

DNA REPLICATION

(TRANSCRIPTION & TRANSLATION)

DONE BY BIOCHEMISTRY TEAM

ننصح بمشاهدة الفيديوهات من اليوتيوب لتثبيت المعلومات

وذلك بعد مذاكرة المحاضرة كاملة

MODEL FOR DNA REPLICATION

لا يوجد اوبجكتفز لهذه المحاضرة لذا وضعنها من العناوين الرئيسية لكل سلايد

- *Prokaryotic DNA Polymerases
- *Features of DNA Replication
- *Mechanism of DNA Replication
- *Transcription
- *Post-Transcriptional Modifications
- *Translation
- *The Genetic Code

MOLECULAR BIOLOGY

REPLICATION OF DNA

DONE BY
ABDULLAH ALATAWI

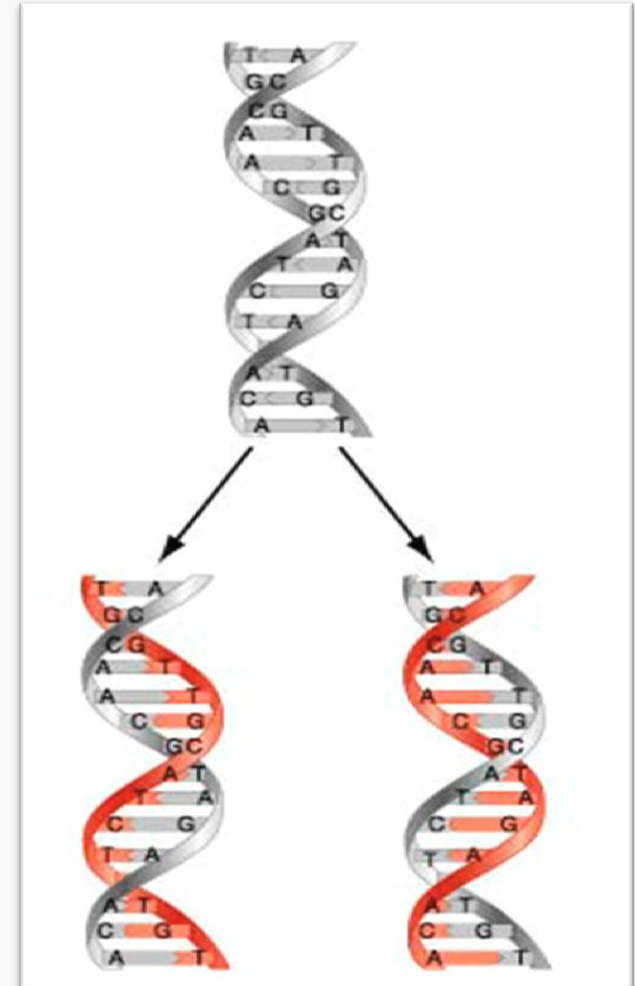
MODEL FOR DNA REPLICATION

SEMICONSERVATIVE MODEL:

• DAUGHTER DNA MOLECULES CONTAIN:

- one parental strand and.
- one newly-replicated strand.

نوع الاستنساخ هنا يمكن تسميته بالنوع {شبه المحافظ} حيث ينتج لدينا شريط مزدوج نصفه من الخلية الأم والنصف الآخر تم انشاؤه حديثاً

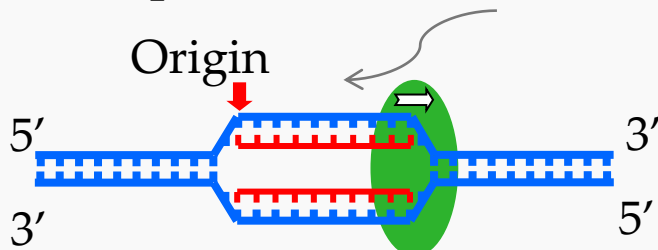


❖ Prokaryotic DNA Polymerases :

