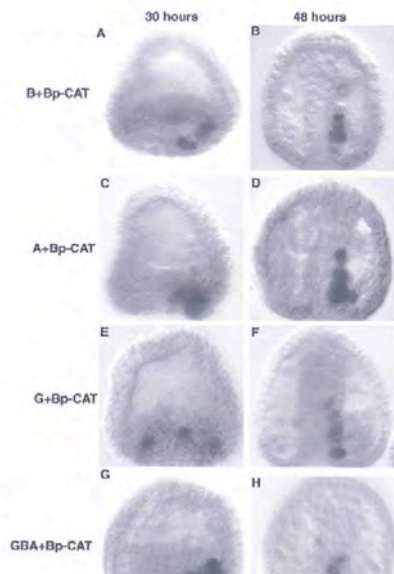
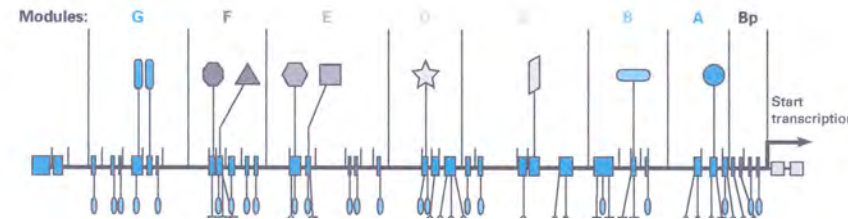


# Quantitative Measurement of Gene Expression: Where?

- Developmental biology is one of the most compelling arenas for thinking about **spacetime** gene expression.



Fruit fly embryo



Sea urchin embryo

Series	X is	Constructs	Fold Relative CAT Activity	
			-10.0	+10.0
X+Bp (2)	-	Bp-CAT	1.00	1.00
	C	C+Bp-CAT	1.06	1.06
	D	D+Bp-CAT	1.83	1.83
	E	E+Bp-CAT	2.03	2.03
	F	F+Bp-CAT	1.06	1.06
	DC	DC+Bp-CAT	4.00	4.00
	EDC	EDC+Bp-CAT	8.66	8.66
GXBA+Bp (3)	-	GBA+Bp-CAT	10.03	10.03
	F	GFBA+Bp-CAT	5.00	5.00
	E	GEBA+Bp-CAT	5.30	5.30
	DC	GDCBA+Bp-CAT	4.72	4.72
	FEDC	GFEDCBA+Bp-CAT	7.53	7.53
XA+Bp (3)	-	A+Bp-CAT	4.01	4.01
	F	FA+Bp-CAT	1.20	1.20
	E	EA+Bp-CAT	2.02	2.02
	DC	DCA+Bp-CAT	1.25	1.25
	EDC	EDCA+Bp-CAT	3.13	3.13
	FEDC	FEDCA+Bp-CAT	1.05	1.05
XB+Bp (2)	-	B+Bp-CAT	2.67	2.67
	F	FB+Bp-CAT	4.03	4.03
	E	EB+Bp-CAT	1.41	1.41
	DC	DCB+Bp-CAT	5.16	5.16
GX+Bp (2)	-	G+Bp-CAT	2.23	2.23
	F	GF+Bp-CAT	1.79	1.79
	FE	GFE+Bp-CAT	1.54	1.54
	FEDC	GFEDC+Bp-CAT	1.07	1.07
GXB+Bp (2)	-	GB+Bp-CAT	3.30	3.30
	F	GF+Bp-CAT	1.40	1.40
	E	GEB+Bp-CAT	3.69	3.69
	DC	GDCB+Bp-CAT	4.56	4.56

*Battle cry: quantitative measurements demand quantitative models.*



# The Lac Operon: The Hydrogen Atom of Gene Regulation

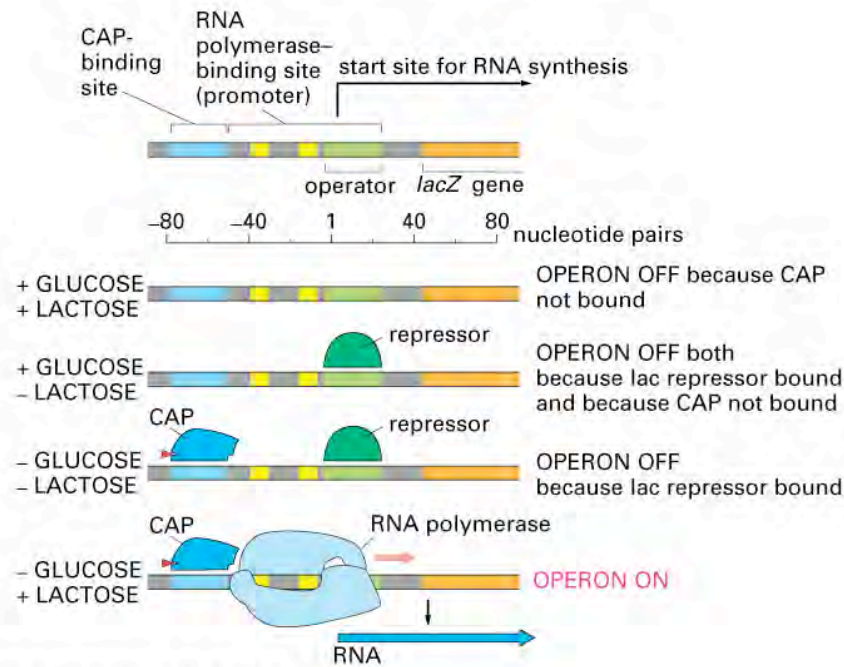


Figure 8-9 Essential Cell Biology, 2/e. (© 2004 Garland Science)

