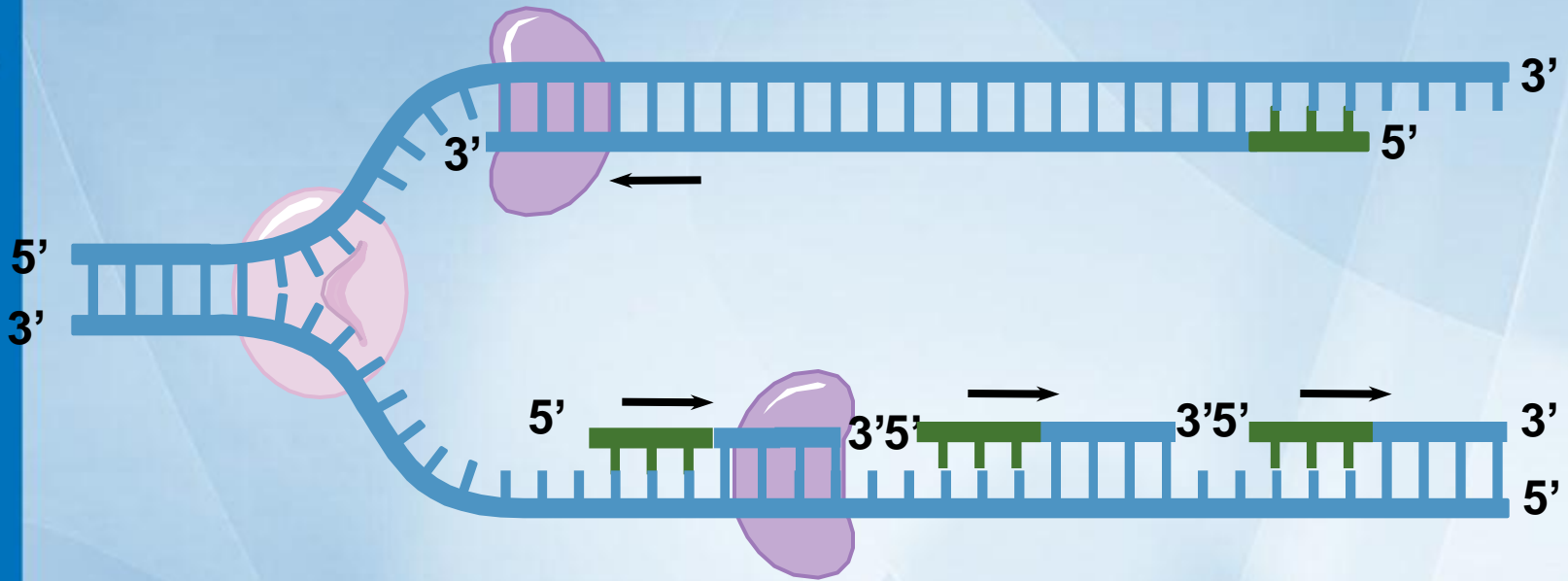


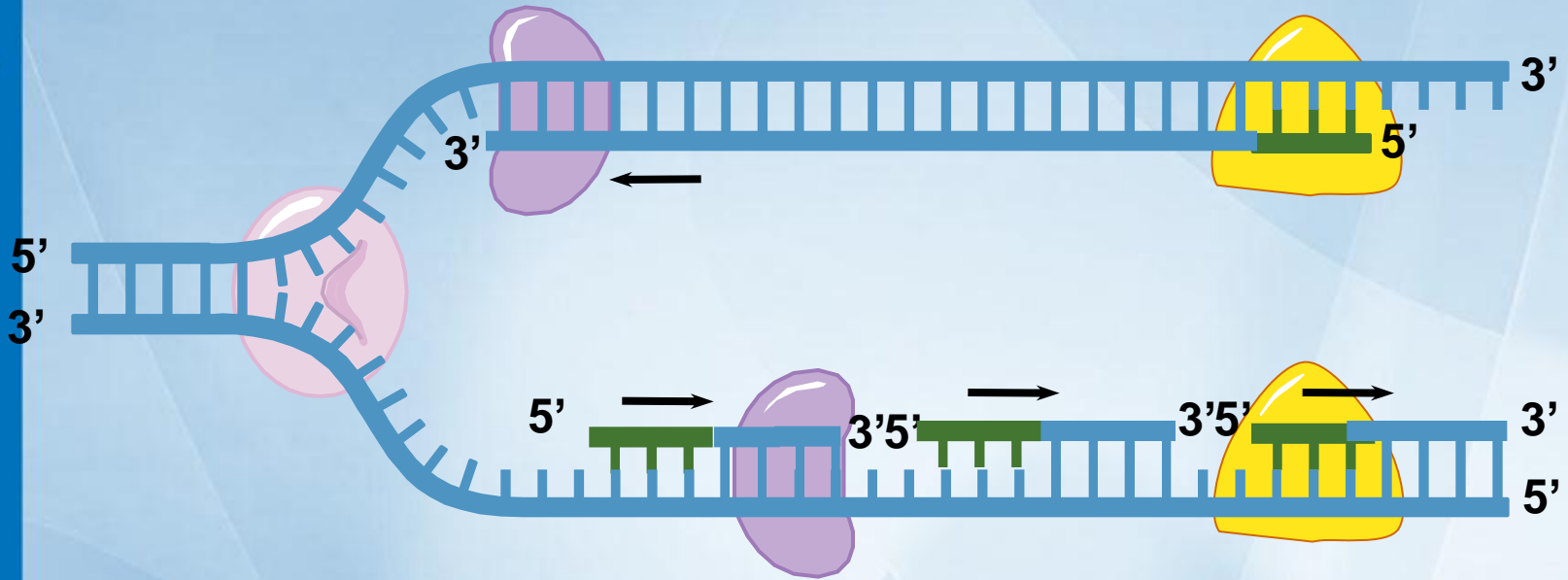
Replication



Leading strand synthesis continues in a 5' to 3' direction.

Discontinuous synthesis produces 5' to 3' DNA segments called Okazaki fragments.

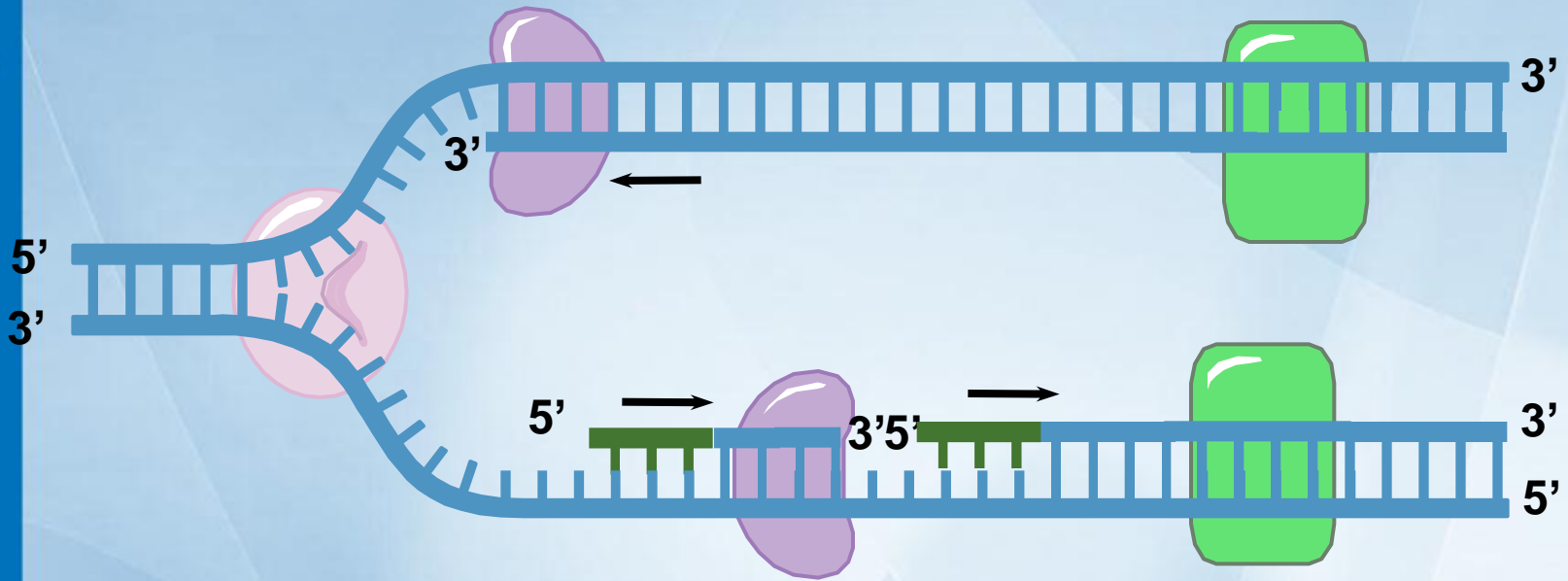
Replication



5- DNA polymerase I

DNA pol 1: المسئول عن ازالة RNA primer ويقوم بملئ الفراغات او الفجوات الصغيرة بين شظايا او كازاكي التي تتكون على الشريط المتلكئ

Replication



Ligase forms bonds between sugar-phosphate backbone.

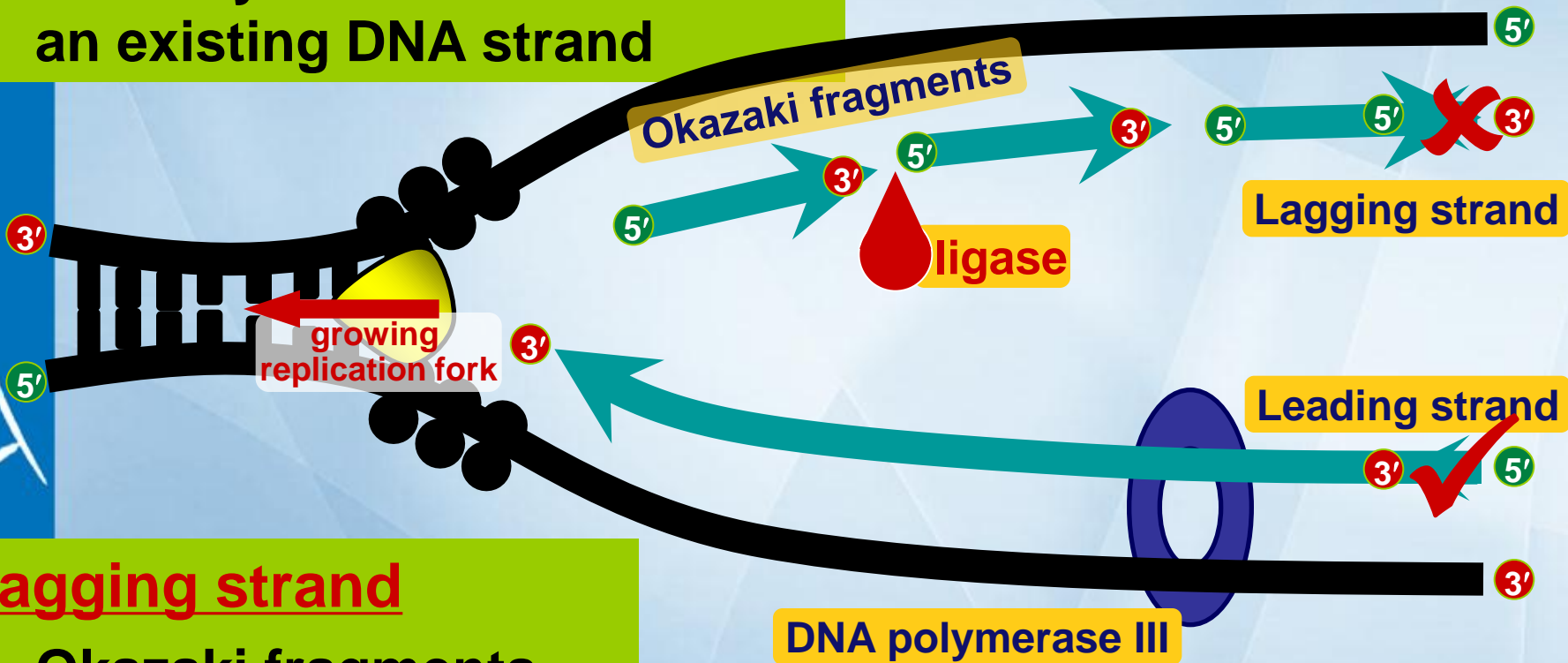
DNA pol II: يلعب دور في إصلاح الأخطاء الناجمة عن التلف الذي قد يحدث في جزيء DNA.



Leading & Lagging str

Limits of DNA polymerase III

- ◆ can only build onto 3' end of an existing DNA strand



Lagging strand

- ◆ Okazaki fragments
- ◆ joined by **ligase**
 - “spot welder” enzyme

Leading strand

- ◆ continuous synthesis

A 3D molecular model of a protein structure. The protein backbone is represented by a blue ribbon, and the side chains are shown as red ball-and-stick models. The structure is complex and folded, with various loops and helices. The background is black.

