



## Lecture 10

## **Bacterial genome replication and expression**

## **Regulation of bacterial cellular processes**

## **JING YUAN**





## **Chapter 10 Molecular Genetic**

# **10.1 Griffith Experiment**

# Griffith实验 1928

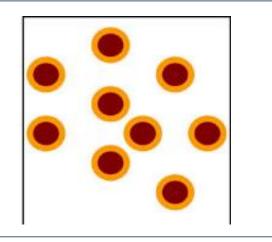
#### Griffith Frederick (1879-1941) 英国细菌学家和流行病学家



# 肺炎球菌(Diplococcus pneumoniae)



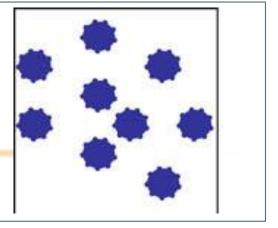
- 体外培养时,细胞产生荚膜, 细菌菌落光滑;
- 感染人体导致肺炎;
- 感染小鼠导致败血症并且死亡。



粗糙型菌株 (Rough, 简称R型)

 体外培养时,细胞不产生荚膜, 菌落粗糙;

• 感染人和小鼠,不发病。



### Griffith实验

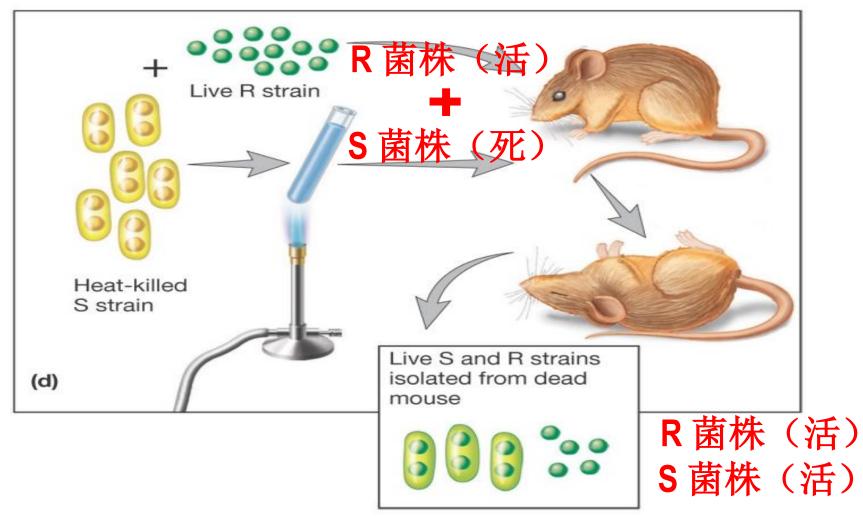
- 实验— S 菌株感染小鼠, 致死
- 实验二 R 菌株感染小鼠, 正常
- 实验三 S 菌株热灭活后感染小鼠,正常

## 实验结果符合预期

### Griffith实验

- 实验一 S 菌株感染小鼠, 致死
- 实验二 R 菌株感染小鼠, 正常
- 实验三 S菌株热灭活后感染小鼠,正常
- 实验四 S 菌株热灭活 + R 菌株 , 混合 后感染小鼠 , 什么结果 ?

实验四的意外发现:细菌转化



## 细菌转化(Transformation) **Heat-killed** Living S type **R** type Living Living **ype** pe

# 逻辑推导:肺炎球菌细胞中存在"转化物质" 转化物质 **Heat-killed** S type Living Living S type **R** type



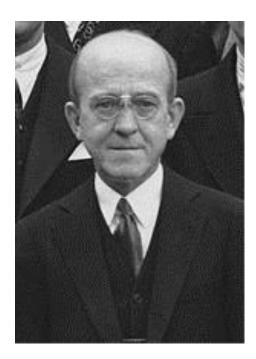


## **Chapter 10 Molecular Genetic**

# **10.2 Avery Experiment**

## 肺炎球菌中的转化物质具体是什么? What is the transforming agents in *D. pneumoniae*?

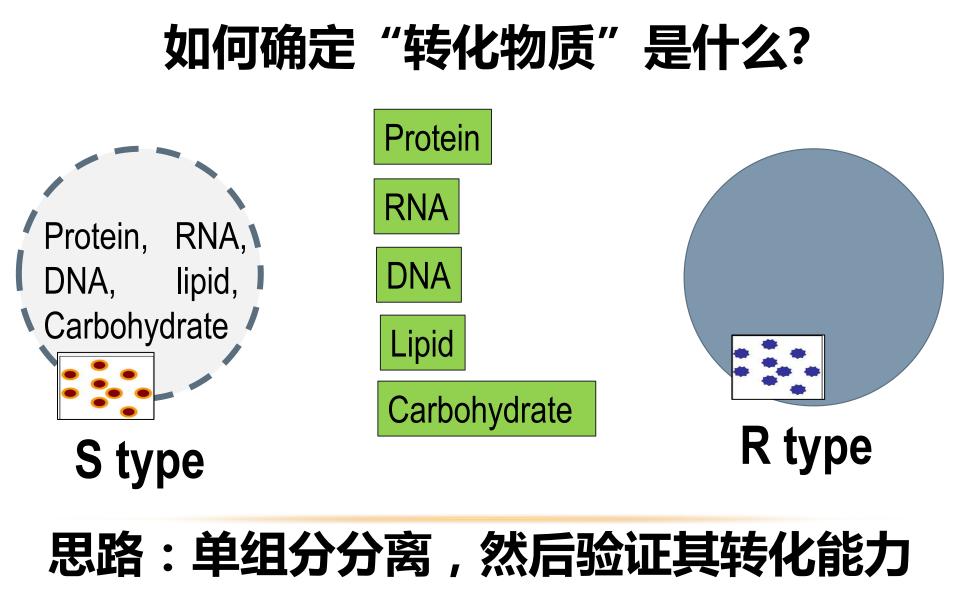
# 肺炎球菌转化物质的化学本质研究



#### 年代: 1944 杂志: J. Experimental Medicine 作者: Avery, MacLeod, and McCarty

#### **Oswald Avery**

美国细菌学家 1877---1955



# Avery实验之功能获得分析

- Killed S-type cell+R type cell->S type colony
  - - + R type cell  $\rightarrow$  R type colony
- Purified DNA + R type cell -> S type colony

分离纯化的单组分

**Purified protein** 

**Purified lipid** 

**Purified RNA** 

# Avery实验之功能缺失分析

- R type cell + (S cell extract )
- R type cell + (S cell extract + 蛋白酶) → S type colony
- R type cell + (S cell extract + 脂酶)
- R type cell + (S cell extract + RNA酶)
- R type cell + (S cell extract + DNA酶)

细胞提取物 降解酶

-> S type colony

 $\rightarrow$  S type colony

→ S type colony

→ R type colony

# 结论:DNA是肺炎球菌的遗传转化物质

**R** type

**Heat-killed** Protein, RNA, DNA, lipids, Carbohydrate S type

#### 1850s 孟德尔发现看不见的因子

1928 Griffith发现细菌转化

1943 Avery揭示DNA是转化物质

1953 Crick/Waston 揭示DNA的双螺旋结构





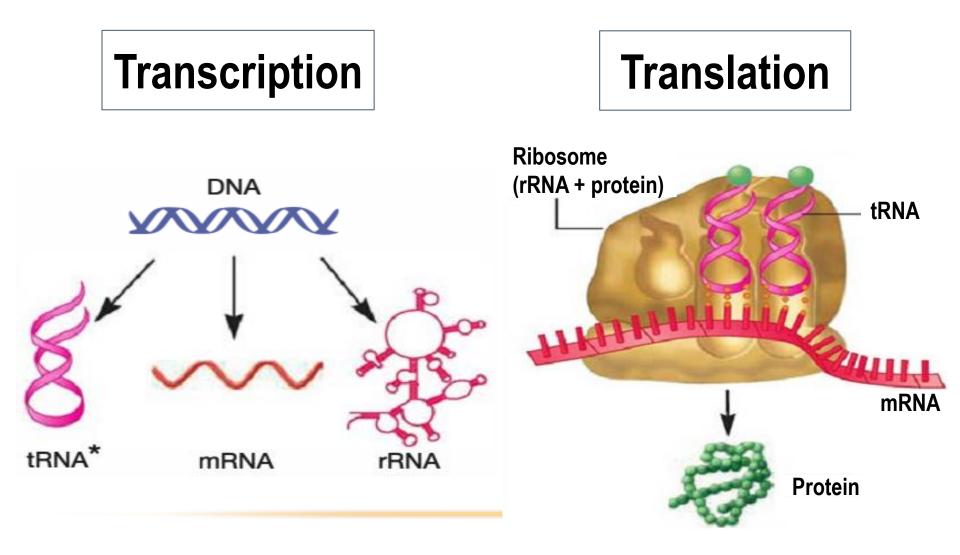
## Chapter 10

## 10.3 Bacterial Gene Classification and Structure 细菌基因的分类和结构

# Concept of "Gene"

One gene -----One protein
One gene -----One polypeptide

Transfer RNA (tRNA) gene
Ribosome RNA (rRNA) gene



# Concept of "Gene"

- One gene -----One protein
- One gene -----One polypeptide
- Transfer RNA (tRNA) gene
- Ribosome RNA (rRNA) gene
- Non-coding RNA genes

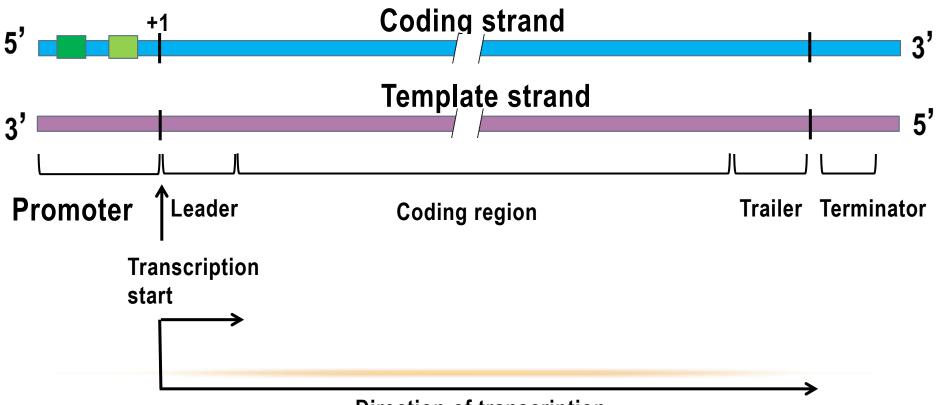
### Gene: The basic unit of genetic information

• Protein-coding genes

• tRNA and rRNA genes

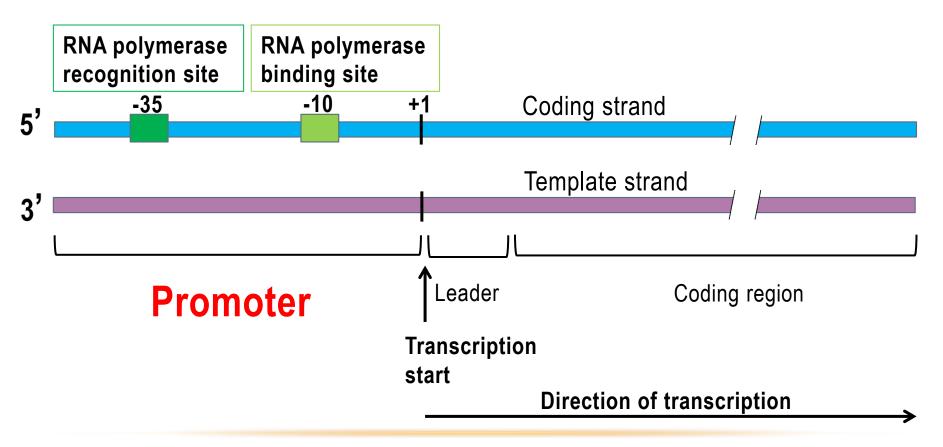
• Non-coding RNA genes

## **A Bacterial Protein-coding Gene Structure**



**Direction of transcription** 

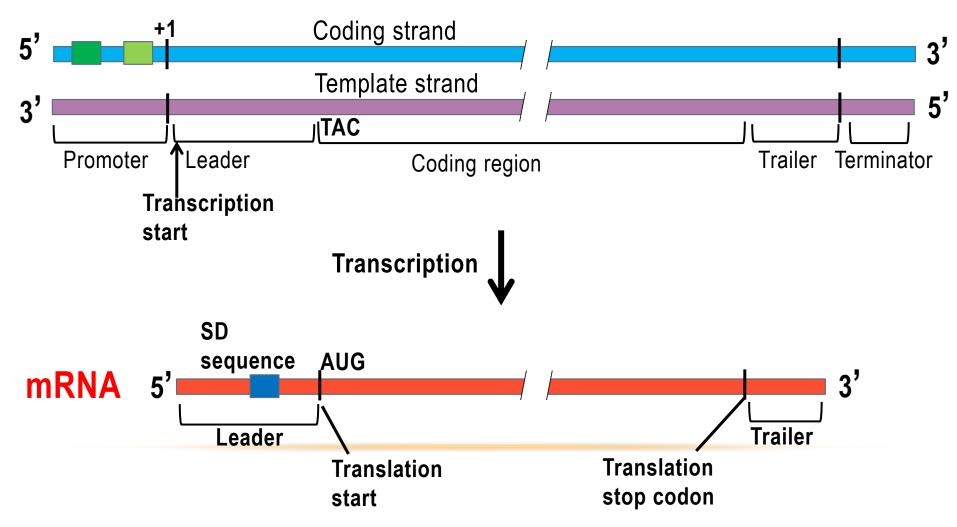
# Promoter



# Gene promoter

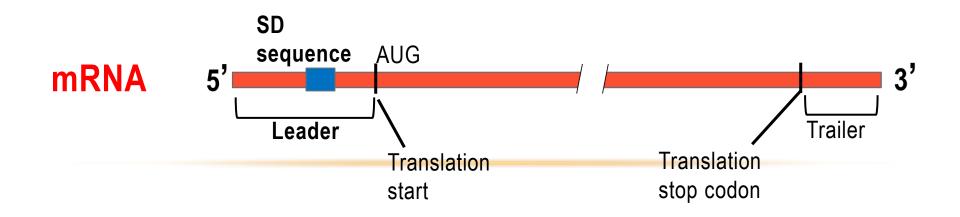
- Promoter is locating upstream of the gene.
- Promoter contains the recognition and binding sites for RNA polymerase.
- Promoter functions to orient the RNA polymerase for transcription.