Monod

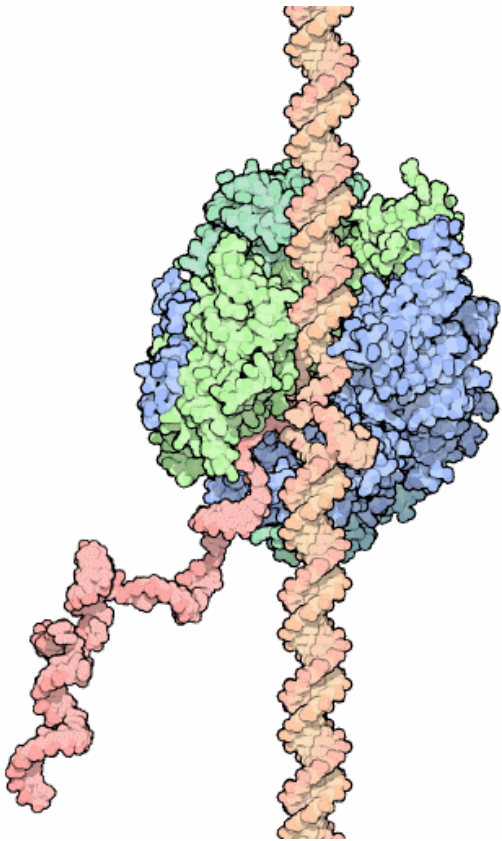


*“Tout ce qui est vrai pour le Colibacille est vrai pour l'éléphant”*

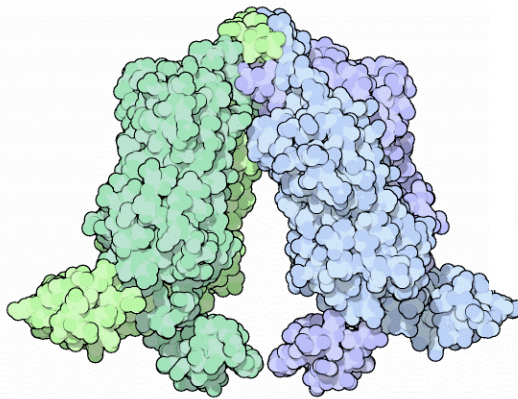


# The Single Molecule Census

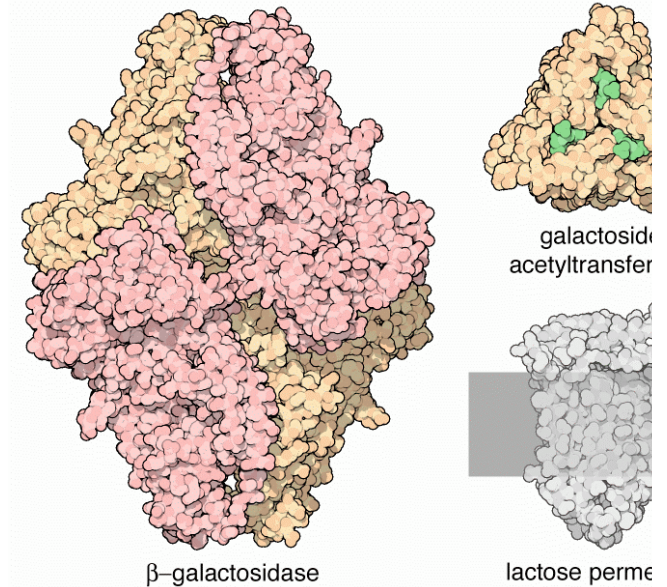
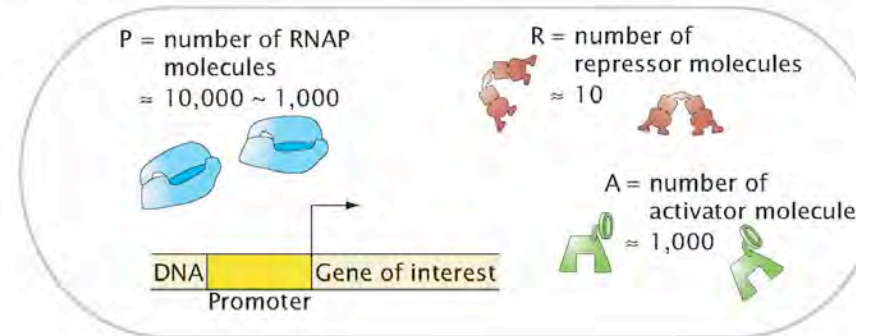
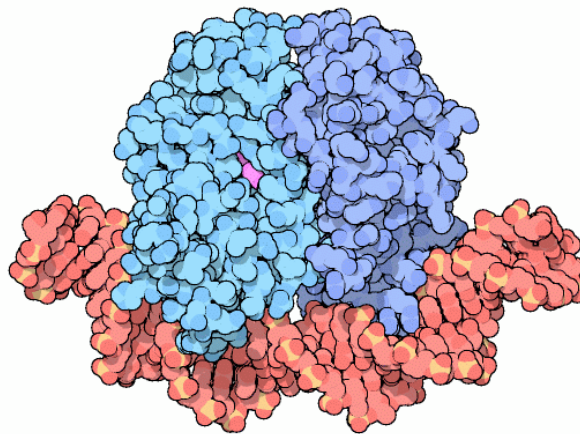
RNAP+DNA+mRNA



