VIBE PROJECT

MODULE 3: FROM CELL GENOME TO PROTEOME

3.1. Nucleic acids – Structure, Function and Organization in the Cell

3.2. DNA Replication

3.3. Transcription

3.4. Translation

3.5. Post-Translational Modifications of Proteins

3.6. Regulation of Gene Expression

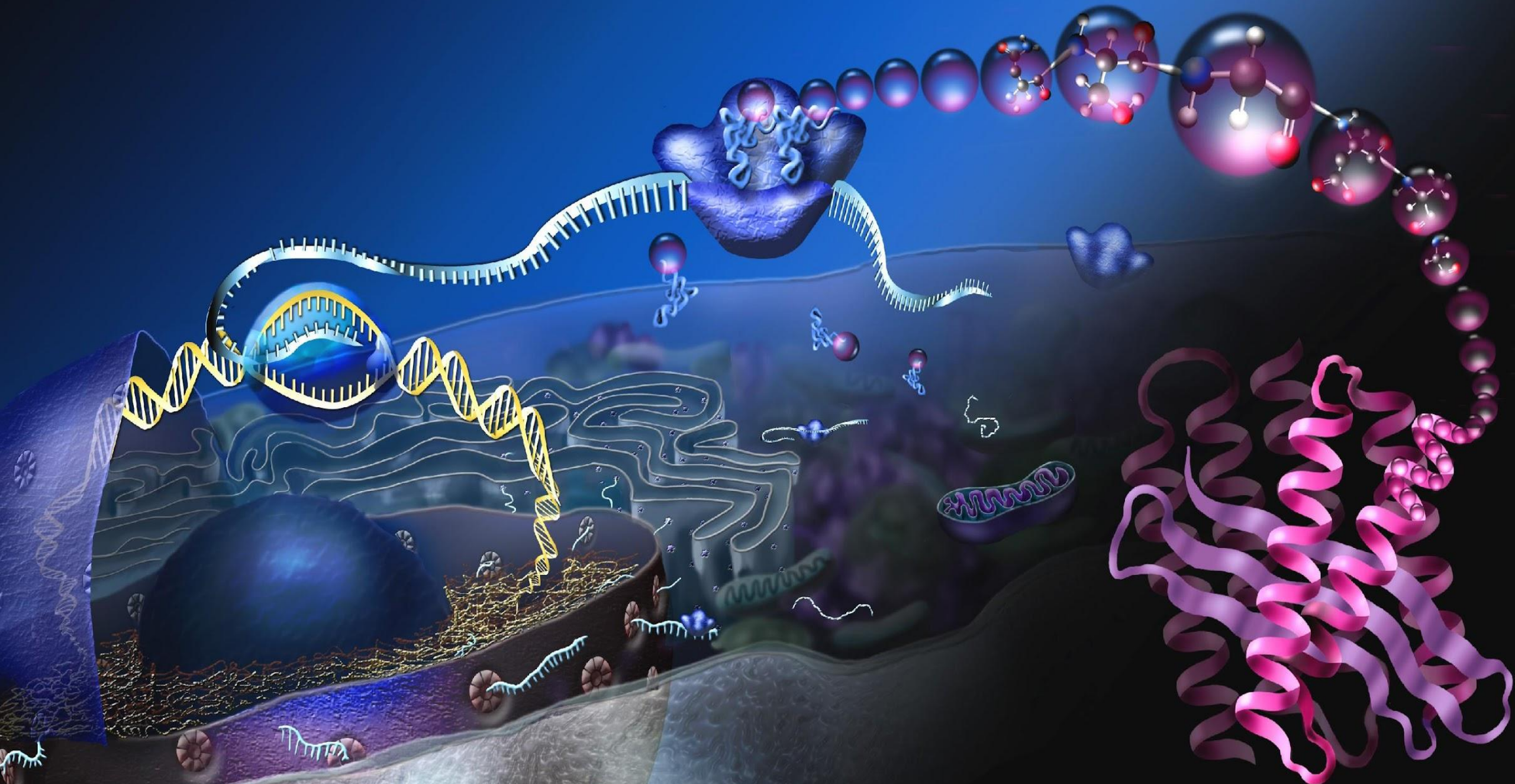
VIBE PROJECT

FROM CELL GENOME TO PROTEOME

3.1. Nucleic acids – Structure, Function and Organization in the Cell

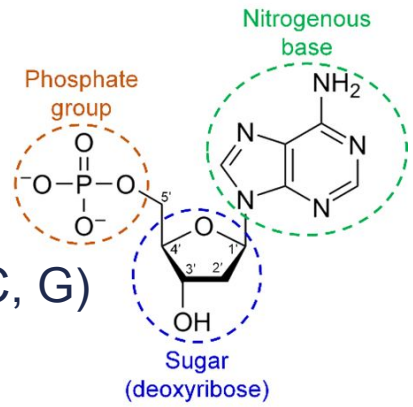
EXPLORING THE MYSTERIES OF LIFE: AN INTRODUCTION TO CELL BIOLOGY

What are nucleic acids?

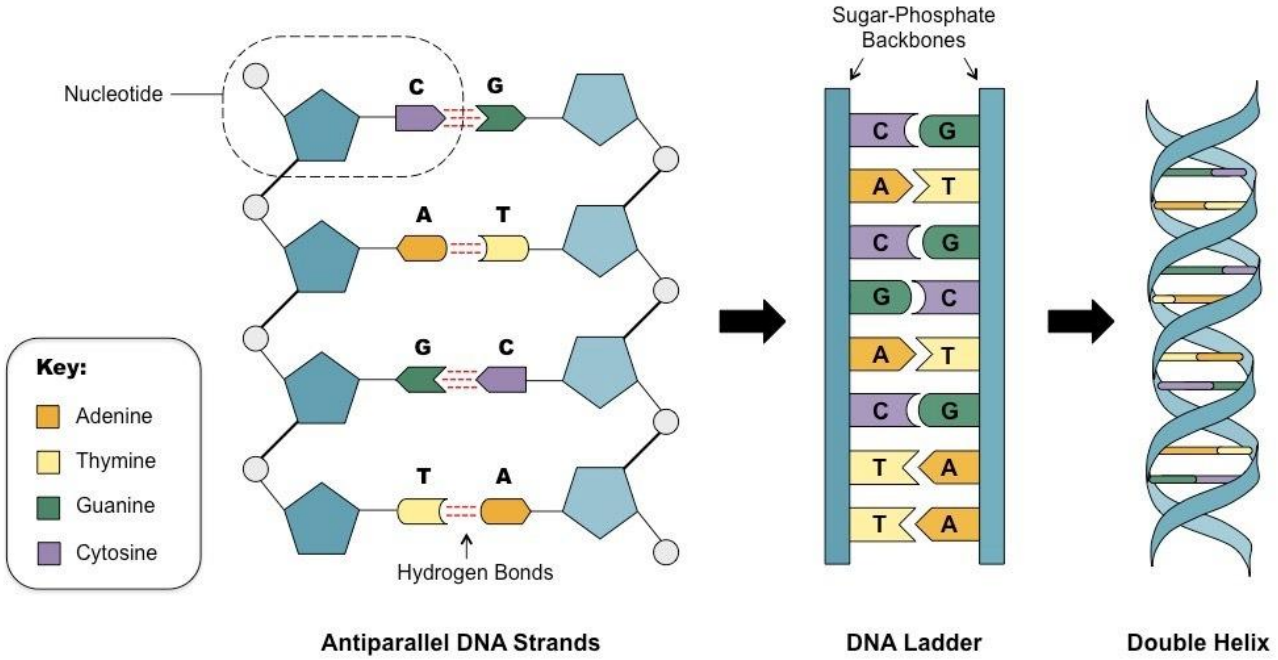


Structure of DNA

- **Double helix**: Two strands twisted together
- **Complementary base pairing**:
  - Adenine (A) pairs with Thymine (T)
  - Cytosine (C) pairs with Guanine (G)
- **Nucleotide components**:
  - Sugar (deoxyribose)
  - Phosphate group
  - Nitrogenous base (A, T, C, G)

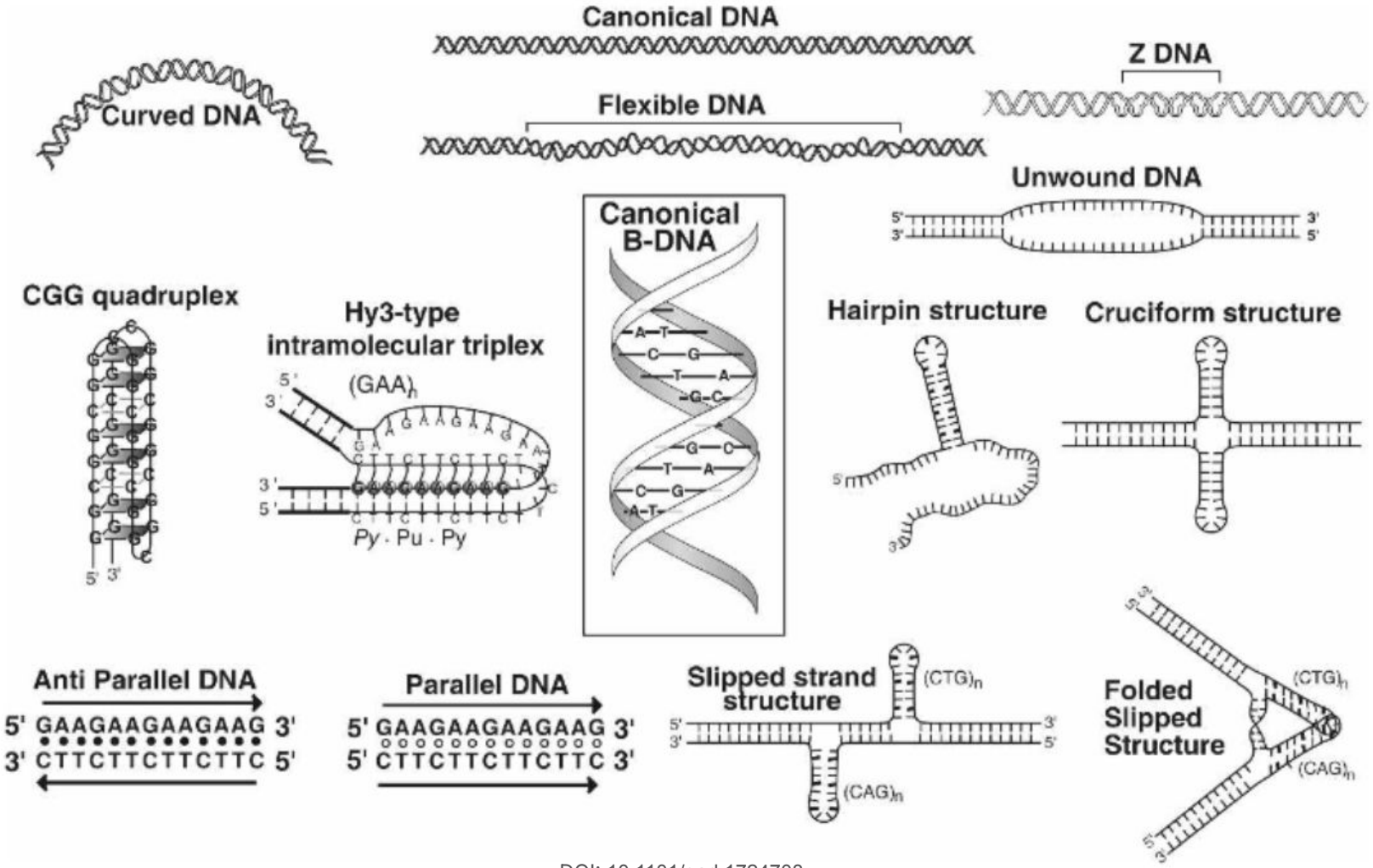


https://microbenotes.com/watson-and-crick-dna-model/



https://quizlet.com/519511920/dna-structure-diagram/?x=1jqt

Structure of DNA



DOI: 10.1101/gad.1724708

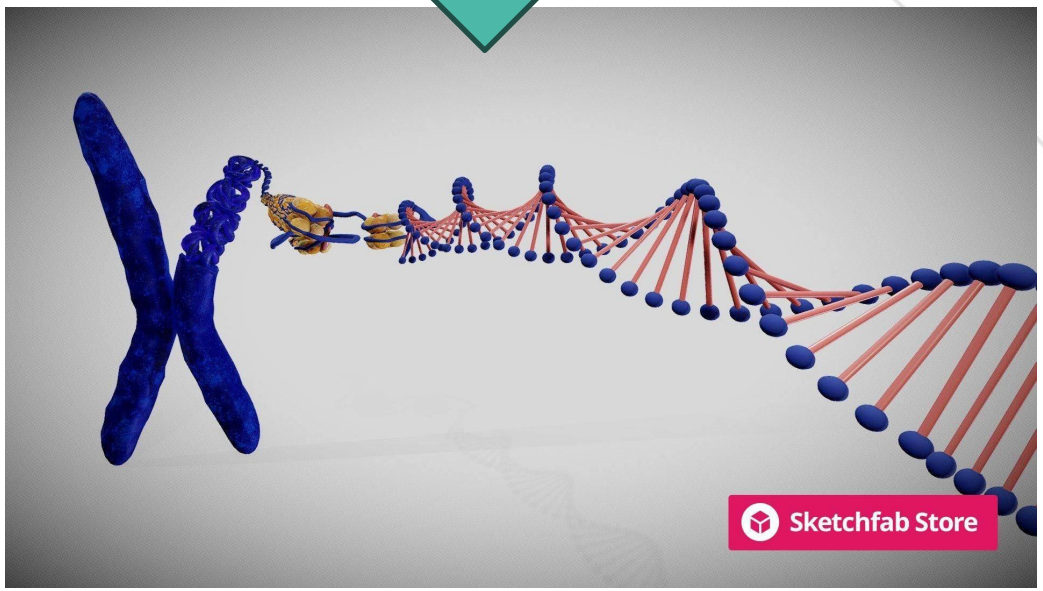
Cell Genome

GENOME:
Complete set of an organism's genetic material, encoded in DNA (or RNA in some viruses). It contains all the information required for the growth, development, and functioning of that organism.