Gene Expression

1- Transcription

2- Translation

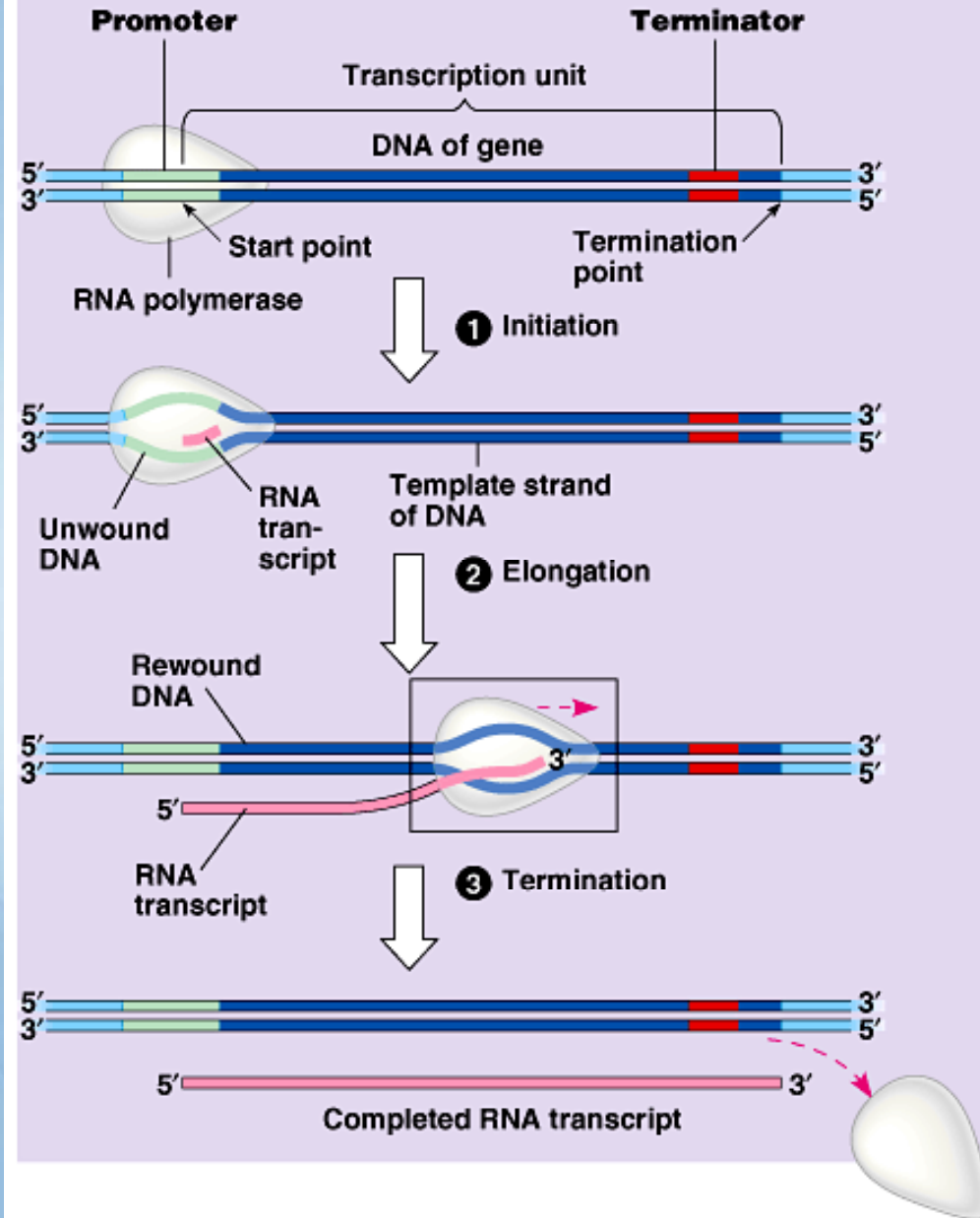
Stages of Transcription

Promoter Binding

Initiation

Elongation

Termination



Gene sequences

The gene contains •

coding strand (sense / non-template strand)
and

non-coding strand (non-sense / template
strand)

G A A C T G G G A T T C T C G G (Sense)

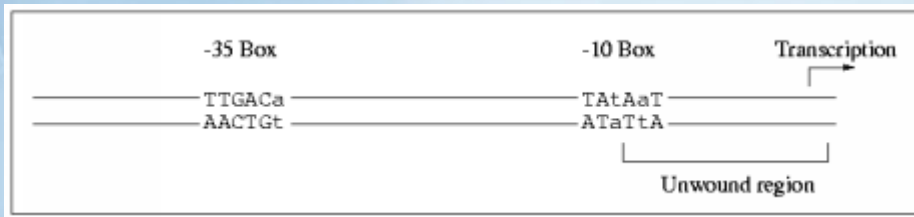
(Non-
template)

G A A C U G G G A U U C U C G G mRNA

C T T G A C C C T A A G A G C C (Non-

Promoter in prokaryotic

A site on DNA to which RNA polymerase can bind and begin transcription



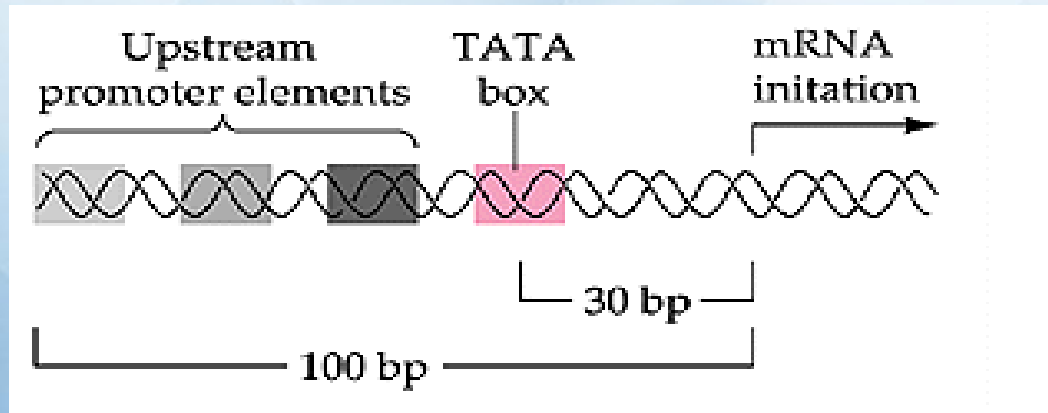
The first region **-10 box** ----- TATA box (**pribnow box**)

