

# Gene regulation in prokaryotes

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# Today we will discuss models of bacterial gene regulation

**Lac operon (LacI repression):** dual regulation involving cAMP induction and inducer exclusion

**Arabinose operon (AraC activation):** repression and activation by changes in DNA conformation

**Antibiotic efflux (TetR repression):** repression and interaction with other regulators

**Metal reduction/transport (MerR activation):** DNA distortion to align -35 and -10 sites

**LysR activation:** (N-term HTH, C-term effector binding) bind inducer → bend DNA to activate RNA polymerase

**Tryptophan operon:** repression and attenuation

95% of bacterial regulators bind DNA using a helix-turn-helix domain

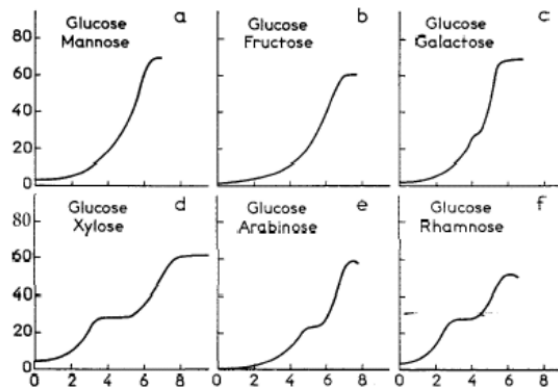
# Basic concepts: carbon catabolite repression to prioritize growth substrates

Jacques Monod's experiments on diauxic growth (1941)

## Keys to bacterial fitness:

1 choose carbon source that supports fastest growth.

2 don't produce enzymes for carbon sources that aren't available.



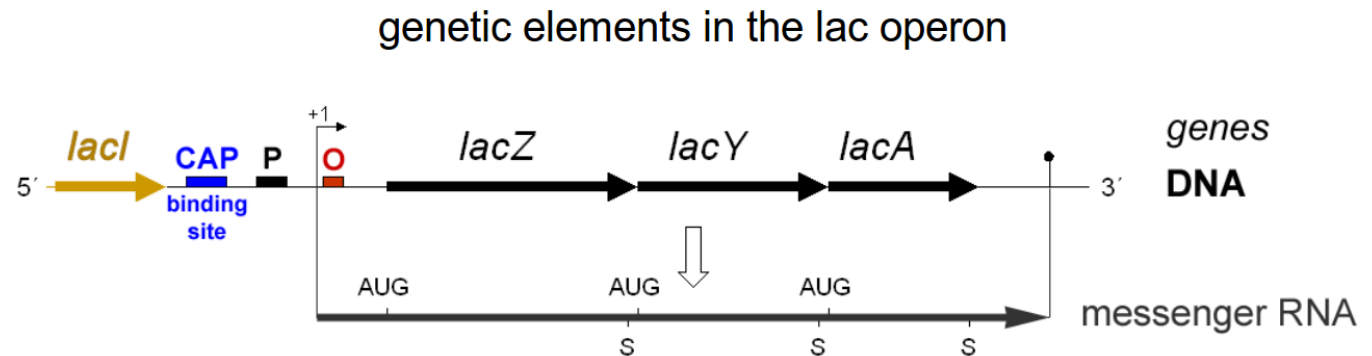
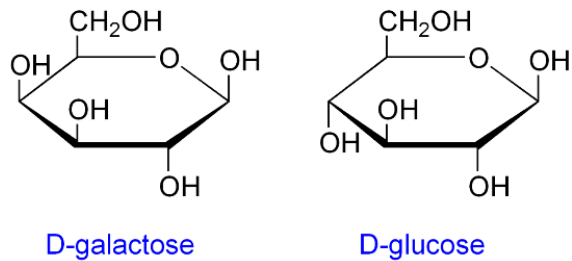
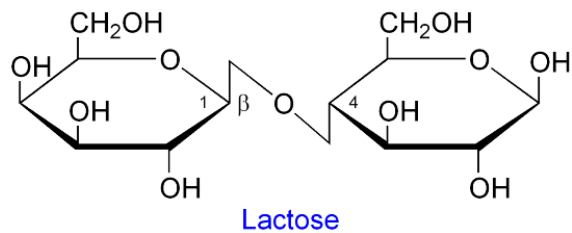
diauxic growth=growth in 2 phases

Fig.1. Growth of *Escherichia coli* in the presence of different carbohydrate pairs serving as the only source of carbon in a synthetic medium<sup>30</sup>.