Lac Repressor



CRP and DNA

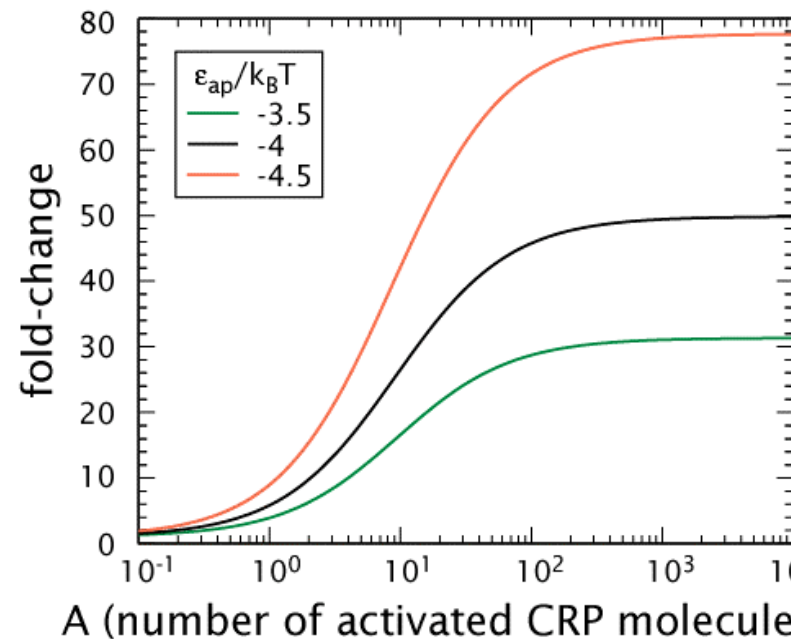


(Beautiful work of David Goodsell)

# The Notion of Fold-Change

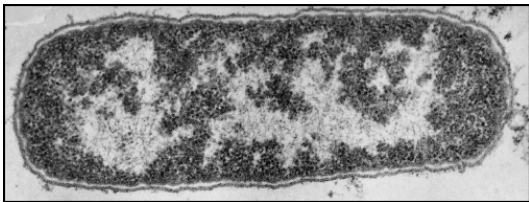
- *The idea: by how many fold is the expression increased or decreased relative to some reference value.*
- *To measure fold-change one can measure the expression level (for example using fluorescent reporter molecules) for the case of interest and for the reference state.*

$$\text{fold-change in promoter occupancy} = \frac{\rho_{\text{bound}}(A \neq)}{\rho_{\text{bound}}(A =)}$$

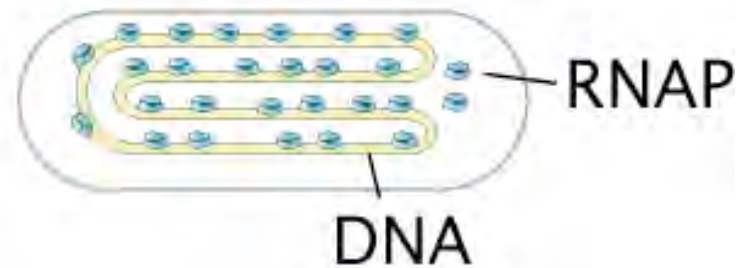


# Statistical Mechanics of Promoter Occupancy

- *The goal: compute the probability of promoter occupancy as a ratio of promoter occupied states to all of the states available to all of the polymerase molecules.*
- *Number of ways of arranging the polymerase molecules is a classic problem in statistics.*