The second region **-35** bases from the start codon TTGACA

Promoter in eukaryotic

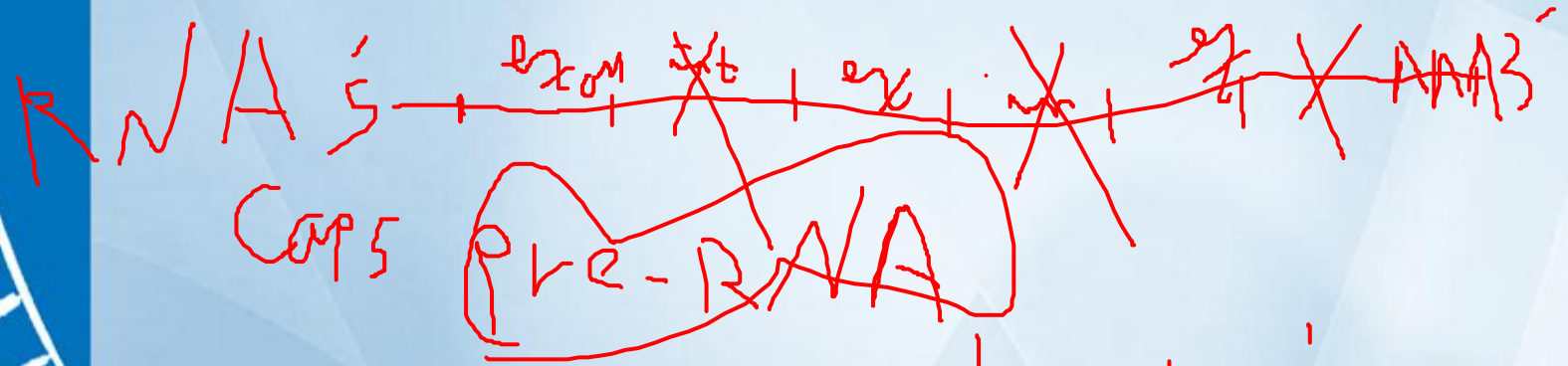
-25 region TATA box

-80 region CAAT

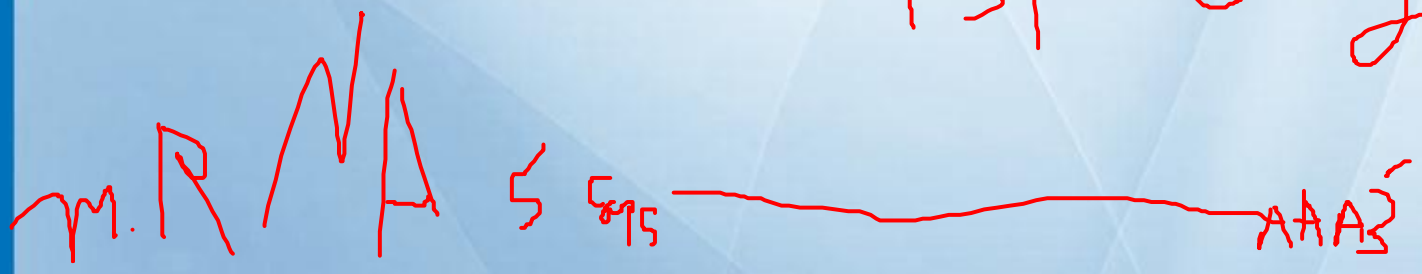


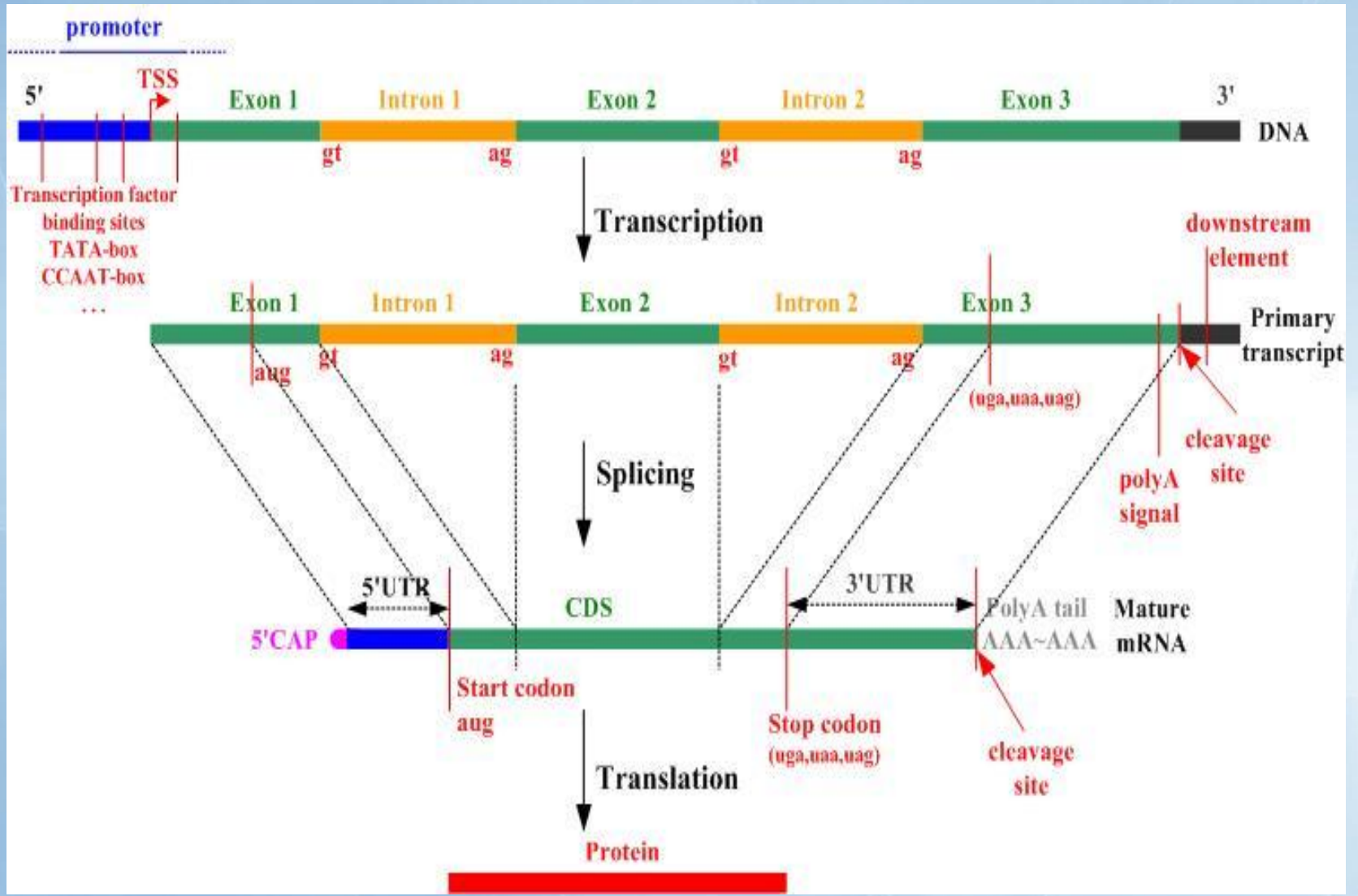


RNA processing

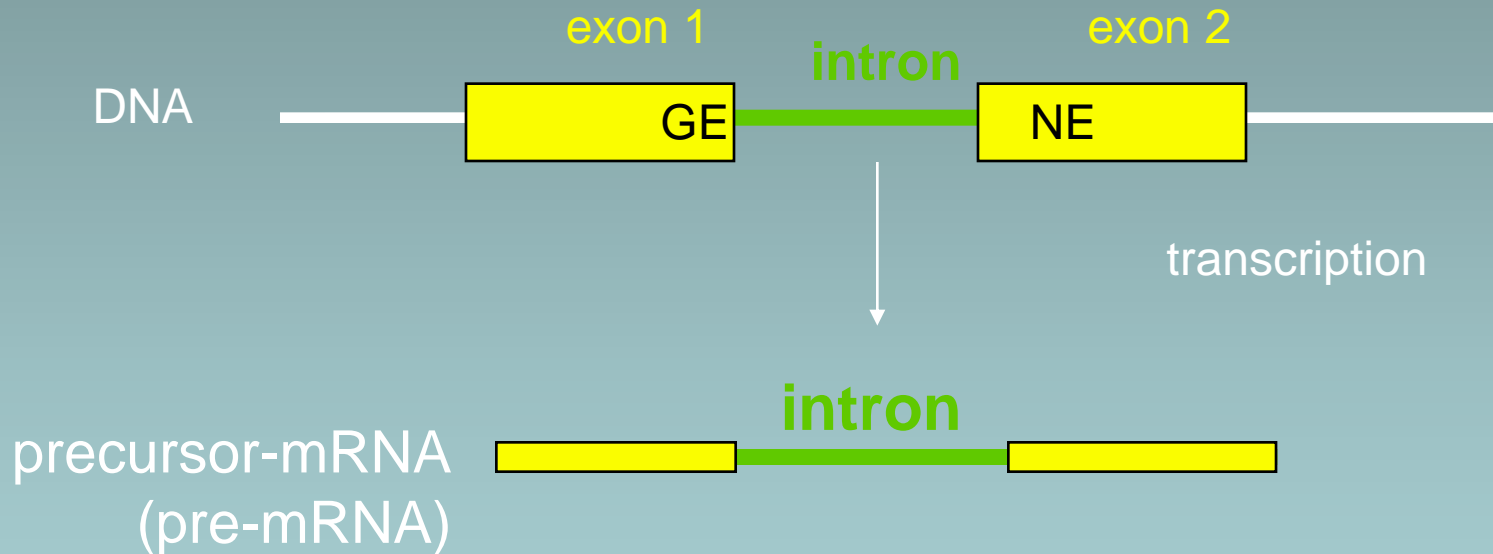


Splicing



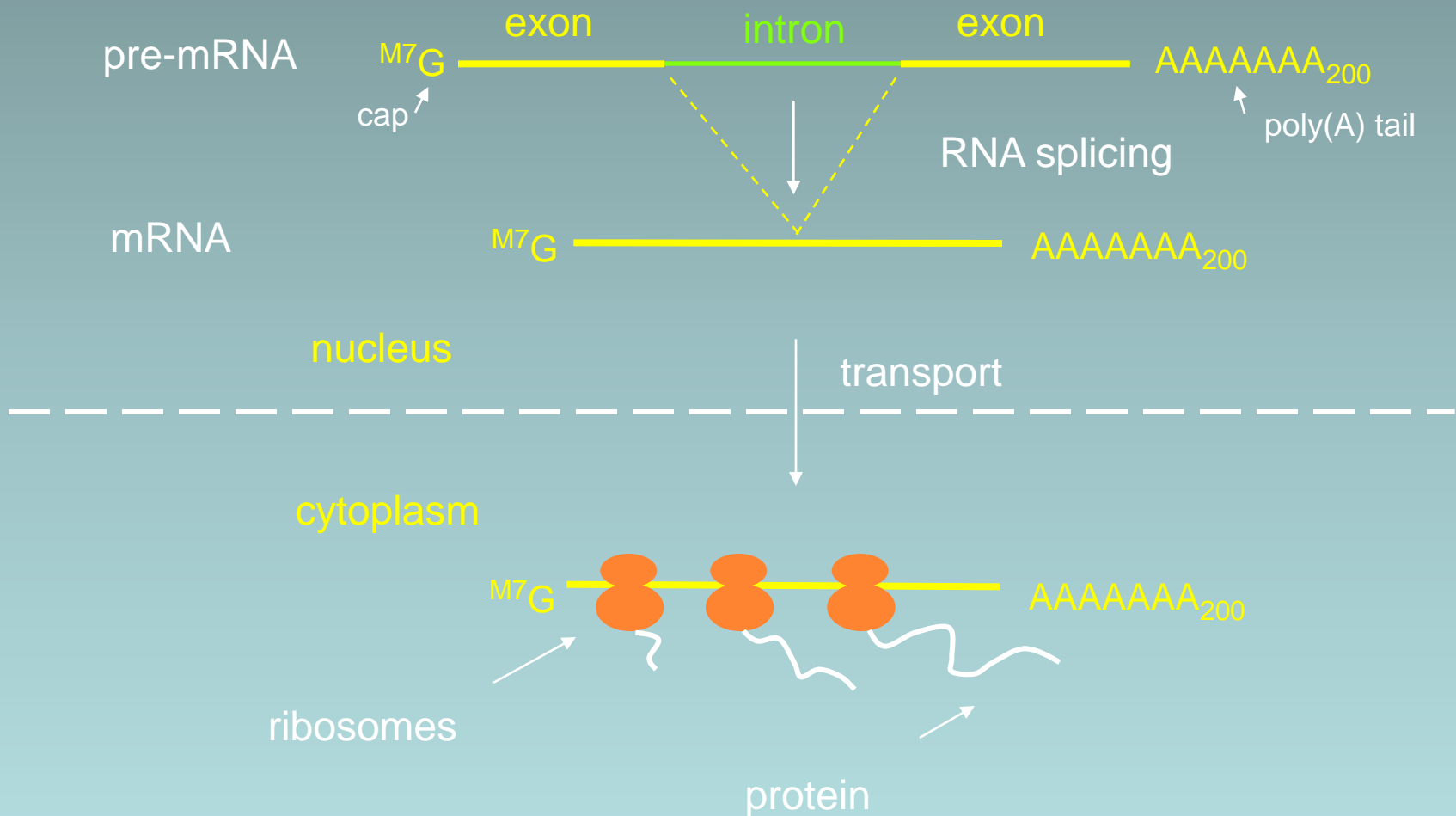


Some genes have their protein-coding information interrupted by non-coding sequences called introns. The coding sequences are then called "exons"



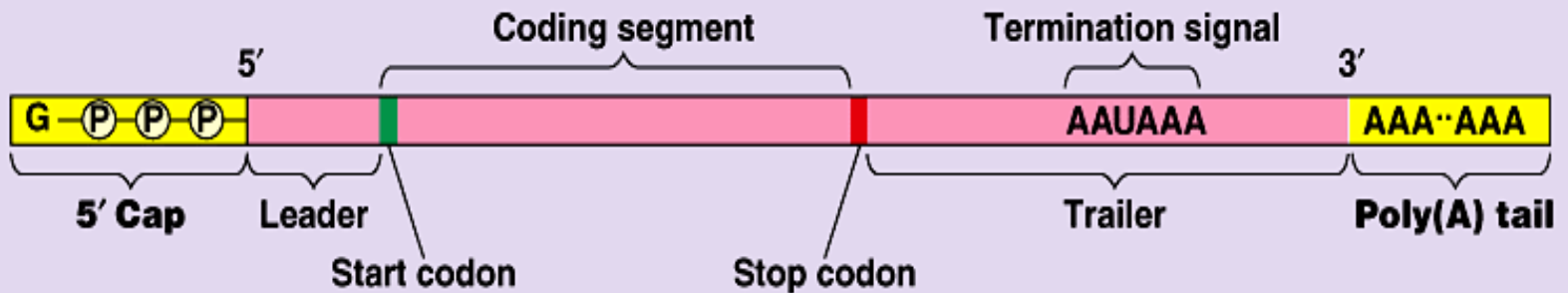
The intron is also present in the RNA copy of the gene and must be removed by a process call "RNA splicing"

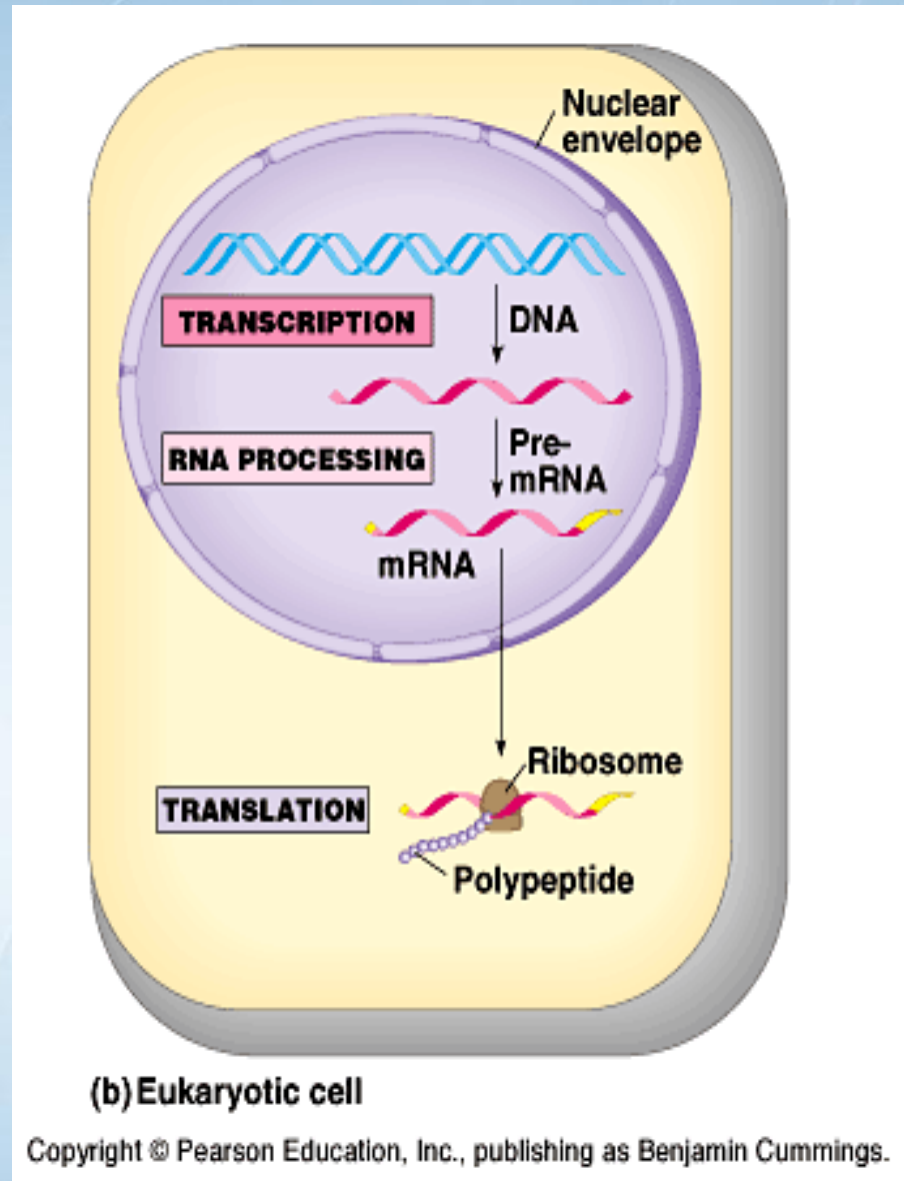
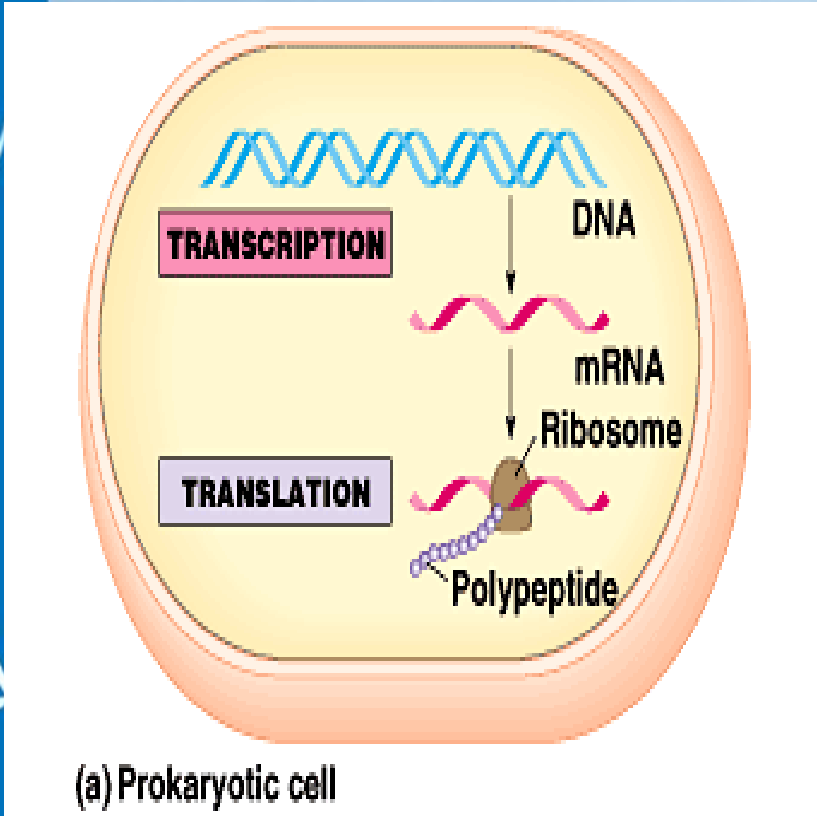
Pre-messenger RNA Processing



a) 5' CAP: CAPPED WITH MODIFIED GUANINE – WHY?

b) POLY A TAIL: 50 – 250 ADENINE NUCLEOTIDES – WHY?