## Growth rates:

glucose=mannose=fructose>galactose>>xylose,arabinose,rhamnase

# Metabolism of lactose by the lac operon



**LacI** represses expression of lac operon

**CAP** site binding site for Crp activator

**P** promoter

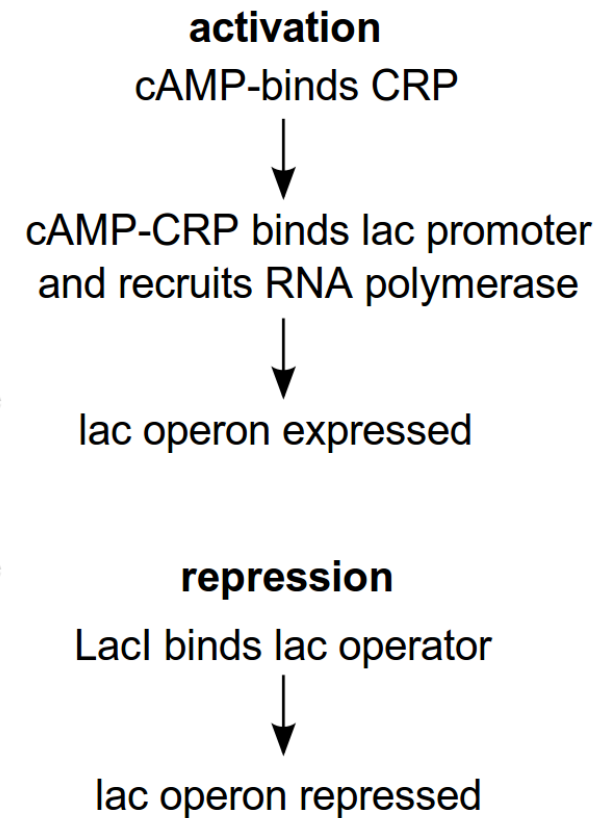
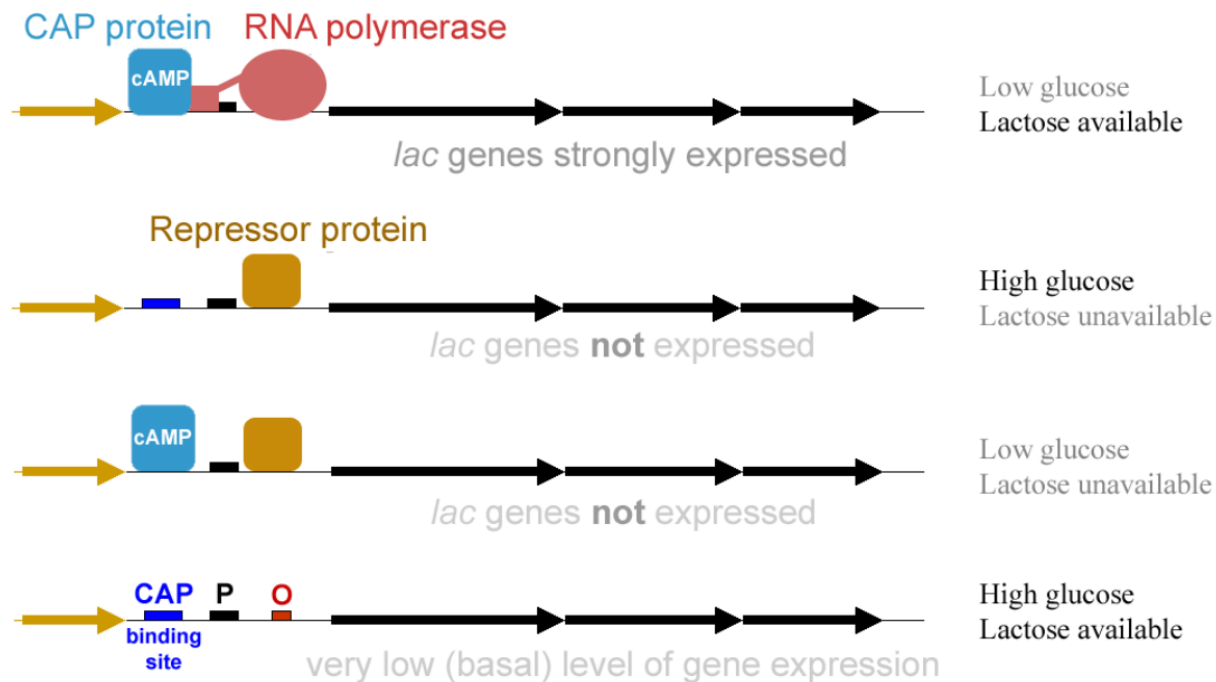
**O** binding site for LacI (operator)

**lacZ** b-galactosidase enzyme (cutting)

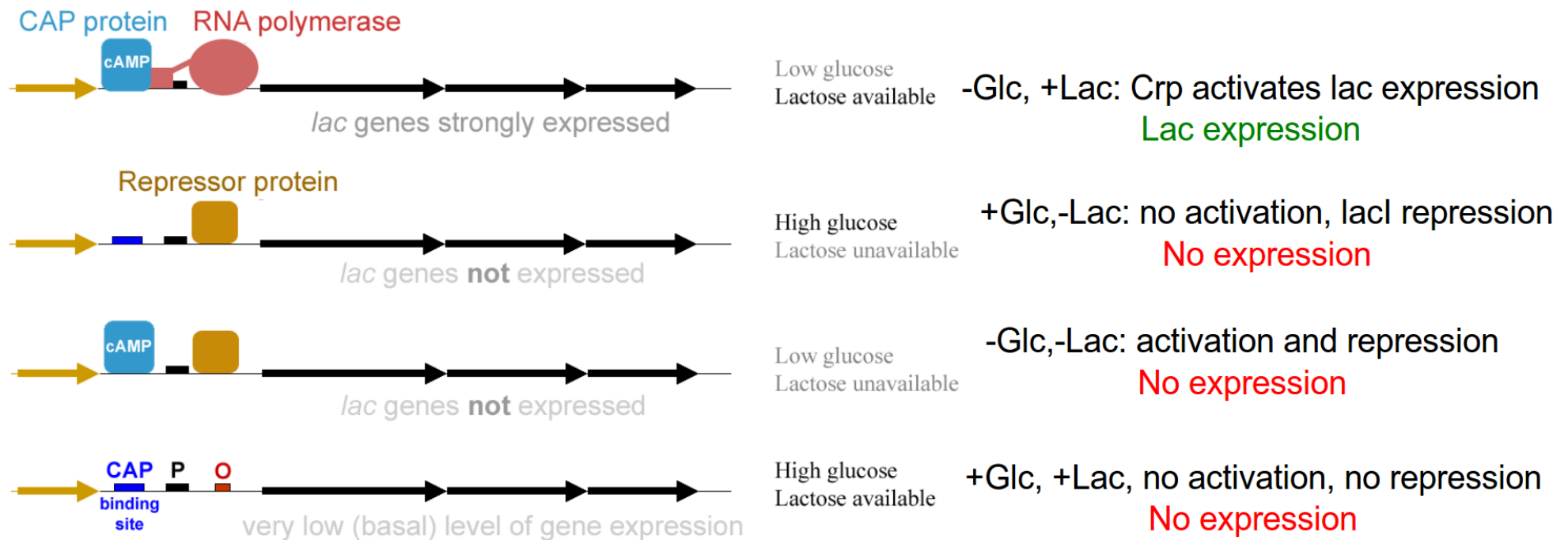
**lacY** lactose permease (transport)

**lacA** galactoside O-acetyltransferase (unknown)

# Dual regulation (activation and repression) of lac operon



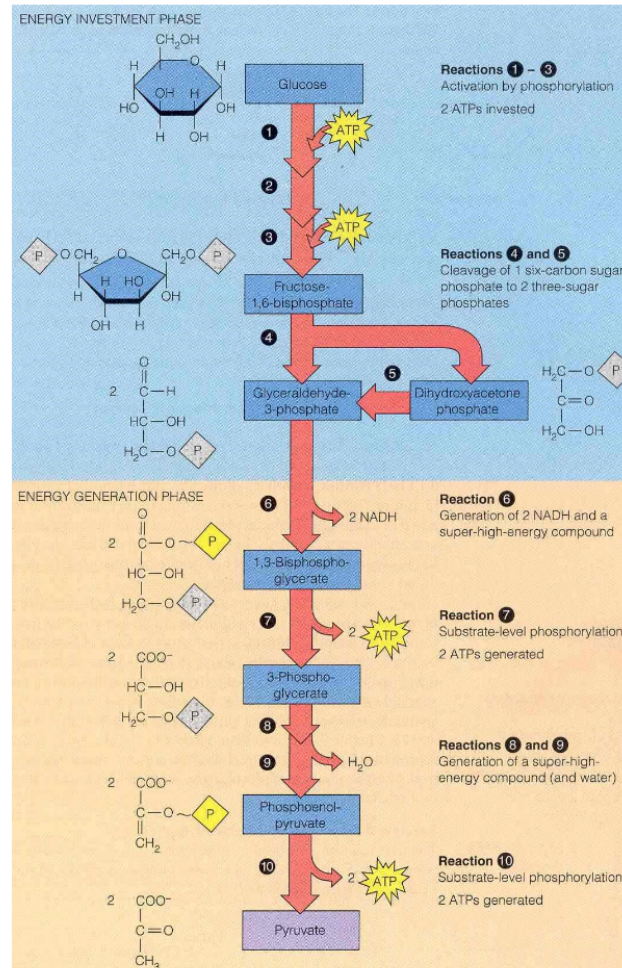
# Lac expression only in presence of lactose and absence of glucose



Crp activates in presence of cAMP  
 LacI represses in absence of lactose

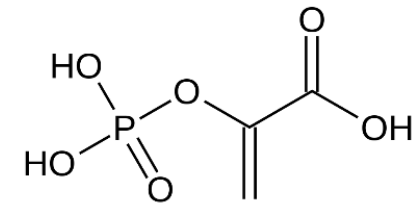
So how does cell control concentrations of cAMP (activator)  
and lactose (inducer)?