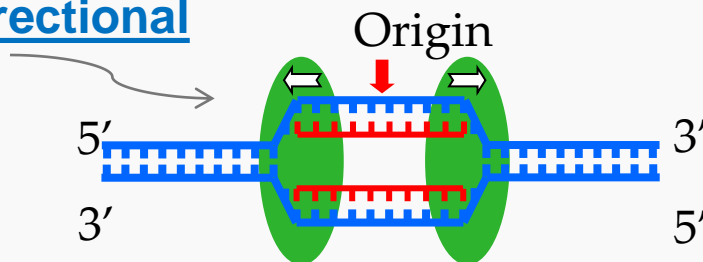
5 types of DNA polymerases are found in **E. coli**

	The type	The function
Replication activity is only at I & III	DNA polymerase I	functions in repair and replication
	DNA polymerase II	functions in DNA repair
	DNA polymerase III	main DNA replication enzyme
	DNA polymerase IV	functions in DNA repair
	DNA polymerase V	functions in DNA repair

Replication can be **Unidirectional**



or **Bidirectional**



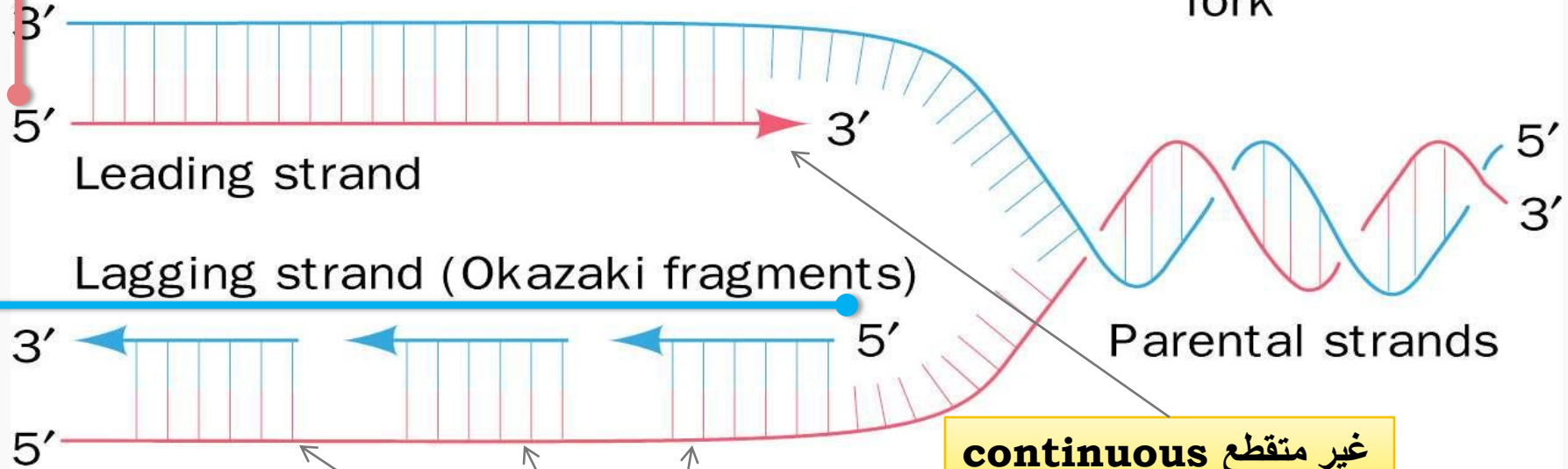
Features of DNA Replication :

- Semiconservative محافظ جزئياً
- Bidirectional ثنائي الإتجاه
- Semidiscontinuous شبه متقطع

DNA IS SYNTHESIZED OR REPLICATED IN ((5' TO 3')) DIRECTIONS

مهم

Motion of replication fork



Leading strand

Lagging strand (Okazaki fragments)