## A Bacterial Gene and Its mRNA Product



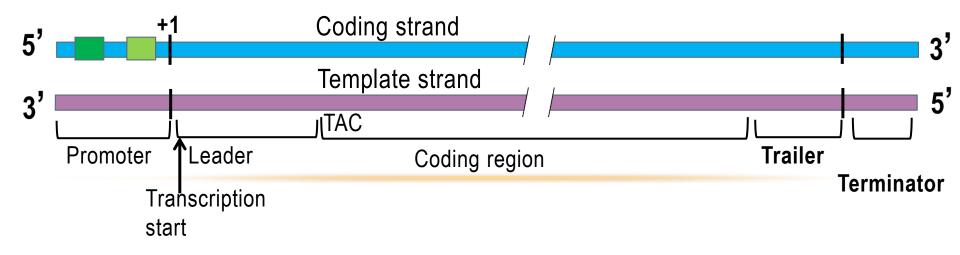
# **Gene structure**

- Leader sequence is transcribed into mRNA, but is not translated into amino acids.
- In bacteria, the leader sequence includes a region called the Shine-Dalgarno sequence, which is important for initiation of protein translation.



# **Gene structure**

- **Trailer** sequence is transcribed but not translated. It contains sequences that prepare the RNA polymerase for release from the DNA template strand.
- **Terminator** is a sequence that signals the RNA polymerase to stop transcription.



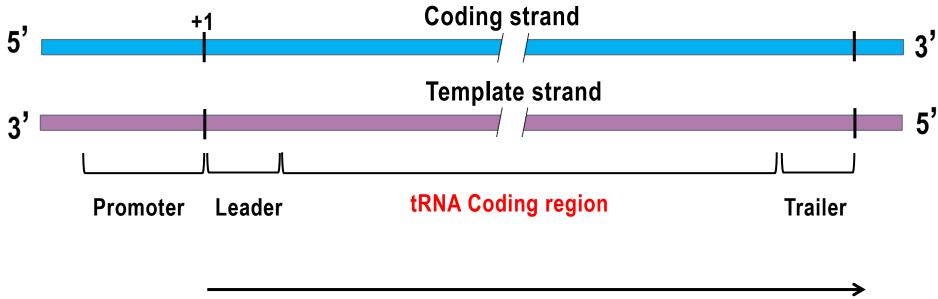
# **Coding region**

- Linear sequence of nucleotides with a fixed start point and end point
- <u>Codons</u> are found in DNA coding strand and code for single amino acids

# Gene structure in Bacteria

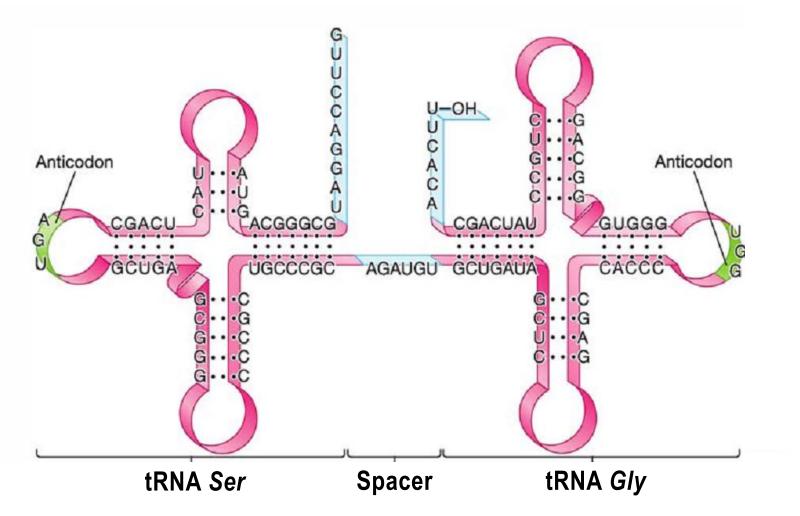
- Bacterial and archaea coding information in gene is normally continuous.
- In eukaryotic, genes that code for proteins (exons) are often interrupted by noncoding regions (introns), which must be removed by splicing.

### **Bacterial tRNA Gene Structure**

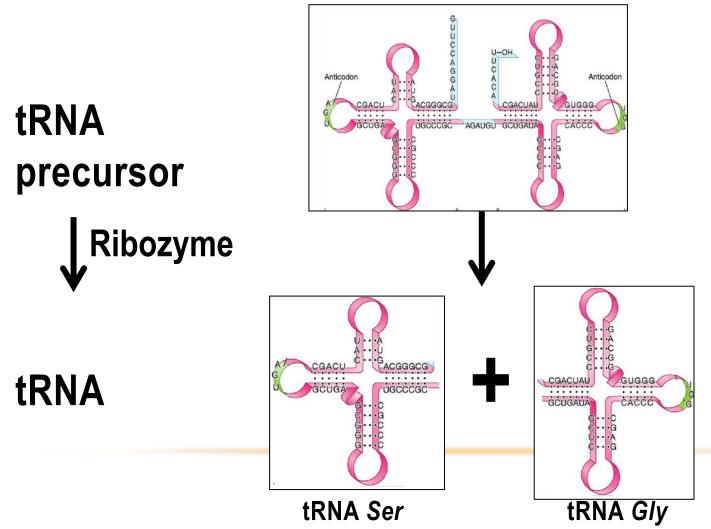


Direction of transcription

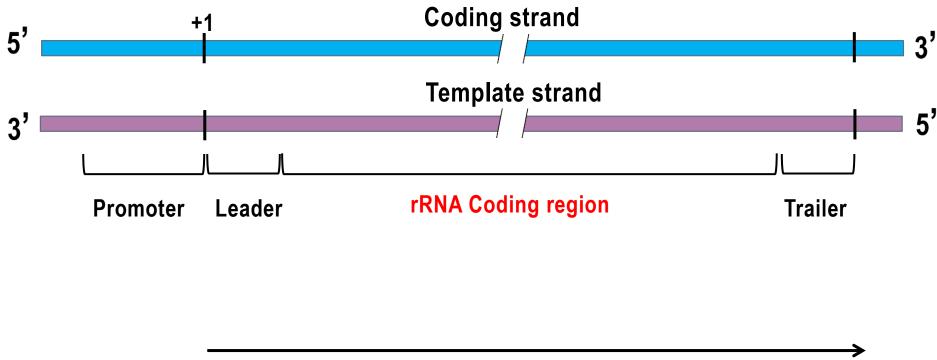
#### A tRNA precursor from *E.coli*



## A tRNA precursor from E.coli

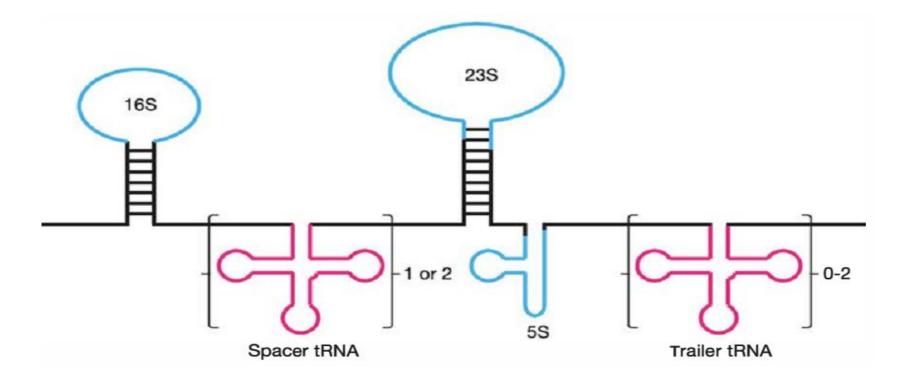


## **Bacterial rRNA Gene Structure**

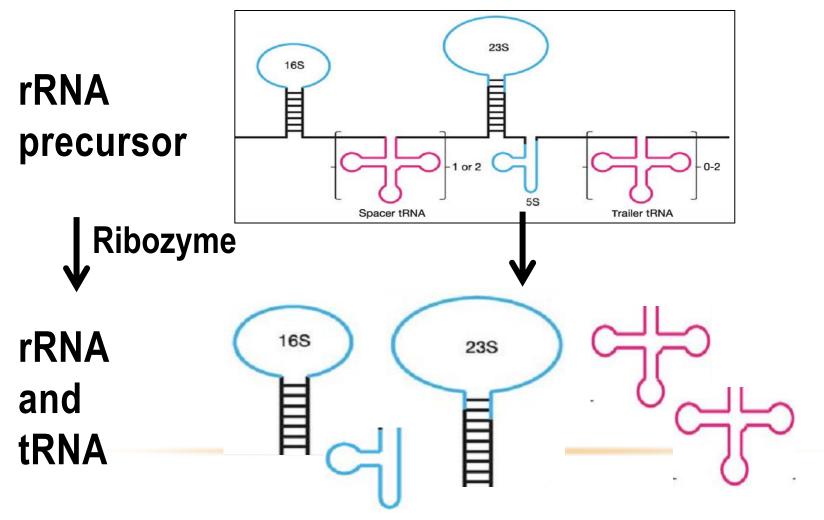


**Direction of transcription** 

### A rRNA precursor from *E.coli*



## A rRNA precursor from E.coli



#### tRNA and rRNA genes

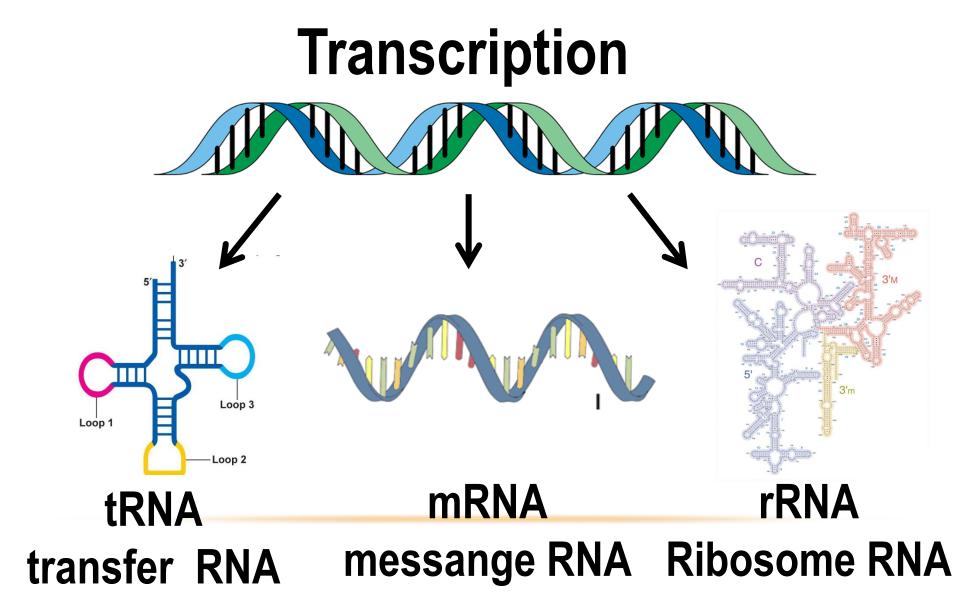
- tRNA genes code for more than one single or one type of tRNA molecule.
- rRNA genes (5S, 16S, 23S) are transcribed as single and large precursor.
- Spacers between the coding regions are removed after transcription, via special ribonucleases called ribozymes.