# Glycolysis: breakdown of glucose (C6) into pyruvate (C3)



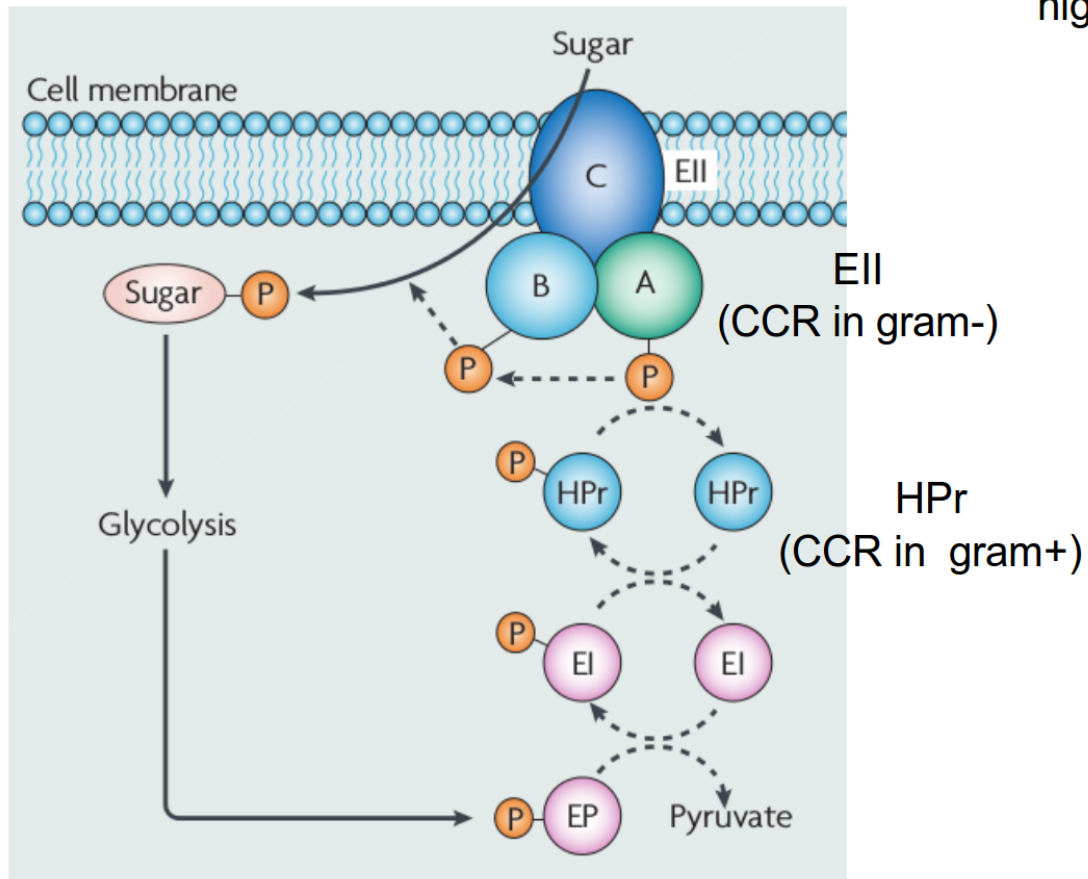
high glucose leads to high PEP/pyruvate ratio

PEP=phosphoenolpyruvate





# Sugar transport by the phosphotransferase system (PTS)



high glucose leads to high PEP (glycolysis intermediate)

PEP transfers Pi to EI

EI transfers Pi to HPr

HPr transfer Pi to EII (A,B,C subunits)

EII transfers Pi to sugar

transport and phosphorylation  
of sugar (glucose)

Glucose → PEP → sugar transport/  
phosphorylation

PMID 18628769

# Carbon catabolite repression (*E. coli*)

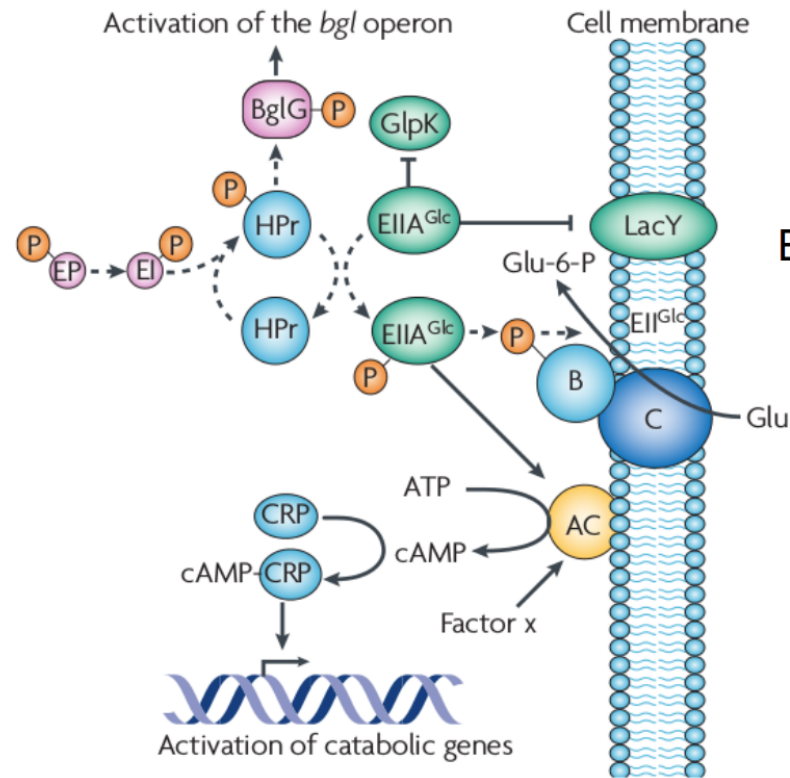
## glucose (repression by inducer exclusion)