Types of RNA polymerases

- prokaryotic → One type of RNA poly.
- Eukaryotic → three RNA polymerase

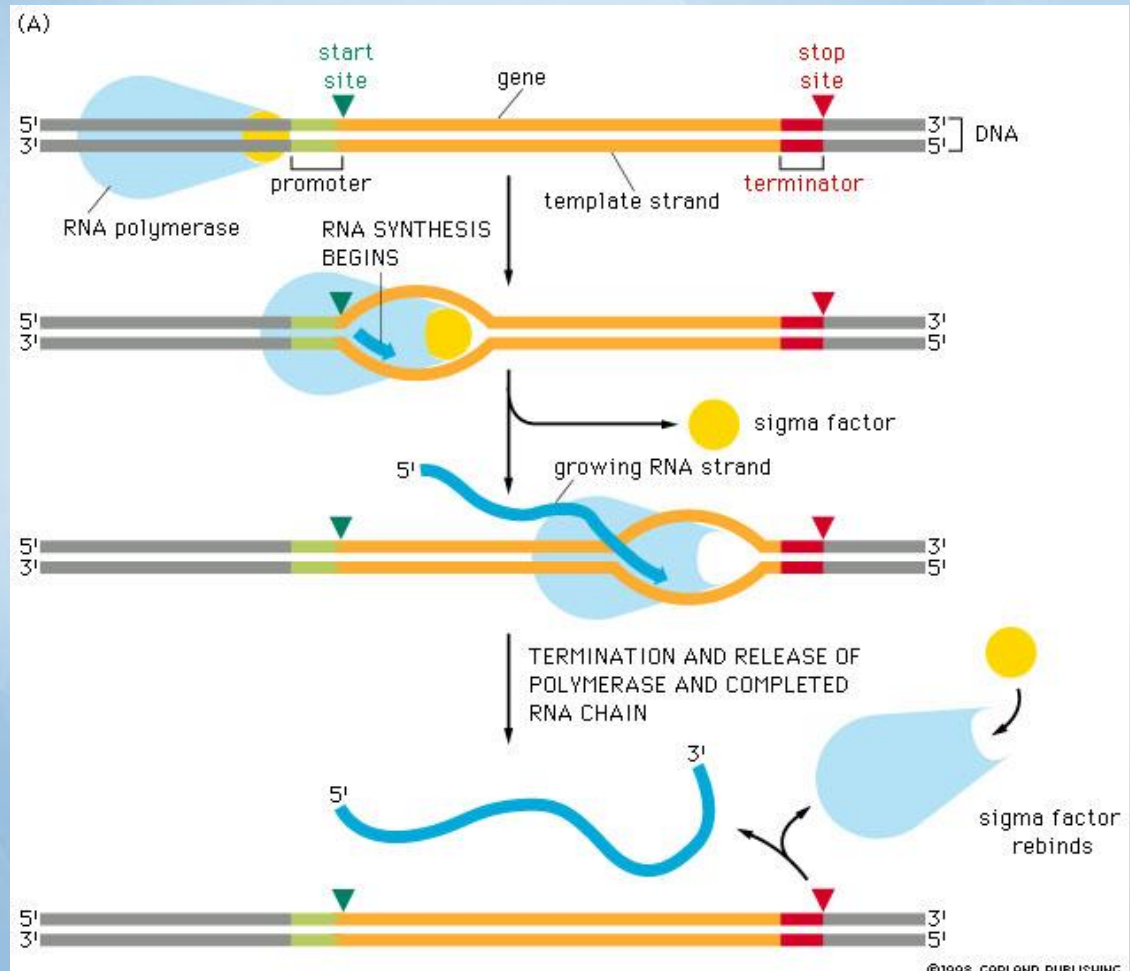
RNA poly.i → rRNA

RNA poly.ii → mRNA

RNA poly.iii → tRNA

Messenger RNA (mRNA)

An RNA molecule that contains the genetic information necessary to encode a particular protein



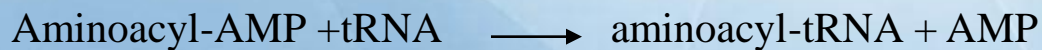
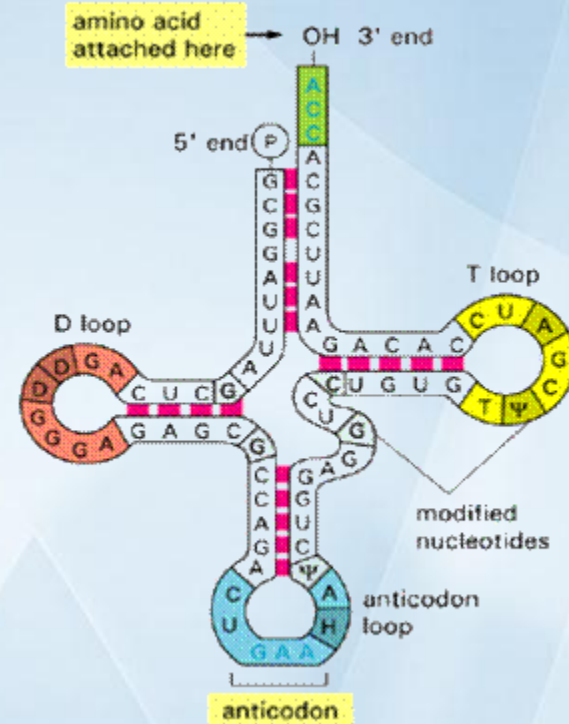
Transfer RNA (tRNA)

An adaptor molecule used in translation that has specificity for both a particular amino acid for one or more codons

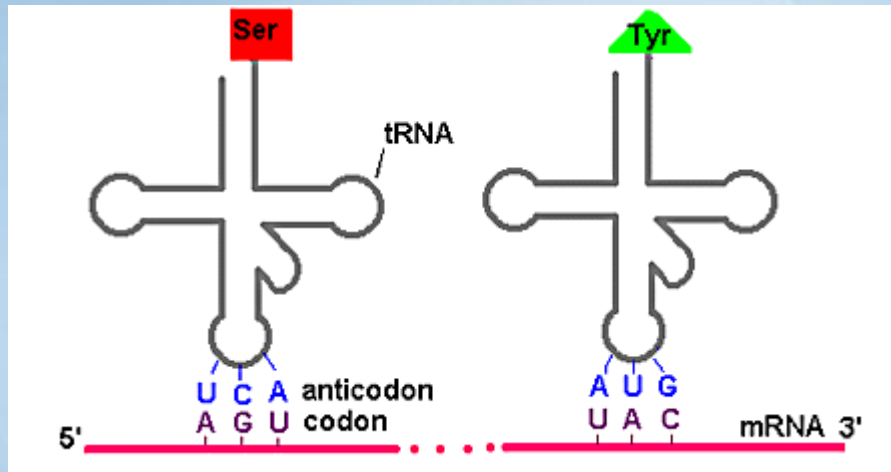
73-93 nucleotides

Acceptor end

Anticodons



EX: alanyl-tRNA synthetase

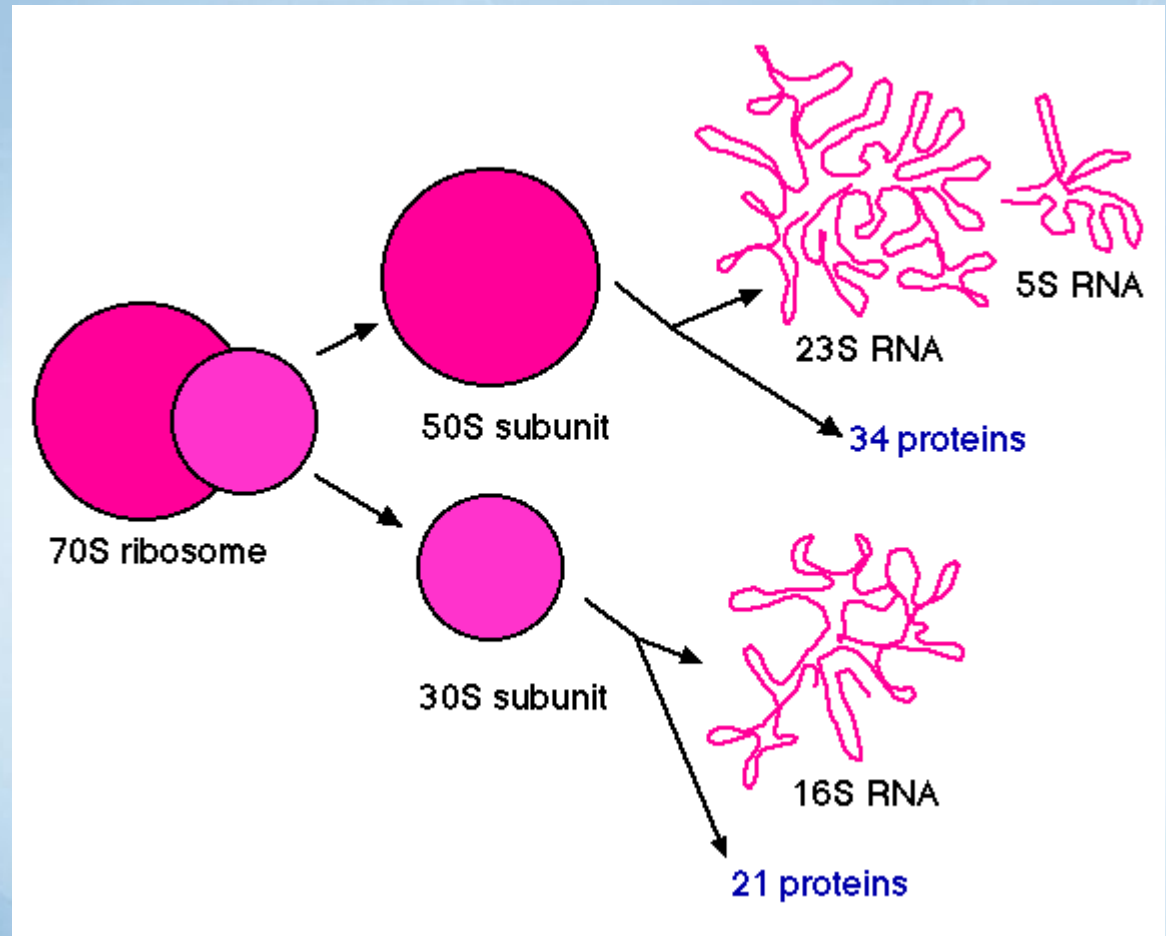


Codon : a sequence of three bases in mRNA that encodes an amino acid

Anticodon : a sequence of three bases in tRNA molecule that base-pairs with codon during protein synthesis

Ribosomal RNA (rRNA)

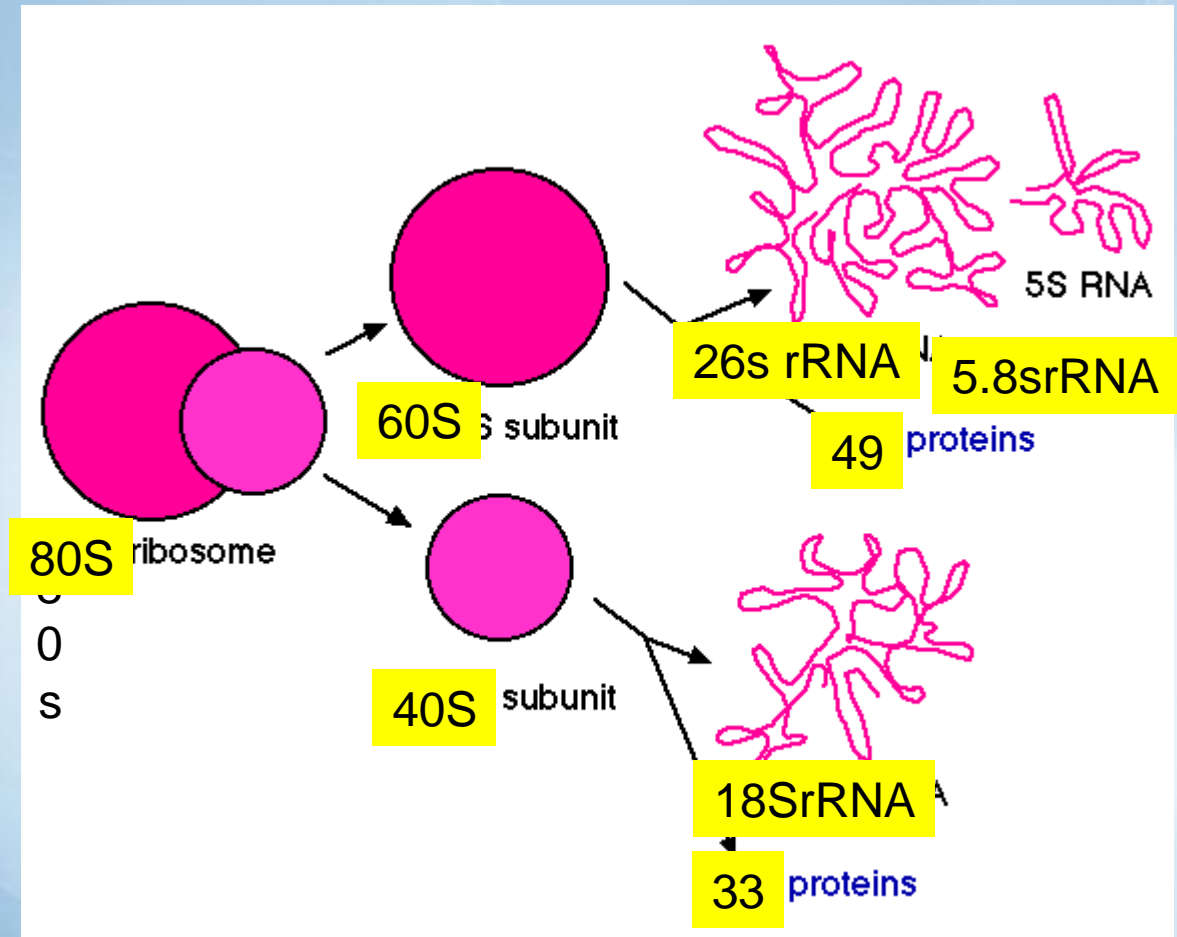
Prokaryotic cell



Euokaryotic cell: Ribosomal RNA consists of 40S + 60S = 80S

Ribosomal RNA (rRNA)

Eukaryotic cell



Eukaryotic cell: Ribosomal RNA consists of 40S + 60S = 80S



Differences between **DNA and RNA**

V. Differences between DNA and RNA

1. RNA has uracil and DNA has thymine.
2. RNA is a single helix and DNA is a double helix.
3. RNA is very small and DNA is very large.
4. RNA can travel between the nucleus and the cytoplasm, DNA is only in the nucleus.
5. RNA has ribose sugar and DNA has deoxyribose.