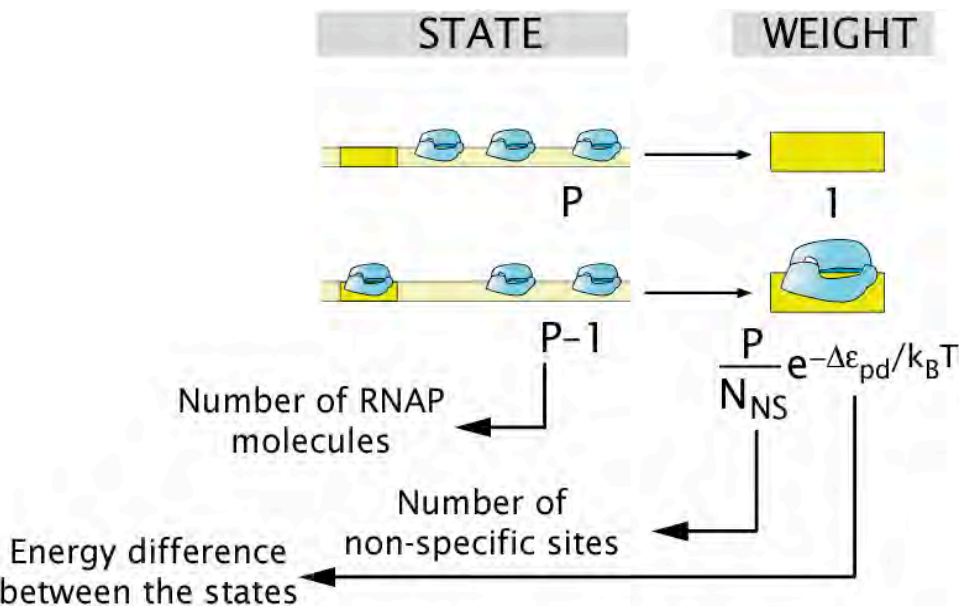
Non-specific DNA is  
RNAP's reservoir



$$Z_{unbound} = \frac{N_{NS}!}{P!(N_{NS}-P)!} e^{-\beta P \epsilon_{pd}^{NS}}$$

# Reckoning Promoter Occupancy

- We construct the ratio of weights for bound and unbound states.



$$p_{bound} = \frac{Z_{bound}}{Z_{bound} + Z_{unbound}}$$

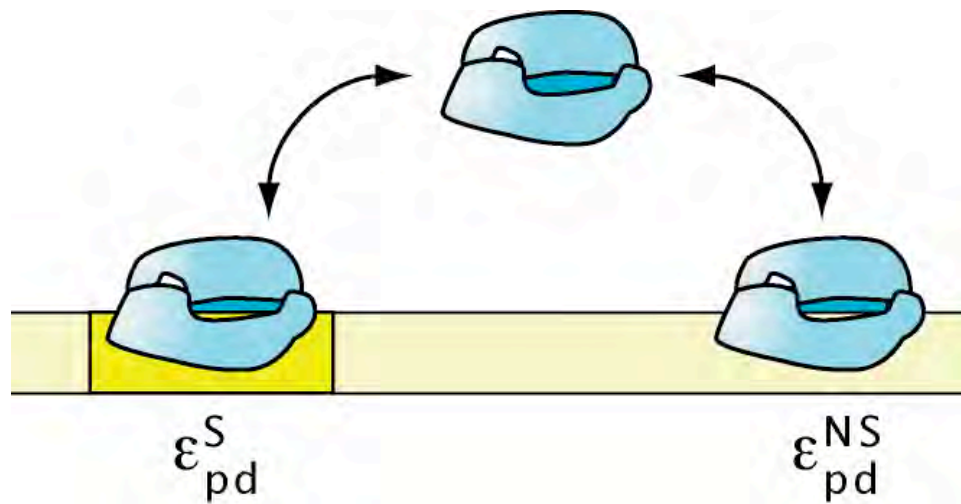
$$Z_{unbound} = \frac{N_{NS}!}{P!(N_{NS}-P)!} e^{-\beta P}$$

The Outcome:

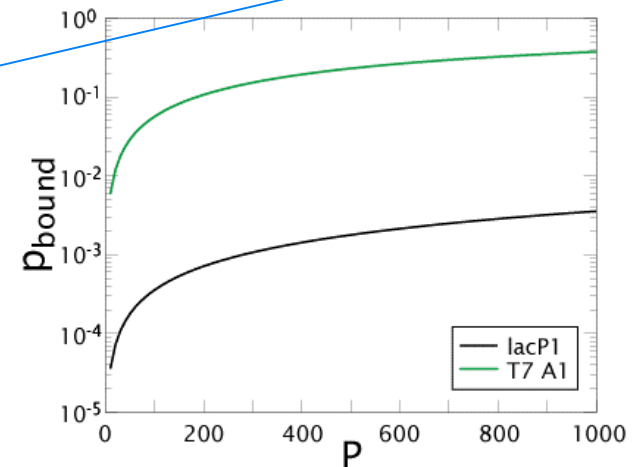
$$p_{bound} = \frac{1}{1 + \frac{N_{NS}}{P} e^{\beta \Delta\epsilon}}$$