EII phosphorylates glucose

EII binds and inactivates  
lactose transport (LacY)

no lactose inducer  
in presence of glucose

LacI represses  
lac operon



## No glucose (cAMP activates lac expression)

EII retains Pi in absence of glucose

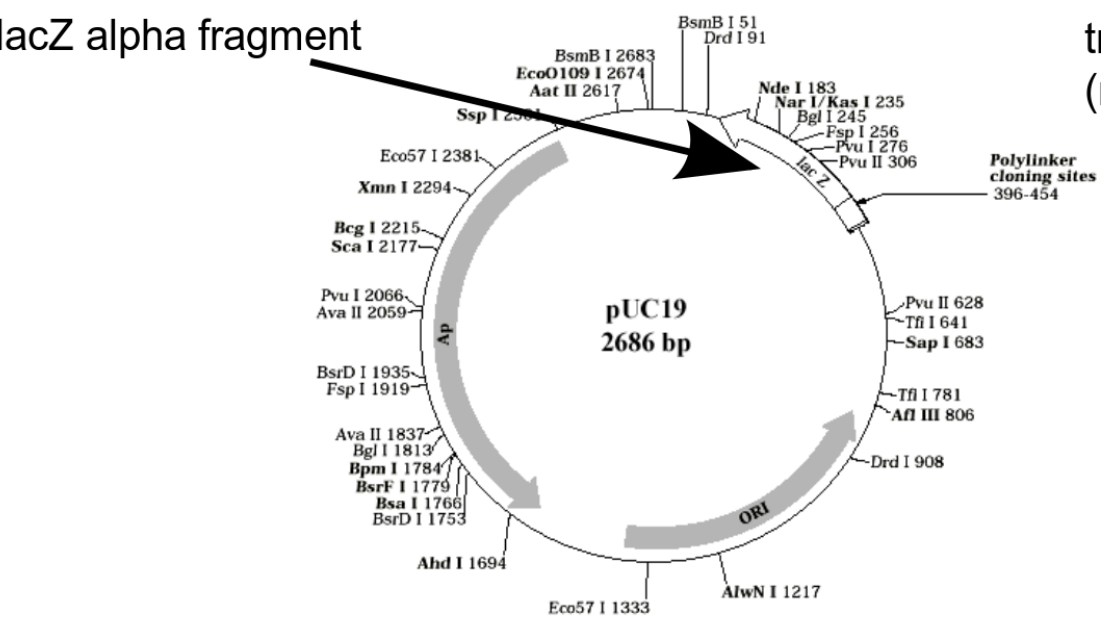
EII-P activates adenylate cyclase (AC)

cAMP formed

cAMP binds CRP

cAMP-CRP activates  
lac operon

# Alpha complementation with pUC19



transform pUC19 into *E.coli* with lacZalpha deletion (missing residues 11-41)

add IPTG (inducer) and X-gal (turns blue when cut by B-gal)

blue colonies

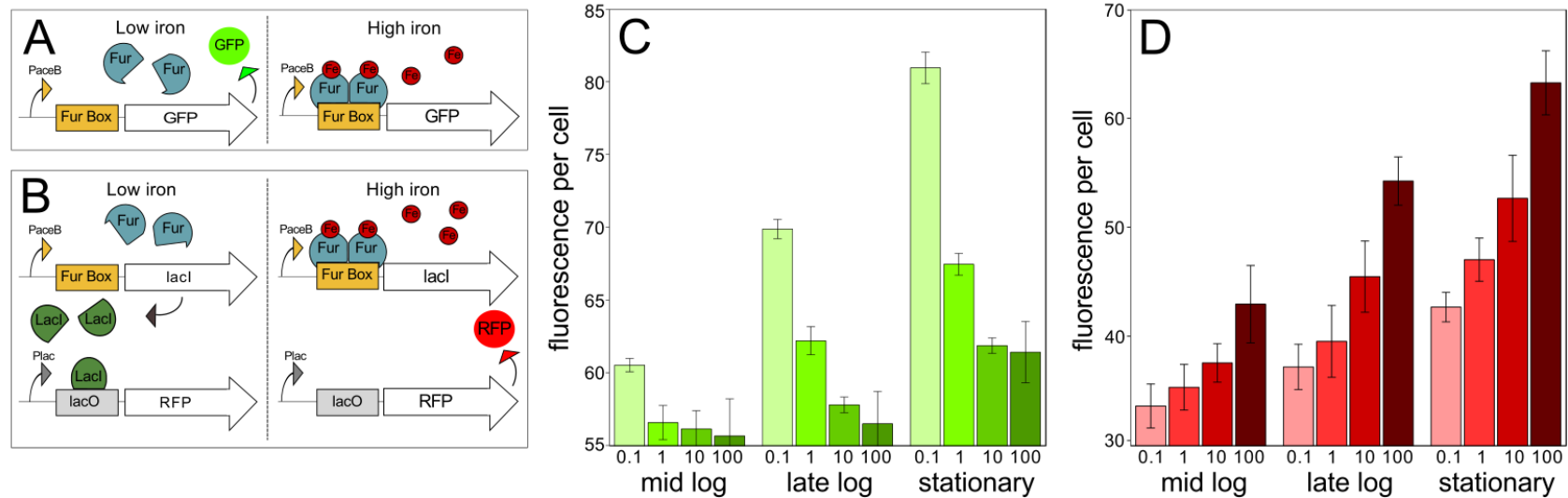
clone gene into MCS between Plac and lacZalpha

disrupt lacZ alpha expression

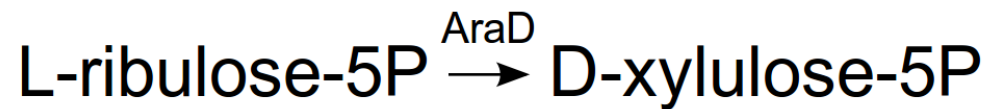
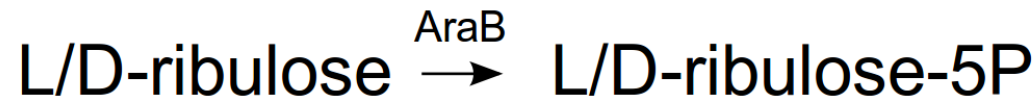
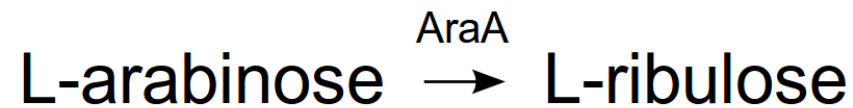
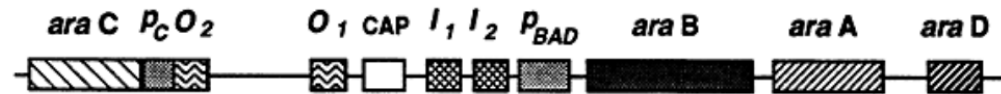
white colonies in +IPTG, +X-gal