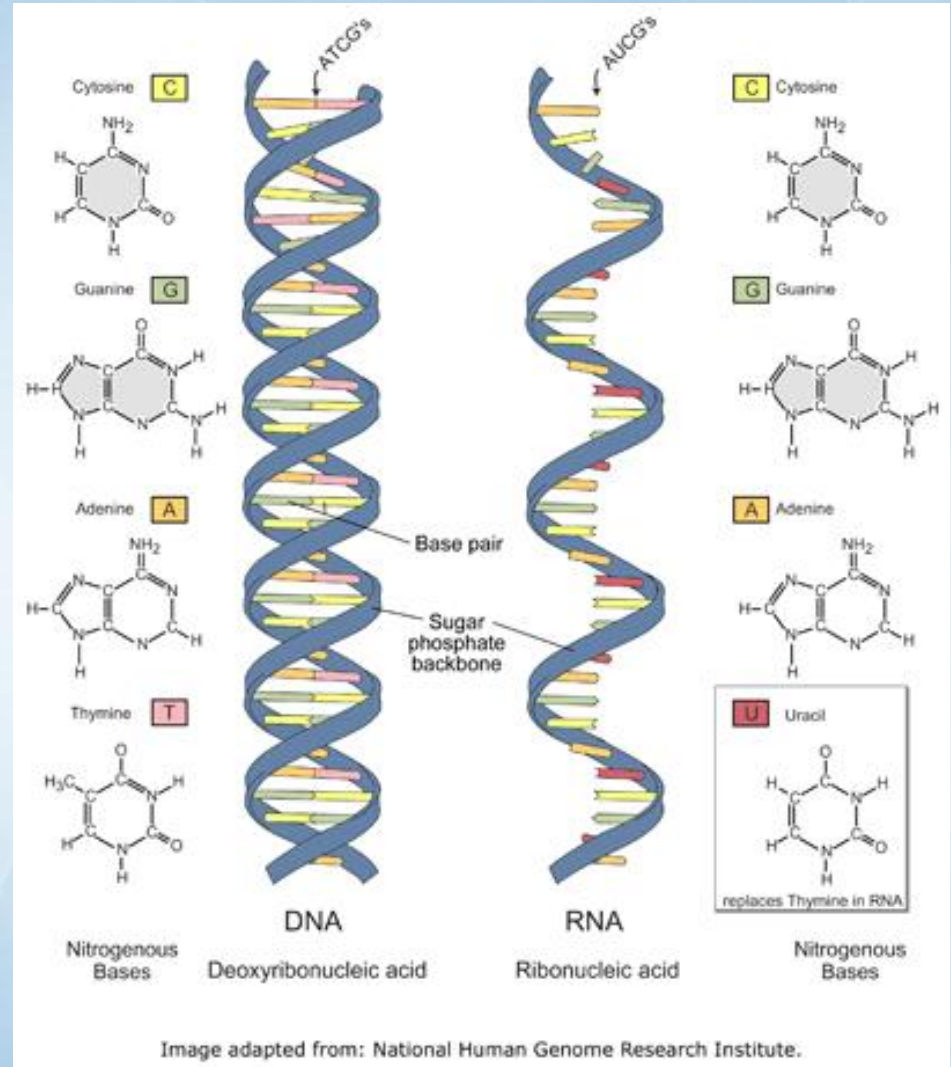


Image adapted from: National Human Genome Research Institute.

translation



Genetic Code

Colinearity between base sequences in DNA and amino acid sequences in protein

Start codon = AUG

Formylmethionine

Methionine

Stop codons = Nonsense codons

UAA

UGA

UAG

The Genetic Code

	U	C	A	G	
U	UUU Phenylalanine UUC Phenylalanine UUG Leucine UUA Leucine	UCU Serine UCC Serine UCA Serine UCG Serine	UAU Tyrosine UAC Tyrosine UAA Stop UAG Stop	UGU Cysteine UGC Cysteine UGA Stop UGG Tryptophan	U C A G
C	CUU Leucine CUC Leucine CUA Leucine CUG Leucine	CCU Proline CCC Proline CCA Proline CCG Proline	CAU Histidine CAC Histidine CAA Glutamine CAG Glutamine	CGU Arginine CGC Arginine CGA Arginine CGG Arginine	U C A G
A	AUU Isoleucine AUC Isoleucine AUA Isoleucine AUG Methionine	ACU Threonine ACC Threonine ACA Threonine ACG Threonine	AAU Asparagine AAC Asparagine AAA Lysine AAG Lysine	AGU Serine AGC Serine AGA Arginine AGG Arginine	U C A G
G	GUU Valine GUC Valine GUA Valine GUG Valine	GCU Alanine GCC Alanine GCA Alanine GCG Alanine	GAU Aspartic acid GAC Aspartic acid GAA Glutamic acid GAG Glutamic acid	GGU Glycine GGC Glycine GGA Glycine GGG Glycine	U C A G