Parental strands

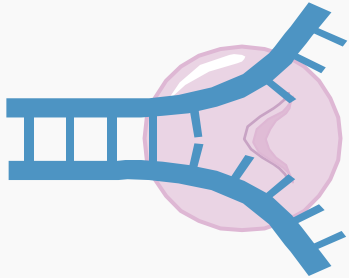
continuous غير متقطع

discontinuous متقطع

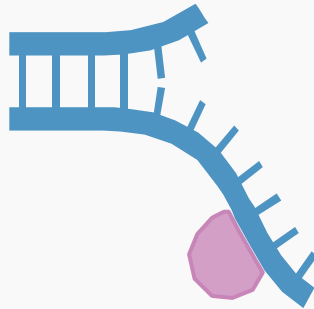
Semi-discontinuous شبه متقطع
((لأنه يجمع بين المتقطع والغير متقطع))

BOTH DAUGHTER STRANDS (LEADING STRAND RED, LAGGING STRAND BLUE) ARE SYNTHESIZED OR REPLICATED IN THEIR 5' TO 3' DIRECTIONS

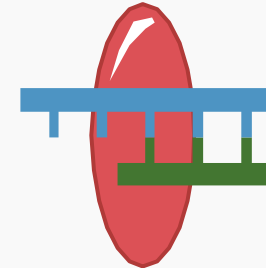
ENZYMES OF DNA REPLICATION



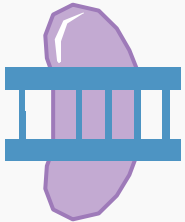
Helicase unwinds parental double helix



Single-strand Binding protein stabilizes separate strands



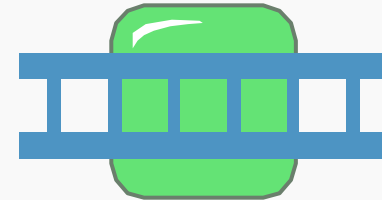
Primase adds a short primer to template strand



DNA polymerase forms new strands



DNA polymerase I (exonuclease) removes RNA primer and inserts the correct bases



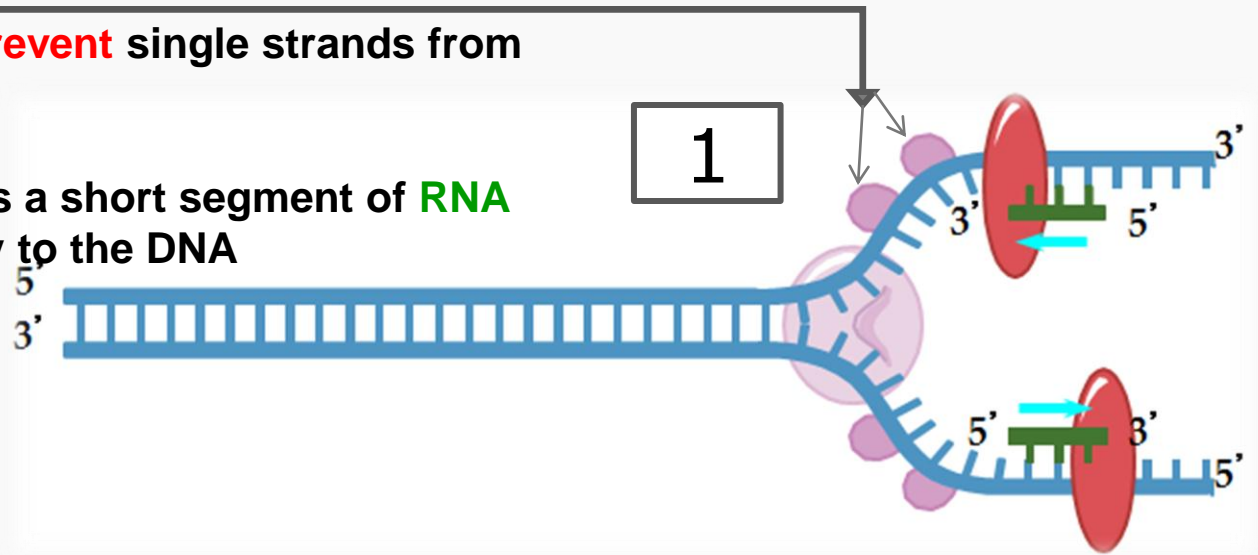
Ligase joins Okazaki fragments and seals gaps in sugar-phosphate backbone