# A LacI-based Fur inverter to activate gene expression in response to iron

iGEM Evry 2013



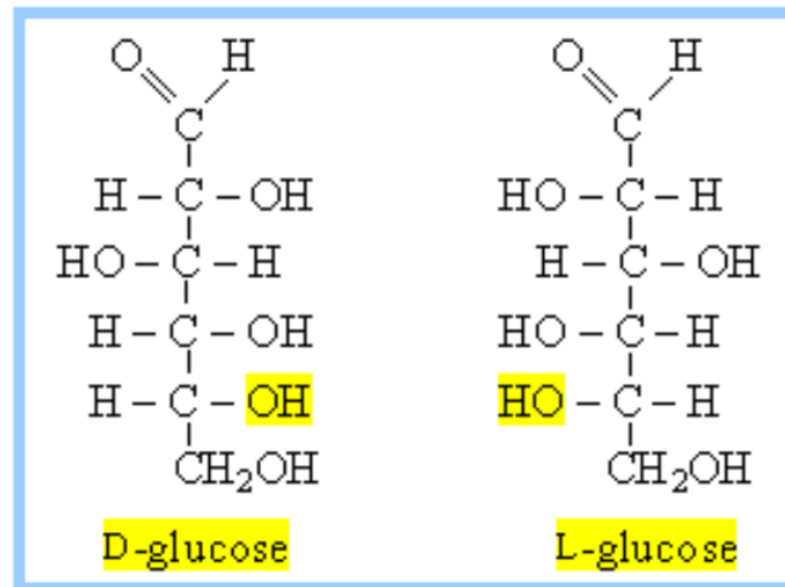
# Regulation of the L-arabinose operon



AraEFGH=arabinose transporters

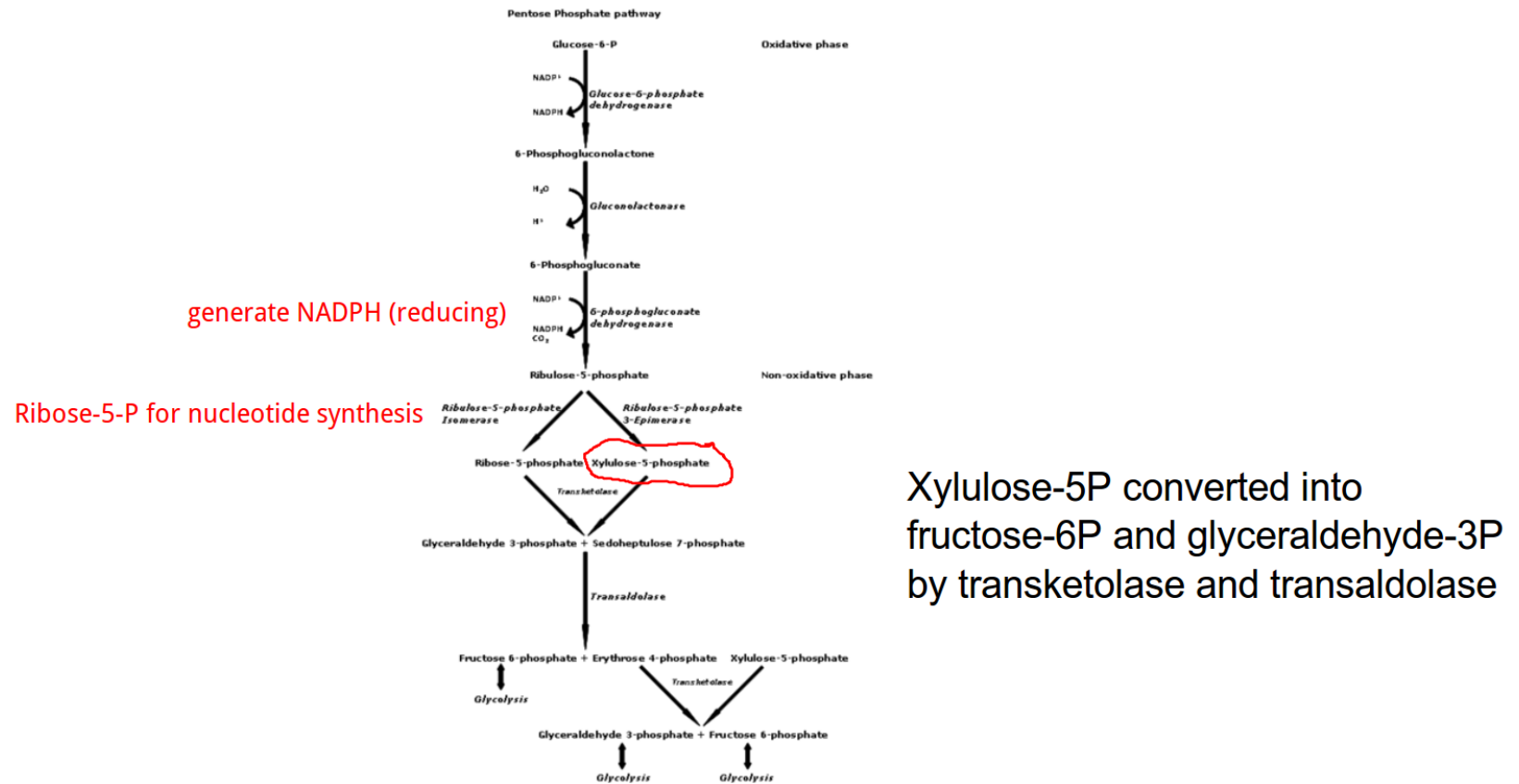
AraC=regulator

# Review: D and L sugars are stereoisomers



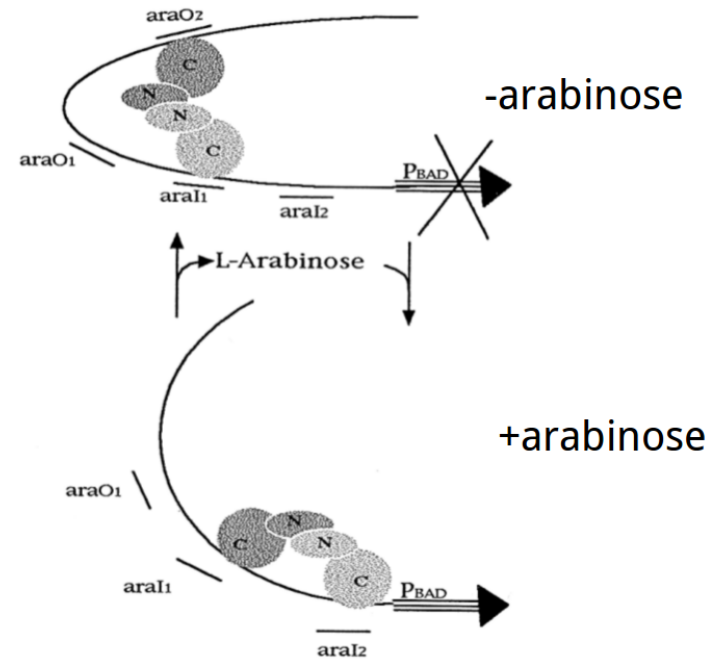
most biological sugars  
are D, but arabinose is L