خصائص الشفرة الوراثية

Characteristics of the genetic code

– خصائص الشفرة الوراثية

– ثلاثية: ثلاثة نيوكليوتيدات متتالية تختصص بحامض أميني واحد

– تتطابق 61 شفرة مع الأحماض الأمينية

– تشفر AUG للميثايونين وتعطي إشارة البدء لعملية النسخ

– تعطي 3 شفرات ”توقف“ إشارة انتهاء عملية الترجمة

– الترادف: قد يوجد أكثر من شفرة لبعض الأحماض الأمينية

– عدم الغموض: أي شفرة لأي من الأحماض الأمينية لا تُستخدم

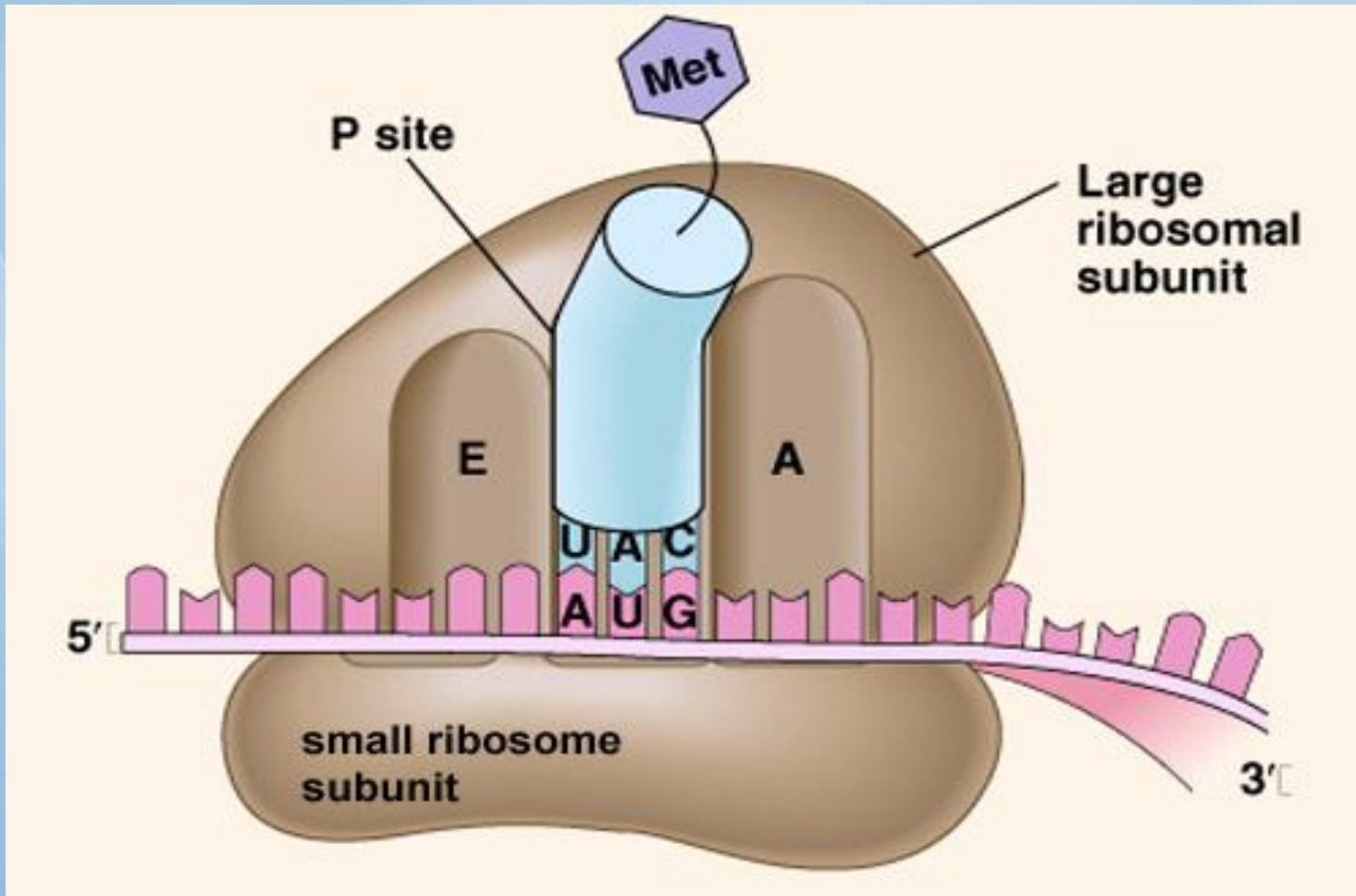
لأي حامض أميني آخر

– لا تحتوي على فراغات أو علامات وقف: الشفرات ملتصقة

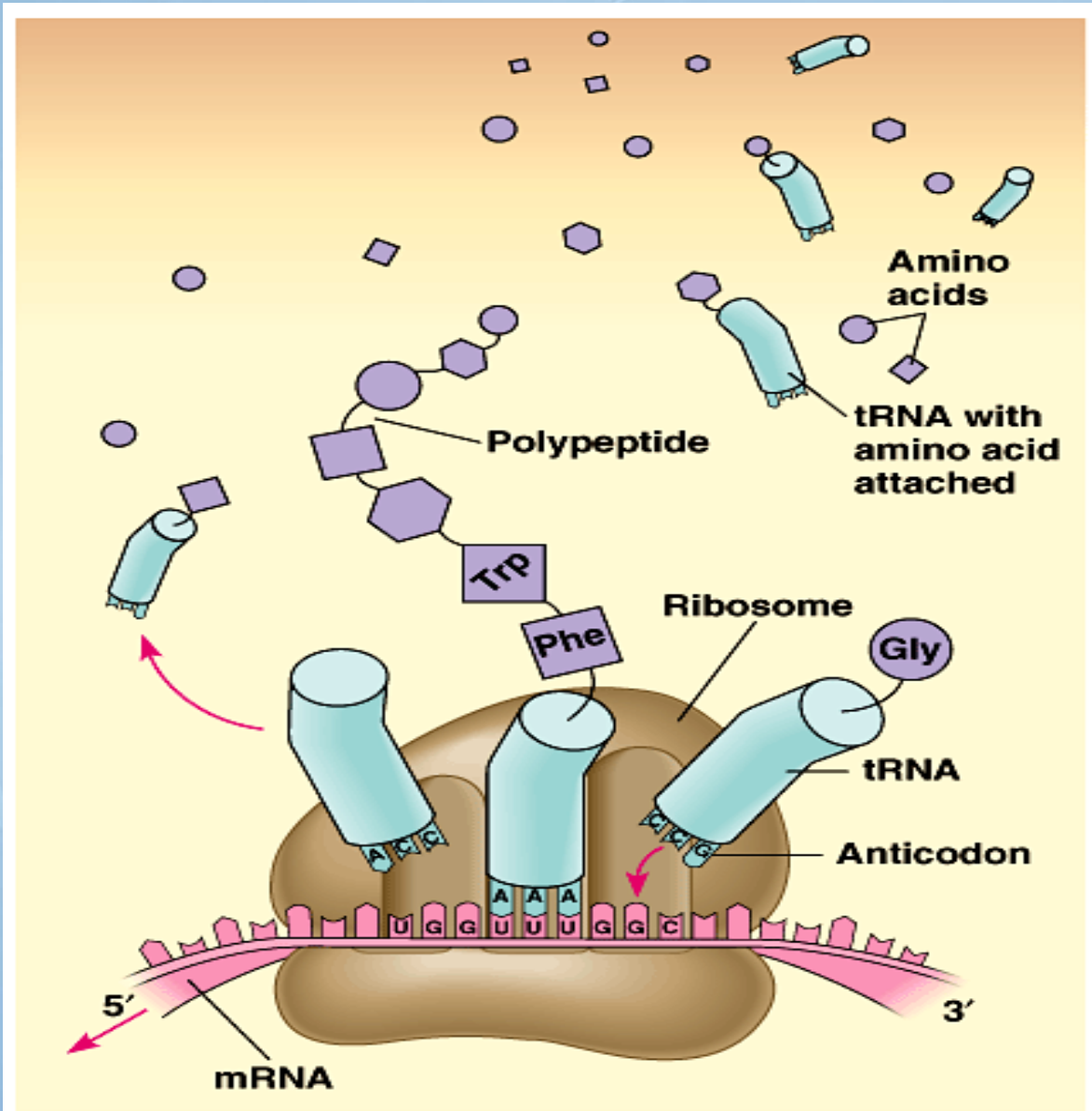
ببعضها البعض بدون أي فراغات بينها

– العمومية والشمول ”تقريباً“

Ribosome



A site = Aminoacyl site P site = peptidyl site E site = Exit site



A site = Aminoacyl site P site = peptidyl site E site = Exit site

2 – Translation

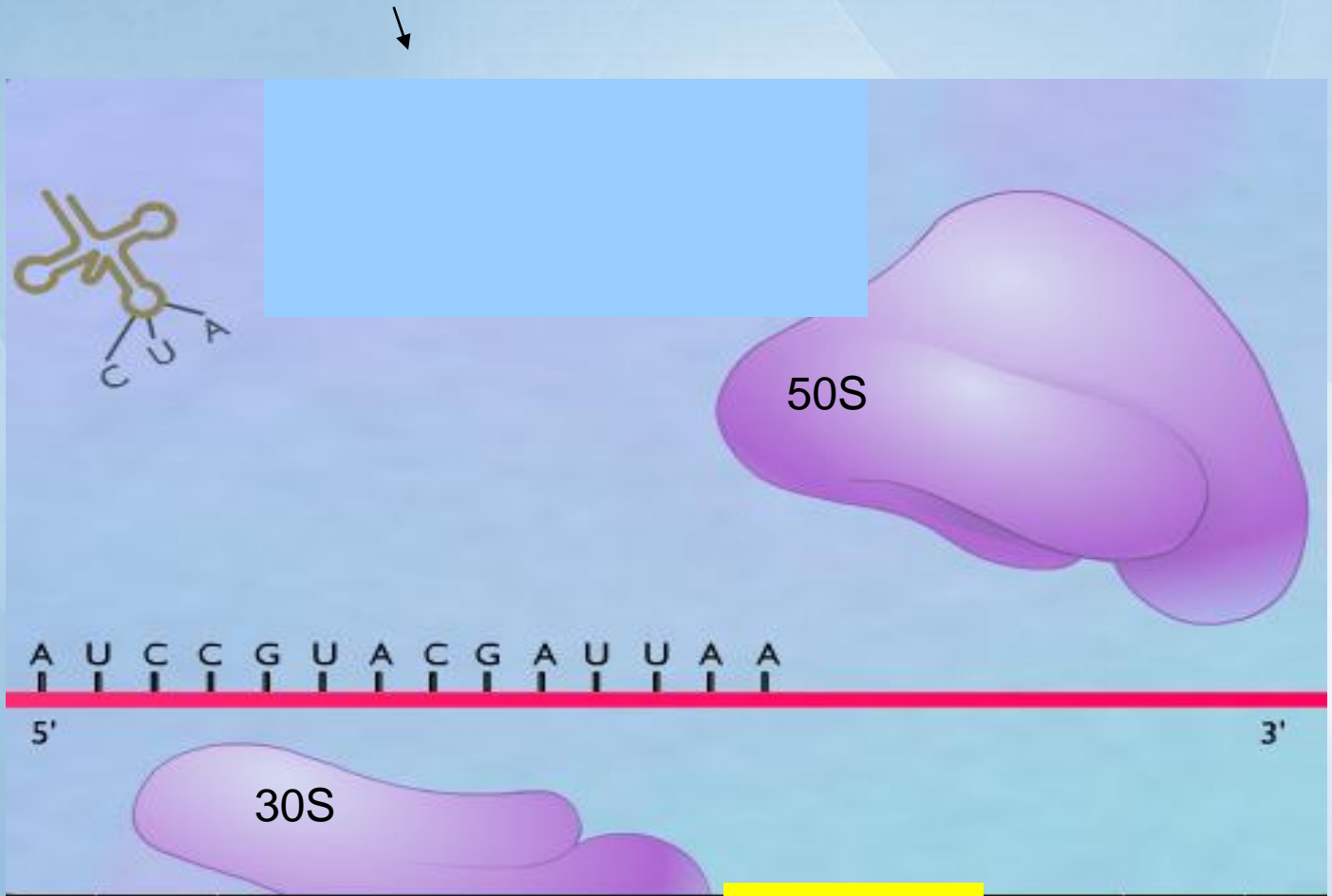
1- Initiation stage

2- Elongation stage

3- Termination stage



1- Initiation stage



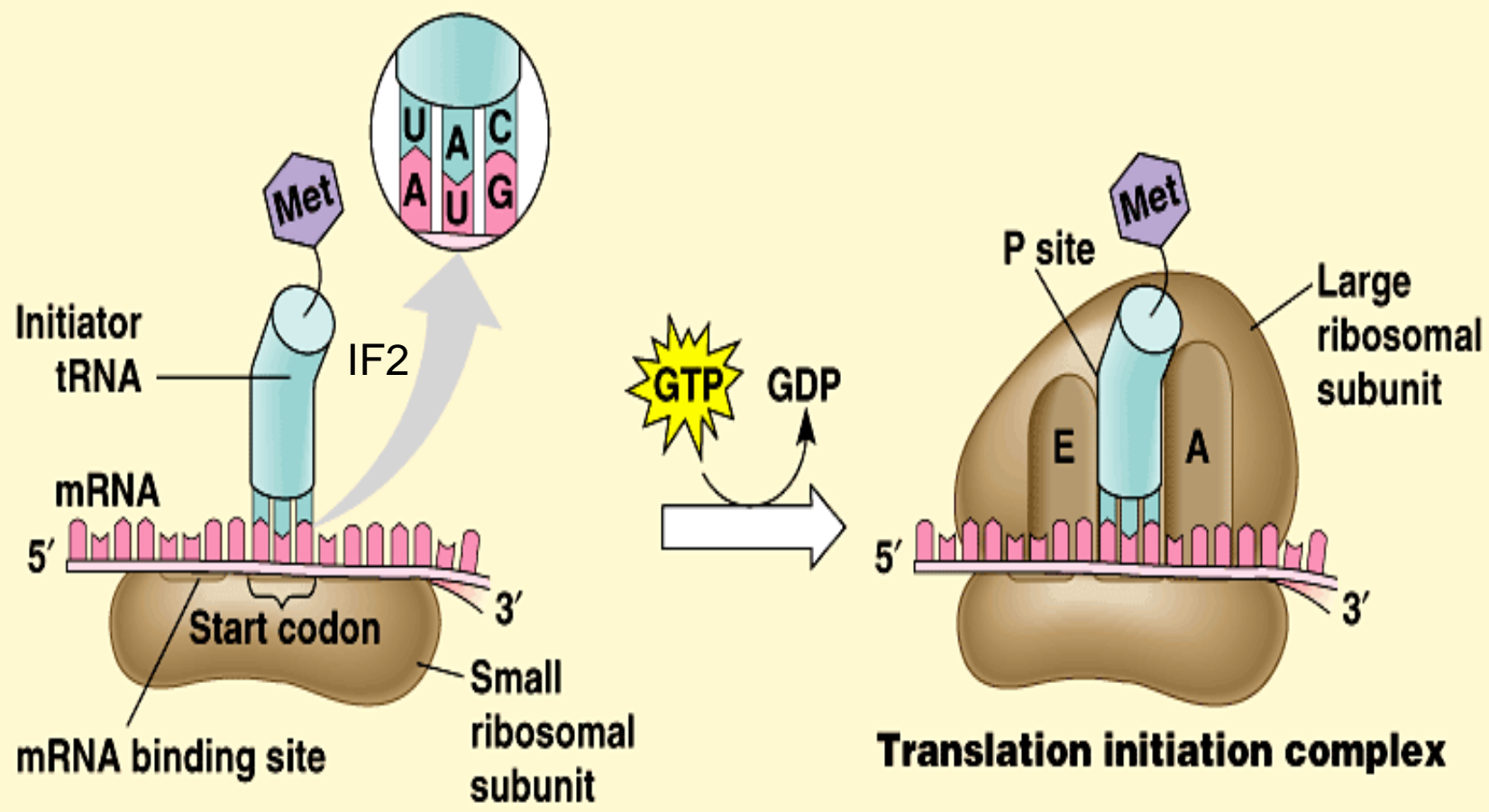
t RNA + mRNA + ribosome

IF1, IF2, IF3

Initiation factors

Initiation complex

1- Initiation stage

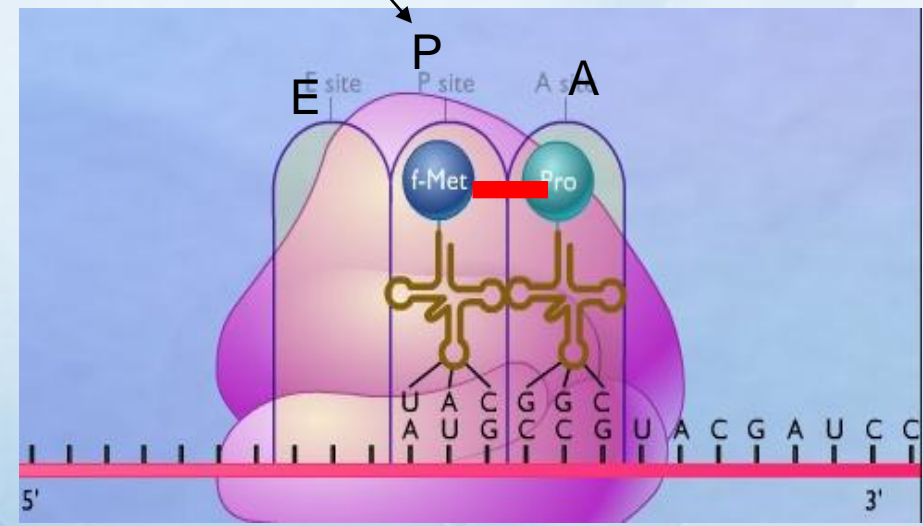
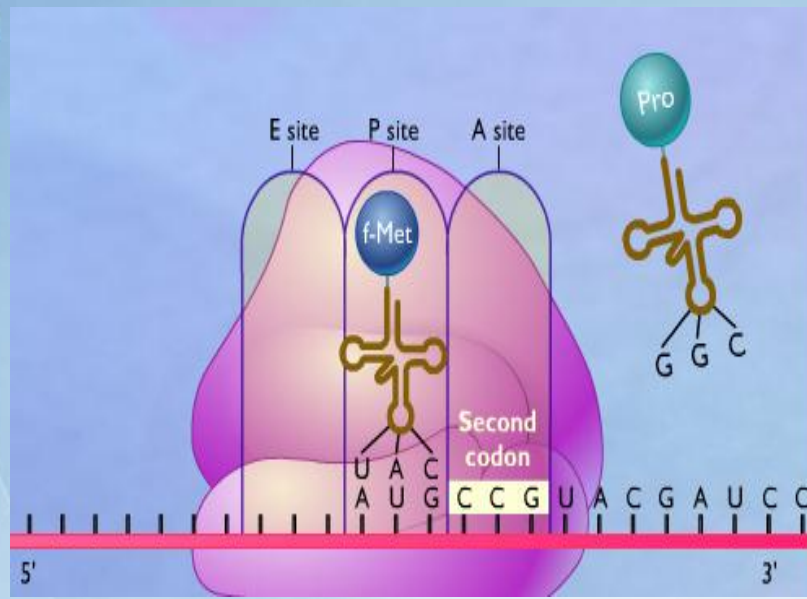


Ribosomal binding site= Shine Dalgarno sequence

- Sequence in mRNA complementary to sequence in r RNA in small ribosomal subunit

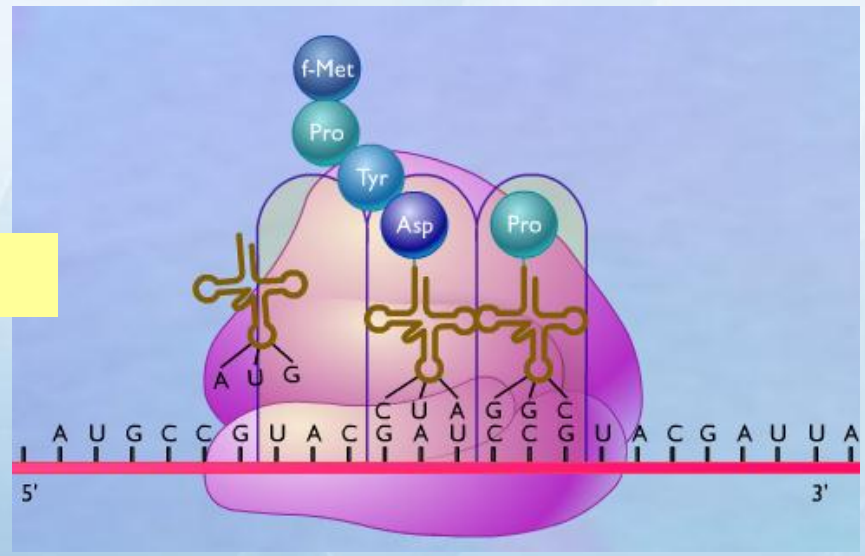
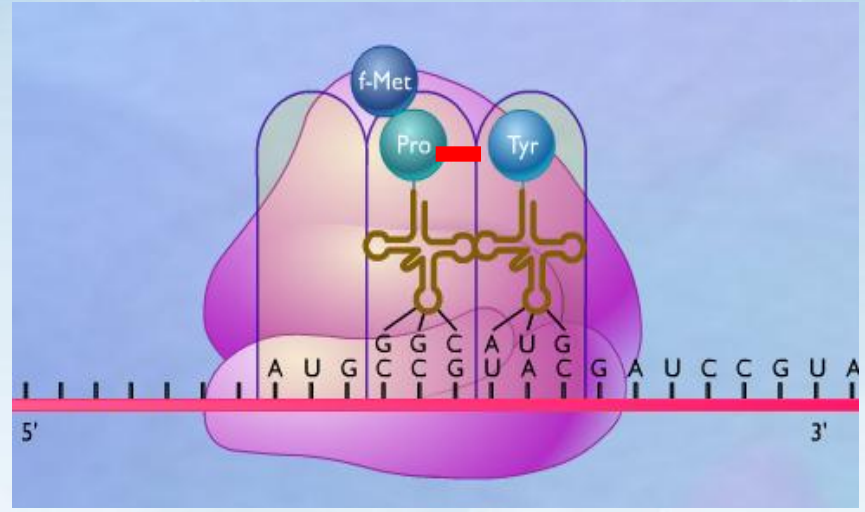
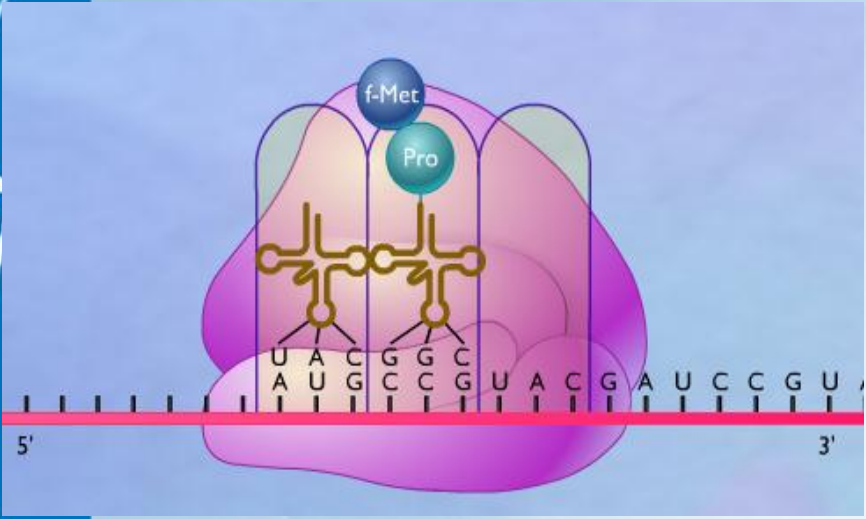
2- Elongation stage