GENES:
Protein-coding and functional RNA sequences within chromosomes

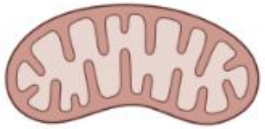
NON-CODING DNA:
- Regulatory elements (e.g., promoters, enhancers)
- Structural elements (e.g., telomeres, centromeres)
- Introns and repetitive sequences

CLICK ON THE IMAGE AND IMMERSE YOURSELF IN THE STRUCTURE OF THE CHROMOSOME



https://bit.ly/37xHBTT

Human Genome features

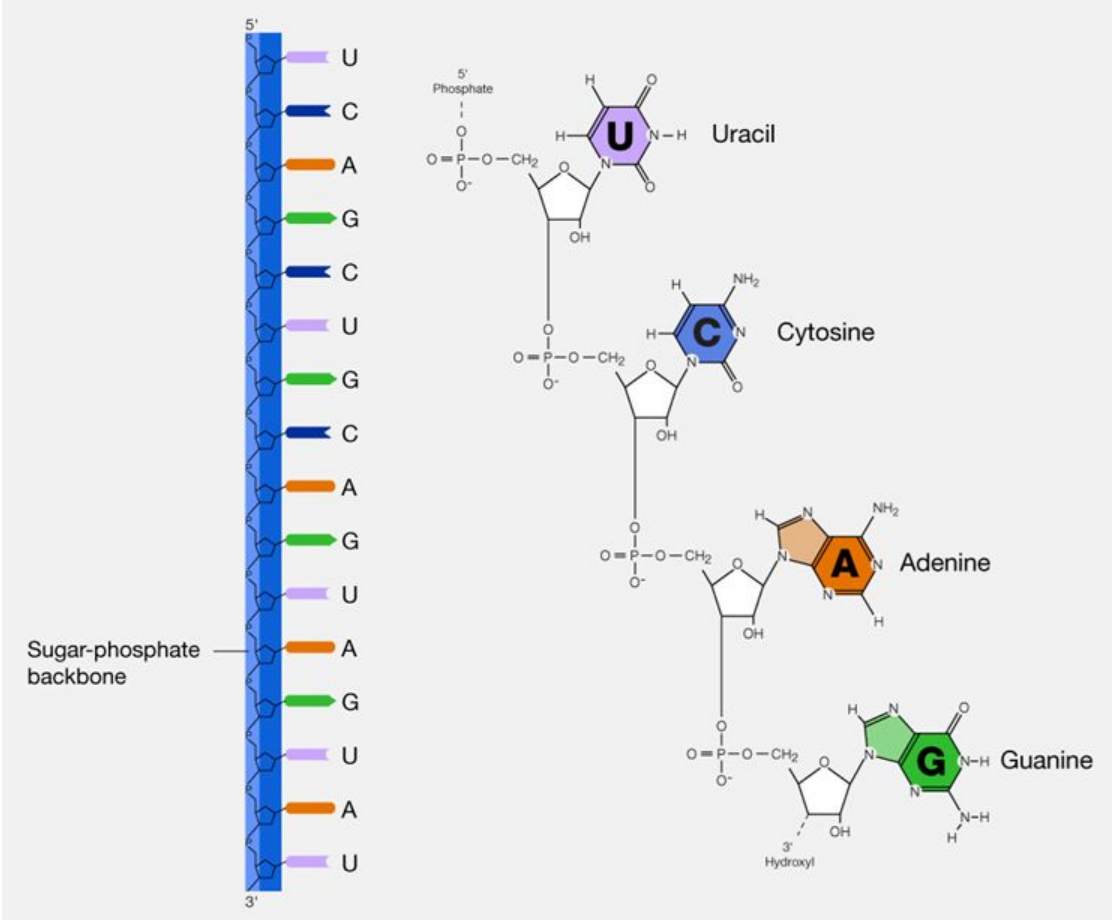
Feature	Nuclear	Mitiochondrial
Location		
Structure	Linear DNA, organized into24 chromosomes (22 autosomes + 2 sex chromosomes)	Circular DNA
Number of copies	Two copies per cell (diploid in somatic cells)	~ 8 0000 copies per cell
Size	~ 3 200 000 000 nucleotides	~ 16 500 nucleotides
Number of genes	~ 25 000 genes	37 genes
Inheritance	Inherited from both parents	Inherited maternally
Function	Codes for most cellular proteins and RNAs	Codes for proteins involved in mitochondrial energy production
Coding DNA	~ 3% (Contains introns, repetitive sequences, and regulatory regions)	~ 93% (Lacks introns, mostly coding regions)

Structure of RNA

•**Single-stranded**: flexible and versatile

• **Bases**:
  Adenine (A)
  Uracil (U)
  Cytosine (C)
  Guanine (G)

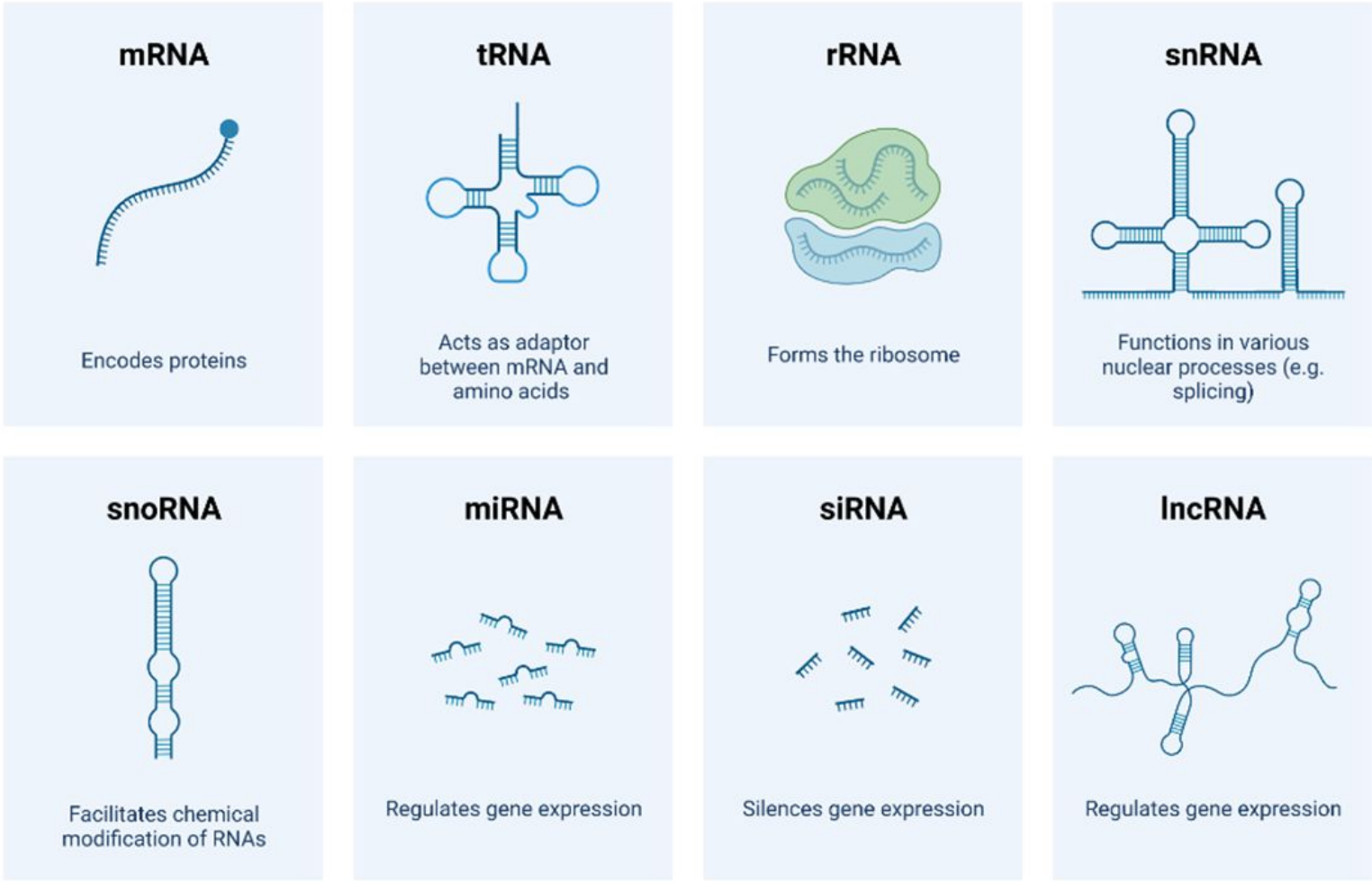
•**Nucleotide components**:
  Sugar (ribose)
  Phosphate group.
  Nitrogenous base (A, U, C, G).



https://www.genome.gov/

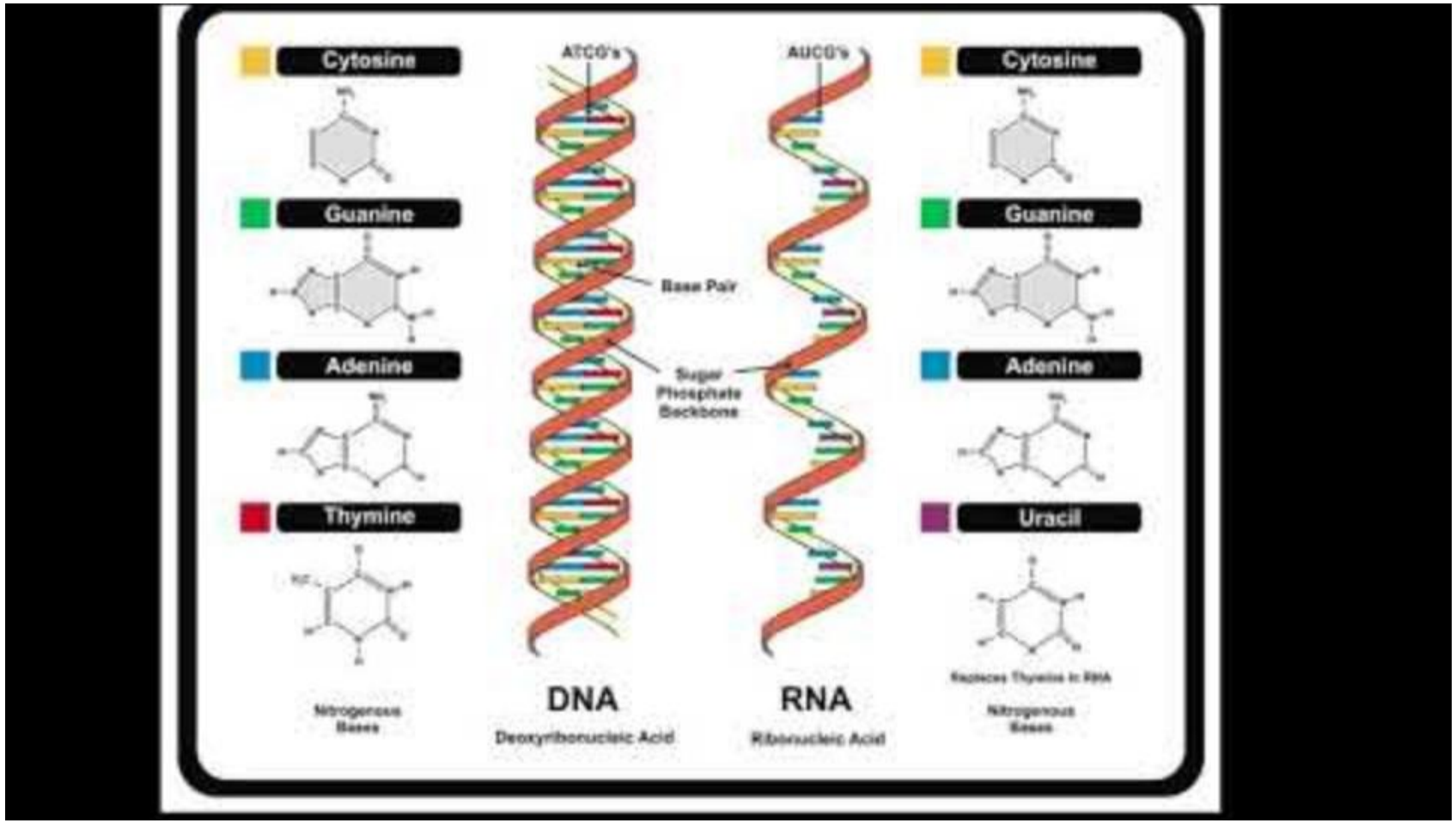
Cell transcriptome

TRANSCRIPTOME:
Complete set of all RNA molecules, including coding and non-coding, transcribed from the DNA of a cell or a population of cells at a specific time.

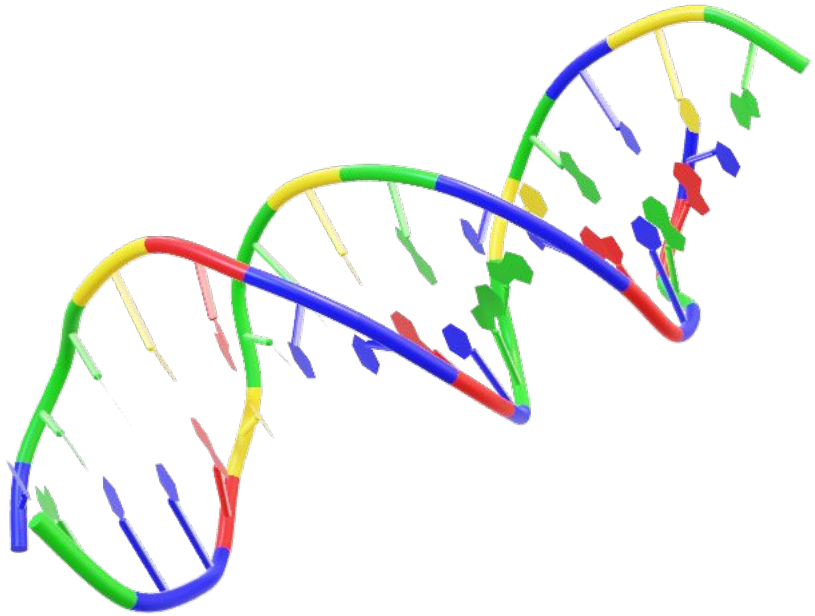


Kim, S. (2021) BioRender

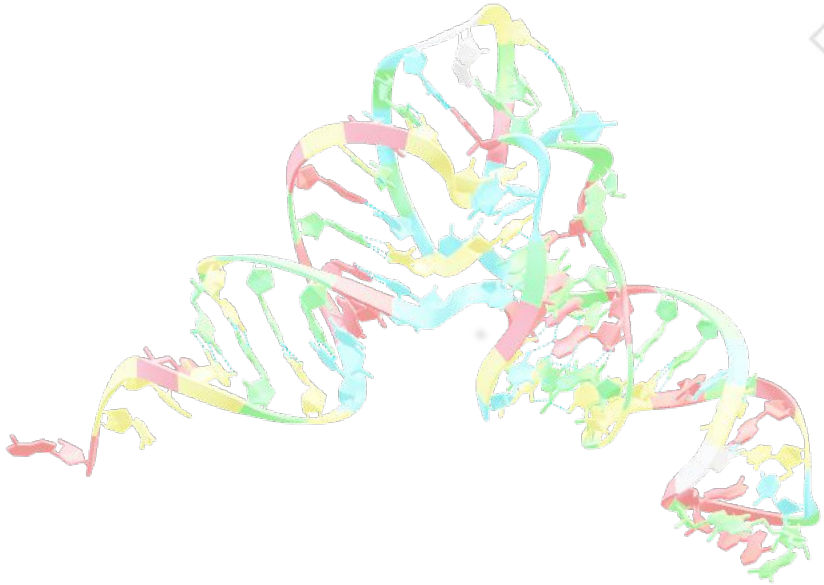
DNA vs. RNA Structure



Grab, Turn, and Explore:



https://skfb.ly/6ZzzZ



https://skfb.ly/oppII

QUIZ

- 10 questions

VIBE PROJECT

Virtual Biomedical and STEM/STEAM Education

2021-1-HU01-KA220-HED-000032251

Funded by the European Union

Funded by the European Union. Views and opinions expressed are however those of the author(s) only and do not necessarily reflect those of the European Union or the European Education and Culture Executive Agency (EACEA). Neither the European Union nor EACEA can be held responsible for them.