# Review: D-xylulose-5P is assimilated by the pentose phosphate pathway



# Repression of arabinose operon by 'no arabinose'

**No arabinose**  
 AraC dimer binds I1, O2  
 ↓  
 AraC on O2 and I1 multimerize  
 ↓  
 DNA bends to block  
 transcription of arabinose operon



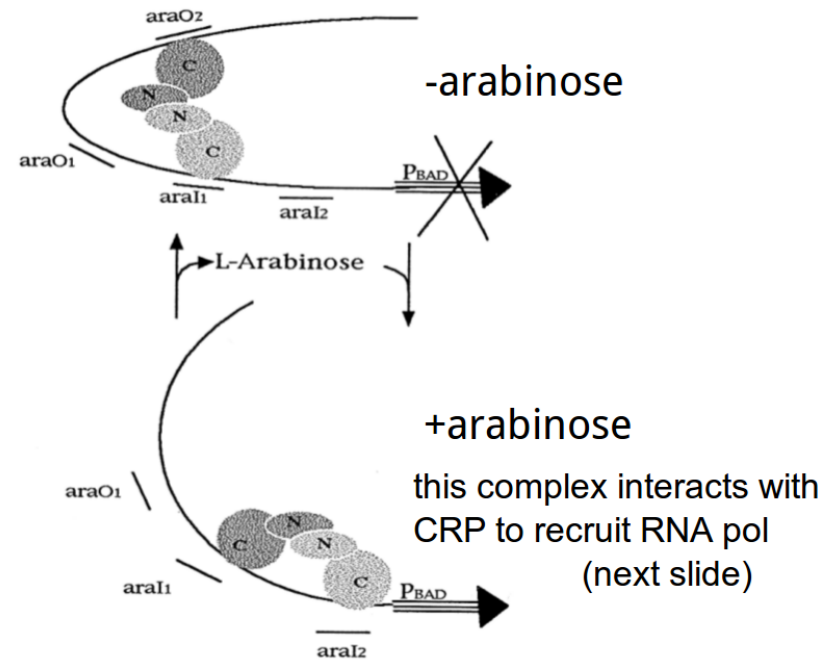
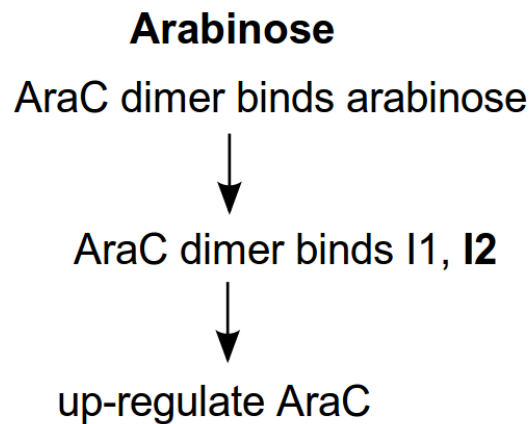
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AraC domain structure: residues 1-170 bind arabinose and dimerize protein; 170-8 flexible linker; 178-286 site-specific DNA binding and RNA polymerase recognition.

AraC consensus binding site: AGC-N7-TCCATA



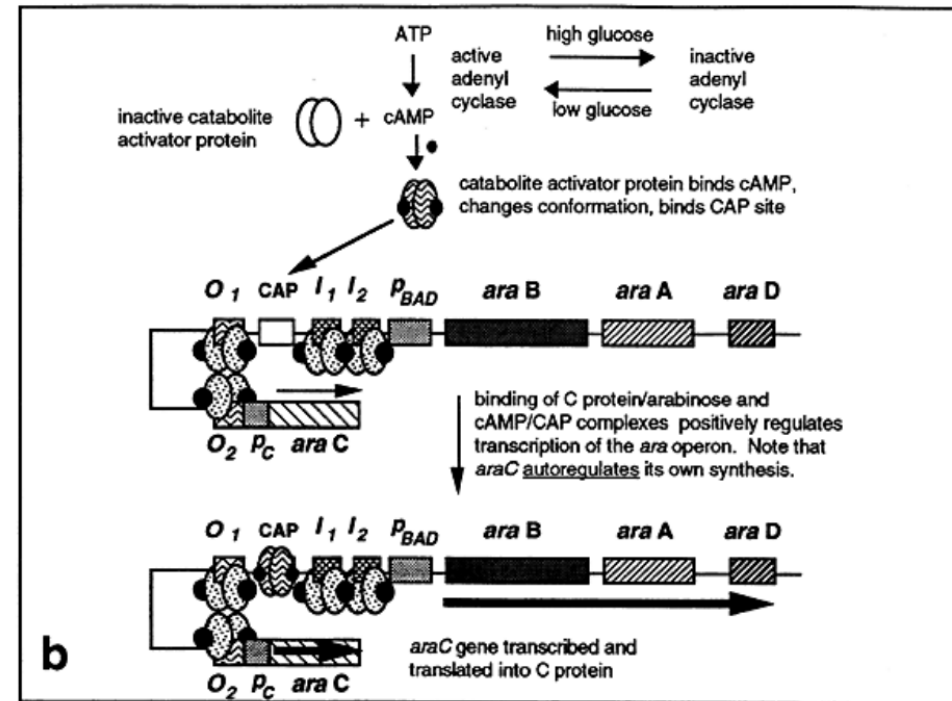
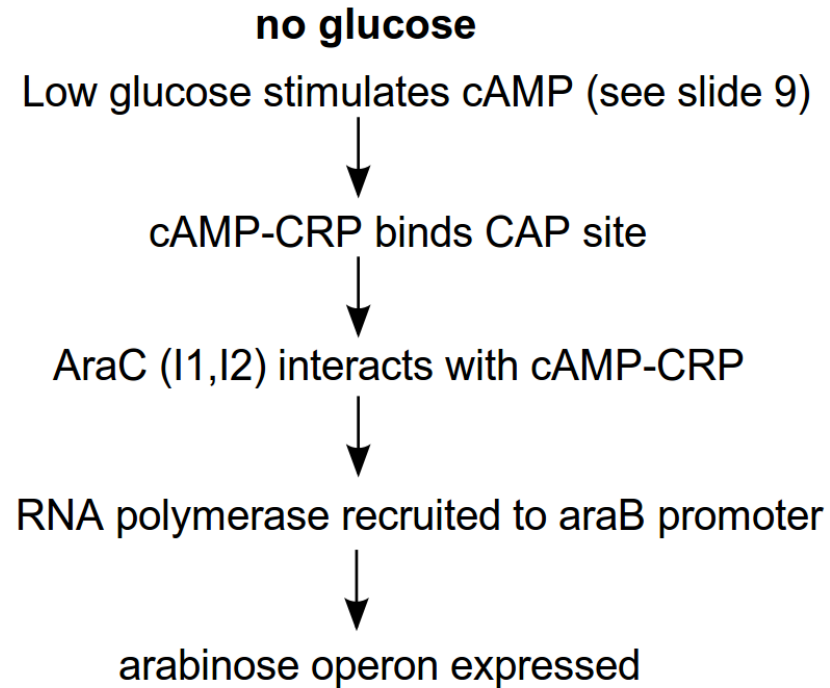
# Activation of *araC* by arabinose



\*Arabinose binds AraC->change affinity of AraC for spatial orientation of binding sites.