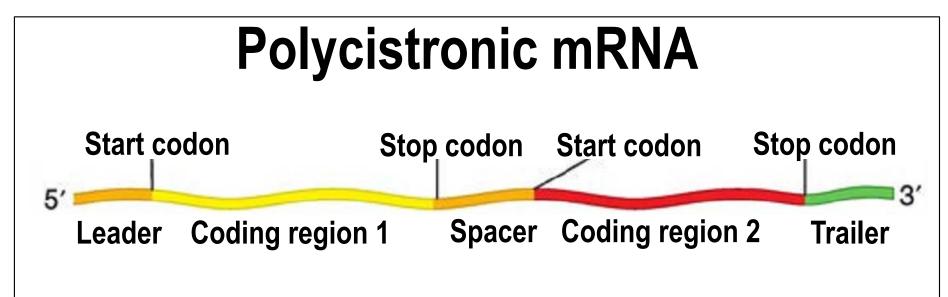


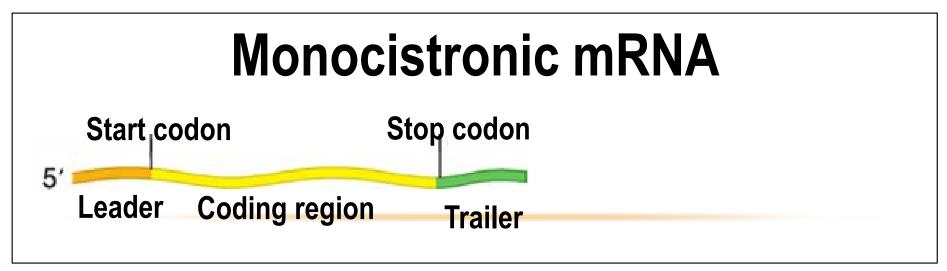


### Chapter 10

## 10.4 Transcription in Bacteria 细菌基因的转录











Volume 73, Issue 3, 7 May 1993, Pages 521–532

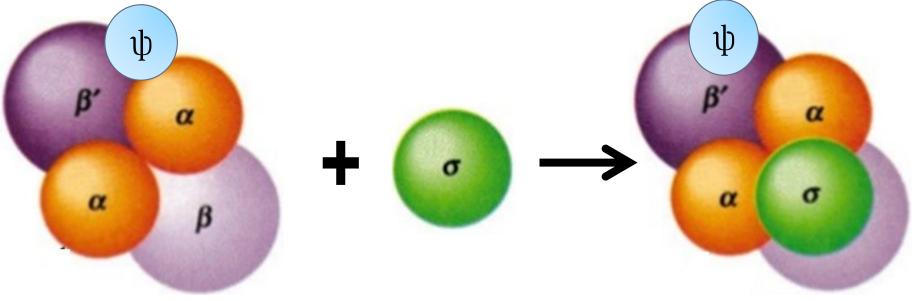
#### Article Operons in C. elegans: Polycistronic mRNA precursors are processed by trans-splicing of SL2 to downstream coding regions

John Spieth, Glenn Brooke, Scott Kuersten, Kristi Lea, Thomas Blumenthal

Department of Biology Indiana University Bloomington, Indiana 47405 USA

Received 25 January 1993, Revised 1 March 1993, Available online 19 April 2004

## Bacterial DNA-Dependent RNA Polymerase



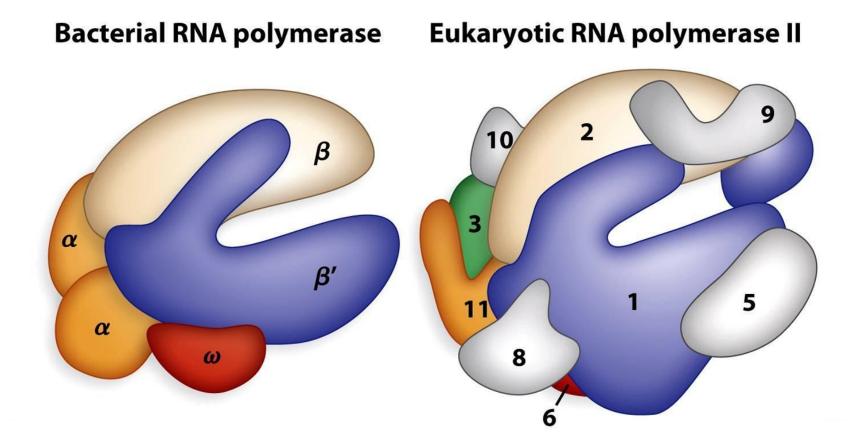
#### **Core enzyme**

Th RNA polymerase core enzyme is composed of fie polypeptides (two a subunits, Holoenzyme

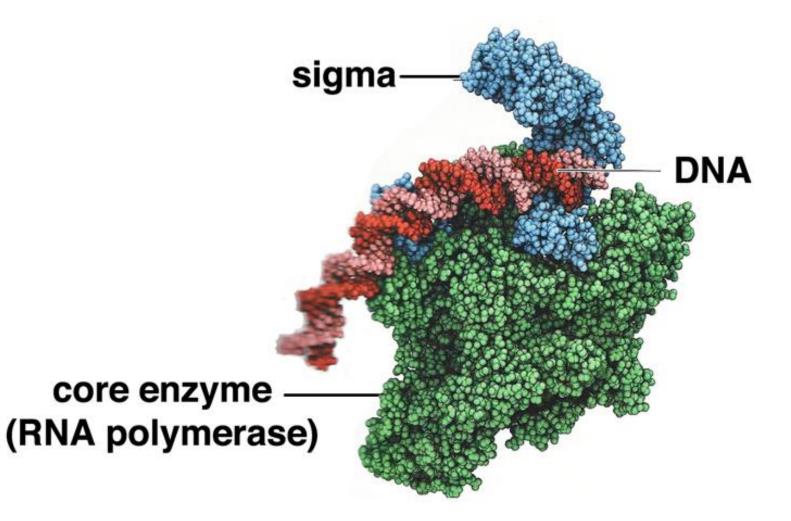
#### **Bacterial DNA-Dependent RNA Polymerase**

- RNA polymerase core enzyme is composed of five polypeptides and catalyzes RNA synthesis.
- Sigma factor has no catalytic activity but helps the core enzyme recognize the promoter.
- Holoenzyme is required for correct initiation of transcription.

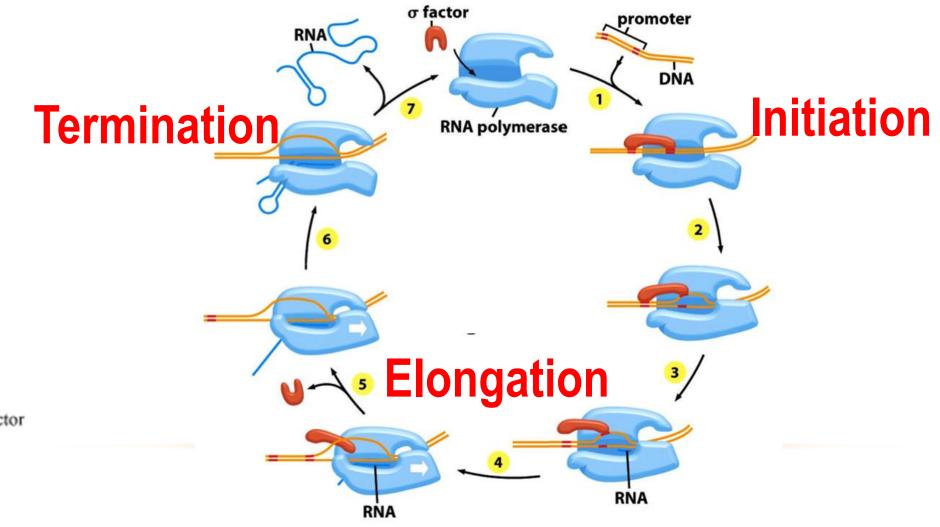
#### **Bacterial and Eukaryotic RNA Polymerase**



#### **Bacterial RNA Polymerase and binding DNA**



#### **The Bacterial Transcription Cycle**

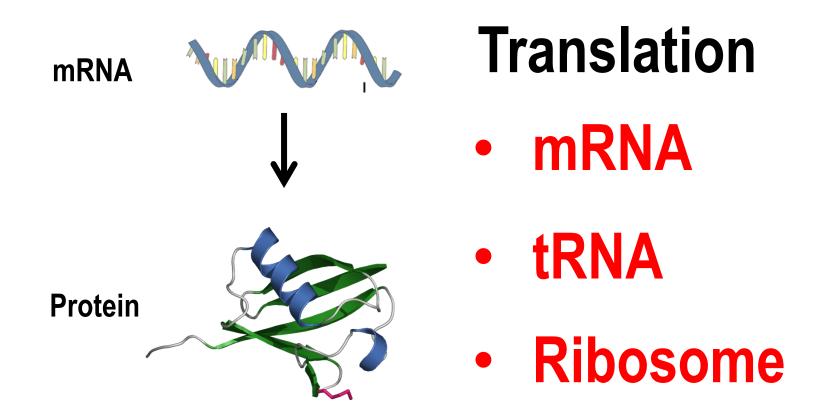






### Chapter 10

## 10.5 Translation in Bactria 细菌的翻译

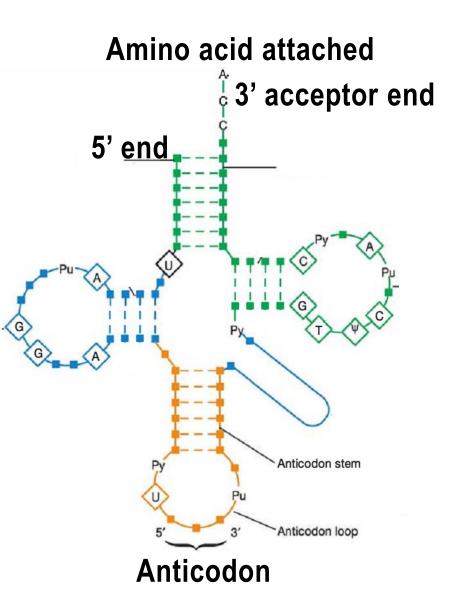


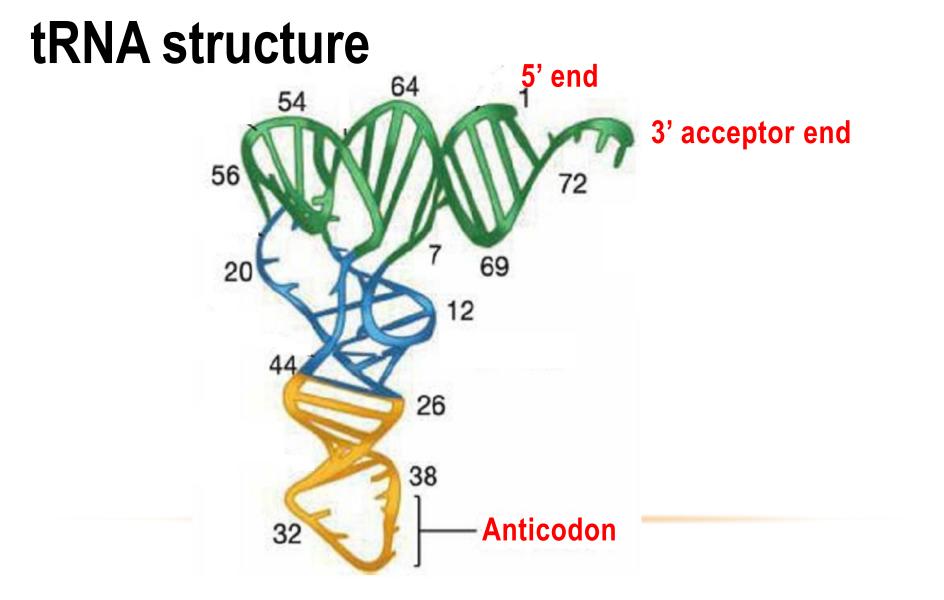
## tRNA structure

 Cloverleaf conformation;

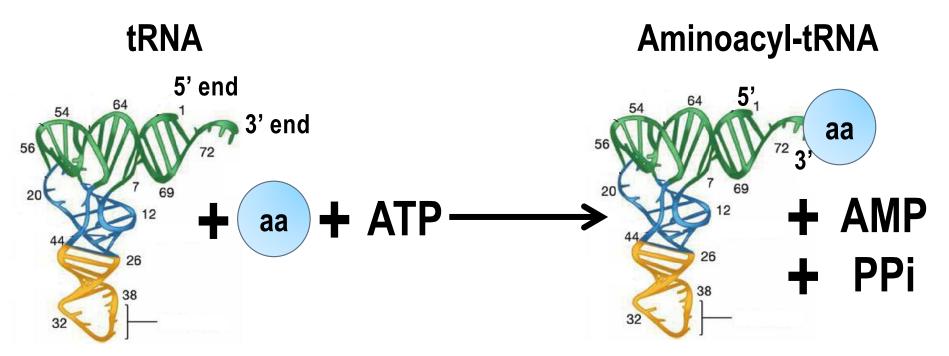


- In E. coli, the 3' end of all tRNAs has the same 5'-C-C-A-3' sequence;
- Anticodon is complementary to the mRNA codon.





## **Amino Acid Activation**



#### Aminoacyl-tRNA Syntheses 氨酰tRNA合成酶

## **Ribosome: Translation machine**

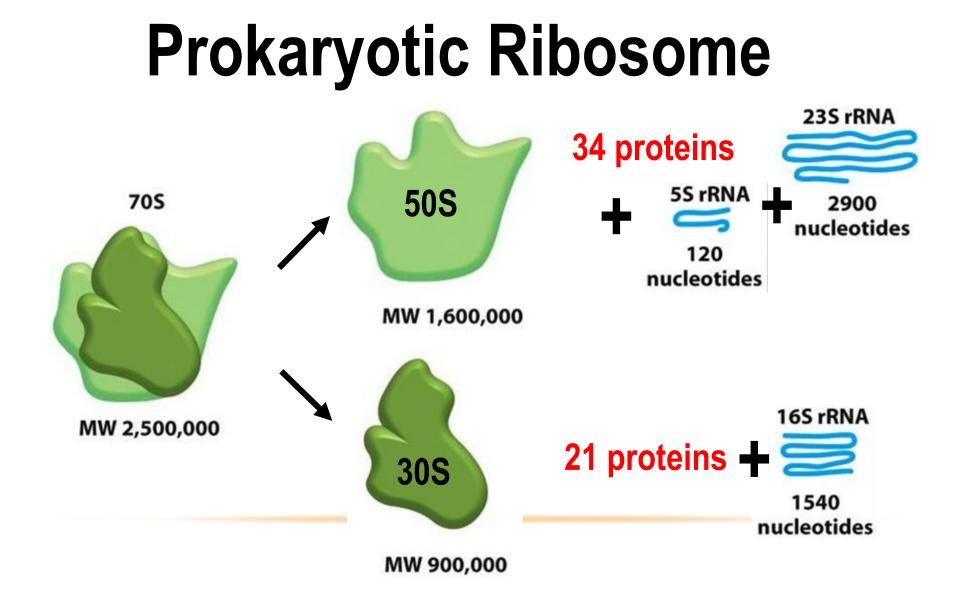
505

30S

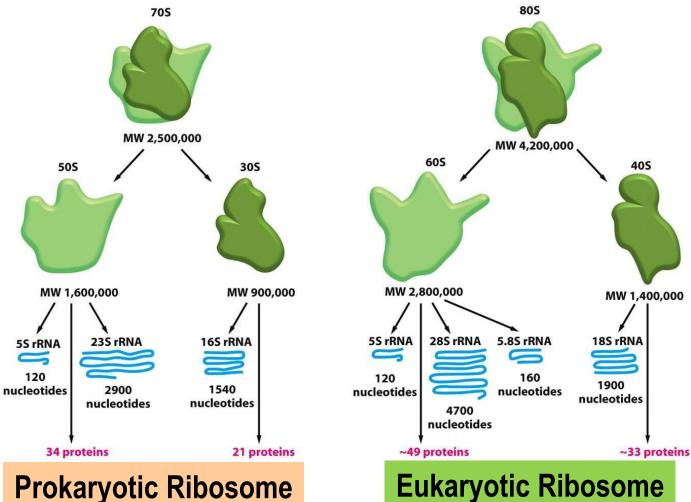
#### 50S subunit (Large)