# Statistical Mechanics of Polymerase Binding: Basal Transcription



$$10^6 p_{\text{bound}} = \frac{1}{1 + \frac{N_{NS}}{P} e^{\beta \Delta}}$$

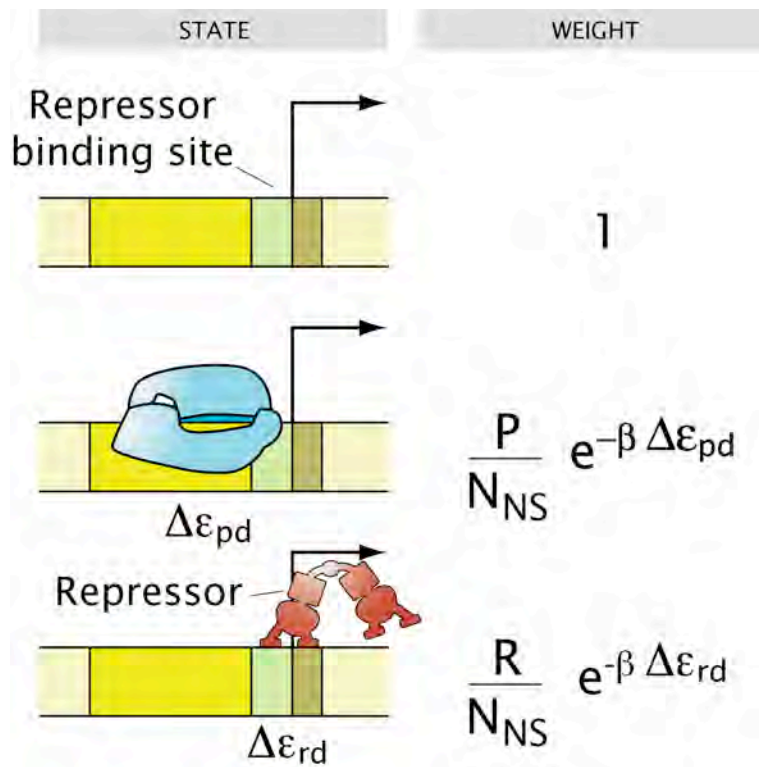


- Key insight: RNAP NOT bound in absence of helper molecules for "normal" promoters.
- $F_{\text{reg}}$  accounts for the presence of regulatory proteins and features such as looping.

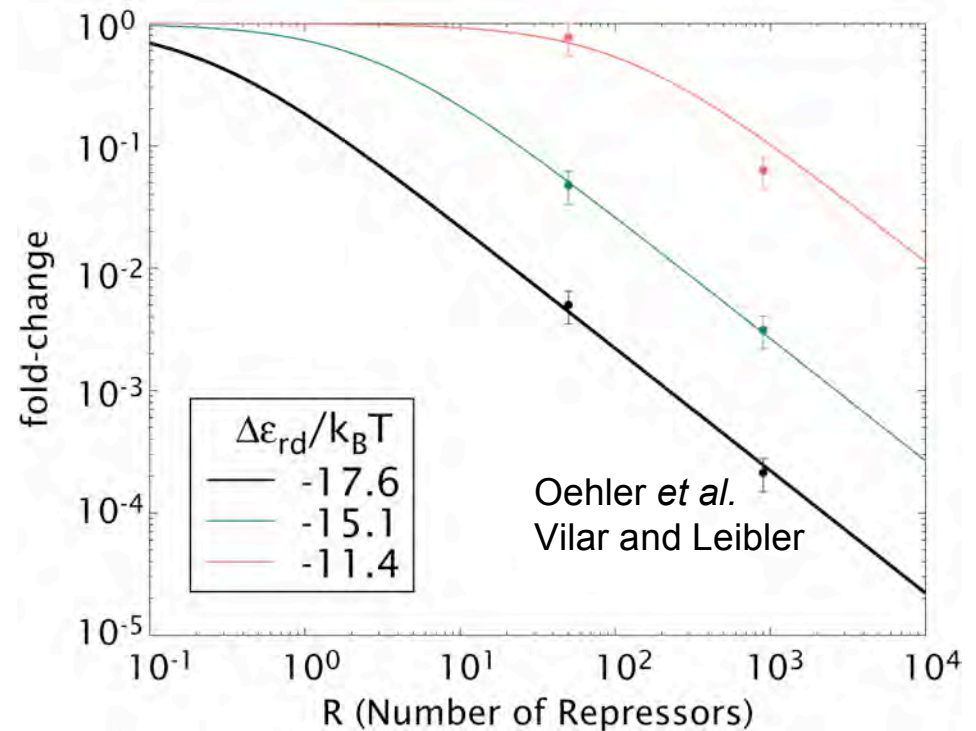
Action of transcription factors: the regulation factor

$$p_{\text{bound}} = \frac{1}{1 + \frac{N_{NS}}{P F_{\text{reg}}} e^{\beta \Delta \epsilon}}$$

# Statistical Mechanics of a Single Repressor Binding Site



$$F_{reg} = \left(1 + \frac{R}{N_{NS}} e^{-\beta \Delta\epsilon_{rd}}\right)$$



- Model predicts concentration dependence of repression for a single repressor binding site.
- Extent of repression depends upon the strength of the binding site.