- ✓ **Helicase** protein binds to DNA sequences called **origins** and unwinds **يفك** DNA strands

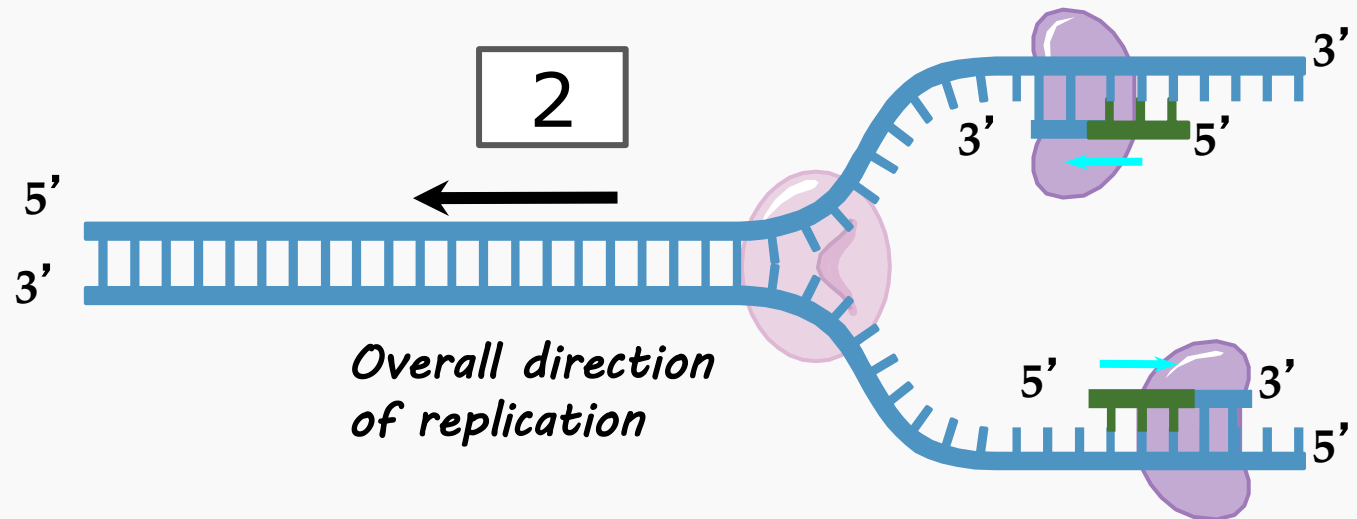
- ✓ **SS binding proteins** **prevent** single strands from rewinding **اعادة الالتصاق**.