#### 30S subunit (Small)

#### **Protein/ribosome RNA complex**



## **Ribosome in Evolution**

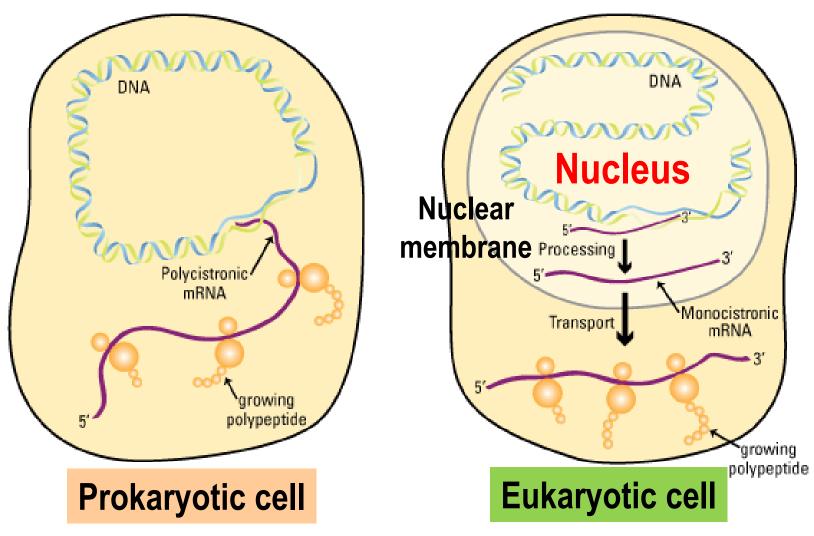


## Translation

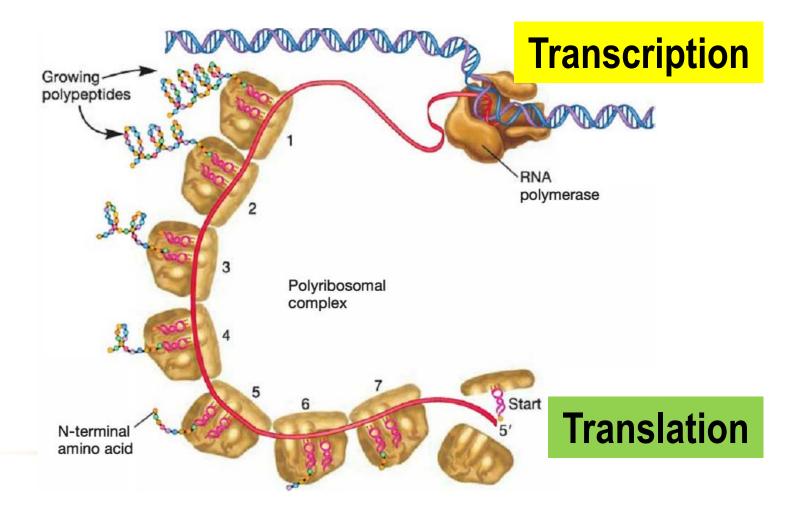
- mRNA
- Aminoacyl-tRNA
- Ribosome

## Initiation **Elongation Termination**

#### **No Nucleus Structure in Bacteria**



#### **Coupled Transcription and Translation in Bacteria**



#### Rapid Protein Synthesis in Bacterial

 In E. coli, synthesis occurs at a rate of at least 900 amino acids added per minute;

 Translation in Eukaryotic is slower, about 100 amino acids residues per minute.





### Chapter 11

## 11.1 Regulation levels of Gene Expression 基因表达的不同水平调控

## **Regulation of gene expression**

mRNA 🗤

Protein

Transcription initiation
 Transcription elongation
 Transcription termination

Translation initiation
 Translation elongation

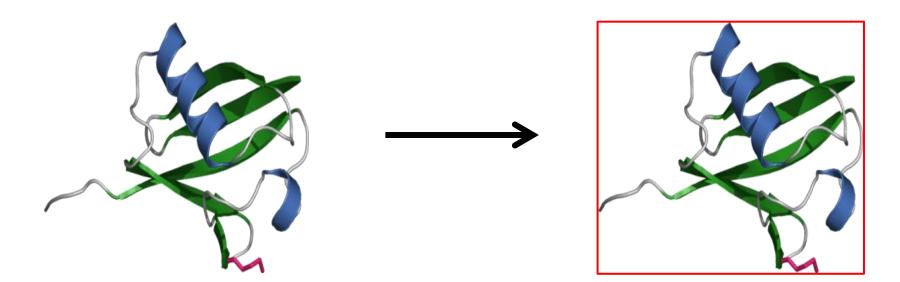
#### **Transcription Regulation**

- Genetic regulatory proteins can bind to the DNA and control whether or not transcription.
- Attenuation: Transcription can terminate very early after it has begun due to the formation of a transcriptional terminator.
- **Binding of a metabolite to a Riboswitch** in mRNA can cause premature termination of transcription.

#### **Translation Regulation**

- Translational repressor proteins can bind to the mRNA and prevent translation from starting.
- Antisense RNA can bind to mRNA and control whether or not translation begins.
- Binding of a metabolite to a riboswitch in mRNA can block translation.

## **Posttranslational Regulation**



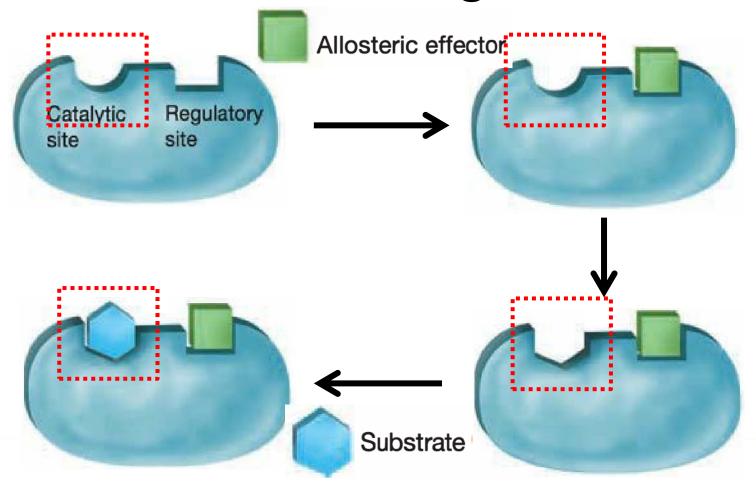
## Nonfunctional protein/enzyme

## Functional protein/enzyme

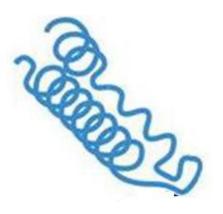
## **Posttranslational Regulation**

- Allosteric Regulation: small molecules can bind (noncovalently) to a protein and affect its function.
- Covalent Modification: the structure and function of a protein can be altered by covalent changes to the protein.

## **Allosteric Regulation**



## **Covalent Modification**



- Glycosylation
- Lipidation
- Phosphorylation
- Methylation
- Acetylation





### Chapter 11

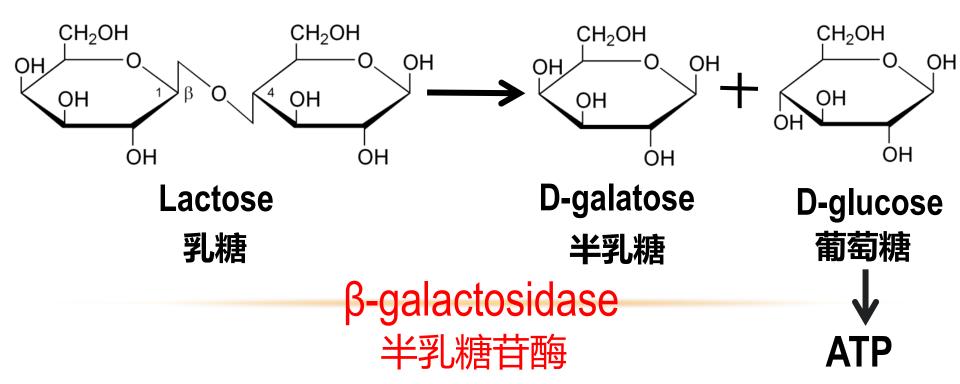
## 11.2 Regulation of Transcription Initiation I 转录起始的调控一

## **Regulation of gene expression**

Constitutive genes: express continuously

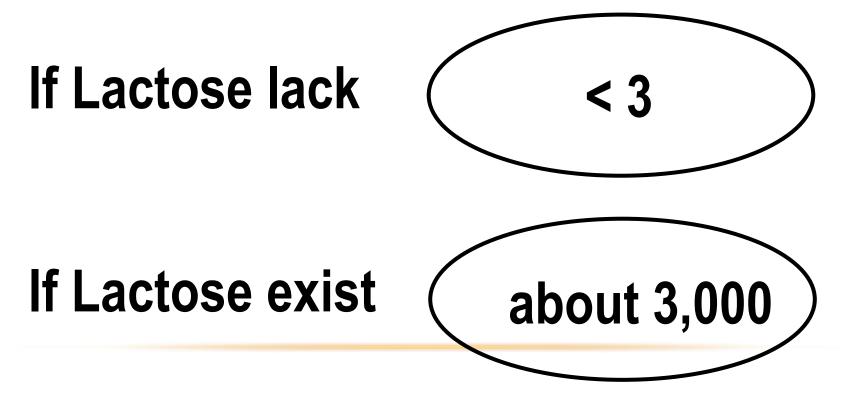
• Regulated genes: express only needed

# Only Lactose available and catabolism needed, galactosidase expresses in Bacteria



#### **Observing in bacteria cell:**

#### Galactosidase molecules



## **Regulatory Decision in Bacteria**

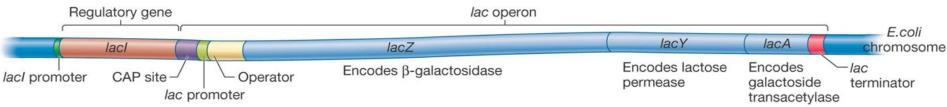
 When No Lactose in the environment No expression of Lactose catabolism enzymes

 When Lactose present in the environment Expression of Lactose catabolism enzymes

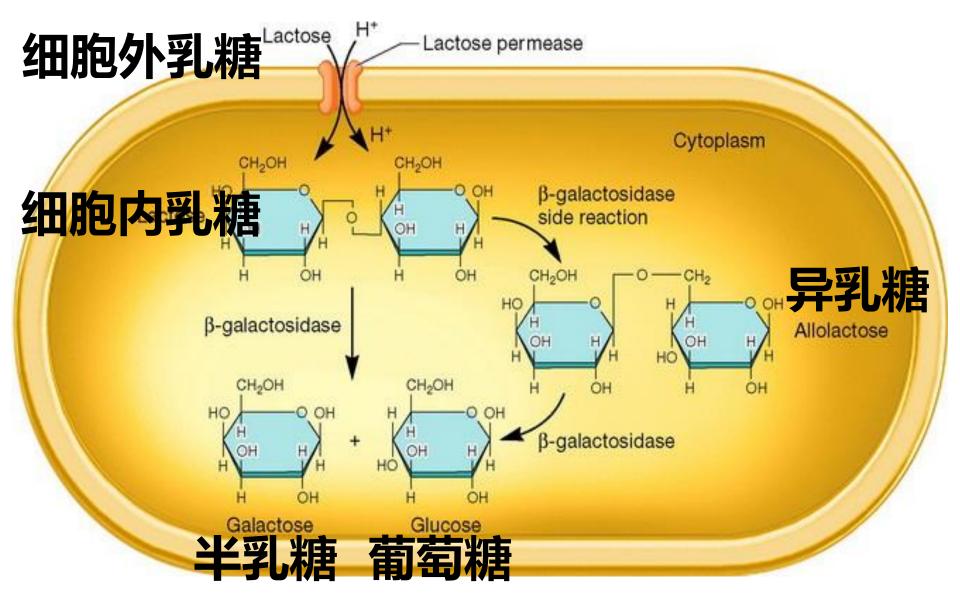


- In bacteria, an operon is a functioning unit of genomic DNA containing a cluster of structural genes under the control of a regulatory DNA including promoter and operator.
- Its expression is regulated as a single unit.
- Lactose Operon (乳糖操纵子)