# Exploring Regulatory Diversity

**Table 1**  
Regulation factors for several different regulatory motifs.

Case	Regulation factor ( $F_{reg}$ )	Regulation factor ( $F_{reg}$ )
1. Simple repressor	$(1+r)^{-1}$	$\left(1 + \frac{ R }{K_R}\right)^{-1}$
2. Simple activator	$\frac{1 + \frac{a_{10}P}{k_B T}}{1+a}$	$\frac{1 + \frac{ A }{K_A} f}{1 + \frac{ A }{K_A}}$
3. Activator recruited by a helper (H)	$\frac{1 + \frac{a_{10}P}{k_B T}}{1 + \frac{1 + \frac{a_{10}P}{k_B T}}{1+h}}$	$\frac{1 + \frac{ H }{K_H} + \frac{ A }{K_A} f + \frac{ A }{K_A} \frac{ H }{K_H} f_{10}}{1 + \frac{ H }{K_H} + \frac{ A }{K_A} + \frac{ A }{K_A} \frac{ H }{K_H} f_{10}}$
4. Repressor recruited by a helper (H)	$\left(1 + \frac{1 + \frac{a_{10}P}{k_B T}}{1+h} r\right)^{-1}$	$\frac{1 + \frac{ H }{K_H}}{1 + \frac{ H }{K_H} + \frac{ R }{K_R} + \frac{ R }{K_R} \frac{ H }{K_H} f}$
5. Dual repressors	$(1+r_1)^{-1}(1+r_2)^{-1}$	$\left(1 + \frac{ R_1 }{K_{R_1}}\right)^{-1} \left(1 + \frac{ R_2 }{K_{R_2}}\right)^{-1}$
6. Dual repressors interacting	$\left(1 + r_1 + r_2 + r_1 r_2 \frac{r_1 r_2}{k_B T}\right)^{-1}$	$\left(1 + \frac{ R_1 }{K_{R_1}} + \frac{ R_2 }{K_{R_2}} + \frac{ R_1 }{K_{R_1}} \frac{ R_2 }{K_{R_2}} f\right)^{-1}$
7. Dual activators interacting	$\frac{1 + \frac{a_{10}P}{k_B T} + \frac{a_{20}P}{k_B T} + \frac{a_{10}P + a_{20}P}{k_B T}}{1 + a_1 + a_2 + a_1 a_2 \frac{a_{10}P + a_{20}P}{k_B T}}$	$\frac{1 + \frac{ A_1 }{K_{A_1}} f_1 + \frac{ A_2 }{K_{A_2}} f_2 + \frac{ A_1 }{K_{A_1}} \frac{ A_2 }{K_{A_2}} f_{12}}{1 + \frac{ A_1 }{K_{A_1}} + \frac{ A_2 }{K_{A_2}} + \frac{ A_1 }{K_{A_1}} \frac{ A_2 }{K_{A_2}} f_{12}}$
8. Dual activators cooperating via looping	$\frac{1 + \frac{a_{10}P}{k_B T} + \frac{a_{20}P}{k_B T} + \frac{a_{10}P + a_{20}P}{k_B T} + \frac{F_{loop}}{k_B T}}{(1 + a_1)(1 + a_2)}$	$\frac{1 + \frac{ A_1 }{K_{A_1}} f_1 + \frac{ A_2 }{K_{A_2}} f_2 + \frac{ A_1 }{K_{A_1}} \frac{ A_2 }{K_{A_2}} f_{12}}{\left(1 + \frac{ A_1 }{K_{A_1}}\right) \left(1 + \frac{ A_2 }{K_{A_2}}\right)}$
9. Repressor		
10. N no		

**Better census needed!**

P = number of RNAP molecules  
≈ 10,000 ~ 1,000

R = number of repressor molecules  
≈ 10

A = number of activator molecules  
≈ 1,000

DNA Promoter Gene of interest

Regulatory symbol i in terms of regulatory TF we in the conc the RNA

**Key point: We can work out the regulation factor for many other scenarios including other looping scenarios.**




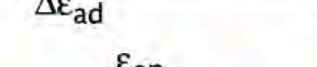
STATE	WEIGHT
	1
	$\frac{P}{N_{ns}} e^{-\Delta\epsilon_{pd}}$
	$\frac{A}{N_{ns}} e^{-\Delta\epsilon_{a_1d}}$
	$\frac{A}{N_{ns}} e^{-\Delta\epsilon_{a_2d}}$
	$\frac{A}{N_{ns}} \frac{A}{N_{ns}} e^{-(\Delta\epsilon_{a_1d} + \Delta\epsilon_{a_2d})}$
	$\frac{P}{N_{ns}} \frac{A}{N_{ns}} e^{-(\Delta\epsilon_{pd} + \Delta\epsilon_{a_1d} + \epsilon_{a_1p})}$
	$\frac{P}{N_{ns}} \frac{A}{N_{ns}} e^{-(\Delta\epsilon_{pd} + \Delta\epsilon_{a_2d} + \Delta\epsilon_{a_2p})}$
	$\frac{P}{N_{ns}} \frac{A}{N_{ns}} \frac{A}{N_{ns}} e^{-(\Delta\epsilon_{pd} + \Delta\epsilon_{a_1d} + \Delta\epsilon_{a_2d} + \epsilon_{a_1p} + \epsilon_{a_2p} + F_{loop})}$