- ✓ **Primase** protein makes a short segment of **RNA**

- ✓ **primer** complementary to the DNA



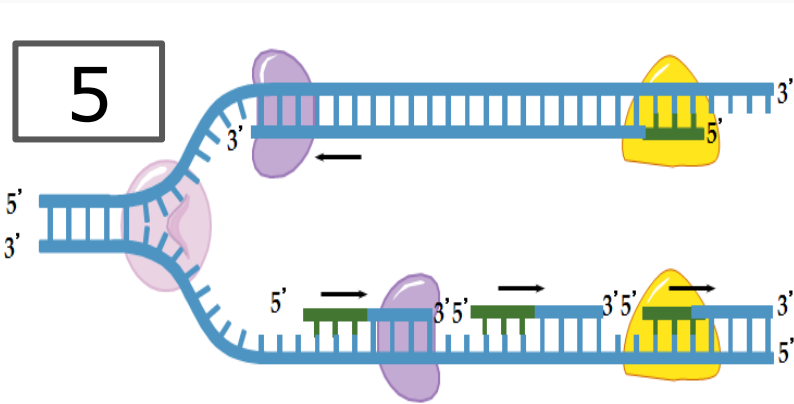
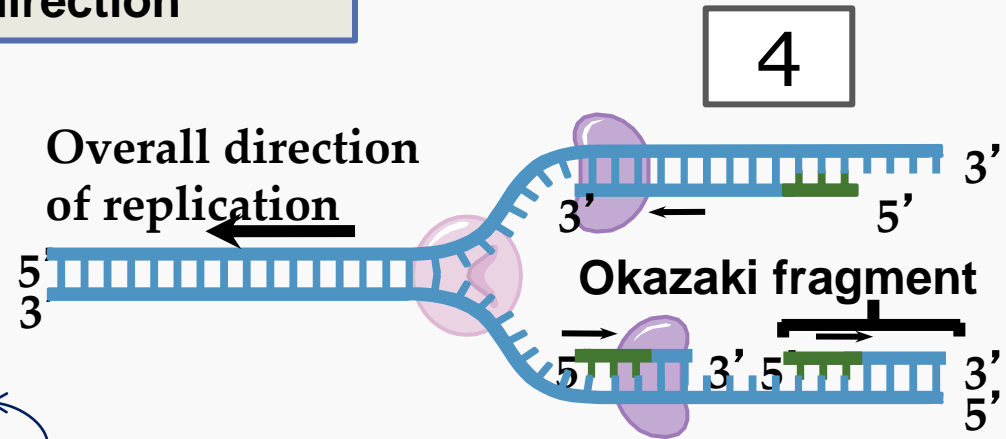
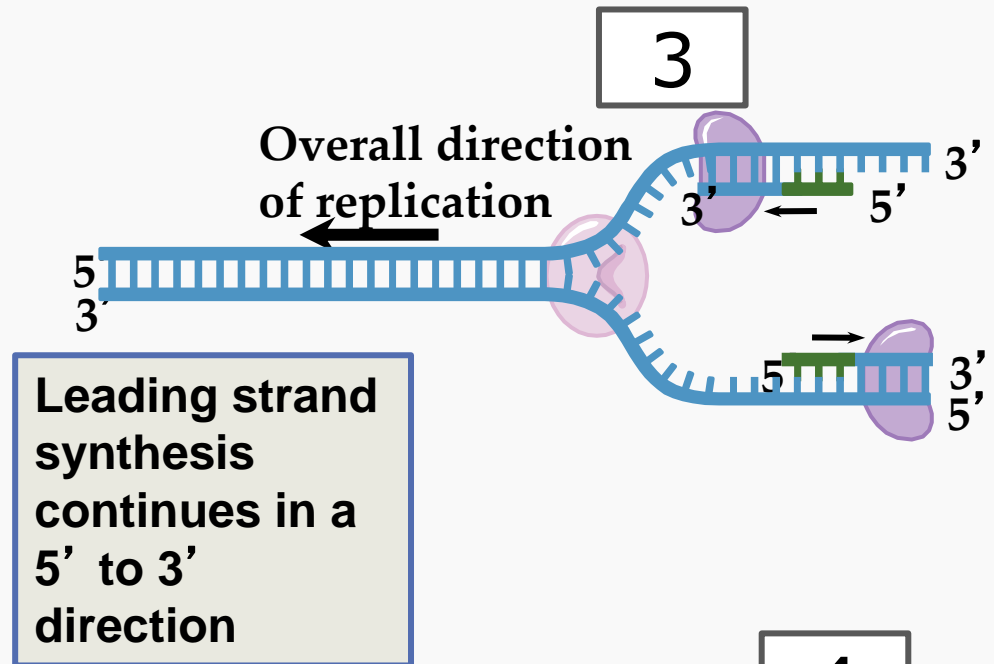
DNA polymerase enzyme adds DNA nucleotides to the RNA primer