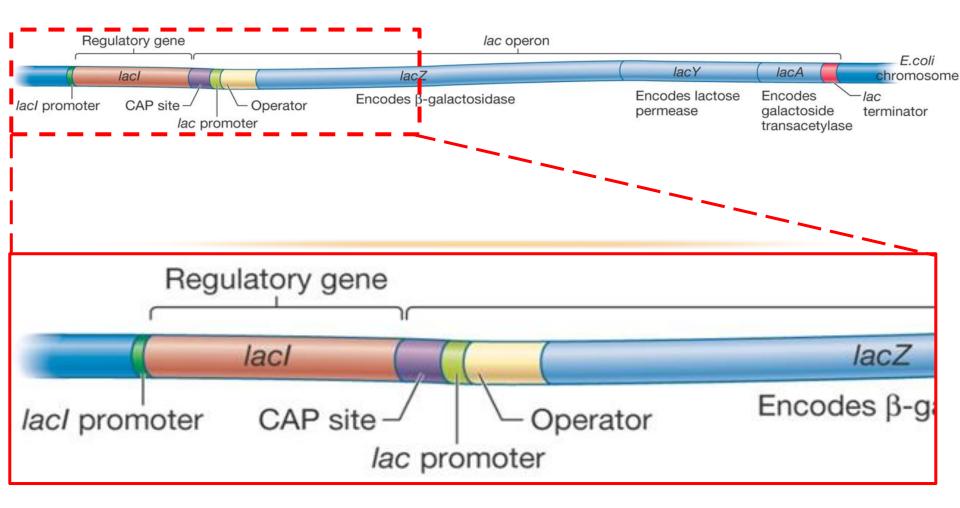
# Lactose Operon



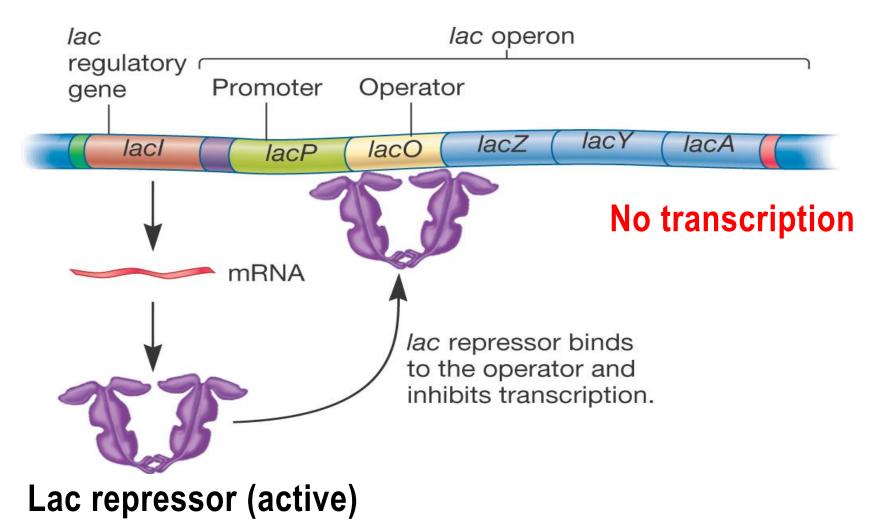
- 1. <u>Regulator</u>- gene that codes for Repressor(阻遏蛋白)
- 2. <u>Regulatory DNA</u>- composed of promoter and operator
- 3. <u>Structural gene cluster</u>- made of three genes each coding for an enzyme needed to catabolize lactose
  - β-galactosidase hydrolyze lactose
  - Permease take lactose across cell membrane
  - β-galactosidase transacetylase –function unknown



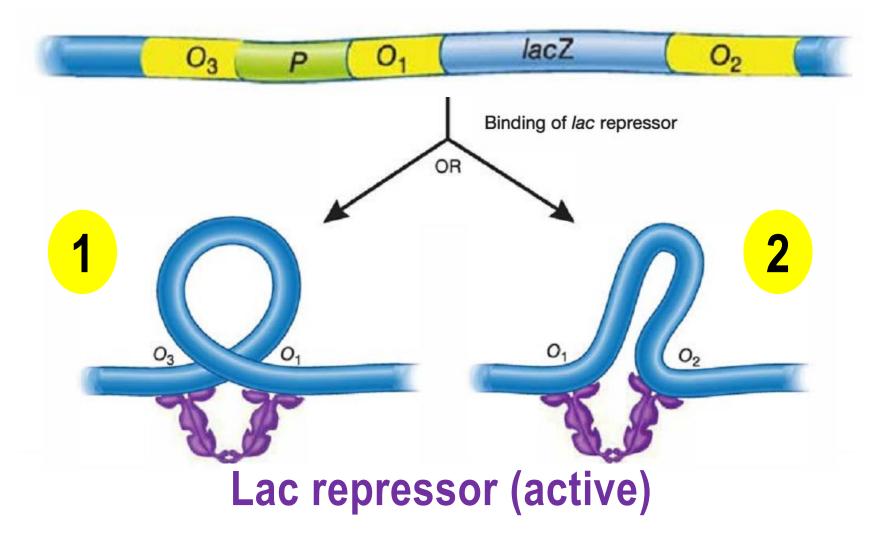
### **Lactose Operon Structure**



#### When No Lactose in the environment



#### **DNA loop forming caused by repressor binding**

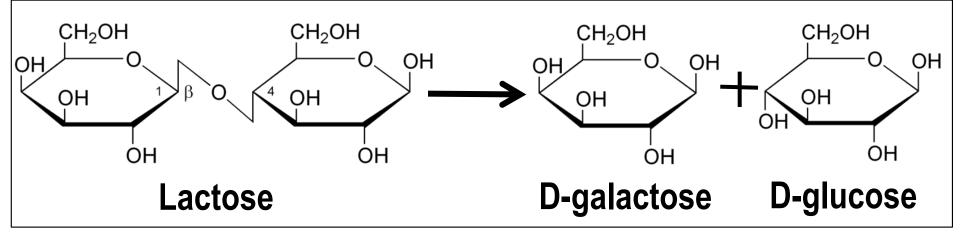


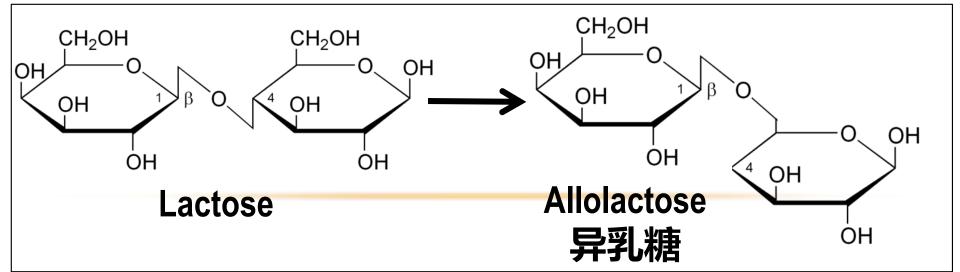
### **Regulatory Decision in Bacteria**

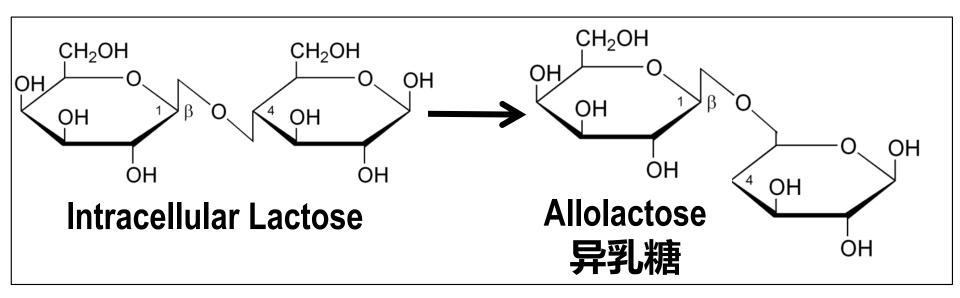
- When No Lactose in the environment
  - No transcription of Lactose Operon

• When Lactose present in the environment Transcription of Lactose Operon

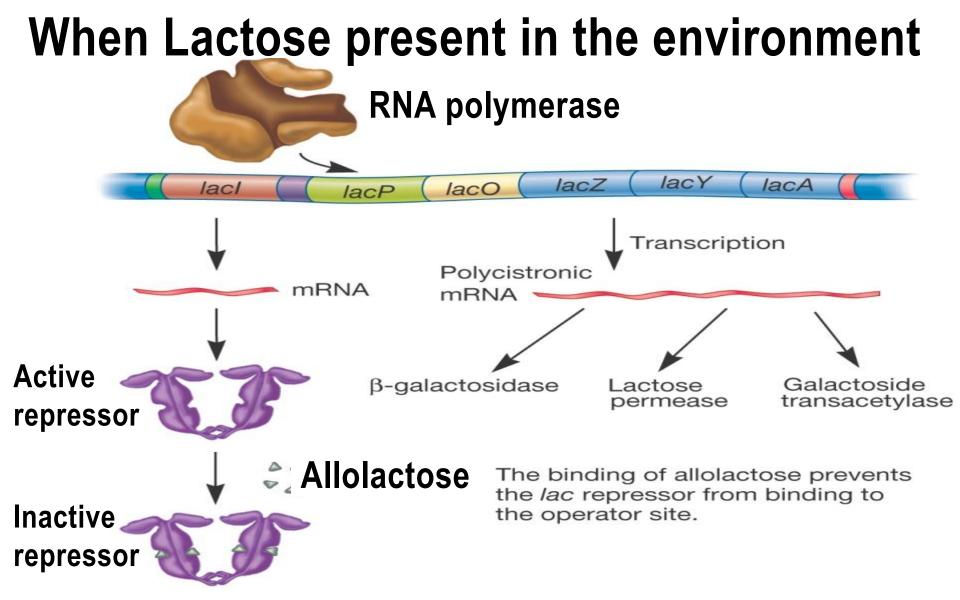
# β-galactosidase 半乳糖苷酶



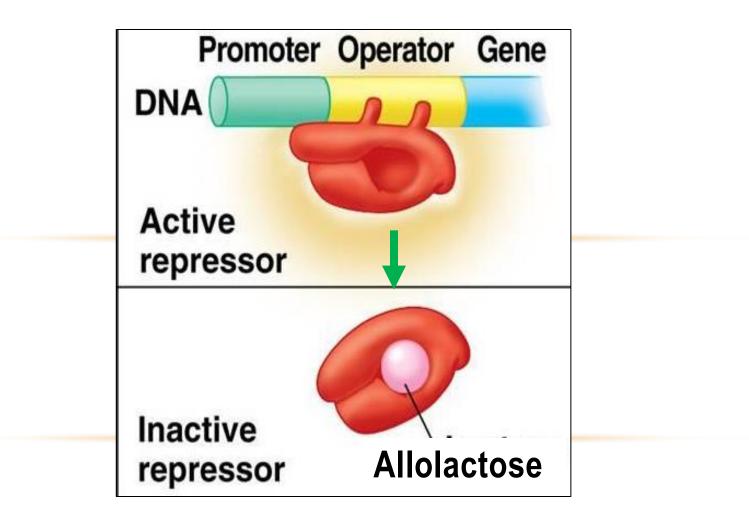




# Allolactose acts as the inducer of lac operon by inactivate repressor protein



### lac operon



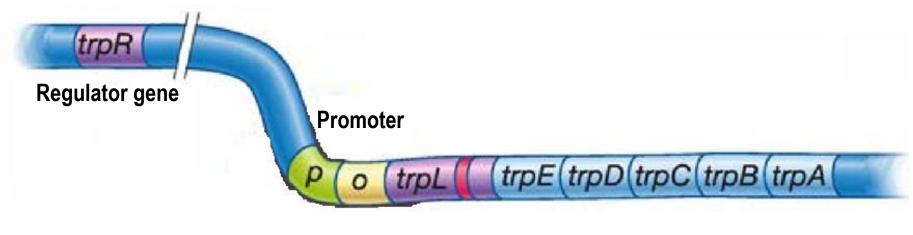
# Lactose Operon

Gene encoding enzyme for catabolism

• Tryptophan Operon 色氨酸

Gene encoding enzyme for synthesizing

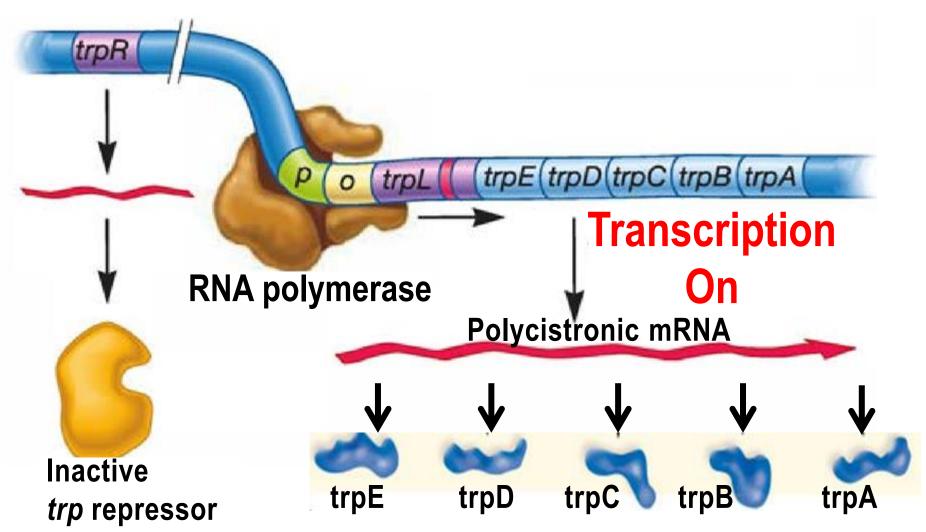
# **Tryptophan Operon**

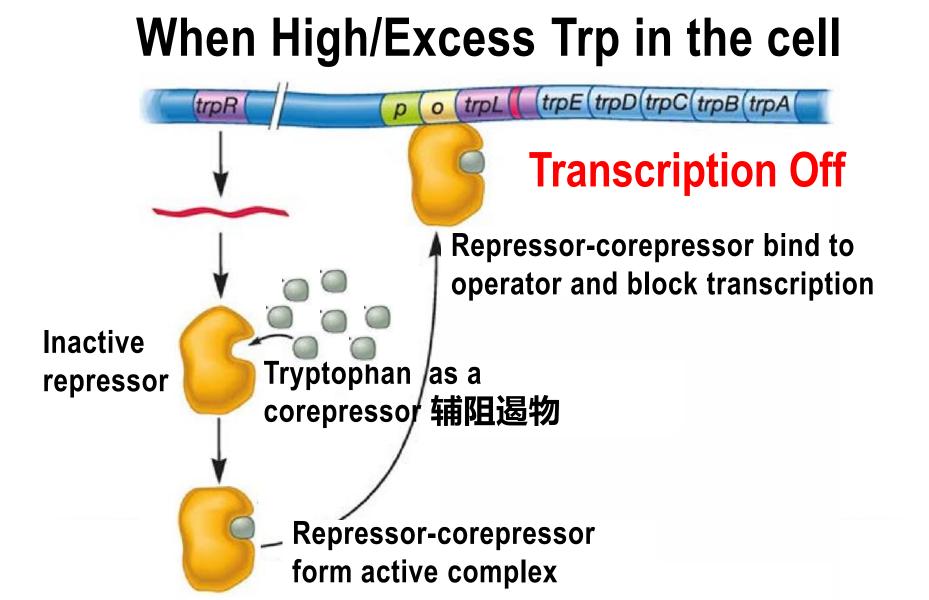


Operator

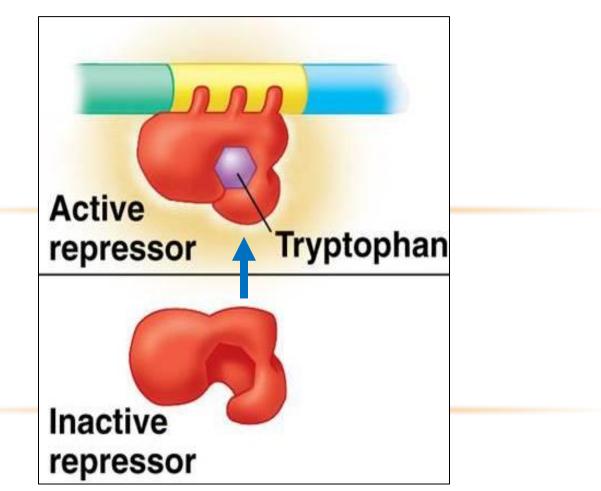
- 1. <u>Regulator</u>- gene encoding Repressor (阻遏蛋白)
- 2. <u>Regulatory DNA</u>- composed of promoter and operator
- 3. <u>Structural gene cluster</u>- made of five genes each coding for an enzyme needed to synthesize tryptophan