PÉCSI TUDOMÁNYEGYETEM
UNIVERSITY OF PÉCS

U.PORTO

Politechnika Śląska

DEX innovation centre

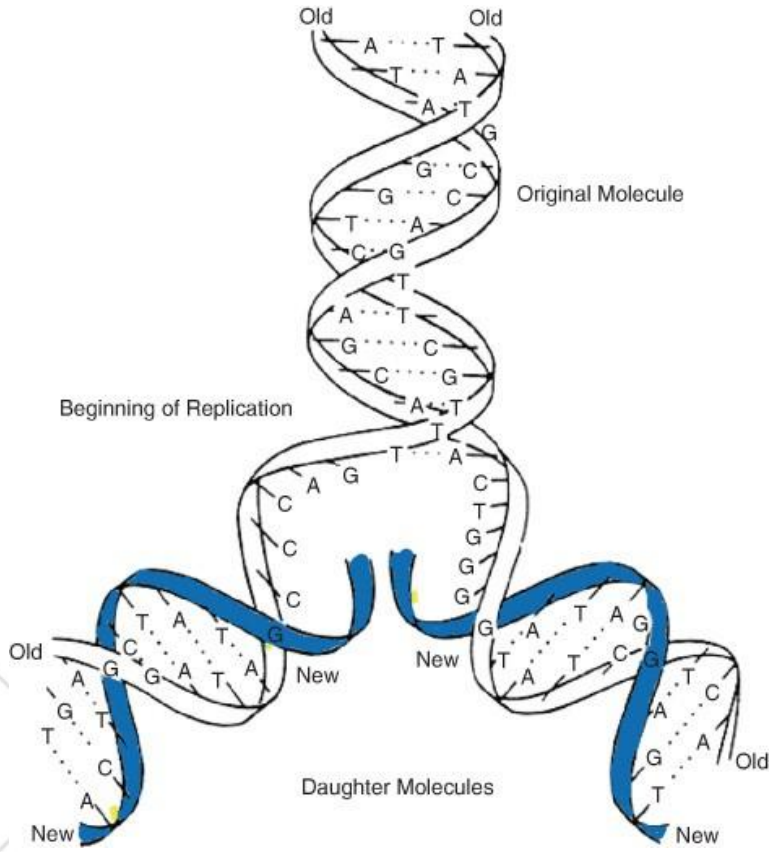
VIBE PROJECT

FROM CELL GENOME TO PROTEOME

3.2. DNA Replication

EXPLORING THE MYSTERIES OF LIFE: AN INTRODUCTION TO CELL BIOLOGY

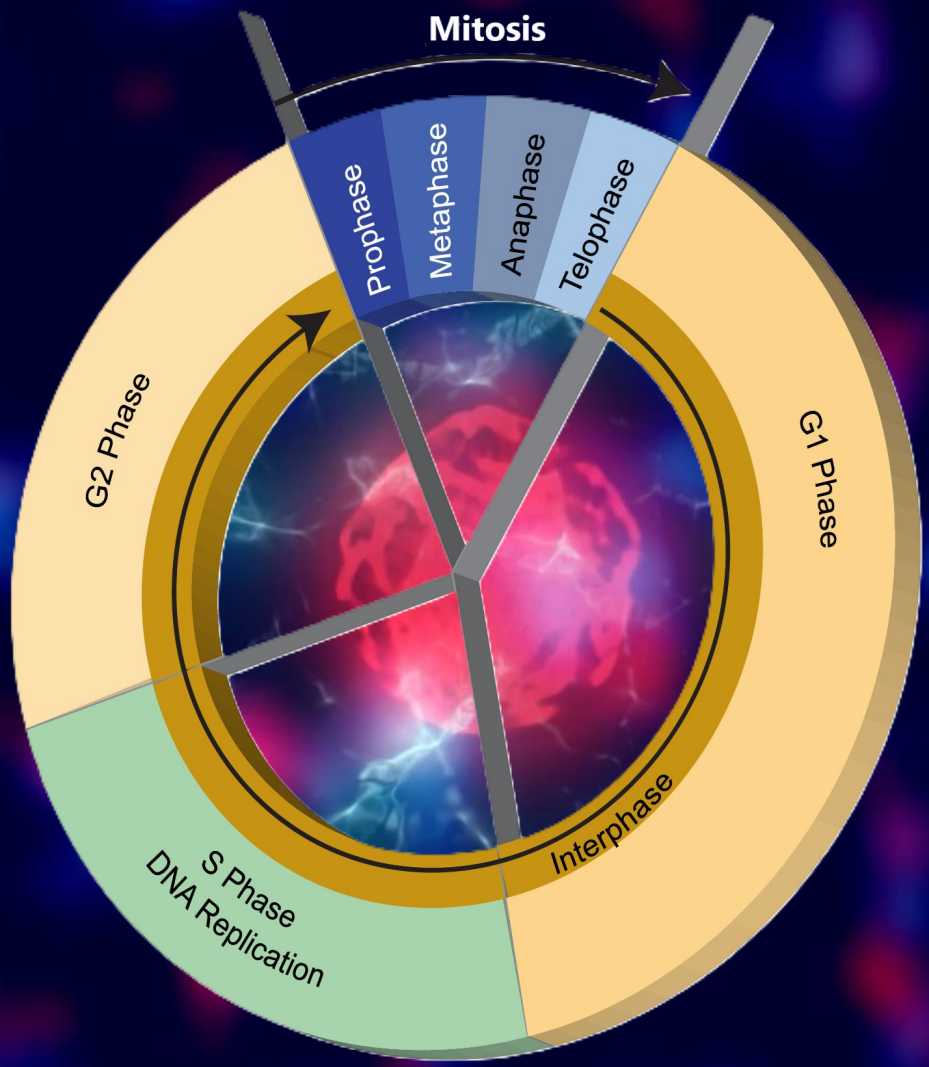
DNA REPLICATION – A SEMI-CONSERVATIVE MECHANISM



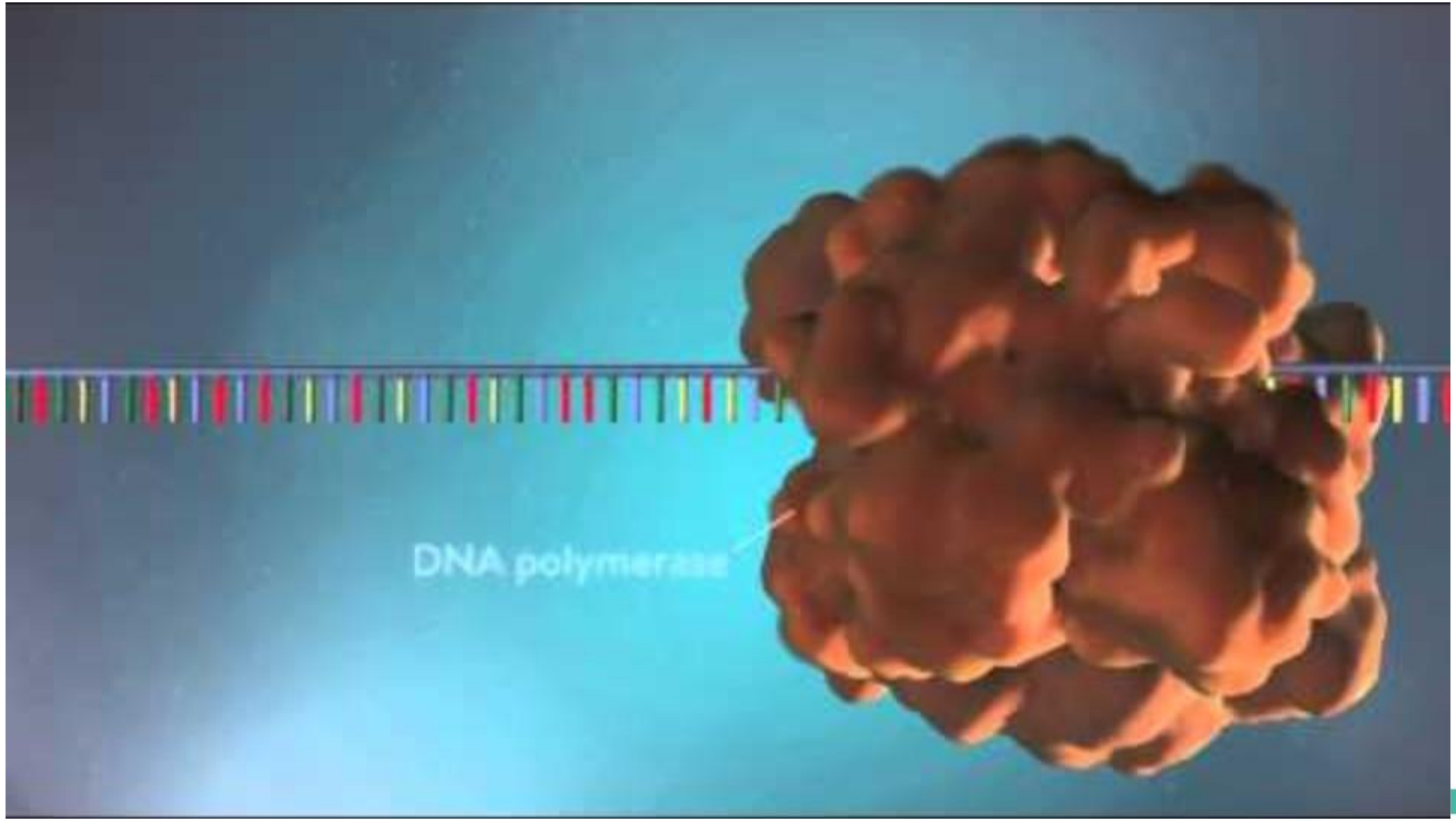
"It has not escaped our notice that the specific pairing we have postulated immediately suggests a possible copying mechanism for the genetic material."

James Watson and Francis Crick (1953)

(2008). Watson and Crick Model. In: Encyclopedia of Genetics, Genomics, Proteomics and Informatics. Springer, Dordrecht. https://doi.org/10.1007/978-1-4020-6754-9_18122



DNA Replication video



STEPS OF DNA REPLICATION

1. **Initiation** - identification of the starting point on the DNA molecule where the replication process begins

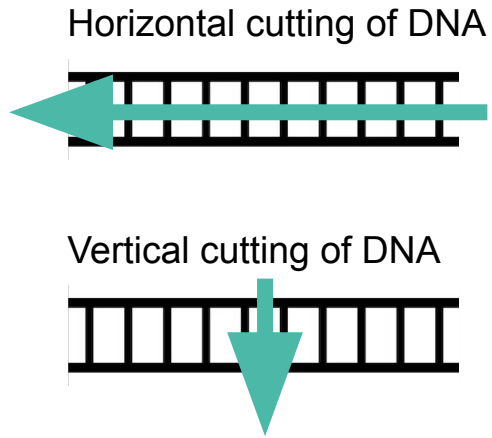
2. **Elongation** - processes related to the action of the replication forks as they copy the parental DNA strands

3. **Termination** - completion and finalization of the new DNA strands

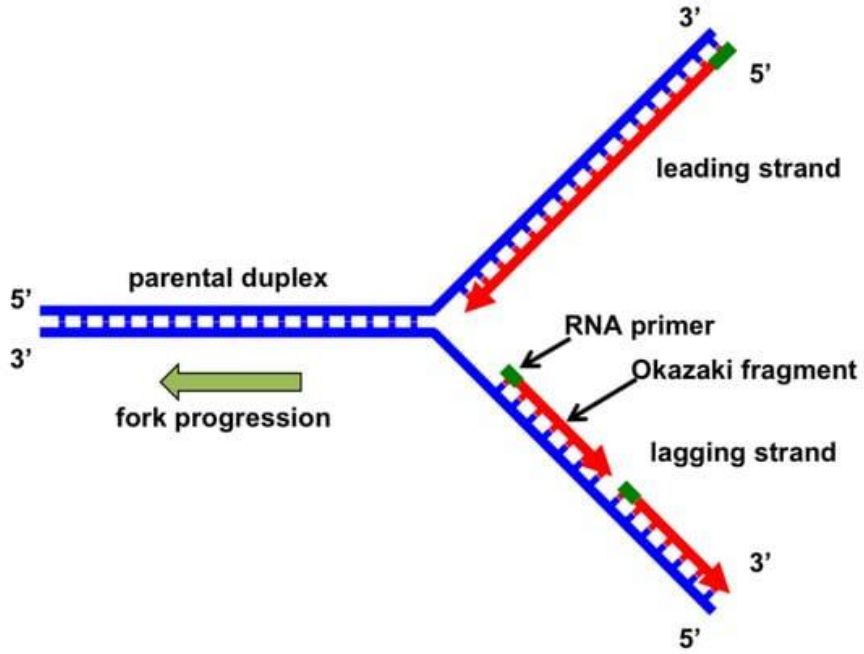
INITIATION

Enzymes involved:

- **Helicases** - unwind DNA double helix, create replication fork
- **Topoisomerases** – prevent DNA supercoiling and facilitate strand separation



Replication fork

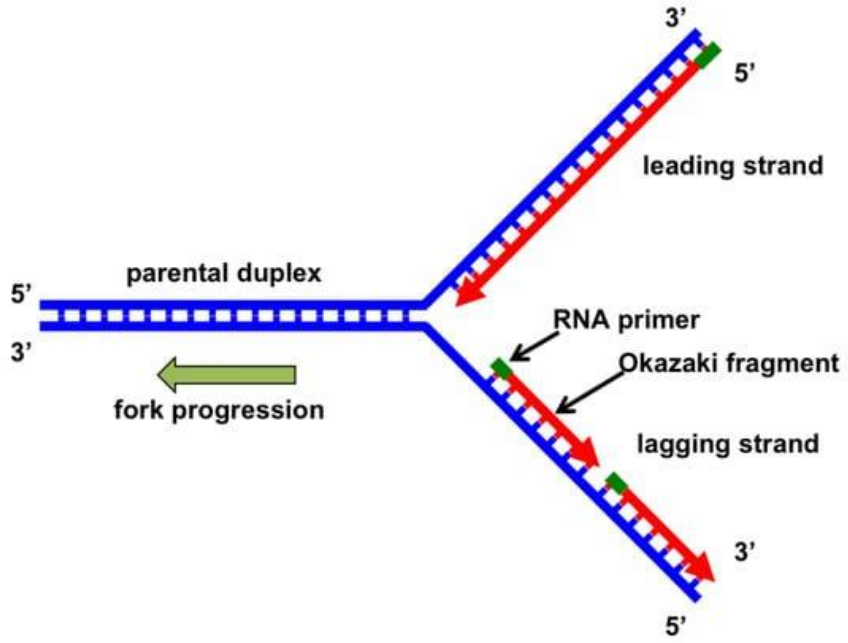


https://doi.org/10.3390/genes4010001

ELONGATION

Replication Forks: Move along DNA strands, enabling genome replication
Directionality: DNA polymerases synthesize DNA only in the 5’->3’ direction
- **Leading Strand:** Synthesized continuously
- **Lagging Strand:** Synthesized discontinuously

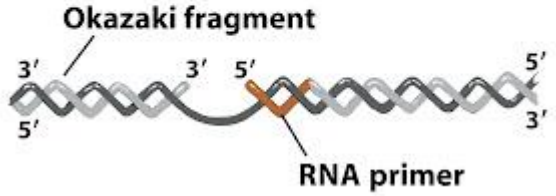
Primers: Required for both strands, made of RNA initially
Enzyme involved:
- **Bacteria:** Primase synthesizes RNA primer; DNA polymerase III extends it
- **Eukaryotes:** Polymerase α synthesizes a short RNA primer and DNA segment; DNA polymerase δ continues synthesis



ELONGATION

The Issue of RNA Primers and Okazaki Fragments

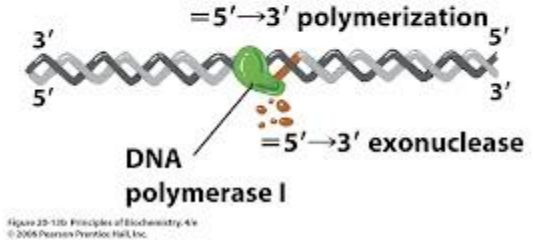
Completion of Okazaki fragment synthesis leaves a nick between the Okazaki fragment and the preceding RNA primer on the lagging strand.