✓ DNA polymerase adds DNA nucleotides to the RNA primer

✓ DNA polymerase proofreads bases added and replaces incorrect nucleotides

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



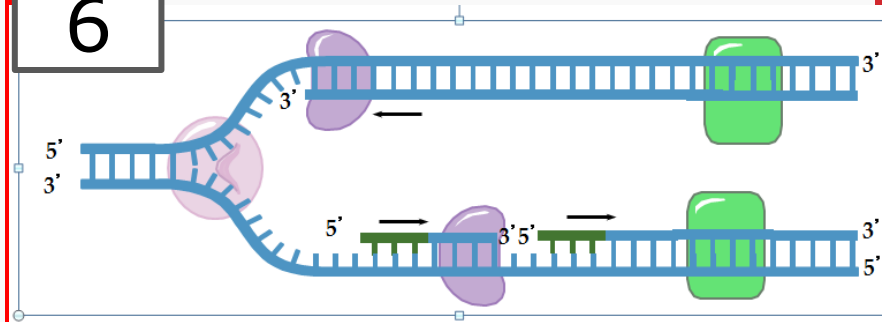
Exonuclease activity of DNA polymerase I removes RNA primers

finally :

Polymerase activity of DNA polymerase I fills the gaps

Ligase forms bonds between sugar-phosphate backbone

6



❖ Eukaryotic DNA Replication Enzymes :5 types of DNA polymerases in Eukaryotes

1. DNA polymerase α
2. DNA polymerase β
3. DNA polymerase γ (*Gama*) → (Mitochondrial DNA replication enzyme)
4. DNA polymerase δ
5. DNA polymerase ϵ

النسخ Transcription

A process of mRNA (messenger RNA) synthesis يصنع from DNA (gene)

The enzyme responsible for this process is RNA polymerase

Only one of the DNA strands is transcribed

A complementary strand of messenger RNA (mRNA), is produced from the DNA template

يتم نسخ جهة واحدة من الشريط المزدوج ويتكون mRNA

The direction of transcription is 5' → 3'

THE GOLDEN RULE : 😊 DNA MAKES RNA MAKES PROTEIN

5' -AATCGCCATACGCACGCA-3'
3' -TTAGCGGTATGCGTGCGT-5'
DNA

↓ Transcription

5' -AAUCGCCAUACGCACGCA-3'
RNA

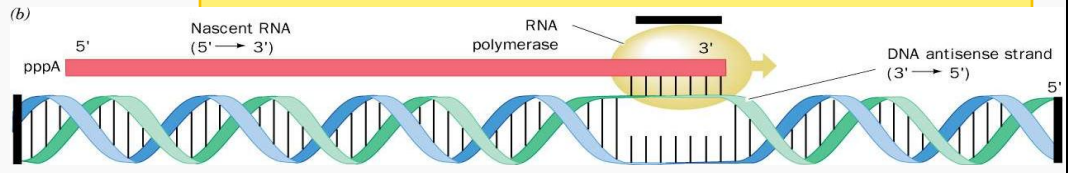
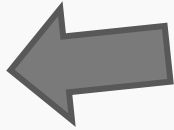
↓ Translation

N-Asn-Arg-His-Thr-His-Ala-C
PROTEIN

CHAIN INITIATION مبدأ الشريط
RNA polymerase
binds to promoter region of DNA to
start transcription

CHAIN ELONGATION تطاول الشريط
portion of DNA template unwinds (opens) at the point of RNA synthesis by **DNA gyrase**
This forms a short length of RNA-DNA hybrid
The unpaired “bubble” of DNA in the open initiation complex travels along the direction of RNA polymerase