#### When No/Low Trp in the bacterial cell

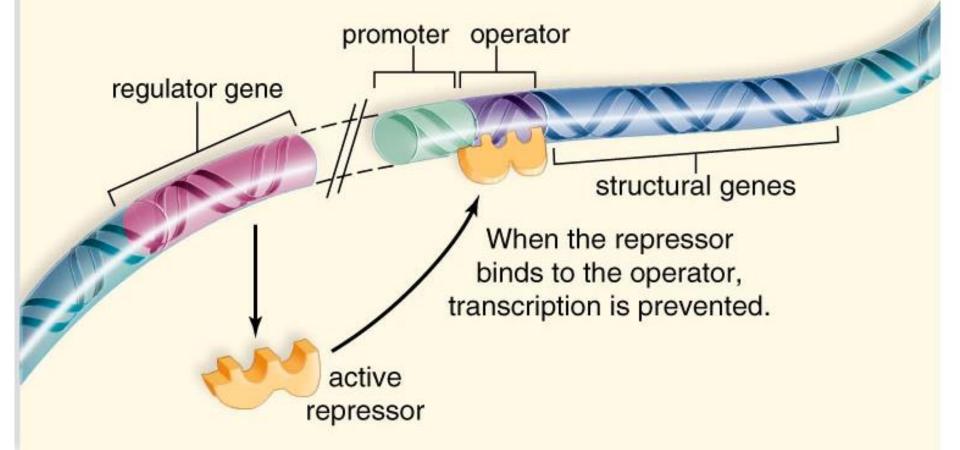




# trp operon

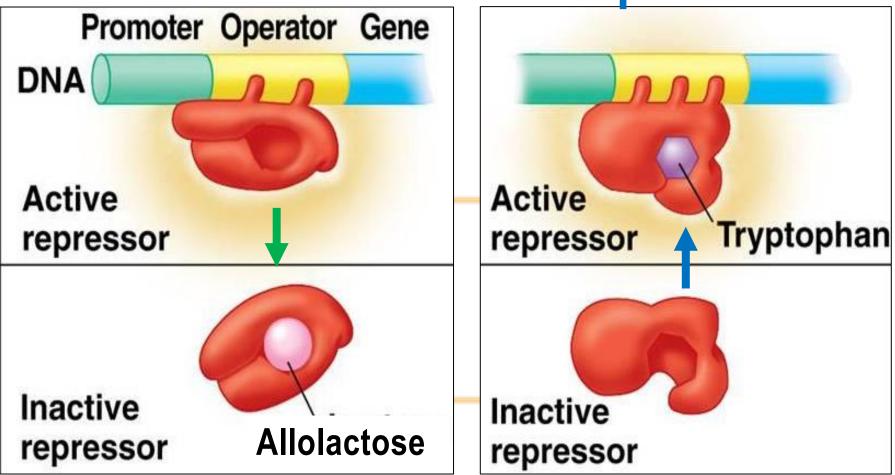


# **Repressor-mediated Negative Regulation of Transcription**



# *lac* operon **Inducible**

### *trp* operon **Repressible**

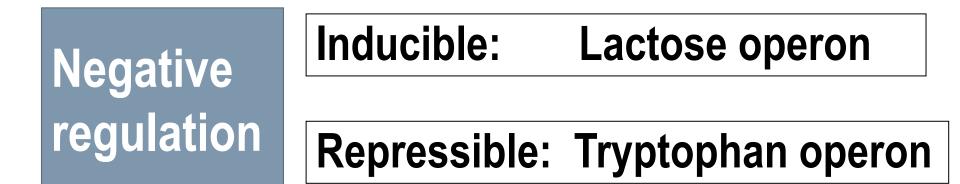






### Chapter 11

# 11.3 Regulation of transcription initiation II 转录起始的调控 二



# Positive regulation



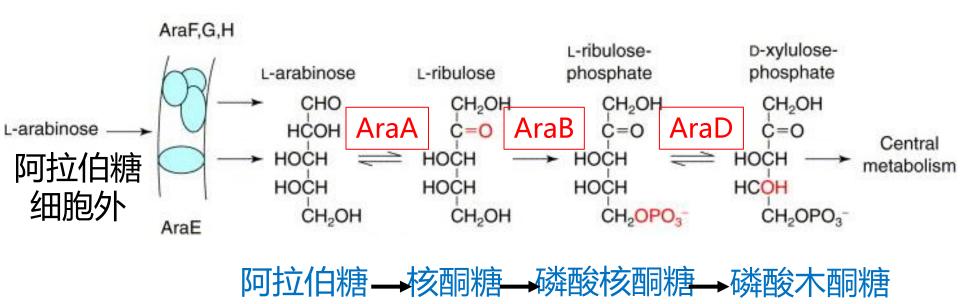
Negative	Inducible:	Lactose operon
regulation	<b>Repressible:</b>	Tryptophan operon

# Positive regulation

#### Arabinose operon 阿拉伯糖

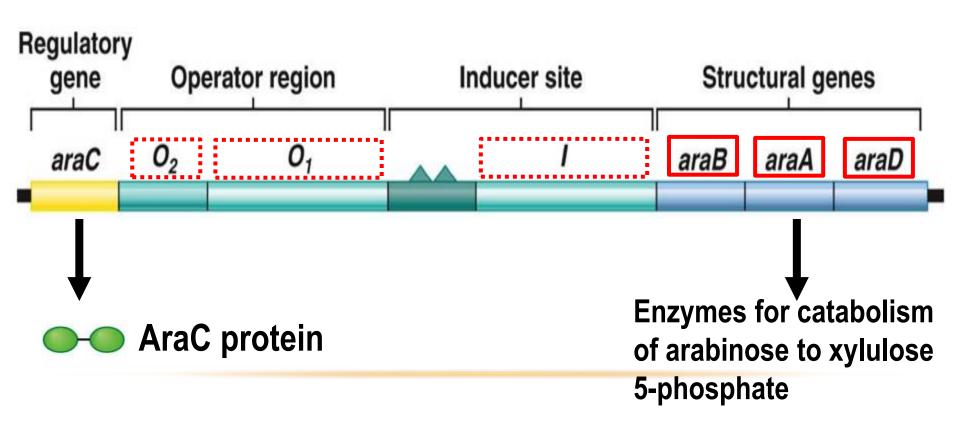
The *ara* operon encodes enzymes needed for catabolism of arabinose.

### Arabinose Metabolism in Bacteria

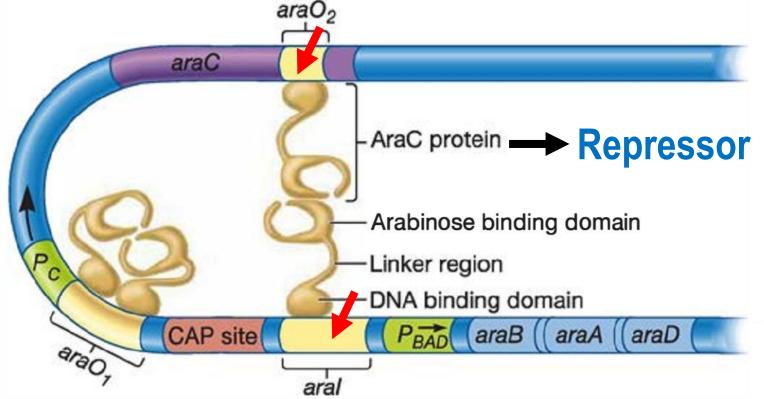


Robert Schleif, 2000, Trends in Genetics

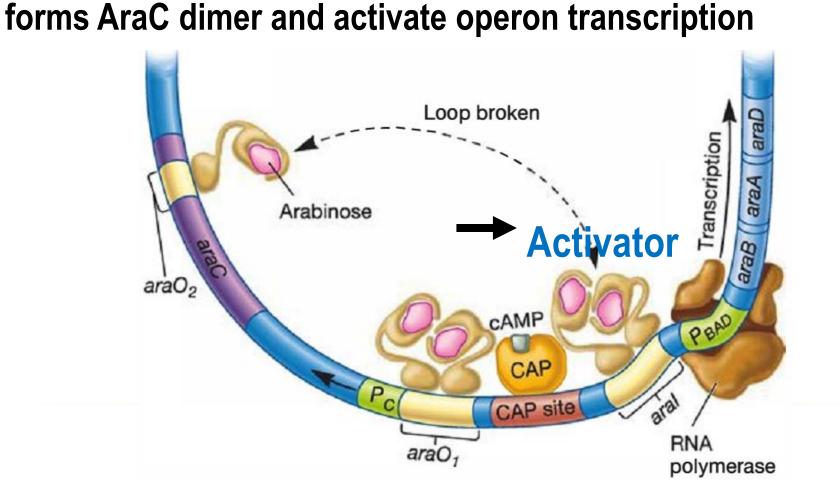
## **Arabinose Operon**



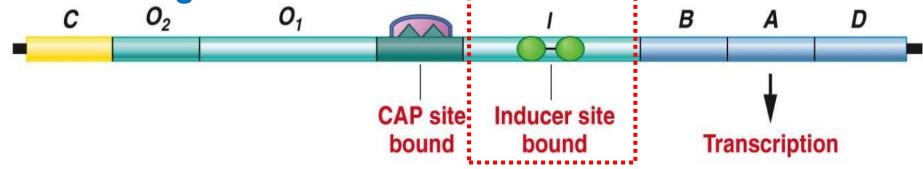
#### Operon inhibited in the absence of Arabinose Negative control-monomers of AraC protein bind to O2 and I looping out the intervening sequence(210bp) & blocking access to the promoter by RNA polymerase



#### Operon activated in the presence of Arabinose Positive control-Arabinose binds AraC to change conformation,



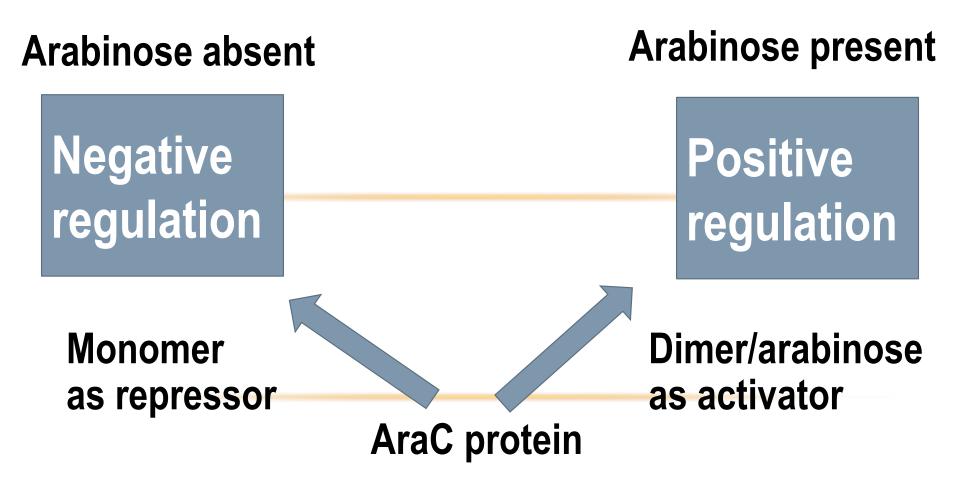
#### Arabinose present; operon is induced. Positive regulation