Okazaki Fragments

Okazaki fragments are short RNA - DNA segments synthesized on the lagging strand during DNA replication, between 1,000 and 2,000 nucleotides long in prokaryotic cells, while in eukaryotic cells, they are much shorter, approximately 200 nucleotides

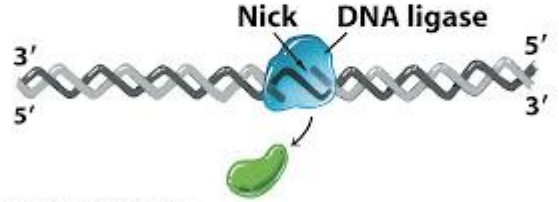
DNA polymerase I extends the Okazaki fragment while its 5′→3′ exonuclease activity removes the RNA primer. This process, called nick translation, results in movement of the nick along the lagging strand.



Removal of the RNA primer and Filling the gap

In eukaryotic cells: enzymes such as RNase H and FEN1 (Flap Endonuclease 1)
In prokaryotic cells: DNA polymerase I

DNA polymerase I dissociates after extending the Okazaki fragment 10–12 nucleotides. DNA ligase binds to the nick.



Ligation by DNA ligase

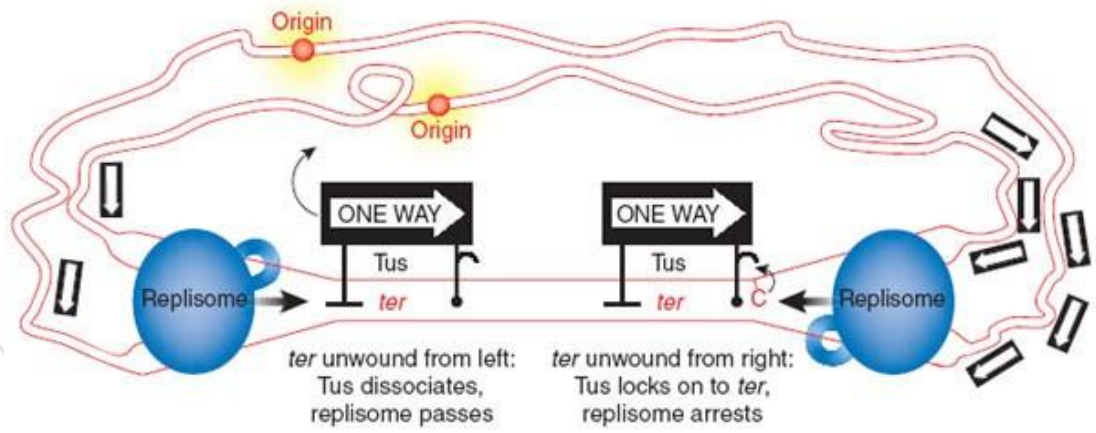
DNA ligase connects the neighboring Okazaki fragments (or fragments on the leading strand) by forming a phosphodiester bond between the 3’-OH end of one DNA fragment and the 5’-phosphate end of another.

Horton, H.R., Moran, L.A., Scrimgeour, K.G., Perry, M.D. and Rawn, J.D. (2006) *Principles of Biochemistry*. Pearson/Prentice Hall, Upper Saddle River, NJ (USA)

TERMINATION

Prokaryotic cells:

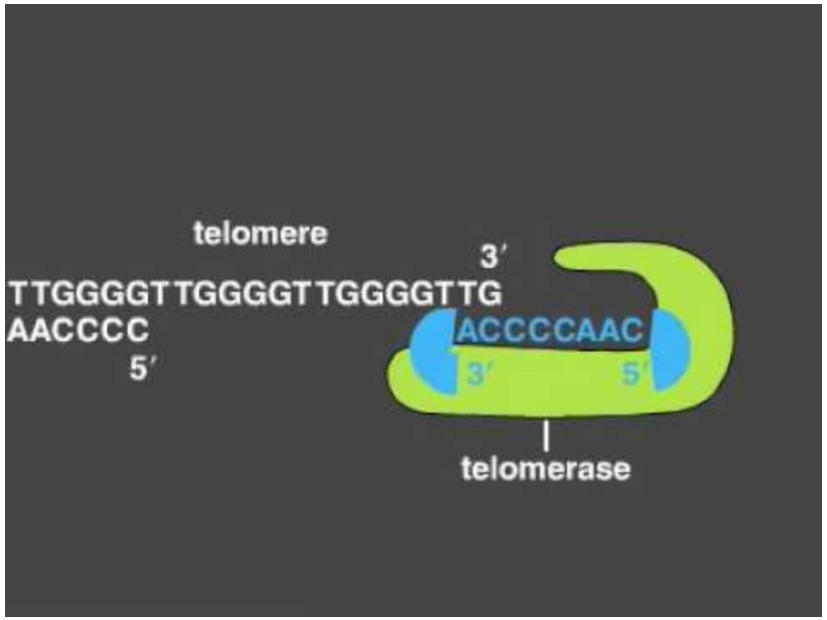
ter sites & Tus proteins



Theis, K. One-way traffic control in replication termination. *Nat Chem Biol* **2**, 455–456 (2006)

Eukaryotic cells:

Telomeres & telomerases



DNA REPLICATION IN PROKARYOTES VS. EUKARYOTES

Feature	Bacteria	Eukaryotic Cells
Genome Structure	Circular DNA with a single origin of replication.	Linear DNA with multiple origins of replication.
Replication Speed	Fast (~1,000 nucleotides/second).	Slower (~50 nucleotides/second).
Enzymes	DNA Polymerase III is the main replicative enzyme.	Multiple DNA polymerases (e.g., δ, ε) involved in replication.
Replication Origins	Single origin of replication (OriC).	Thousands of origins across the genome.
Termination	Replication forks meet at termination sites (ter sites).	Replication forks converge; telomeres require telomerase to complete replication.
Okazaki Fragments	Longer (~1,000-2,000 nucleotides).	Shorter (~100-200 nucleotides).

QUIZ

- 10 questions

VIBE PROJECT

Virtual Biomedical and STEM/STEAM Education

2021-1-HU01-KA220-HED-000032251

Funded by the European Union

Funded by the European Union. Views and opinions expressed are however those of the author(s) only and do not necessarily reflect those of the European Union or the European Education and Culture Executive Agency (EACEA). Neither the European Union nor EACEA can be held responsible for them.