الاستطالة



Peptidyl transferase----peptidyl bound

2- Elongation stage

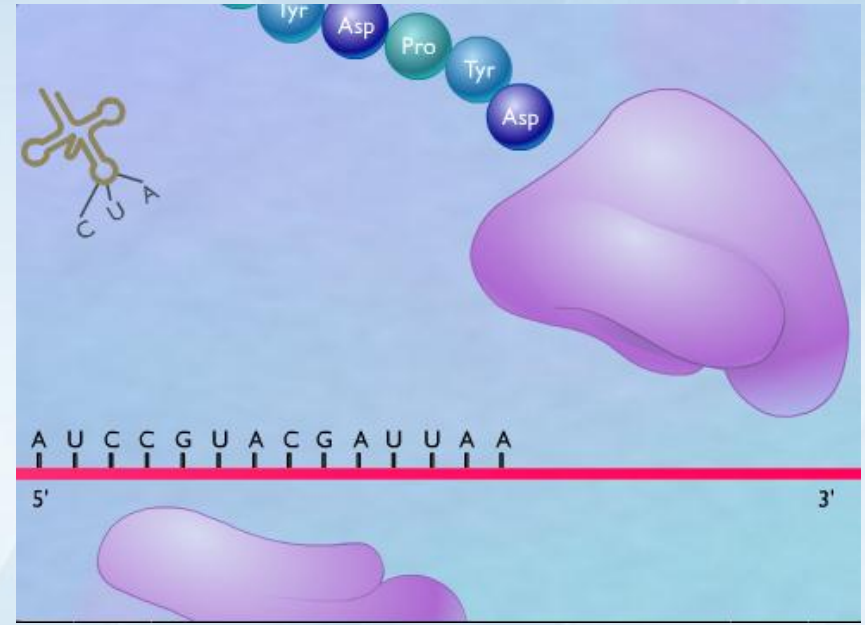
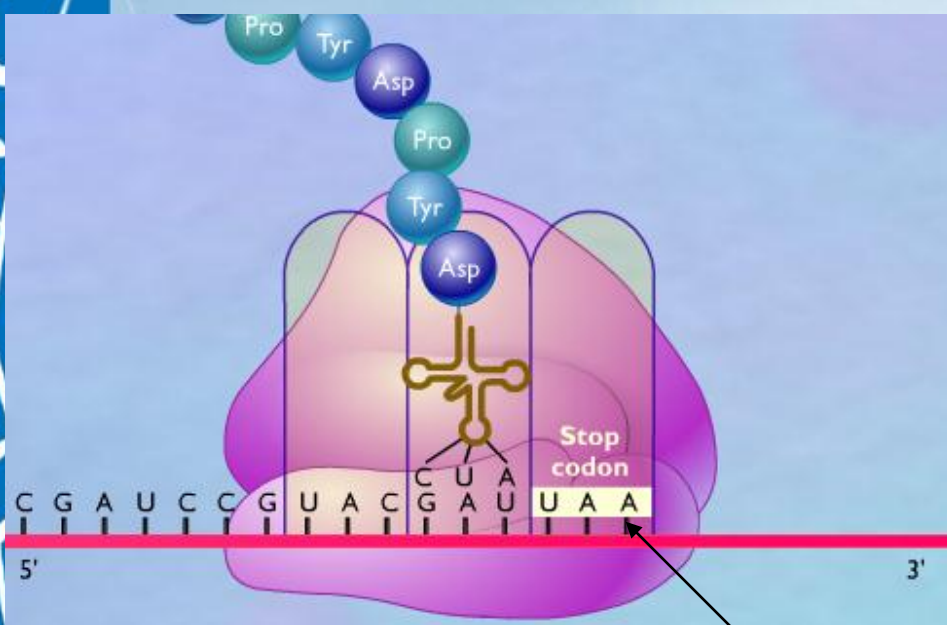


Peptidyl transferase----peptidyl bound

3- Termination stage

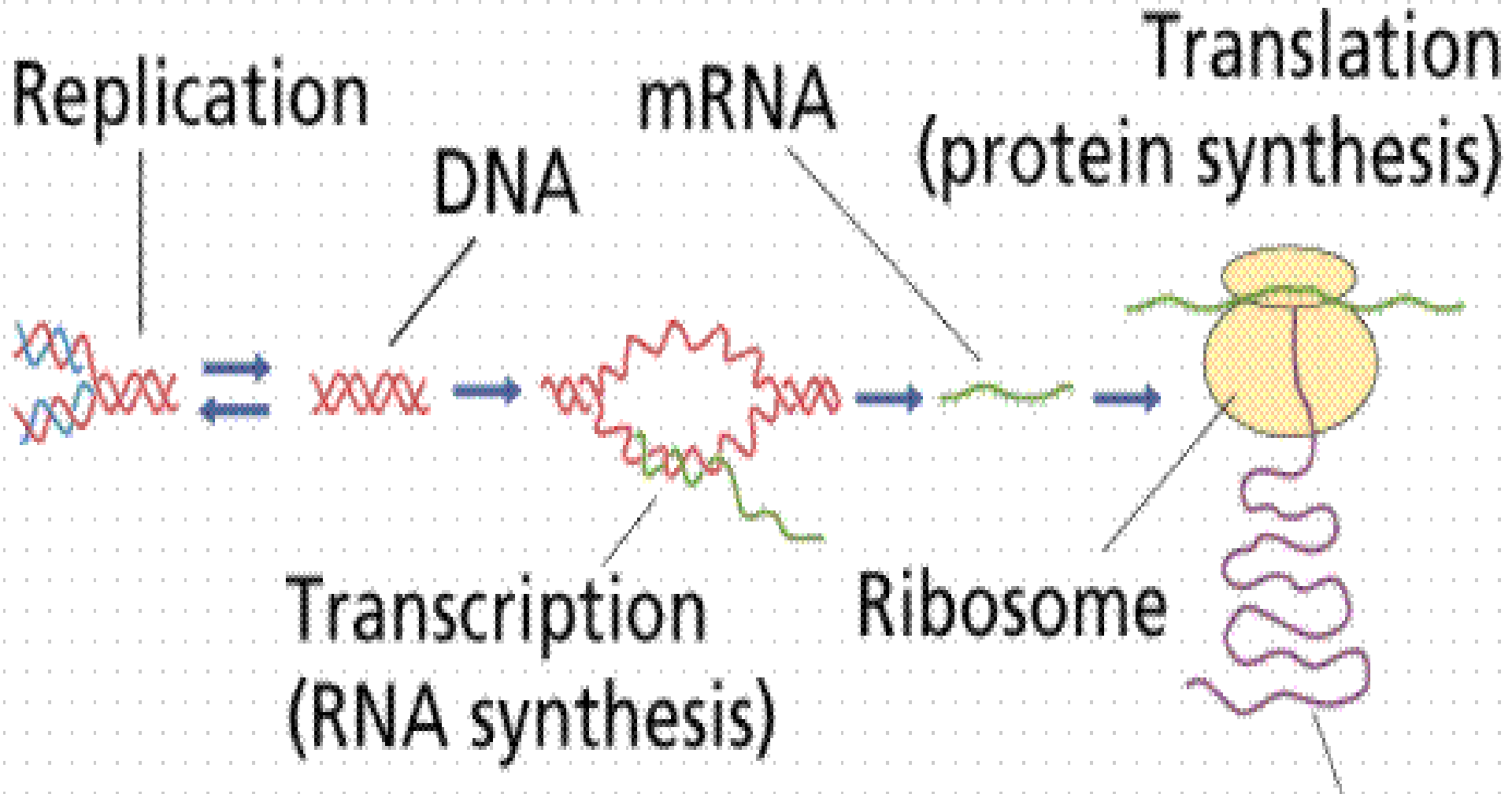
النهاية

Stop codons = nonsense codons: UGA, UAA, UAG

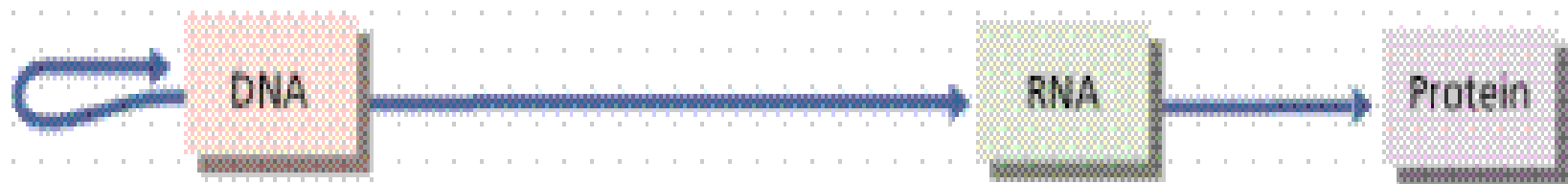


Release factors: prokaryotics -----RF1(UAA), RF2 (UGA,UAG) RF3

Eukaryotics -----eRF (for three stop codons)



العقيدة المركزية **CENTRAL DOGMA** Protein



Practice

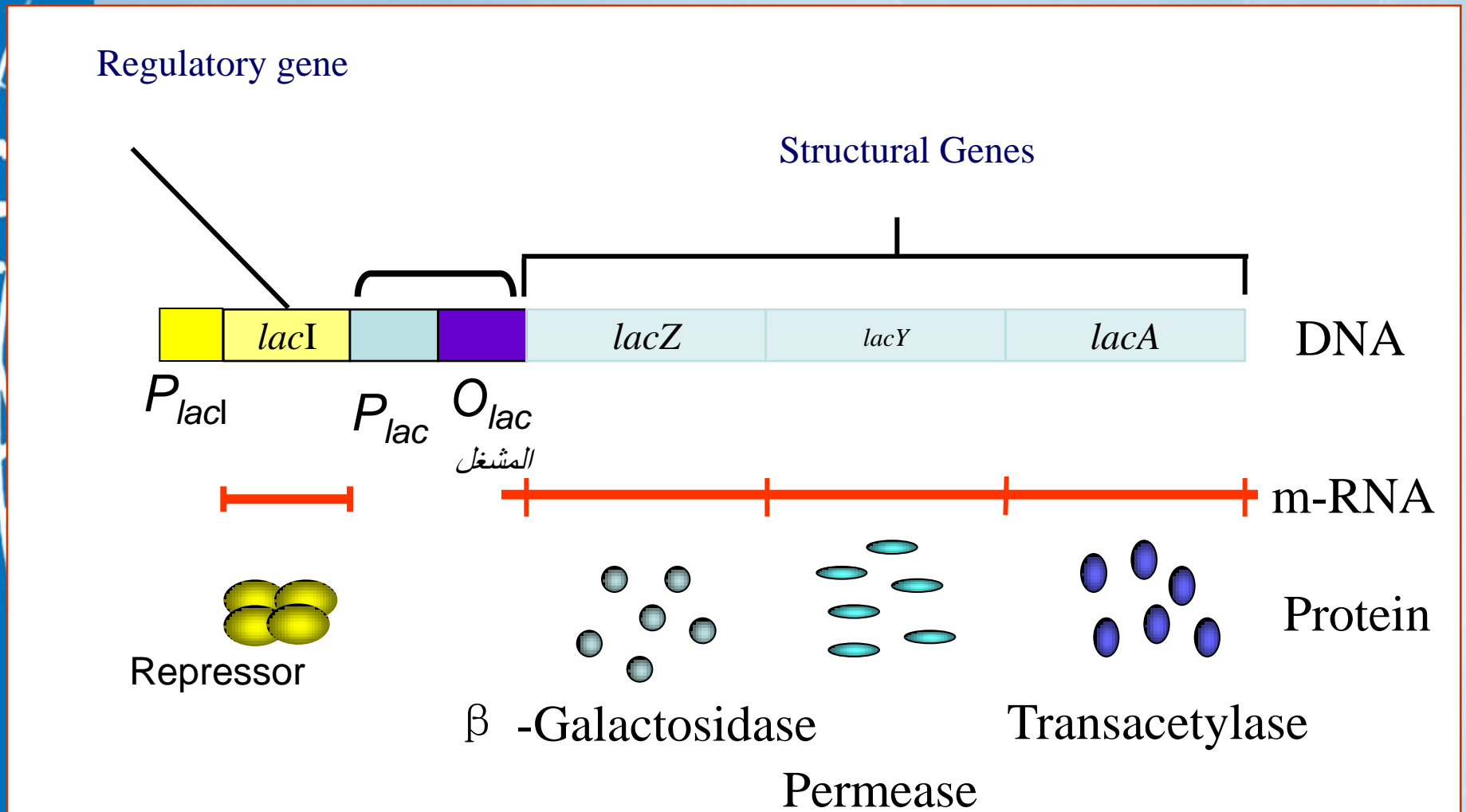
Make the complementary RNA strand for the •
single strand of DNA below: •

ATG GGC TAA CCG TTA
TAC CCG ATT GGC AAT
AUG GGC UAA CCG UUA
TT A G T A G T G C A A

A A T C A T C A C G T T •
U U A G U A G U G C A A •

Gene Regulation in Prokaryotes

Lactose operon: a regulatory gene and 3 structural genes



Operons

An operon is a group of genes that are •
transcribed at the same time.