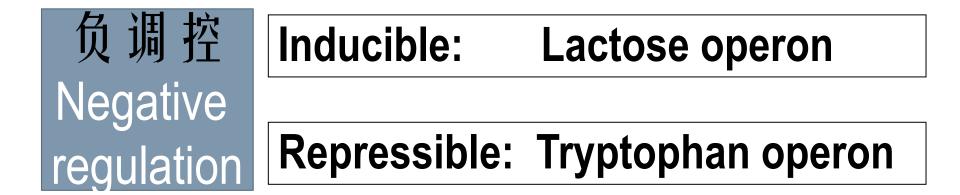


#### Arabinose absent; operon is repressed. Negative regulation CAP CAP

CAP site unbound Inducer site bound No transcription

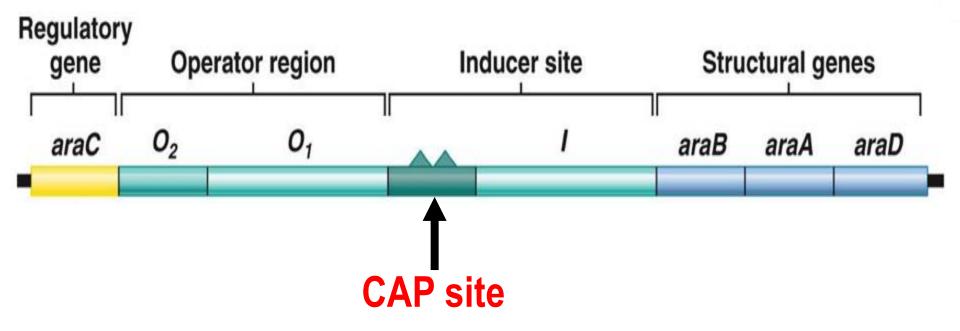
# **Arabinose Operon**







# CAP site for positive regulation in bacteria Operon

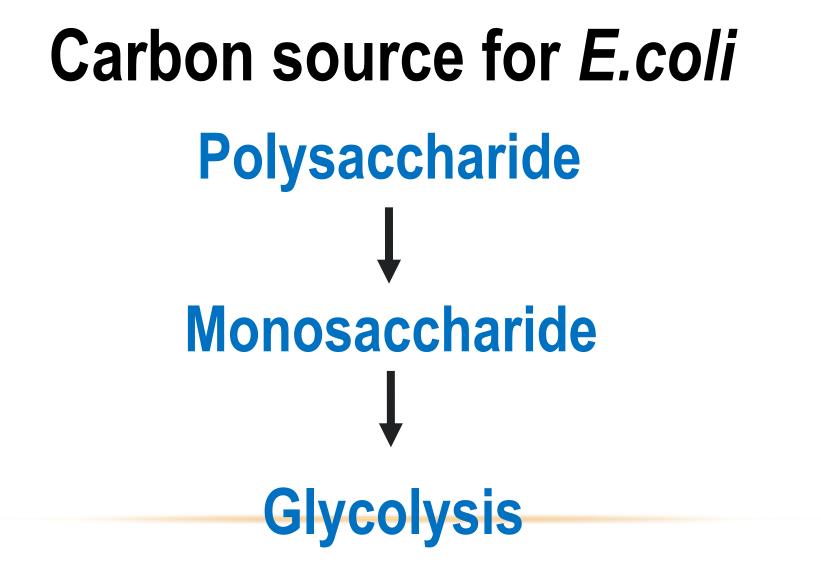






### Chapter 11

# 11.6 Regulating Complex Cellular Processes 复杂细胞过程的调控



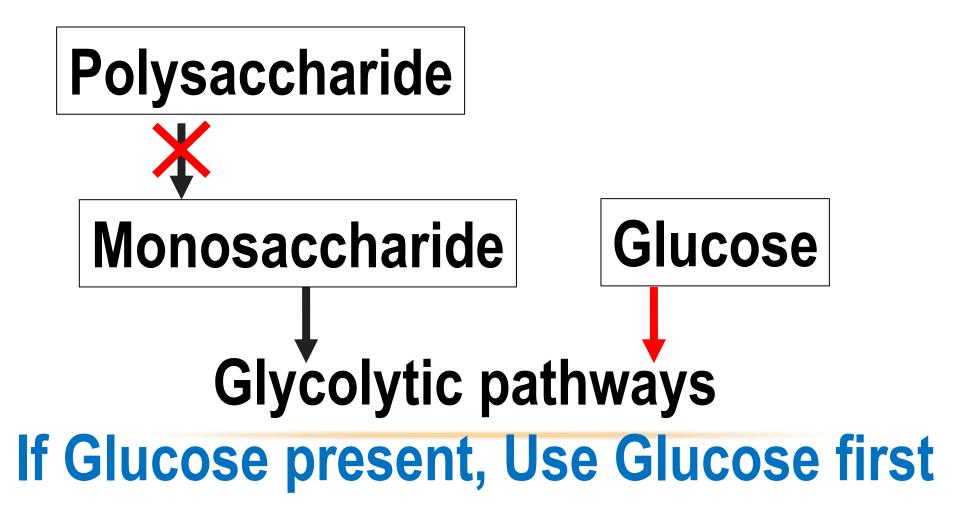
# Carbon Catabolism in *E.coli*

- Constitutive genes: enzyme for glucose catabolism
- Regulated genes: enzyme for catabolism of other carbon source
  - Arabinose(ara) Lactose(lac)
  - Maltose(*mal*) Galactose(*gal*)

## Carbon Catabolism in E.coli

# If Glucose present, Use Glucose first





# **Catabolite Repression**

• The operons that encode enzymes required for the catabolism of carbon sources that must first be modified before entering glycolysis.

 The expression of these catabolite operons is coordinately repressed when glucose is plentiful.

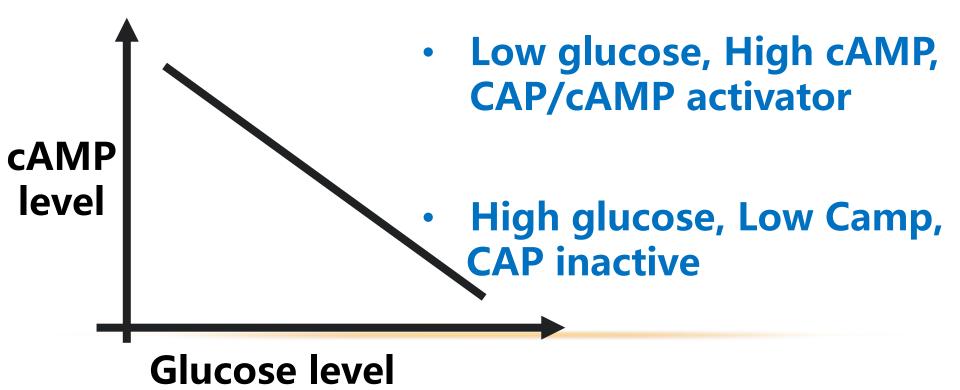
## **Catabolite Activator Protein (CAP)**

 Also named cAMP receptor protein (CRP)

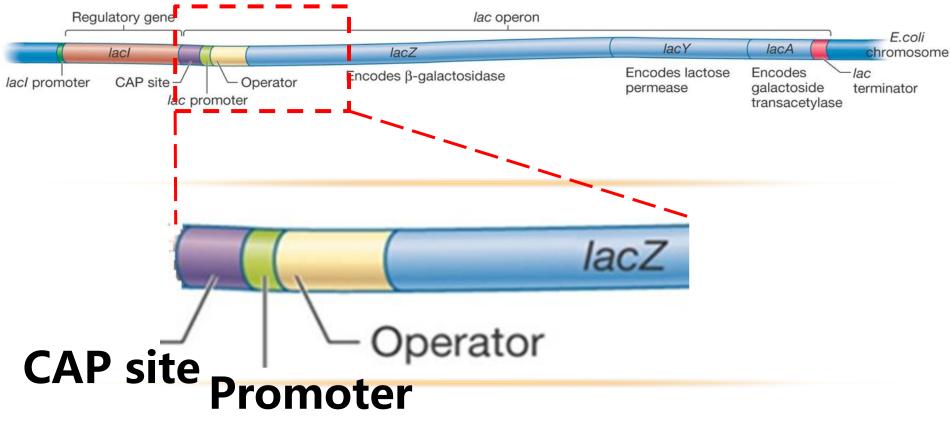
• CAP is active when the cAMP is bound and binding

• CAP is inactive when it is free of cAMP.

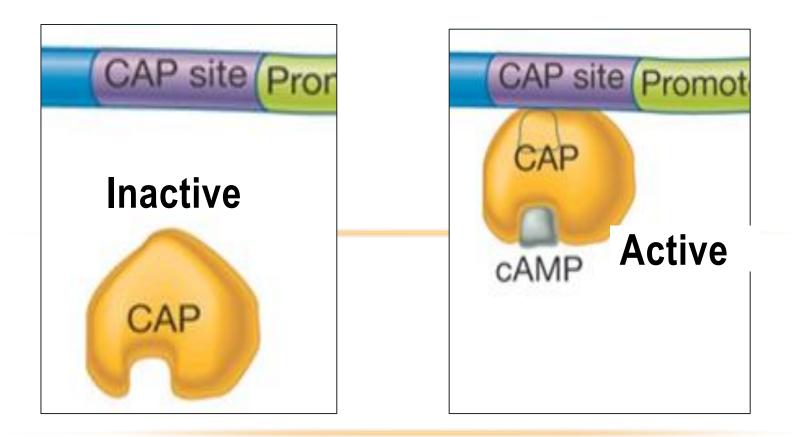
# The level of cAMP varies inversely with that of glucose