PÉCSI TUDOMÁNYEGYETEM
UNIVERSITY OF PÉCS

U.PORTO

Politechnika Śląska

DEX innovation centre

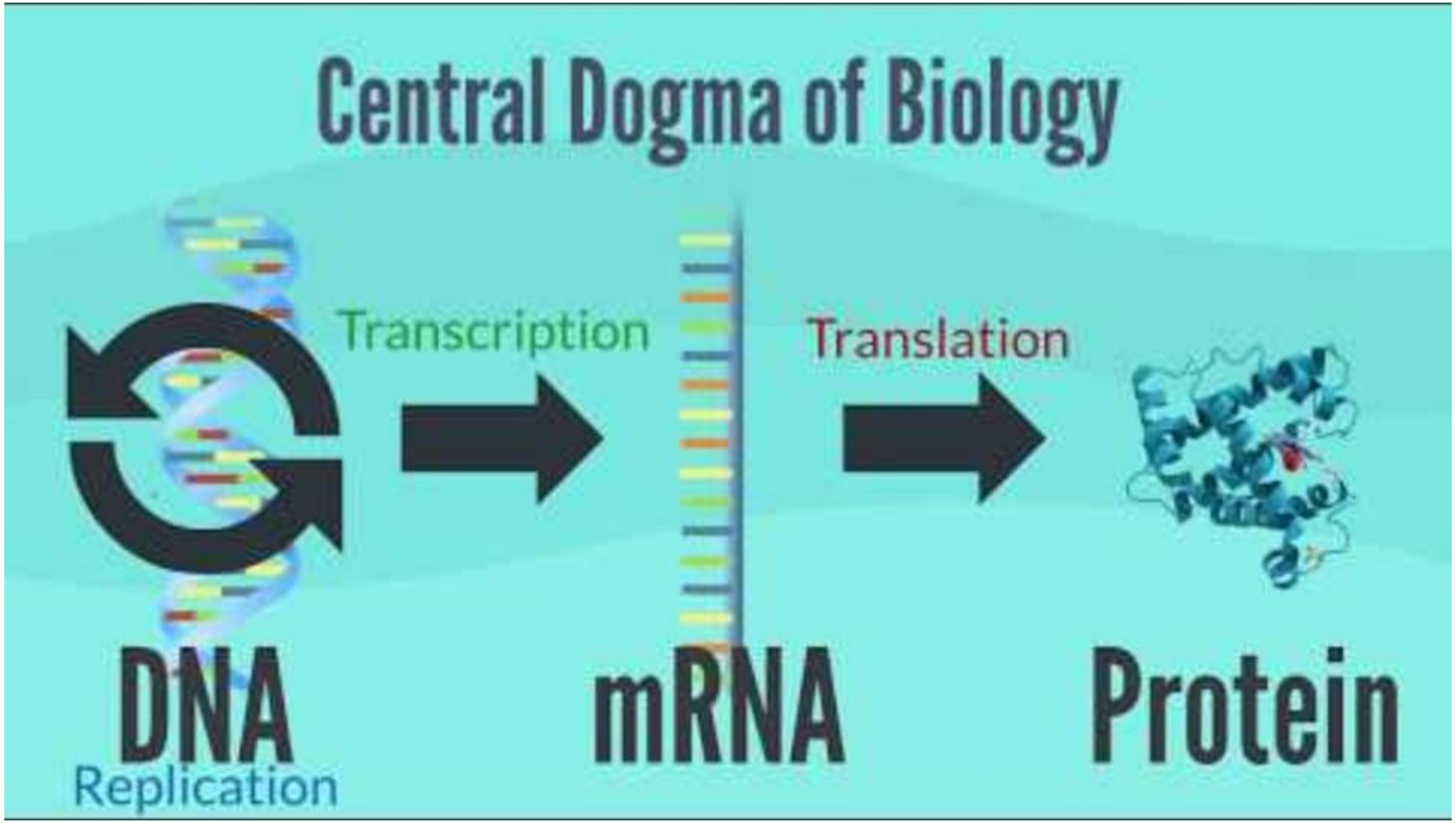
VIBE PROJECT

FROM CELL GENOME TO PROTEOME

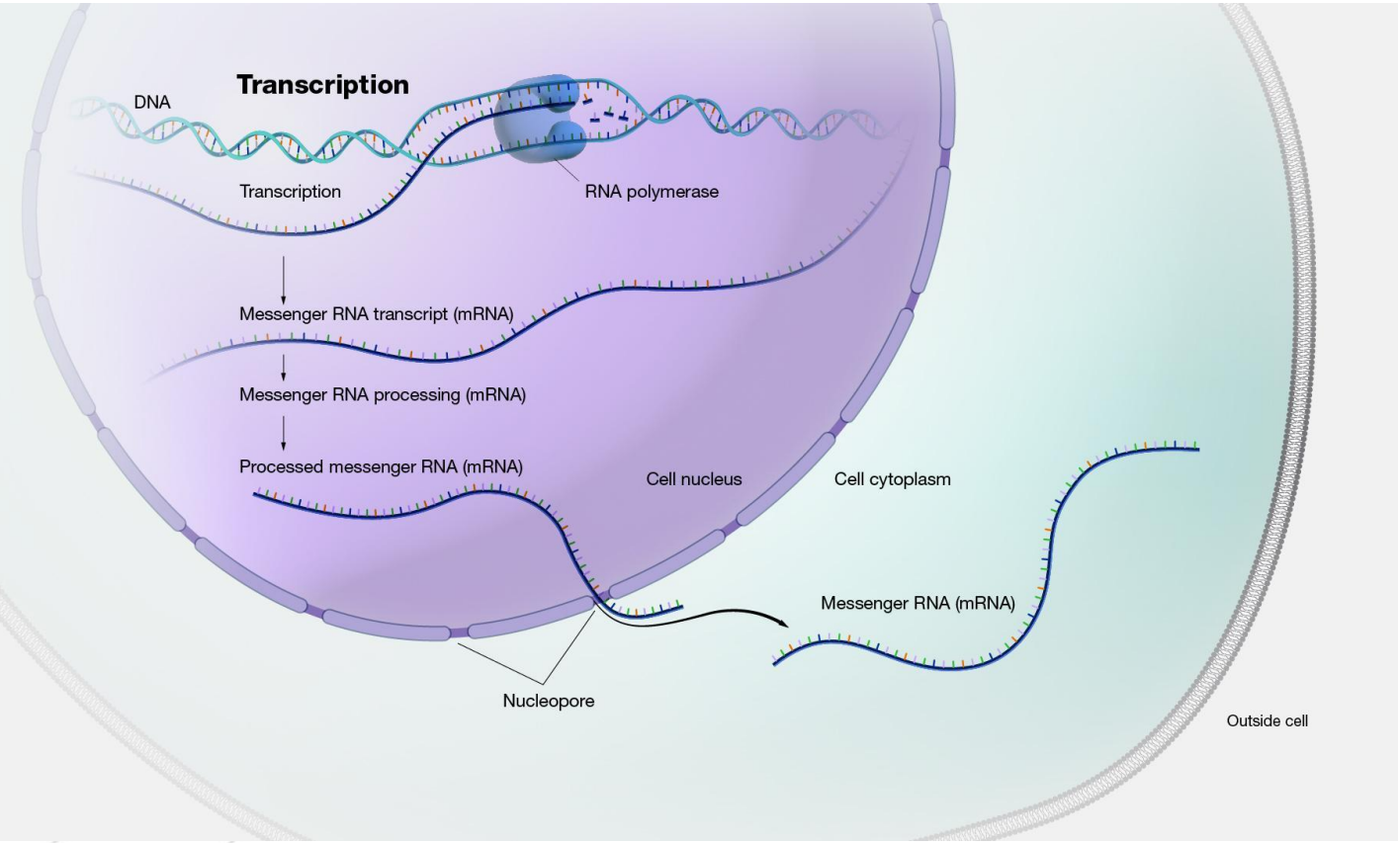
3.3. Transcription

EXPLORING THE MYSTERIES OF LIFE: AN INTRODUCTION TO CELL BIOLOGY

CENTRAL DOGMA OF MOLECULAR BIOLOGY



TRANSCRIPTION



www.genome.gov

Transcription

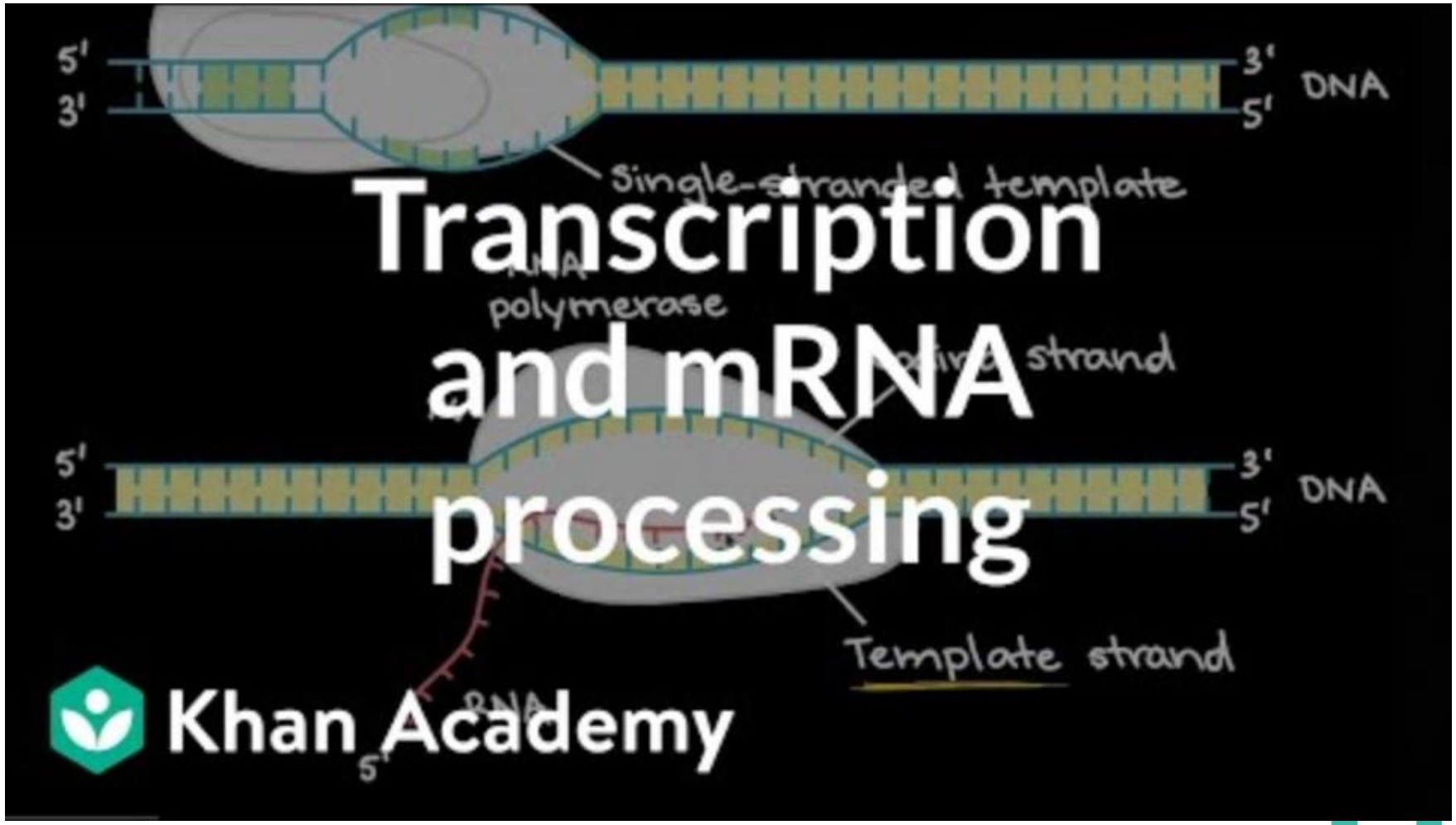
- The process of synthesizing RNA from a DNA template by RNA polymerase
- Produces messenger RNA (mRNA), transfer RNA (tRNA), and ribosomal RNA (rRNA)

Biological Significance

- Converts genetic information from DNA into RNA, making it accessible for protein synthesis
- Regulates gene expression and allows cells to adapt to their environment
- Essential for growth, development, and maintaining cellular functions

Transcription

TRANSCRIPTION IN DETAILS



TRANSCRIPTION IN SUMMARY

STEPS OF TRANSCRIPTION:

1. **Initiation**: RNA polymerase binds to the promoter, unwinding the DNA and beginning RNA synthesis
2. **Elongation**: RNA polymerase moves along the DNA template, synthesizing RNA in the 5’ to 3’ direction
3. **Termination**: Transcription ends when RNA polymerase reaches a termination signal, releasing the RNA transcript

ENZYMES OF TRANSCRIPTION:

RNA Polymerase: The main enzyme responsible for synthesizing RNA from the DNA template strand

Helicase: Unwinds the DNA double helix to allow access to the template strand

Topoisomerase: Prevents DNA from becoming too supercoiled during unwinding by relieving torsional strain

GTFs (General Transcription Factors): In eukaryotes, these factors are required for RNA polymerase to initiate transcription

.

TRANSCRIPTION IN SUMMARY

SEQUENCES OF TRANSCRIPTION:

Promoter: A DNA sequence located at the beginning of a gene where RNA polymerase binds to initiate transcription. It includes key regions like the **TATA box**

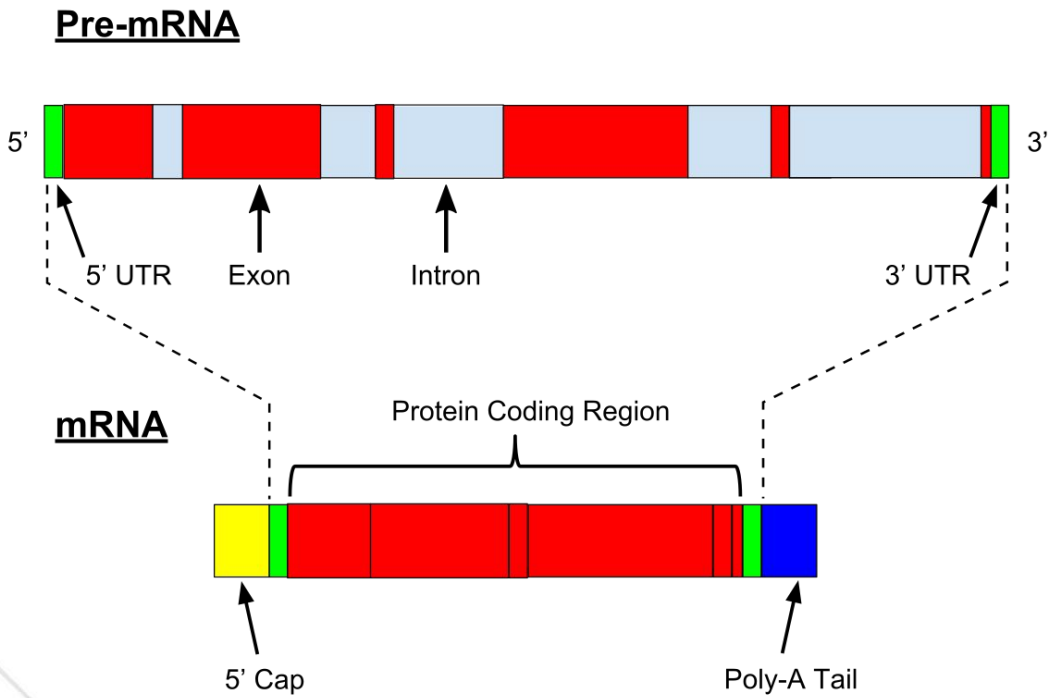
Transcription Start Site (TSS): The position where RNA synthesis begins

Exons: Coding sequences that are transcribed into RNA and later translated into protein

Introns: Non-coding regions within a gene that are transcribed into RNA but are removed during RNA processing

Terminator: A sequence signaling the end of transcription, causing RNA polymerase to detach from the DNA template

POST-TRANSCRIPTIONAL MODIFICATIONS (EUKARYOTES)



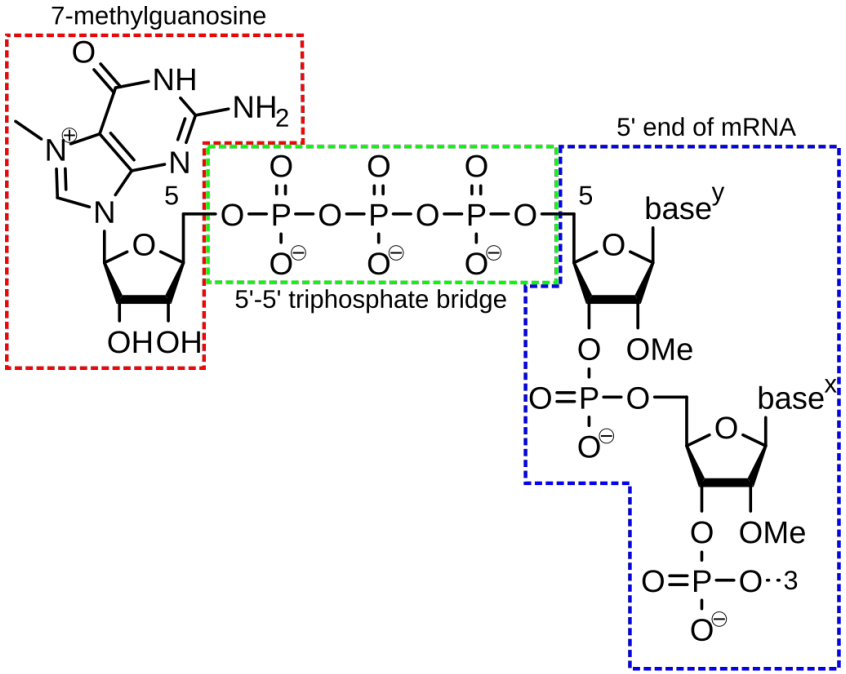
https://en.wikipedia.org/

- **5' Capping**: Addition of a modified guanine nucleotide to the 5' end, protecting RNA from degradation
- **Splicing**: Removal of non-coding introns and joining of coding exons by the spliceosome
- **Poly(A) Tail Addition**: A tail of adenine nucleotides is added to the 3' end to enhance RNA stability and regulate translation

5’ CAPPING PROCESS

Mechanism:

1. Transfer a guanosine triphosphate (**GTP**) to the 5’ end of pre-mRNA by **guanylyltransferase** enzyme, forming characteristic **5' to 5' triphosphate bridge**
2. **Methylation** of the guanine by **methyltransferase enzyme**

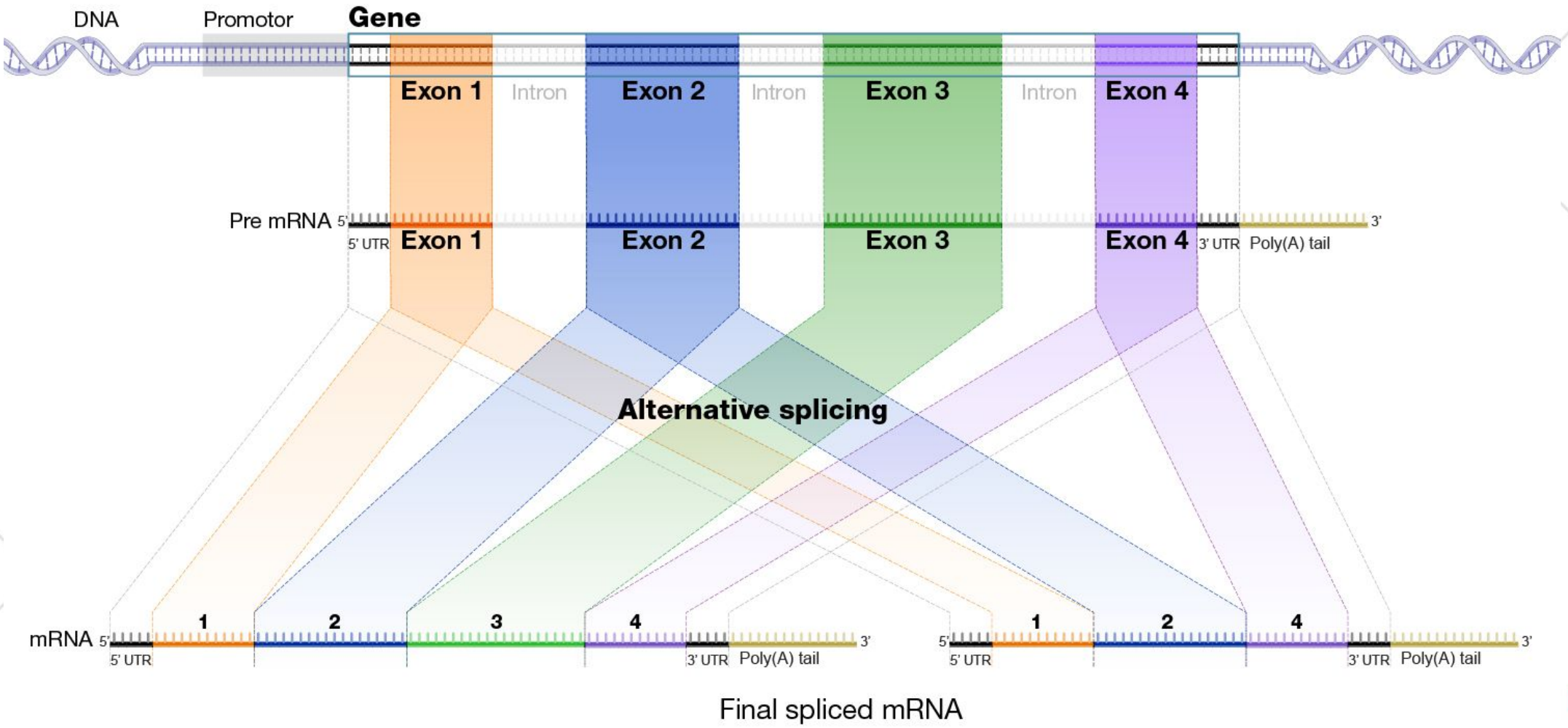


https://en.wikipedia.org/

Biological significance:

- **Protection**
- **Facilitating Export**
- **Translation Initiation**

SPLICING



Final spliced mRNA

www.genome.gov

POLYADENYLATION

Biological significance:

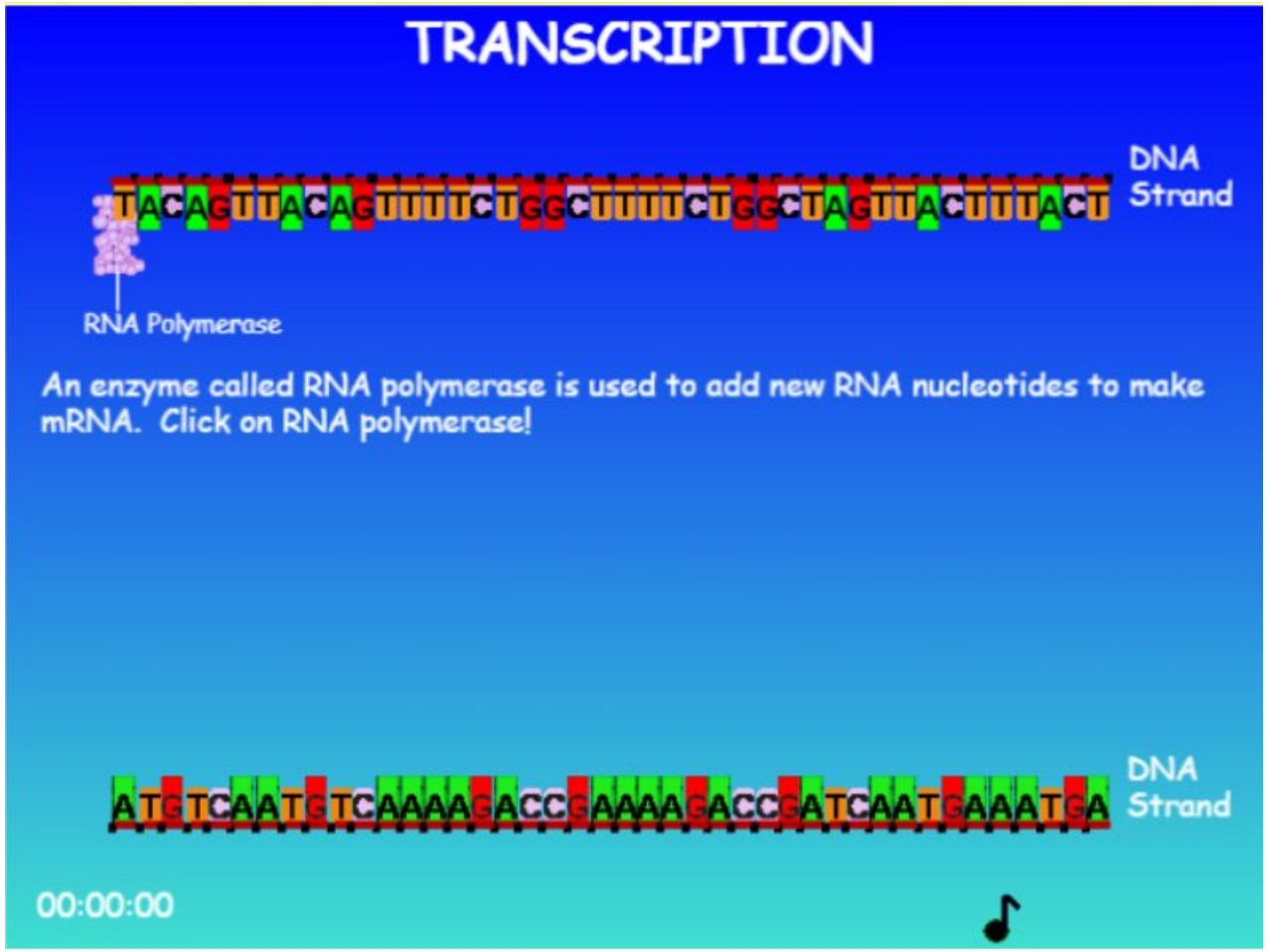
- **Protection**
- **Facilitating Export**
- **Translation Efficiency**

Niazi, A.M., Krause, M., Valen, E. (2021). Transcript Isoform-Specific Estimation of Poly(A) Tail Length by Nanopore Sequencing of Native RNA. In: Picardi, E. (eds) RNA Bioinformatics. Methods in Molecular Biology, vol 2284. Humana, New York, NY.

TRANSCRIPTION IN PROKARYOTES VS. EUKARYOTES

Feature	Prokaryotes	Eukaryotes
Location	Cytoplasm	Nucleus
RNA Polymerases	One type (RNA polymerase)	Three types (RNA polymerases I, II, III)
Initiation	Directly at promoter	Requires transcription factors and promoter elements (TATA box)
mRNA Processing	None; mRNA is ready for translation	Pre-mRNA undergoes splicing, capping, and polyadenylation
Coupling with Translation	Transcription and translation occur simultaneously	Transcription and translation are separated in time and space
Genes	Often organized into operons	Each gene typically transcribed individually

TAKE A BREAK - PLAY THE RNA POLYMERASE SIMULATOR GAME



quiz

- 10 QUESTIONS

VIBE PROJECT

Virtual Biomedical and STEM/STEAM Education

2021-1-HU01-KA220-HED-000032251

Funded by the European Union

Funded by the European Union. Views and opinions expressed are however those of the author(s) only and do not necessarily reflect those of the European Union or the European Education and Culture Executive Agency (EACEA). Neither the European Union nor EACEA can be held responsible for them.

PÉCSI TUDOMÁNYEGYETEM
UNIVERSITY OF PÉCS

U.PORTO

Politechnika Śląska

DEX innovation centre

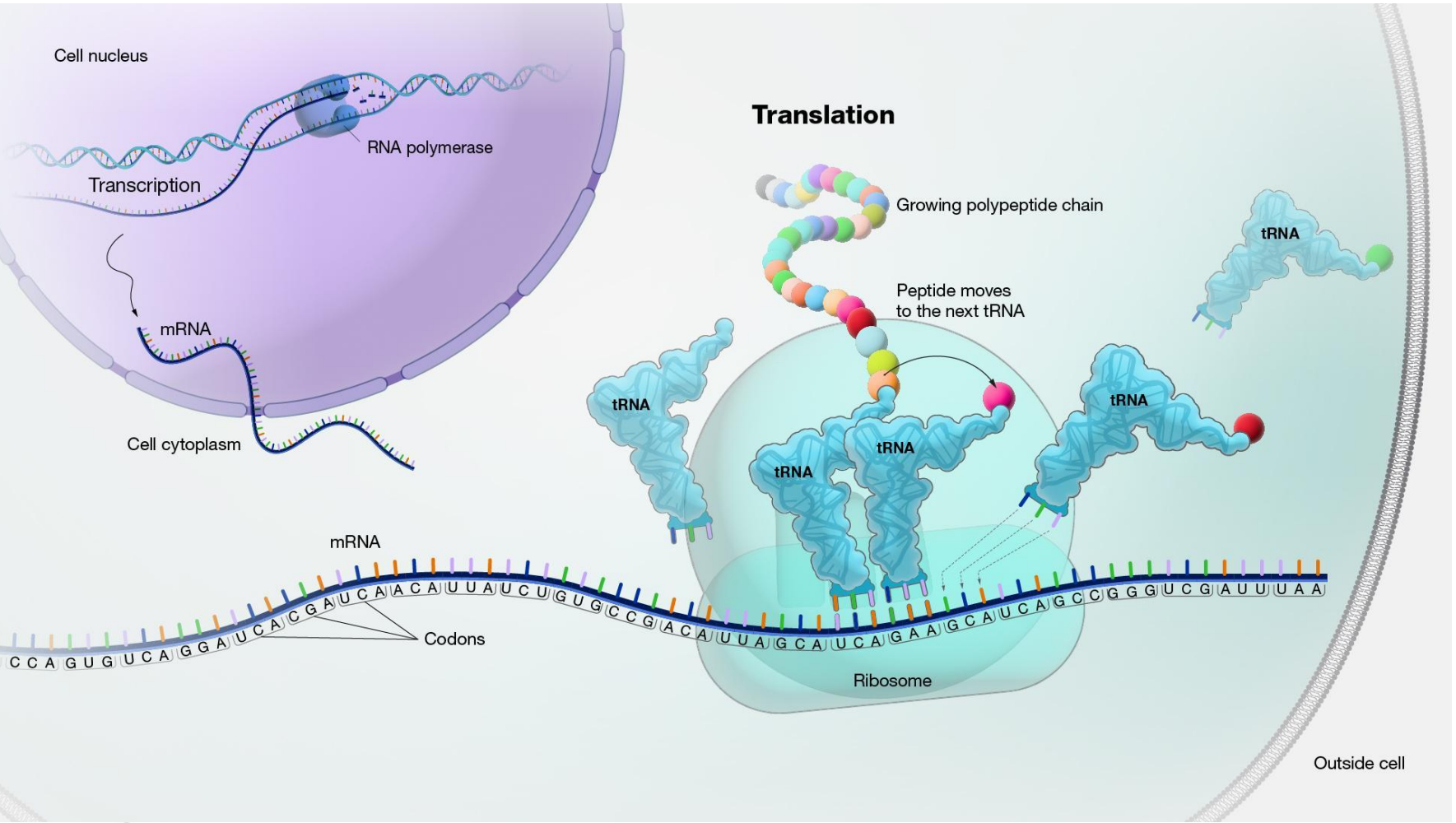
VIBE PROJECT

FROM CELL GENOME TO PROTEOME

3.4. Translation

EXPLORING THE MYSTERIES OF LIFE: AN INTRODUCTION TO CELL BIOLOGY

TRANSLATION



Definition

Translation is the process by which mRNA is decoded by ribosomes to synthesize proteins.

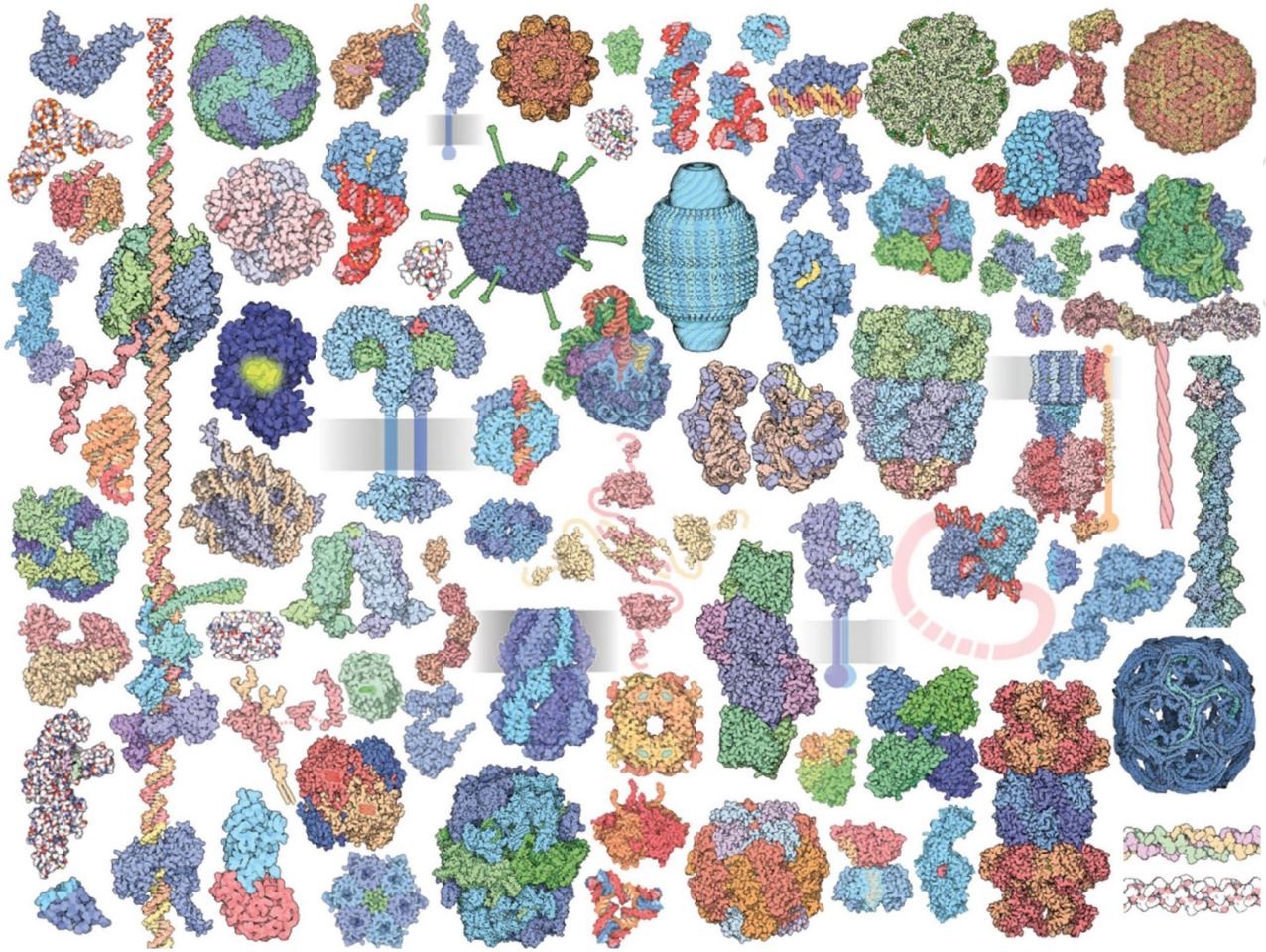
It occurs in the cytoplasm, where ribosomes read mRNA codons and match them with the corresponding tRNA molecules carrying amino acids.These amino acids are linked together to form a polypeptide chain, which folds into a functional protein.

www.genome.gov

TRANSLATION

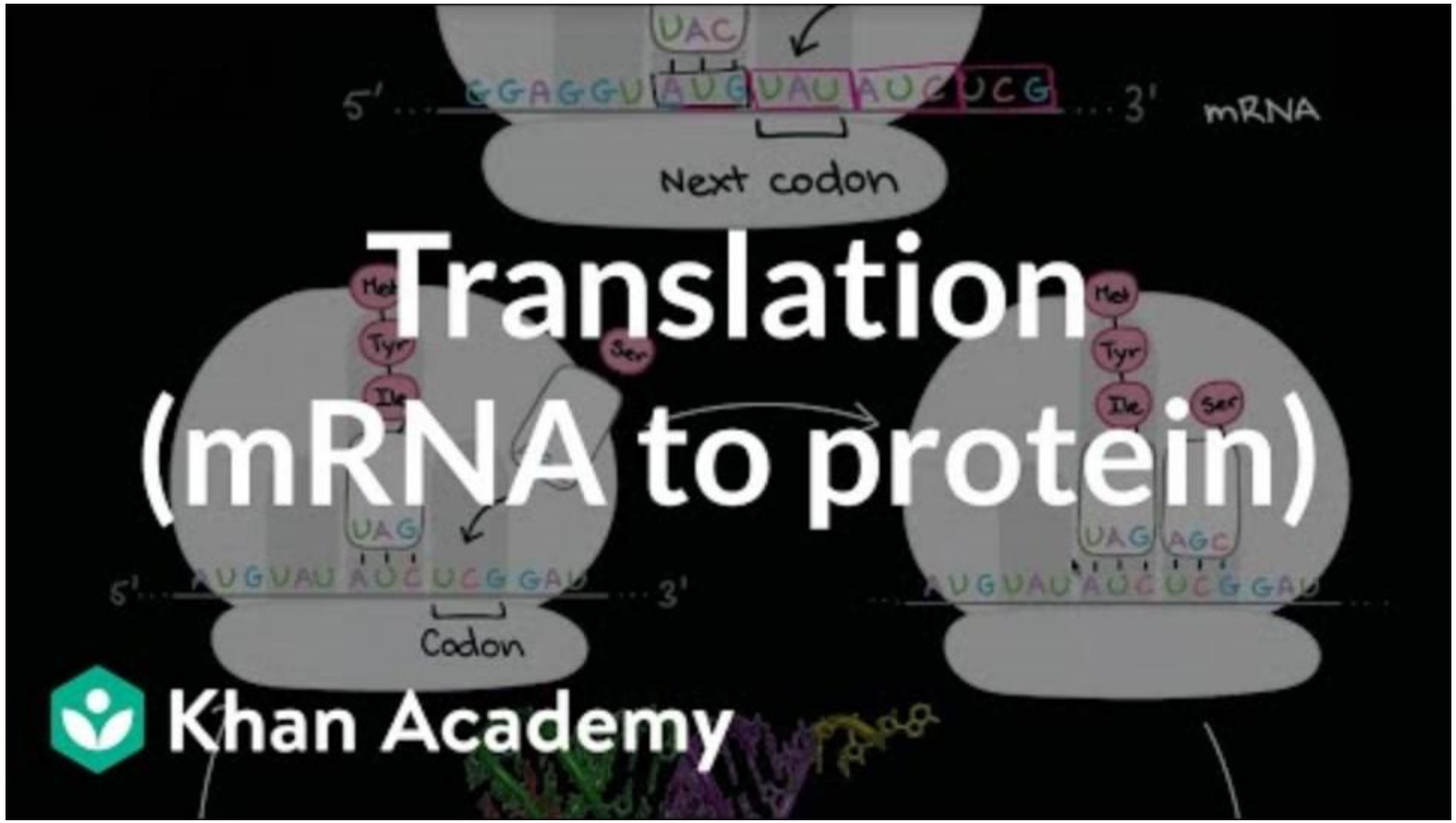
Biological Significance

- Translation is essential for gene expression, converting genetic information from nucleic acids into functional proteins.
- Proteins are crucial for all cellular processes, including enzyme catalysis, signaling, structure, and defense.
- This process is vital for cell growth, reproduction, and responding to environmental changes.