CHAIN TERMINATION انهاء الشريط
DNA contains specific sites which stop transcription
Transcription is terminated at a sequence of 4-10 AT base pairs



POST-TRANSCRIPTIONAL MODIFICATIONS (RNA PROCESSING) تعديلات تطراً على الآر إن أي

Capping :

Addition of a methylated guanine nucleotide at 5' end of mRNA
Function: To prevent mRNA degradation by *exonuclease enzymes*

Polyadenylation :

Addition of a poly A tail (poly Adenylate...AAAAAA...) at 3' end of mRNA
Function:
To protect the mRNA from degradation
For ribosomal RNA recognition

الترجمة (Protein Synthesis) Translation

A process of protein synthesis from mRNA

mRNA has codes for amino acids present in proteins

components of protein synthesis

- the genetic code
- mRNA
- ribosomes
- tRNAs
- amino acids
- enzymes / protein factors

the process

- chain initiation
- chain elongation
- chain termination
- post-translational modifications

**THE
GOLDEN
RULE : 😊
DNA MAKES
RNA MAKES
PROTEIN**

THE GENETIC CODE

A genetic code contains 3 nucleotides

Genetic code is triplet (ثلاثي), like => non-overlapping, (غير متشابك) comma-free

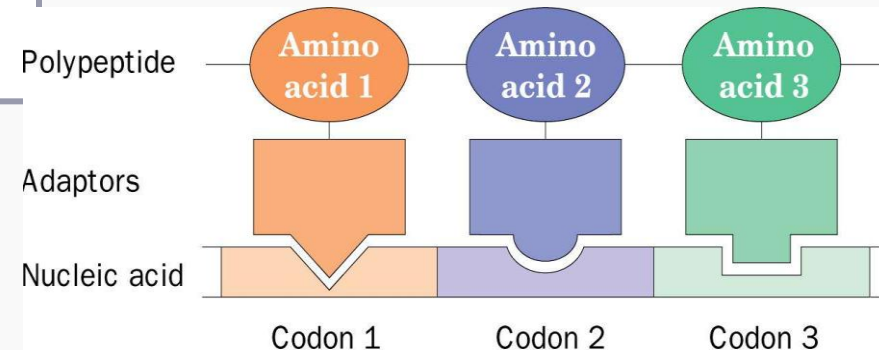
64 possible codons

- 61 codons specify 20 amino acids
- 1 Start codon (also specifies an aa)
- 3 stop codons
- ❖ The genetic code is degenerate
- ❖ One codon can specify only one amino acid
- ❖ One amino acid can be coded for by more than one codon
- ❖ Mitochondrial DNA has different codons

The "Standard" Genetic Code

First position (5' end)	Second position				Third position (3' end)
	U	C	A	G	
U	UUU Phe	UCU Ser	UAU Tyr	UGU Cys	U
	UUC	UCC	UAC	UGC	C
	UUA Leu	UCA	UAA Stop	UGA Stop	A
	UUG	UCG	UAG Stop	UGG Trp	G
C	CUU	CCU Pro	CAU His	CGU Arg	U
	CUC Leu	CCC	CAC	CGC	C
	CUA	CCA	CAA Gln	CGA	A
	CUG	CCG	CAG	CGG	G
A	AUU	ACU Thr	AAU Asn	AGU Ser	U
	AUC Ile	ACC	AAC	AGC	C
	AUA	ACA	AAA Lys	AGA Arg	A
	AUG Met ^b	ACG	AAG	AGG	G
G	GUU	GCU Ala	GAU Asp	GGU Gly	U
	GUC Val	GCC	GAC	GGC	C
	GUA	GCA	GAA Glu	GGA	A
	GUG	GCG	GAG	GGG	G

The genetic code is read by molecules that recognize a particular codon and carry the corresponding amino acid