They are **only found in prokaryotes.** •



• تعريف Operon :

وحدة جينية لتشغيل الجينات اللازم لتكسير اللاكتوز

• العناصر الرئيسية للأوبرون :

• جينات تركيبية Structural genes .

• المشغل Operater : هو الموقع الذي يتحد فيه الـ repressor (ناتج الجين المنظم)

• المحفز Promoter : موقع ارتباط RNA polymerase ويوجد ملاصقاً للـ operator أو متداخلاً معه .

• الجين المنظم (i) Regulator gene : يقوم بالتحكم في إنتاج البروتين المثبط الذي ينتج عن تفاعله مع (o) إحداث تثبيط تناسق و منتظم لجميع الجينات التركيبية معاً و في نفس الوقت بمعنى أن تحدث توقف كمي في تعبير الجينات التركيبية .

Lactose operon (Lac. operon)

β - galactosidase (z)

It transforms lactose into allolactose and also catalyzes the conversion of lactose to glucose and galactose.

β - galactoside permease (y)

β - galactoside transacetylase (a)

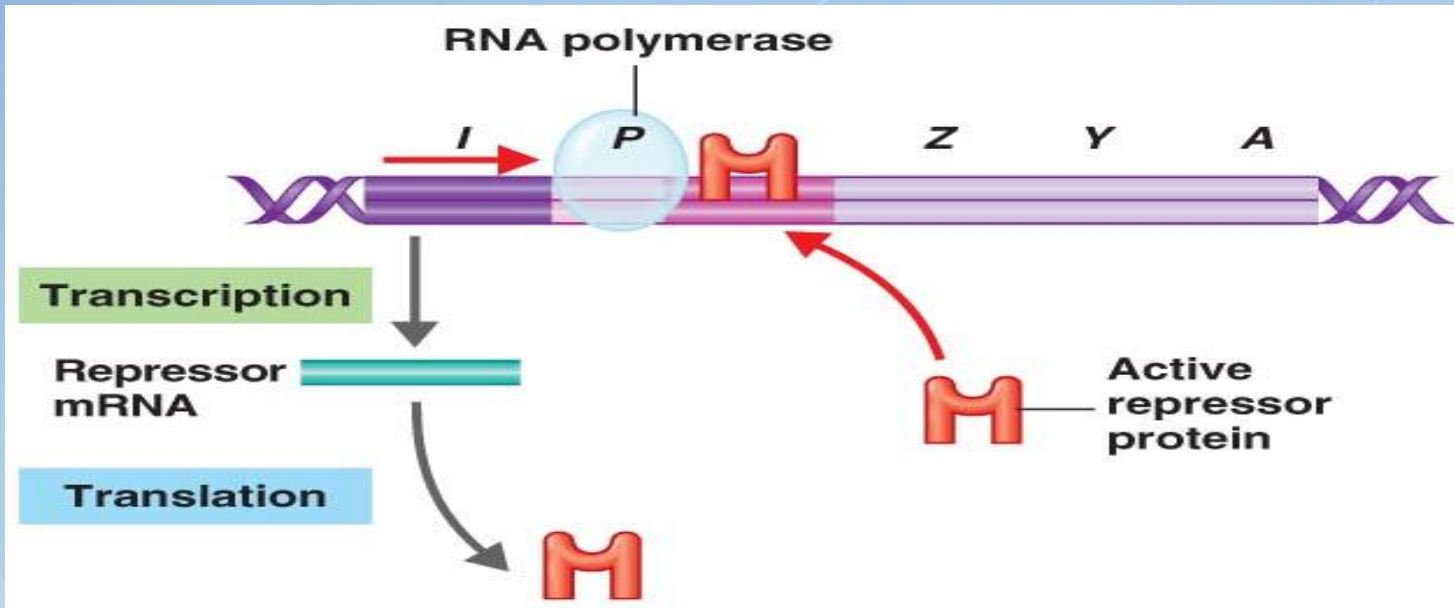
Lactose operon (Lac. operon)

β - galactoside permease (*y*)

Membrane channel protein required to uptake lactose from the environment

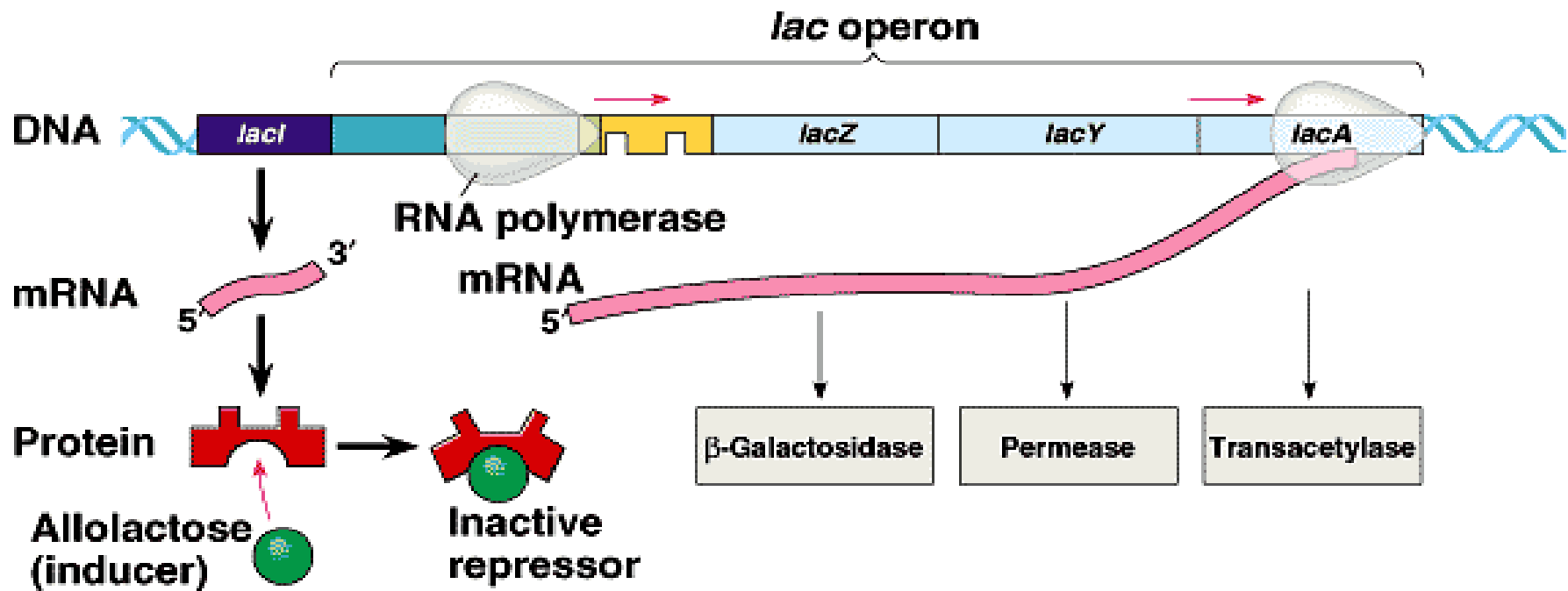
β - galactoside transacetylase (*a*)

It rids the cell of toxic thiogalactosides that also get transported by *lac Y*.



■ When lactose is absent

- The lac **repressor** senses the presence of lactose (more precisely allolactose-an isomer of lactose) in the medium. In the absence of allolactose (A) the repressor protein (R) binds to the operator region (O) and blocks the RNA polymerase from transcribing the structural genes.



(b) Lactose present, repressor inactive, operon on

When lactose is present :

When lactose is present in a medium, some of it will be converted to **allolactose**. This **allolactose binds to the repressor protein**. Binding of allolactose with repressor protein **changes the shape of repressor protein** so it can no longer **binds to the operator region**. This allows the **RNA polymerase to bind** to the promoter site, starting the initiation of **transcription of the structural genes *lacZ*, *lacY*, and *lacA* to produce mRNA**.



Genetic Engineering and Biotechnology

Aim: How do scientists utilize recombinant DNA technology?



Why does Spiderman have these special powers?

What is Genetic Engineering?



Genetic Engineering is a *new* process that scientists use to **alter** the **genetic instructions** in organisms.

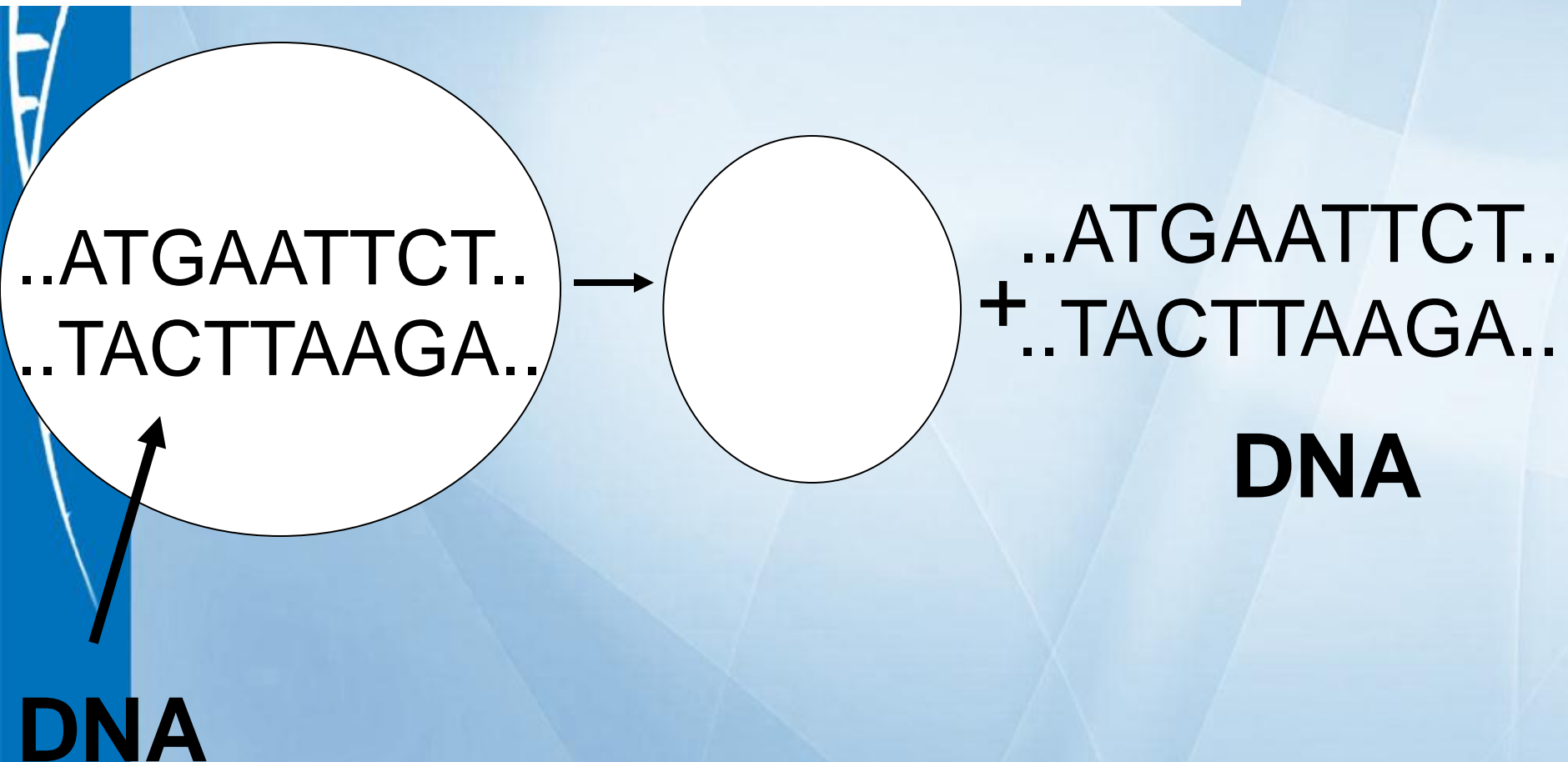
Why would scientists want to alter the genetic instructions of organisms?



Scientists can generate organisms with desired characteristics.

How is DNA Modified?

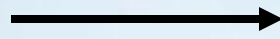
Step 1: DNA is first extracted
(removed) from cells.



How is DNA Modified?

Step 2: DNA is then cut into smaller pieces with **Restriction Enzymes**.

ATGAATTCT
TACTTAA GA



ATG AATTCT
TACTTAA GA



Restriction enzymes are “scissor-like” enzymes that recognize and cut specific sequences in the DNA.

What base sequence was this restriction enzyme specific for? **GA**