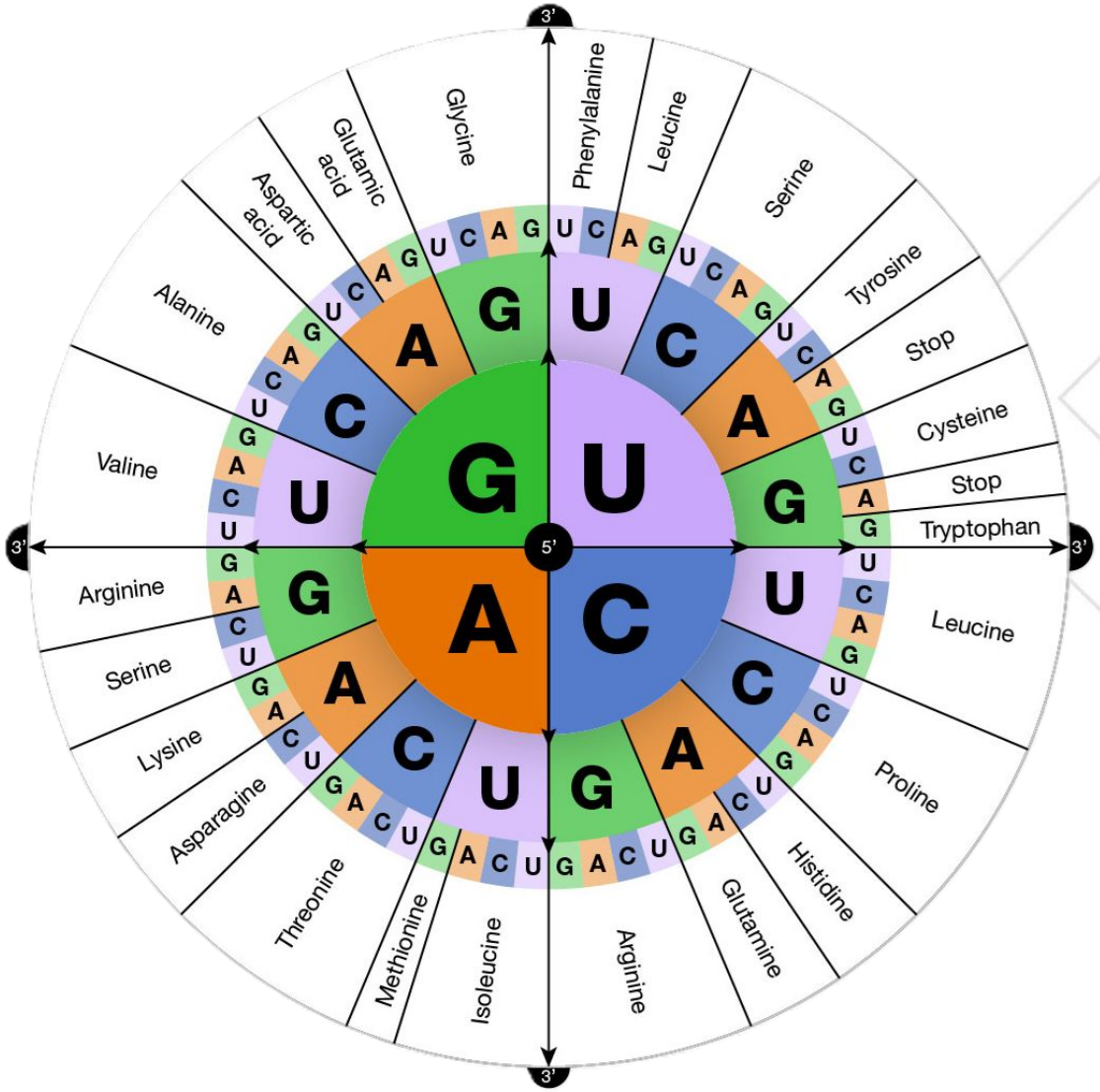
The remarkable diversity and complexity of protein structures. Credit to "RCSB Protein Data Bank" (CC-BY-4.0 license).

TRANSLATION IN DETAILS



GENETIC CODE

- **The Genetic Code** is a set of rules that defines how the sequence of nucleotides in DNA or RNA is translated into a sequence of amino acids in proteins. The code is nearly universal and ensures accurate protein synthesis in all living organisms.
- **Codons** are triplets of nucleotides that code for specific amino acids
- **Start Codon**: The most important start codon is **AUG**, which codes for methionine. It is the signal for the ribosome to begin protein synthesis and sets the reading frame for the rest of the mRNA.
- **Stop Codons**: These include **UAA**, **UAG**, and **UGA**. They do not correspond to any amino acid, but instead, they signal the termination of translation. When the ribosome reaches a stop codon, it releases the newly synthesized polypeptide.

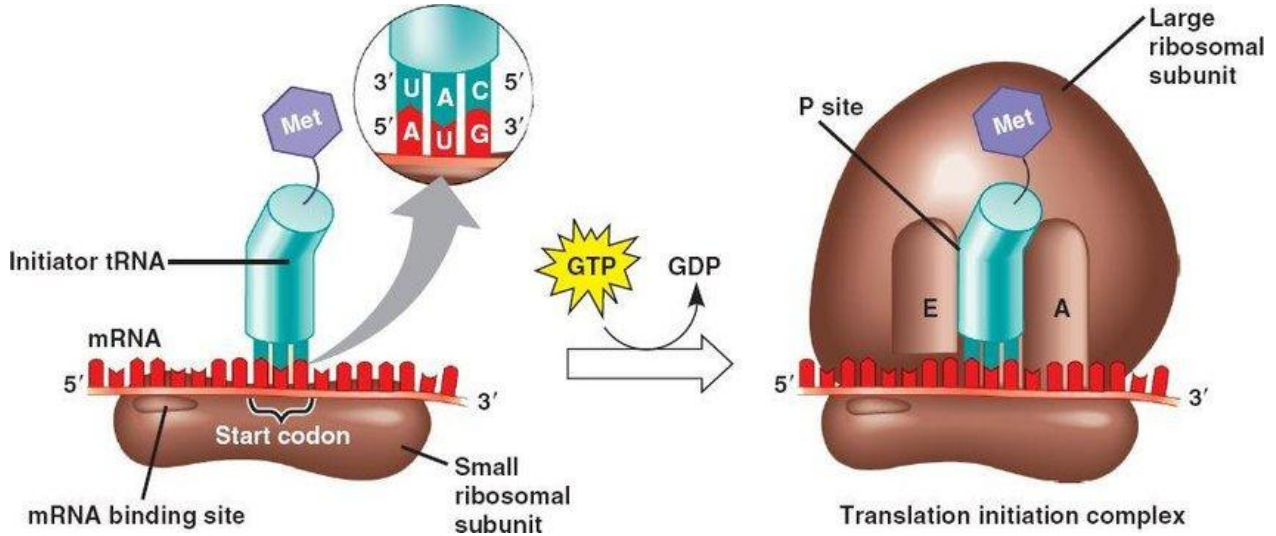


www.genome.gov

TRANSLATION IN SUMMARY

Initiation:

- The process begins when the small ribosomal subunit binds to the mRNA at the 5’ end and scans for the start codon, **AUG** (adenine-uracil-guanine)
- The start codon is recognized by the tRNA carrying methionine, which binds to the mRNA, signaling the beginning of protein synthesis. The large ribosomal subunit then attaches, forming a functional ribosome
- GTP (guanosine triphosphate) plays a critical role in translation by providing the energy required for key steps in the process

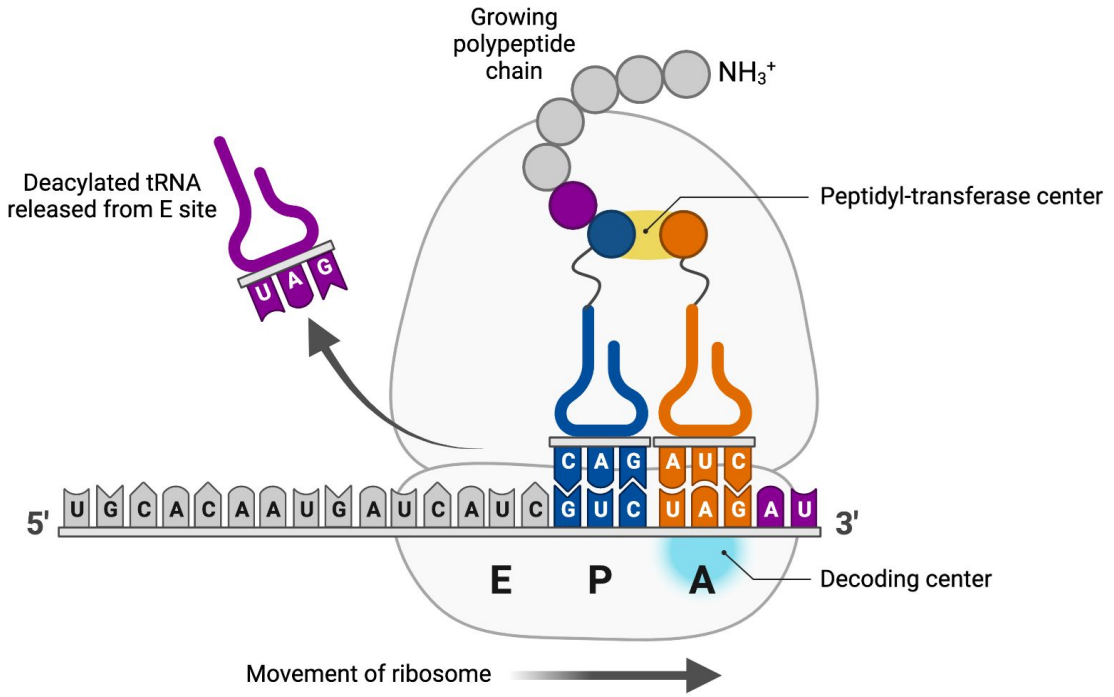


DOI: 10.1088/1742-6596/1836/1/012074

TRANSLATION IN SUMMARY

The elongation cycle involves three main steps:

1. **Codon recognition:** The tRNA with the correct anticodon pairs with the mRNA codon in the ribosome's A-site.
2. **Peptide bond formation:** The ribosome catalyzes the formation of a peptide bond between the amino acid from the A-site tRNA and the polypeptide in the P-site.
3. **Translocation:** The ribosome moves along the mRNA to the next codon, shifting the tRNAs into the E-site (exit site) and P-site, and making room for the next tRNA in the A-site.

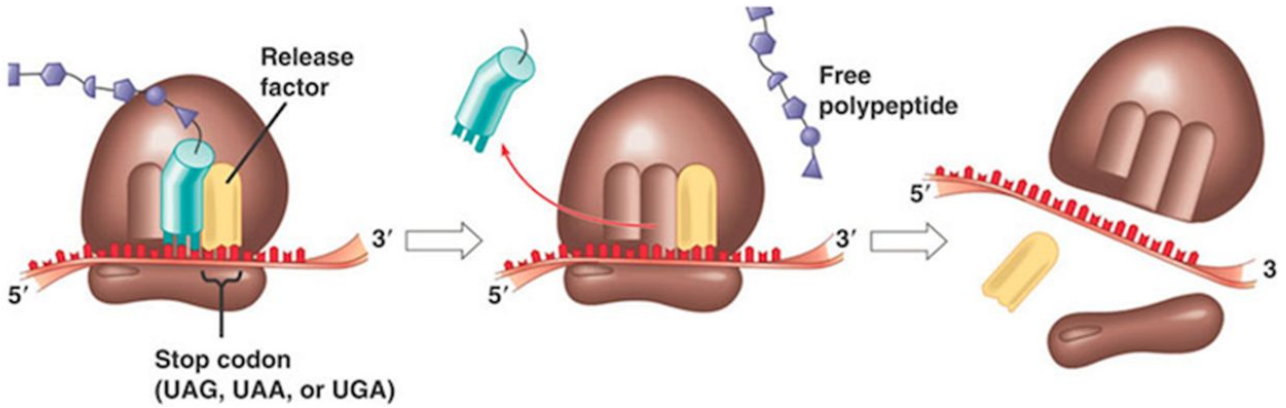


Anthony J.F. Griffiths, University of British Columbia; Susan R. Wessler, University of California, Riverside; Sean B. Carroll, Howard Hughes Medical Institute, University of Wisconsin--Madison; John Doebley, University of Wisconsin--Madison. (2015). Introduction to genetic analysis. New York, NY :W.H. Freeman & Company,