# CAP recognition site in all catabolite operons

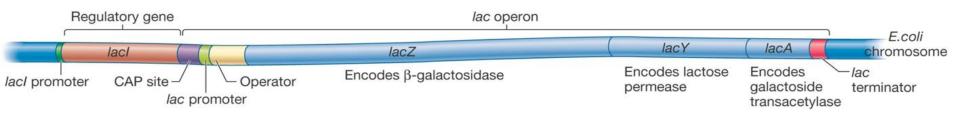


### CAP Site for CAP/cAMP activator binding



High Glucose: Low cAMP Low Glucose: High cAMP

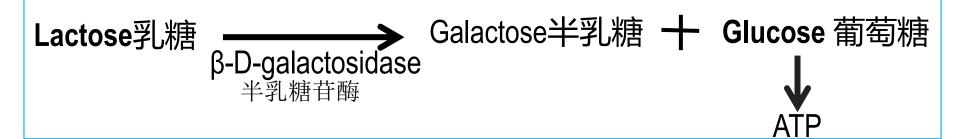
# **Dual regulation in Lactose Operon**



Regulatory protein specific to each operon

 CAP for positive regulation in all catabolite operons

# Regulation of *Lac* Operon in different nutrient environment



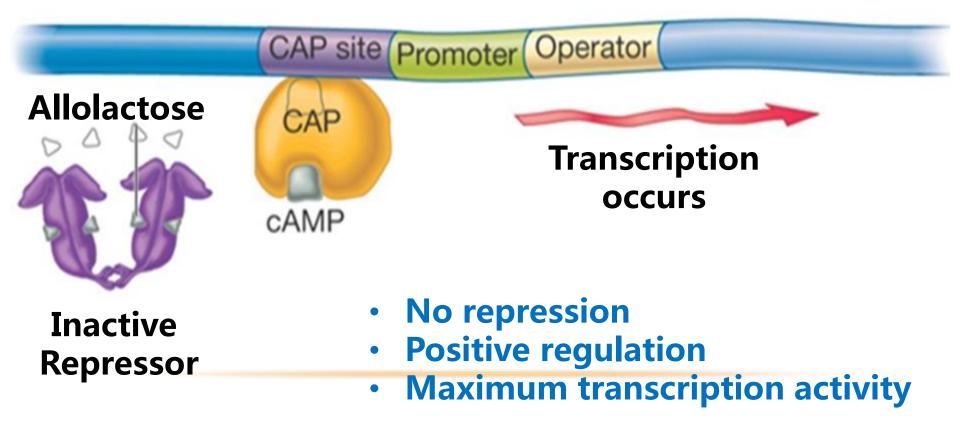
### 1. Only Lactose; No Glucose

### 2. Lactose and Glucose

3. Neither Lactose Nor Glucose

4. No Lactose; Only Glucose

### 1. Only Lactose present; No Glucose



### 2. Both Lactose and Glucose Present



CAP

Inactive

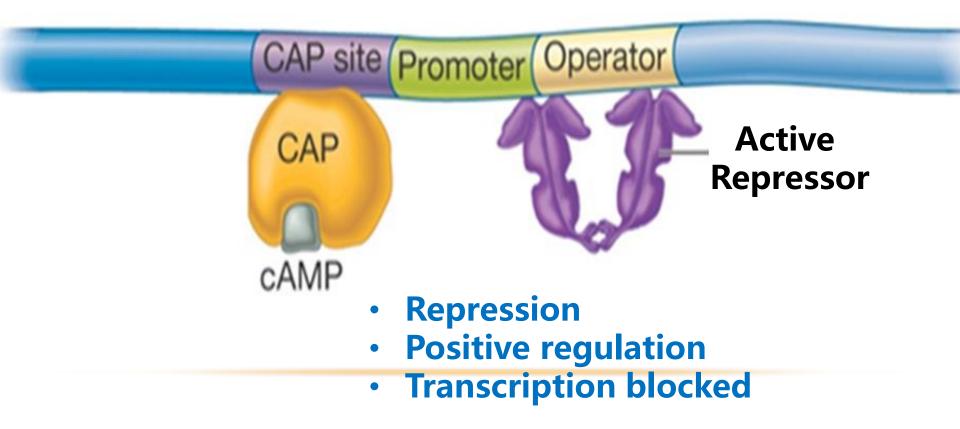
#### Allolactose



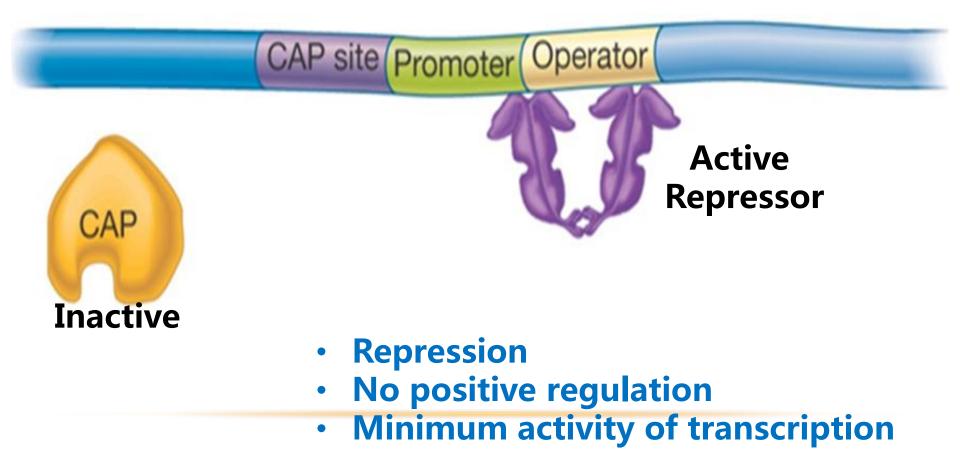
Inactive Repressor No repression

- No positive regulation
  - Low Transcription activity

### 3. Neither Lactose Nor Glucose Present

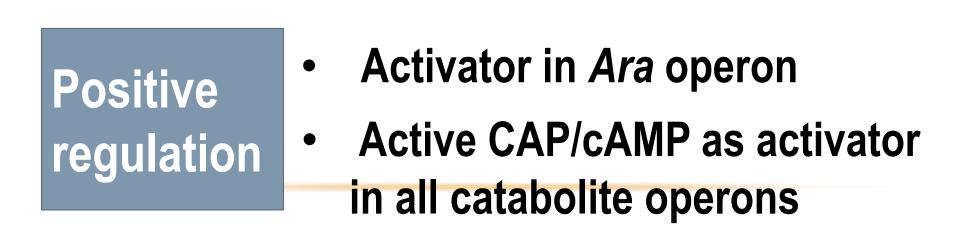


### 4. No Lactose; Only Glucose Present





- **Repression by repressor**
- Attenuation by attenuator
- Riboswitch



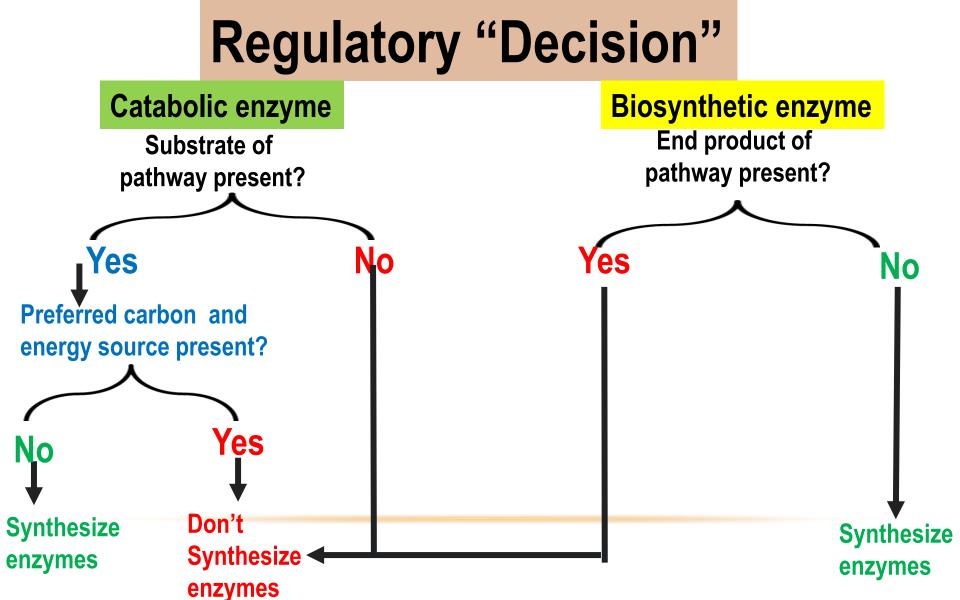
### Inducible Vs Repressible Operon

Inducible operon is turned ON by substrate.

*Lac* operon - enzymes needed to catabolize the nutrient/lactose are produced when needed.

Repressible operon is turned OFF by the product synthesized;

*Trp* operon – enzymes used to synthesize Try stop being produced when they are not needed







## **Chapter 11**

## 11.7 Riboswitch and antisense RNA 核糖开关和反义RNA

# **Regulation Of Gene Expression**

### □ Transcription

- Regulation Of Transcription initiation
   Operon 操纵子
- Regulation Of Transcription elongation
  - Riboswith 核糖开关

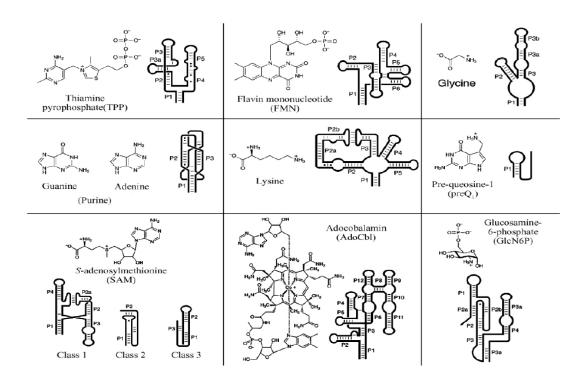
# Translation Riboswith; antisense RNA

### Riboswitch 核糖开关

- Regulatory sequences in the leader of an mRNA both sense and respond to environmental conditions by either prematurely terminating transcription or blocking translation.
- Folding pattern <u>altered</u> in response to mRNA binding of an <u>effector molecule.</u>
- Folding of mRNA leader sequence determines whether transcription will continue or be terminated

### **Riboswitches Bind Specific Metabolites**

- amino acids,
- vitamins,
- glucosamine-6phosphate,
- S-adenosylmethionine,
- thiamine pyrophosphate, ions
- flavin mononucleotide (FMN)

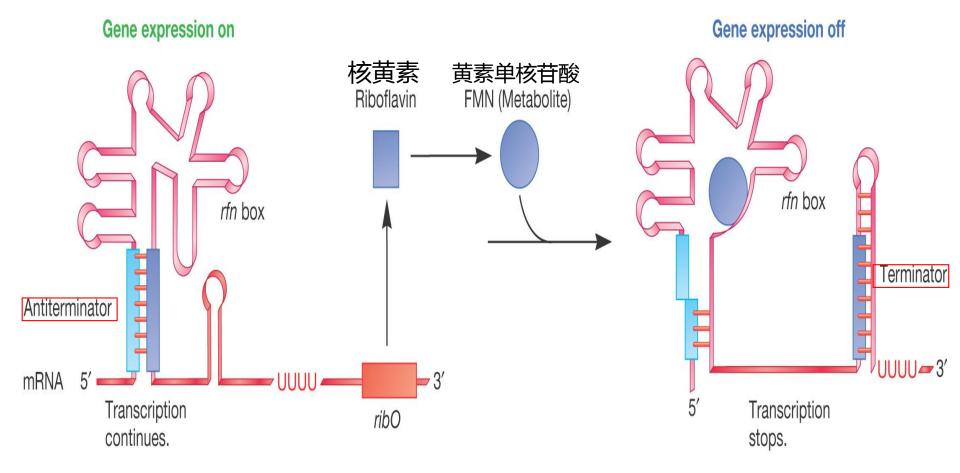


### **Riboswitches in bacteria**

#### Table 13.1Regulation of Gene Expression by Riboswitches

System	Microbe(s)	Target genes encode:	Effector and Regulatory Response
T box	Many gram-positive bacteria	Amino acid biosynthetic enzymes	Uncharged tRNA; anticodon base pairs to 5' end of mRNA, preventing formation of transcriptional terminator
Vitamin B <sub>12</sub> element	E. coli	Cobalamine biosynthetic enzymes	Adenosylcobalamine (AdoCbl) binds to <i>btuB</i> mRNA and blocks translation
THI box	Rhizobium etli E. coli B. subtilis	Thiamine (Vitamin B <sub>1</sub> ) biosynthetic and transport proteins	Thiamine pyrophosphate (TPP) causes either premature transcriptional termination ( <i>R. etli, B. subtilis</i> ) or blocks ribosome binding ( <i>E. coli</i> )
RFN-element	B. subtilis	Riboflavin biosynthetic enzymes 核黄素合成	Flavin mononucleotide (FMN) cases premature transcriptional termination
S box	Low G + C gram- positive bacteria	Methionine biosynthetic enzymes	S-adenosylmethionine (SAM) causes premature transcriptional termination

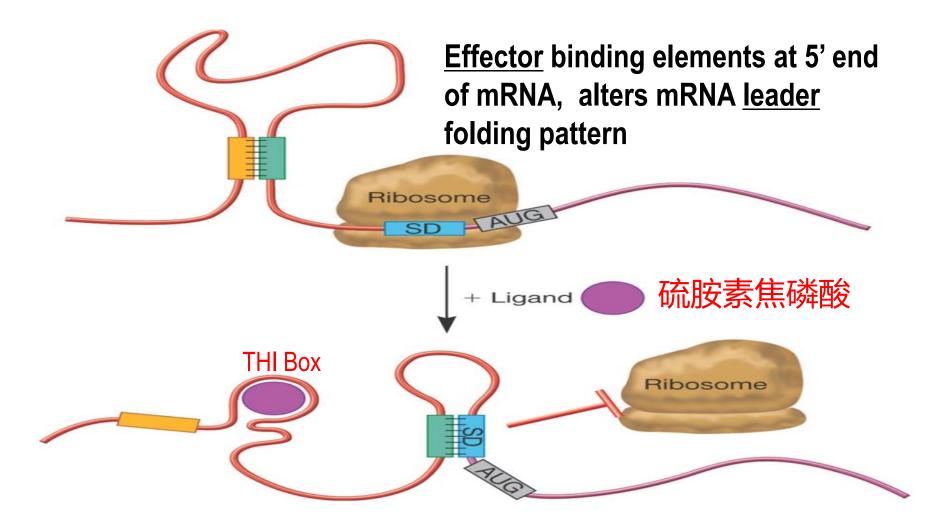
### The riboflavin (*rib*) biosynthetic operon in *bacillus subtilis* 枯草芽孢杆菌

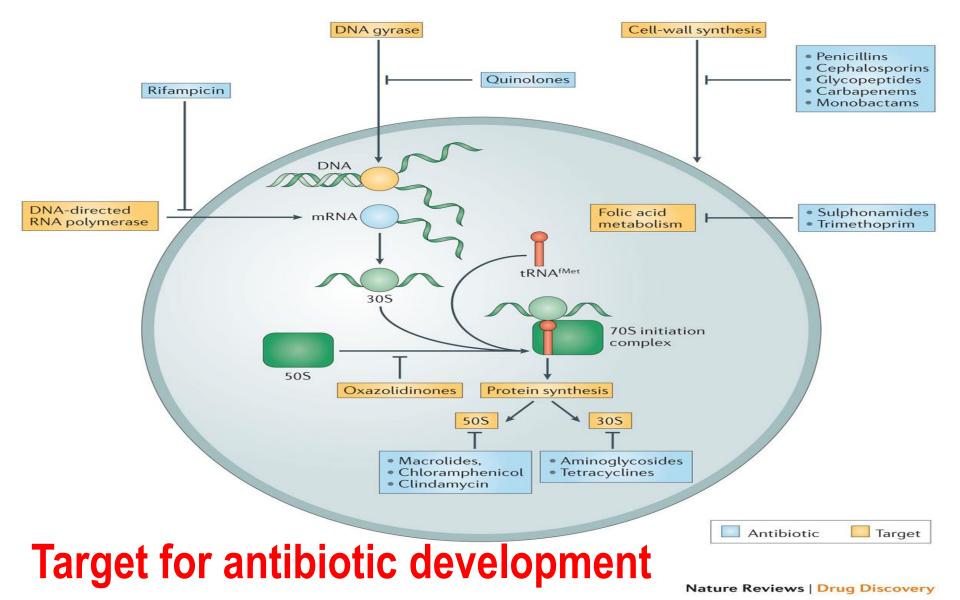


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### **Blocking translation Initiation by a Riboswitch**





# Riboswitches as novel antibiotic target

### ARTICLE

2015 Oct 29

doi:10.1038/nature15542

# Selective small-molecule inhibition of an RNA structural element

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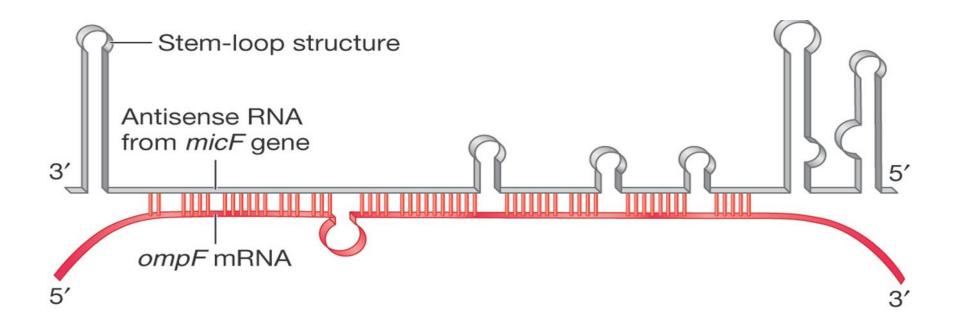
Riboswitches are non-coding RNA structures located in messenger RNAs that bind endogenous ligands, such as a specific metabolite or ion, to regulate gene expression. As such, riboswitches serve as a novel, yet largely unexploited, class of emerging drug targets. Demonstrating this potential, however, has proven difficult and is restricted to structurally similar antimetabolites and semi-synthetic analogues of their cognate ligand, thus greatly restricting the chemical space and selectivity sought for such inhibitors. Here we report the discovery and characterization of ribocil, a highly selective chemical modulator of bacterial riboflavin riboswitches, which was identified in a phenotypic screen and acts as a structurally distinct synthetic mimic of the natural ligand, flavin mononucleotide, to repress riboswitch-mediated *ribB* gene expression and inhibit bacterial cell growth. Our findings indicate that non-coding RNA structural elements may be more broadly targeted by synthetic small molecules than previously expected.

### **Regulation of translation by small RNA molecules** Key

- small (sRNAs) or noncoding (ncRNAs) RNAs
  - Do <u>not</u> function as mRNA, tRNA, or rRNA
  - May inhibit or enhance translation
  - Antisense RNAs are complementary to mRNA and function as translation blocker by base pairing

## Translation repression by "antisense RNA"

Key



#### **Antisense RNA medicines**