**Synergistic Activation**

# How Should We Think About Regulation Quantitatively?

“Thermodynamic Models” –  
Equilibrium Notions

Rate Equation Perspective

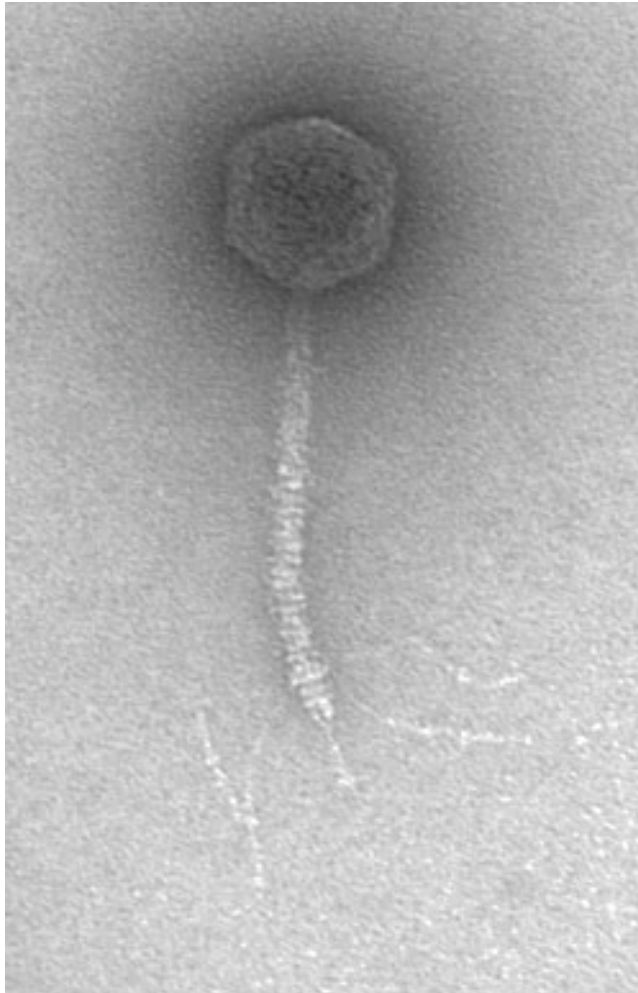
STATE	WEIGHT
 <p>Activator binding site</p>	1
 <p>activated</p> <p><math>\Delta\epsilon_{pd}</math></p>	$\frac{P}{N_{NS}} e^{-\Delta\epsilon_{pd}/k_B T}$
 <p>CRP</p> <p><math>\Delta\epsilon_{ad}</math></p>	$\frac{A}{N_{NS}} e^{-\Delta\epsilon_{ad}/k_B T}$
 <p><math>\Delta\epsilon_{ad}</math></p> <p><math>\epsilon_{ap}</math></p> <p><math>\Delta\epsilon_{pd}</math></p>	$\frac{P}{N_{NS}} \frac{A}{N_{NS}} e^{-(\Delta\epsilon_{pd} + \Delta\epsilon_{ad} + \epsilon_{ap})/k_B T}$

$$\begin{aligned} \frac{d[\text{mRNA}_{\text{Rep}}]}{dt} &= V_{\text{mRNA-Rep}} - (k_{\text{d,mRNA-Rep}} + \mu) \cdot [\text{mRNA}_{\text{Rep}}] \\ \frac{d[\text{Rep}]}{dt} &= V_{\text{Rep}} - (k_{\text{d,Rep}} + \mu) \cdot [\text{Rep}] \\ \frac{d[\text{mRNA}_{\text{ZYA}}]}{dt} &= V_{\text{mRNA-ZYA}} - (k_{\text{d,mRNA-ZYA}} + \mu) \cdot [\text{mRNA}_{\text{ZYA}}] \\ \frac{d[\beta\text{gal}]}{dt} &= V_{\beta\text{gal}} - (k_{\text{d}} + \mu) \cdot [\beta\text{gal}] \\ \frac{d[\text{Perm}]}{dt} &= V_{\text{Perm}} - (k_{\text{d}} + \mu) \cdot [\text{Perm}] \\ \frac{d[\text{Lac}_{\text{out}}]}{dt} &= V_{\text{Lac}} - V_{\text{cat,Lac}} - V_{\text{Lac-Allo}} - \mu \cdot [\text{Lac}_{\text{out}}] \\ \frac{d[\text{Allo}]}{dt} &= V_{\text{Lac-Allo}} - V_{\text{cat,Allo}} - \mu \cdot [\text{Allo}] \\ \frac{d[\text{cAMP}]}{dt} &= V_{\text{cAMP}} - (k_{\text{cat}} + \mu) \cdot [\text{cAMP}] \\ \frac{d[\text{Glu}_{\text{out}}]}{dt} &= (V_{\text{out,Glu}} - V_{\text{I,Glu}}) \cdot X \\ \frac{d[\text{Lac}_{\text{cat}}]}{dt} &= -V_{\text{I,Lac}} \cdot X \\ \frac{dX}{dt} &= \mu X \\ \frac{d[\text{Glu6P}]}{dt} &= V_{\text{I,Glu}} + 2 \cdot (V_{\text{cat,Lac}} + V_{\text{cat,Allo}}) - \frac{\mu}{Y_{X/\text{Glu6P}}} - \mu \cdot [\text{Glu6P}] \end{aligned}$$