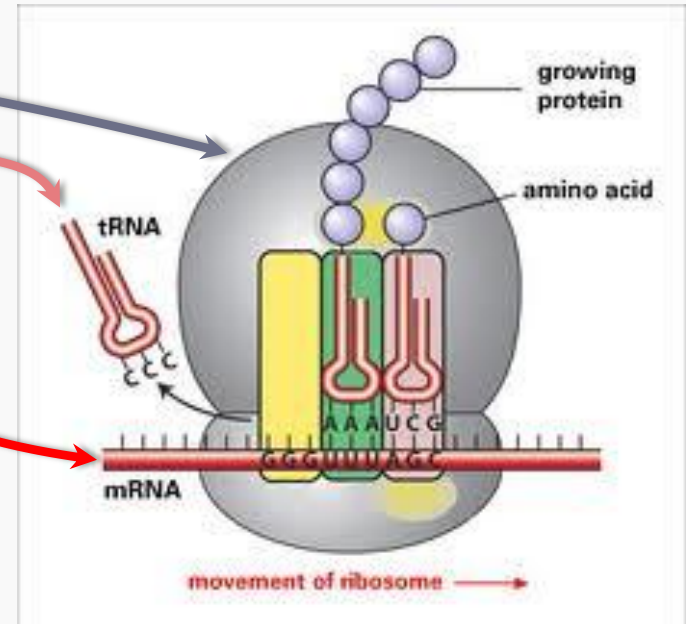
Chain Initiation

Translation is initiated by Initiation Factors:
IF-1, IF-2, IF-3

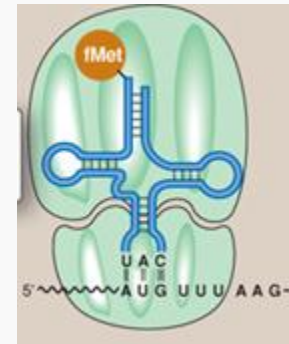
They combine ribosome, mRNA & tRNA
together

The first tRNA binds to AUG (start codon) of mRNA in the P-site (in middle) of ribosome.

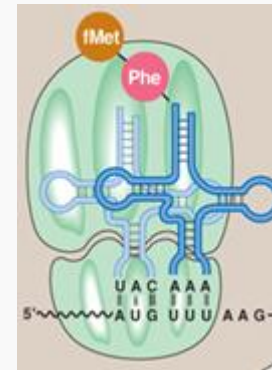
يوجد في اليوتيوب فيديوهات خاصة لهذه
الجزئية بالذات ننصح بمشاهدتها



1) Chain Initiation : The complex forms of combination of ribosome, mRNA and tRNA together .The first tRNA binds to AUG (start codon) of mRNA in the P-site of ribosome



2) chain Elongation: The second tRNA bind to A-site of ribosome Peptide bond formation takes place between two amino acids (transpeptidation)

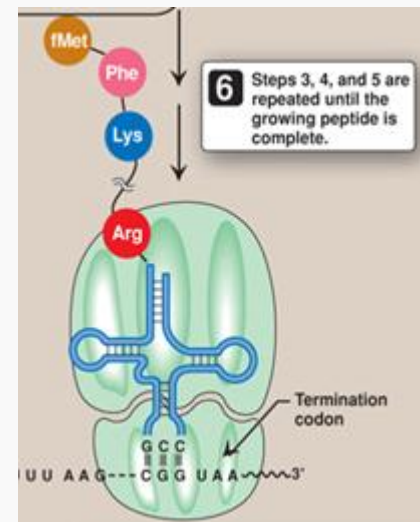


A-site tRNA carries the growing protein chain and moves to P-site (translocation)

3) chain Termination : mRNA contains stop codons (UAA, UAG, UGA)



When ribosomes reads any stops codon, translation is terminated This releases the new protein chain



BIOCHEMISTRY TEAM

وقفنا الله وإياكم