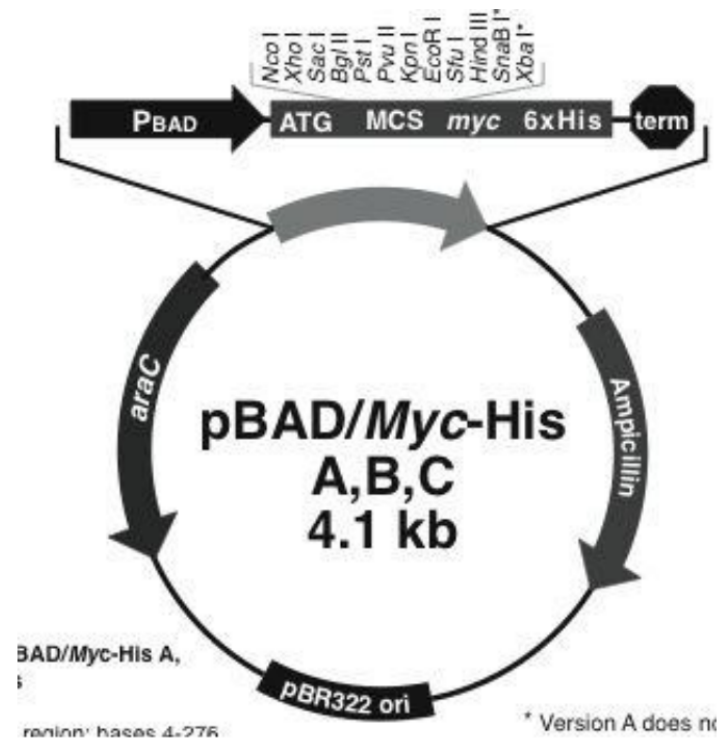
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# Activation of arabinose operon by 'no glucose'



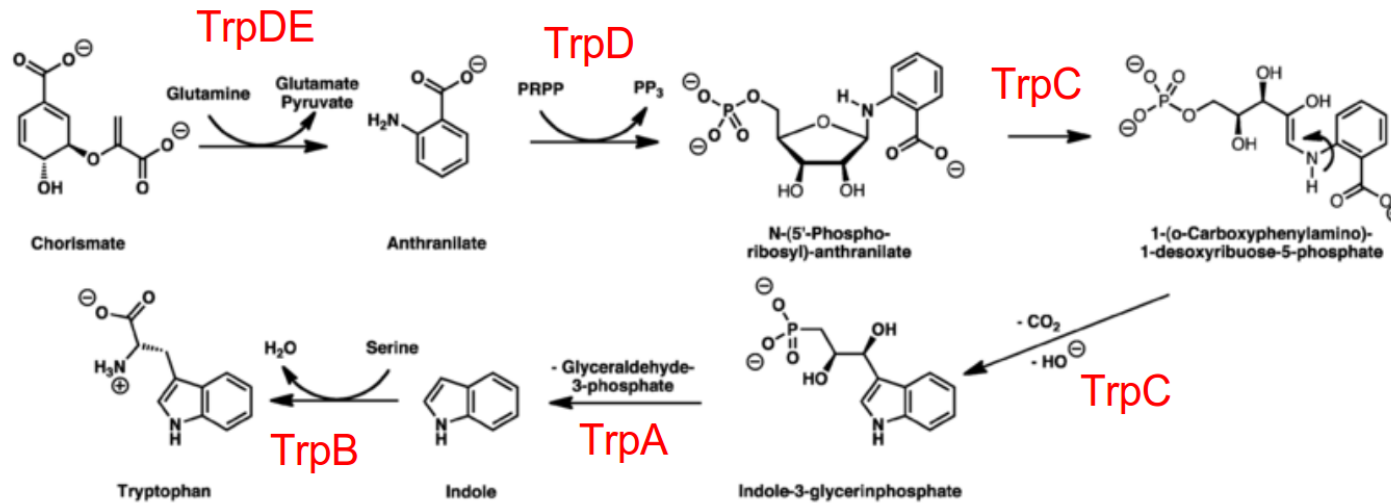
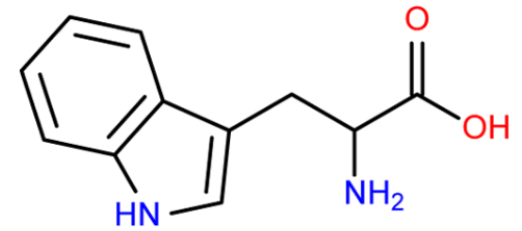
# P<sub>bad</sub> promoter

activate gene expression in +arabinose, -glucose



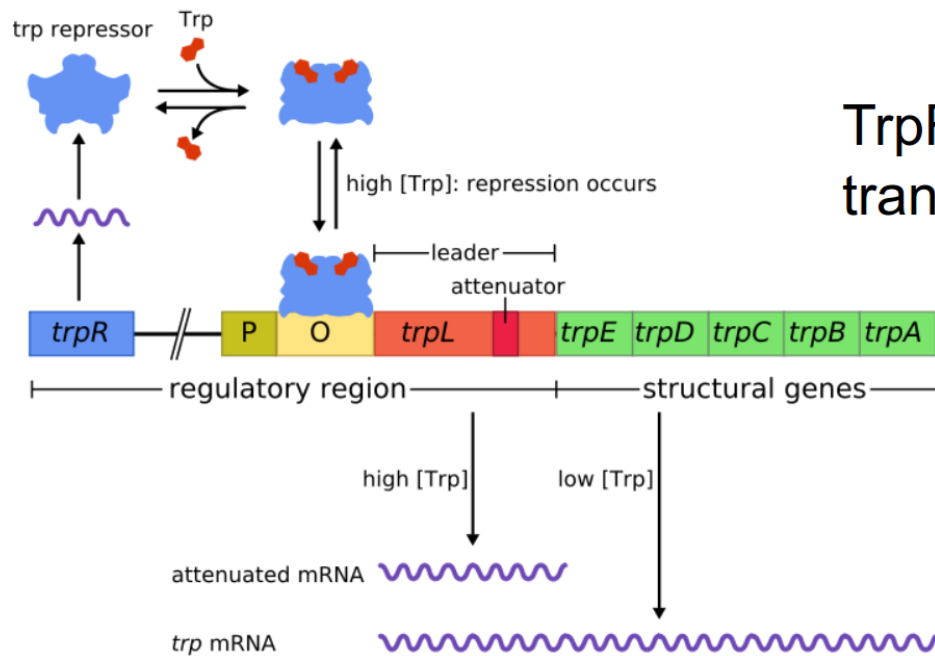
# Trp operon: 5 genes for tryptophan biosynthesis