Wong, Gladney, and Keasling



# *The Lambda Switch: The Other Hydrogen Atom of Gene Regulation*

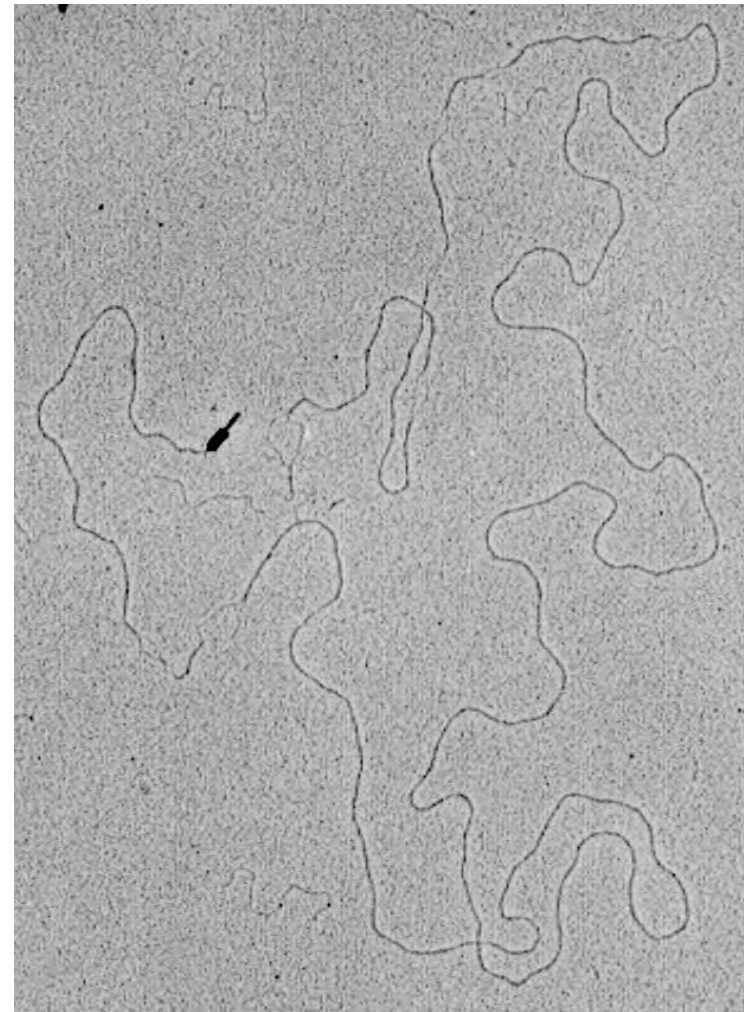
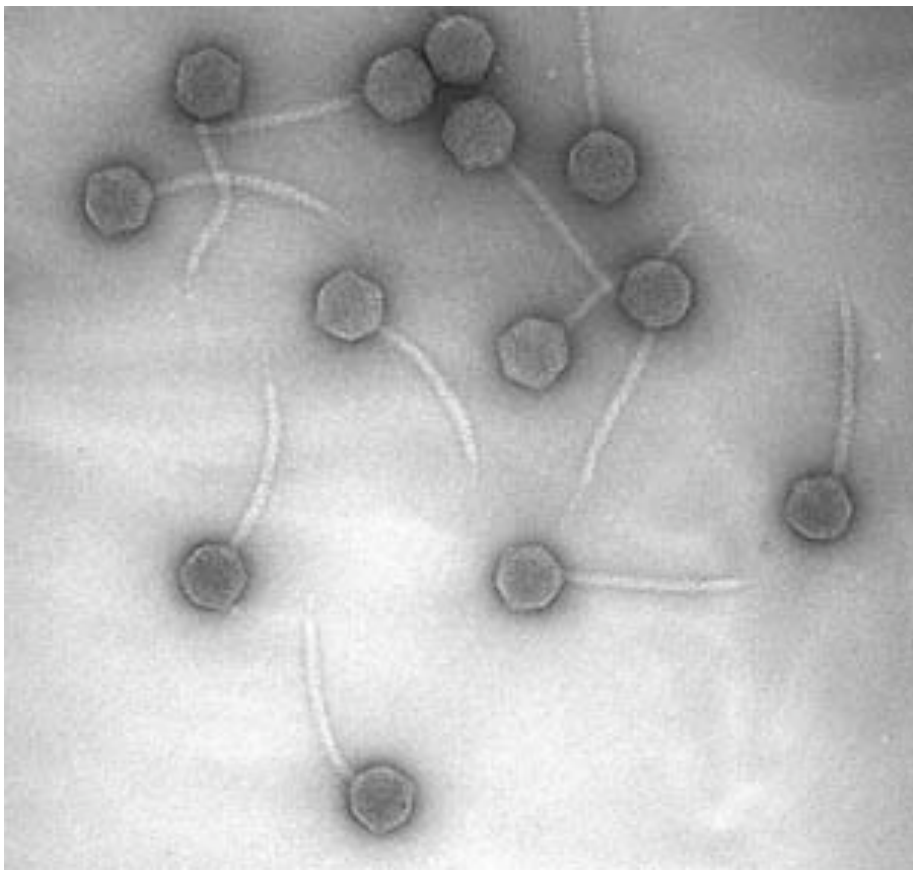


Roger Hendrix



# *Bacteriophage and Their Genomes*

<http://www.biochem.wisc.edu/inman/empics/0020b.j>



# The Life Cycle of Bacteriophage Lambda