synthesis of Trp from chorismate



# TrpR blocks trp operon transcription in +Trp conditions

TrpR constitutively expressed



TrpR-Trp binds operator to block transcription of Trp operon

# Trp regulation by attenuation

## Important points

-simultaneous transcription and translation in bacteria

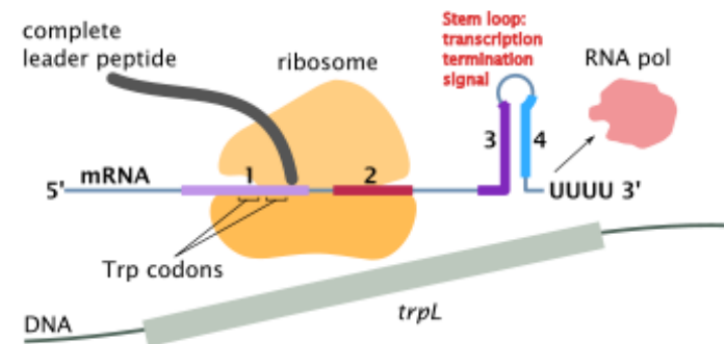
-upstream is tryptophan-rich  
130 bp leader peptide

-two stem loops possible:  
3-4 is a transcription terminator  
(RNA pol falls off DNA)

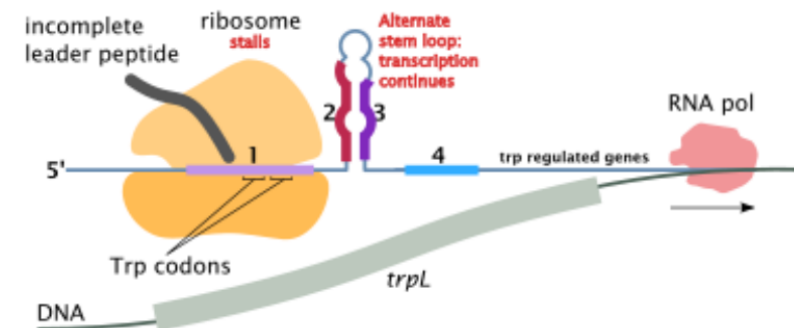
2-3 prevents formation of 3-4  
but does not block transcription

-attenuation senses the amount  
of tRNA-trp

### High level of tryptophan

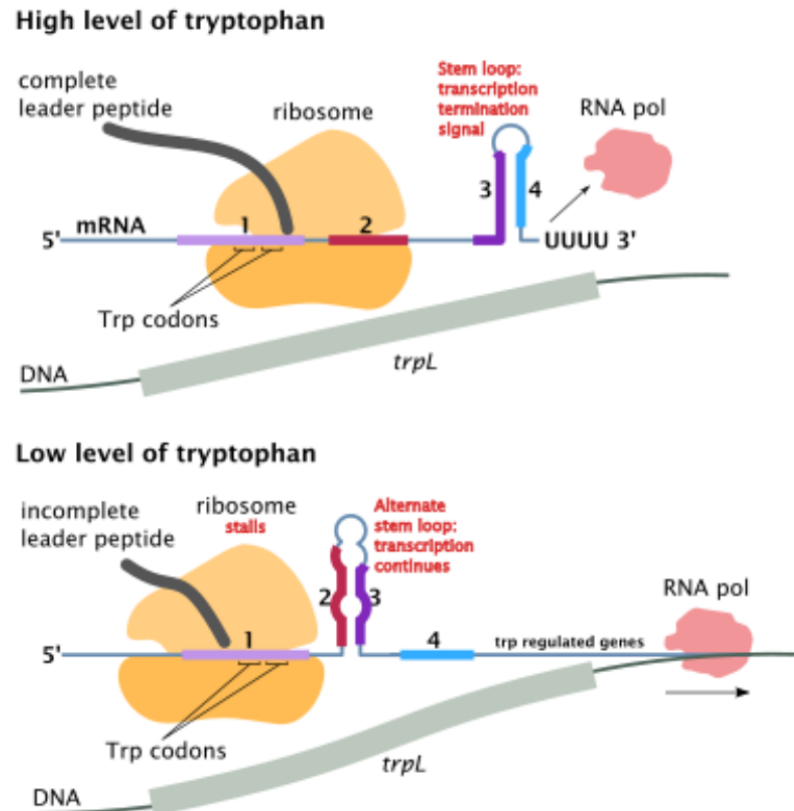
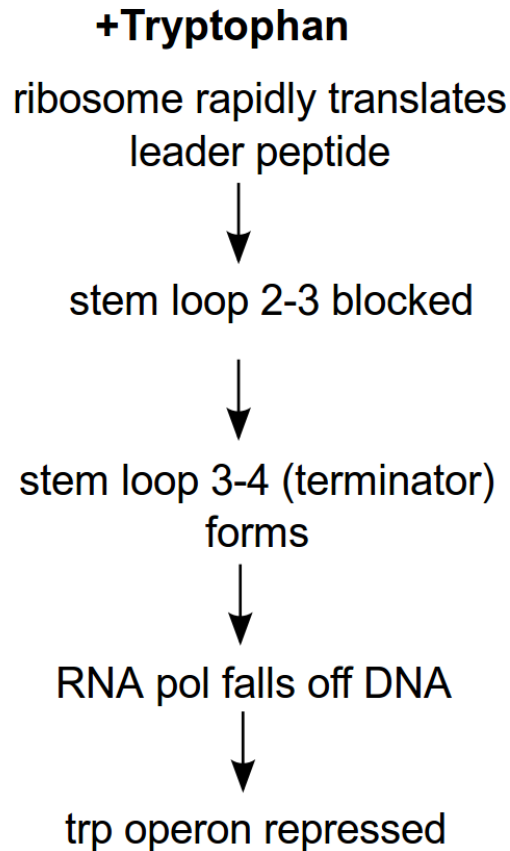


### Low level of tryptophan



# Trp regulation by attenuation

attenuation also controls His, Phe, Thr synthesis



[http://en.wikipedia.org/wiki/Trp\\_operon](http://en.wikipedia.org/wiki/Trp_operon)