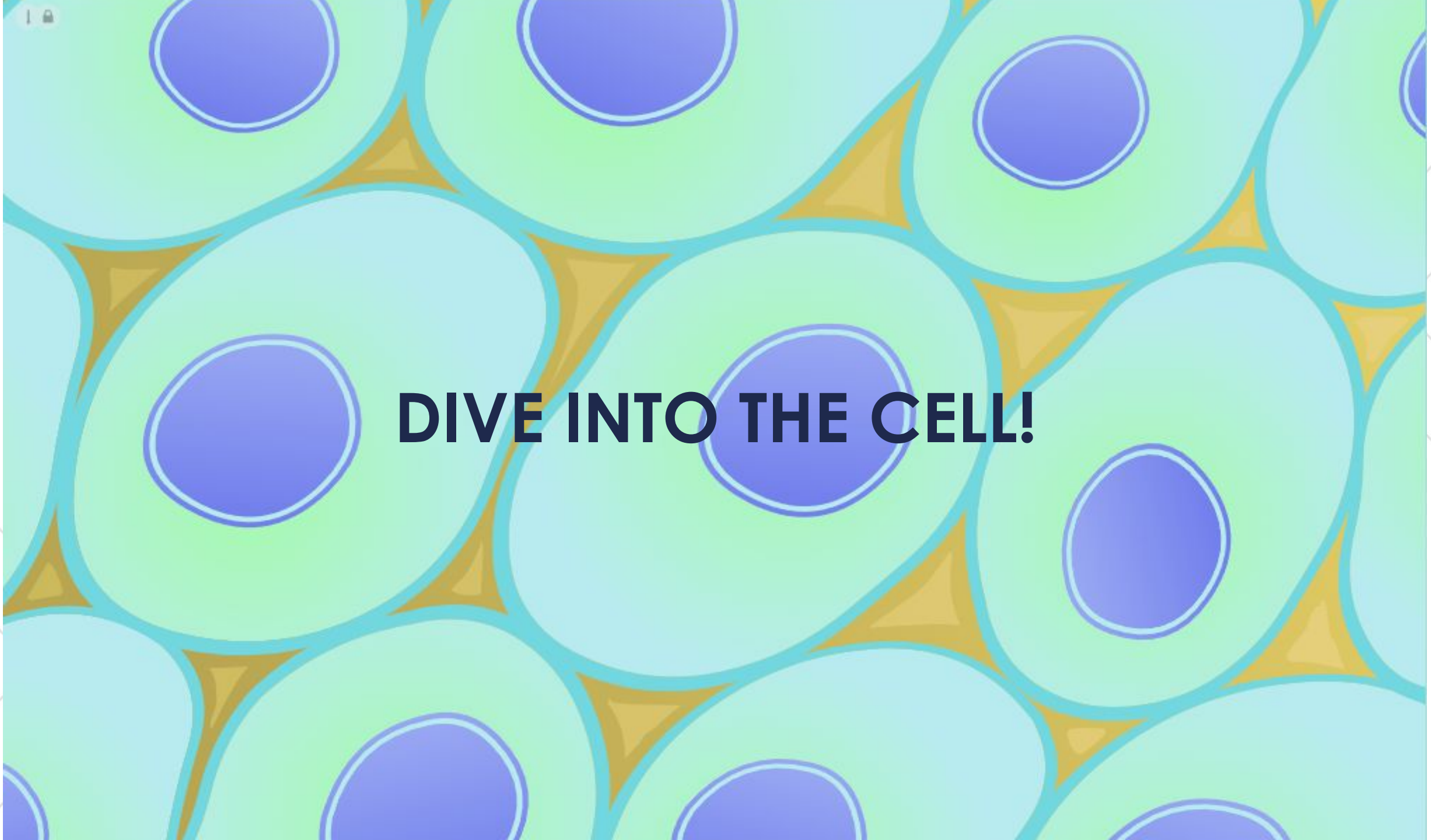
TRANSLATION IN SUMMARY

Termination

- Termination occurs when the ribosome encounters a stop codon (UAA, UAG, or UGA) on the mRNA. These codons do not code for any amino acid, marking the end of the polypeptide synthesis. Instead of a tRNA, a protein known as a **release factor** recognizes and binds to the stop codon in the ribosome's A-site.
- The bond between the polypeptide chain and the tRNA in the P-site is **hydrolyzed**, releasing the completed polypeptide.
- **Ribosome Disassembly:** The ribosome subunits separate, facilitated by additional proteins and energy from GTP hydrolysis. The mRNA and tRNA are also released.



https://quizlet.com/364283576/topic-translation-termination-diagram/?i=3a41pw&x=1jqt


DIVE INTO THE CELL!

QUIZ

- 10 QUESTIONS

VIBE PROJECT

Virtual Biomedical and STEM/STEAM Education

2021-1-HU01-KA220-HED-000032251

Funded by the European Union

Funded by the European Union. Views and opinions expressed are however those of the author(s) only and do not necessarily reflect those of the European Union or the European Education and Culture Executive Agency (EACEA). Neither the European Union nor EACEA can be held responsible for them.

PÉCSI TUDOMÁNYEGYETEM
UNIVERSITY OF PÉCS

U.PORTO

Politechnika Śląska

DEX innovation centre

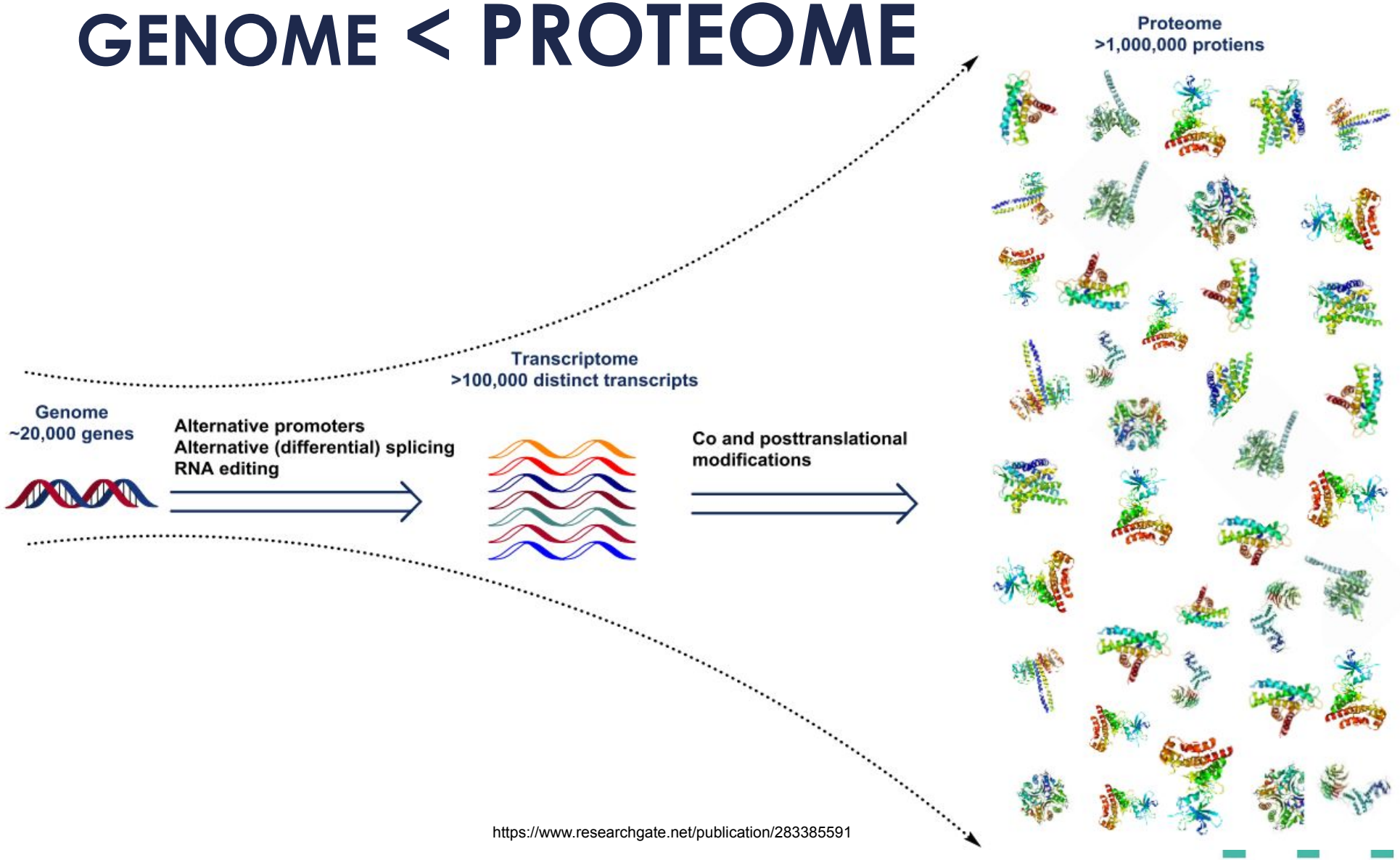
VIBE PROJECT

FROM CELL GENOME TO PROTEOME

3.5. Post-Translational Modifications of Proteins

EXPLORING THE MYSTERIES OF LIFE: AN INTRODUCTION TO CELL BIOLOGY

GENOME < PROTEOME



https://www.researchgate.net/publication/283385591

Post-Translational Modifications (PTMs):

PTM is the covalent process of changing proteins that occurs after their synthesis during translation. These modifications involve the addition or removal of functional groups or the cleavage of peptide bonds, which can significantly alter the protein's activity, stability, localization, and interactions. PTMs may be catalyzed by enzymes or, in some cases, occur spontaneously.

- **Proteolytic cleavage**
- **Chemical modifications**
- **Intein splicing**

Proteolytic cleavage

PROTEASES:

Activation of zymogens (inactive precursors of enzymes)

e.g. digestive proteins (trypsin, chymotrypsin), proteins of coagulation system (prothrombin, plasminogen)

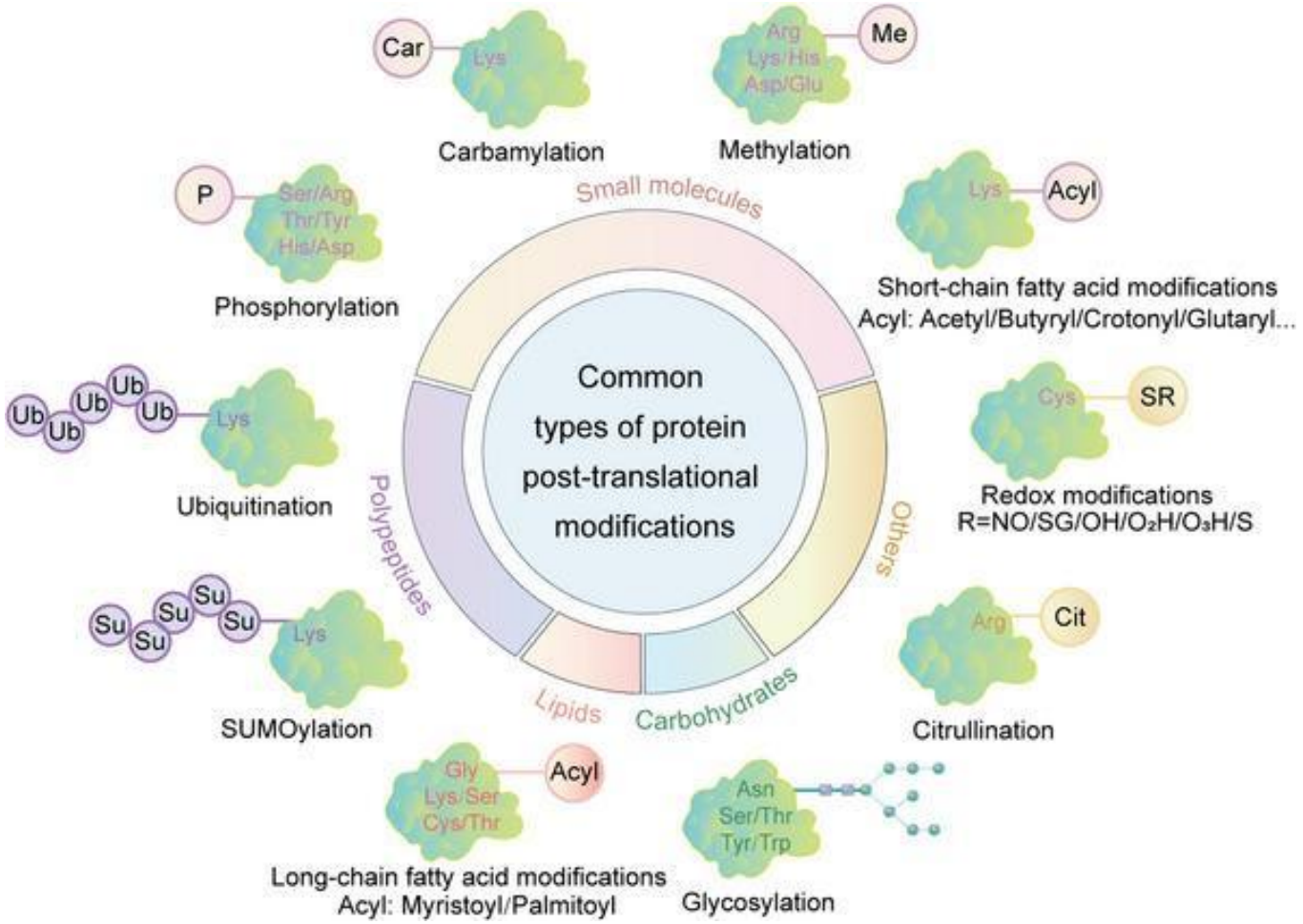
Activation of prohormones (inactive hormones)

e.g. proinsuline

Signal Peptide Removal

e.g. collagen

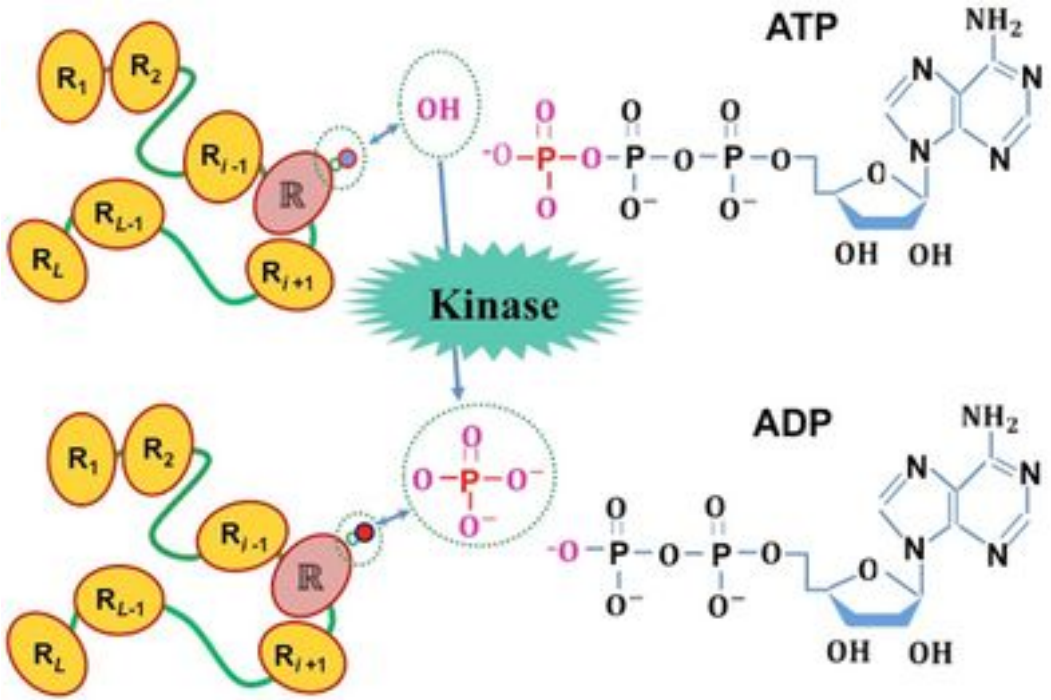
Chemical modifications



doi: 10.1002/mco2.261

Phosphorylation

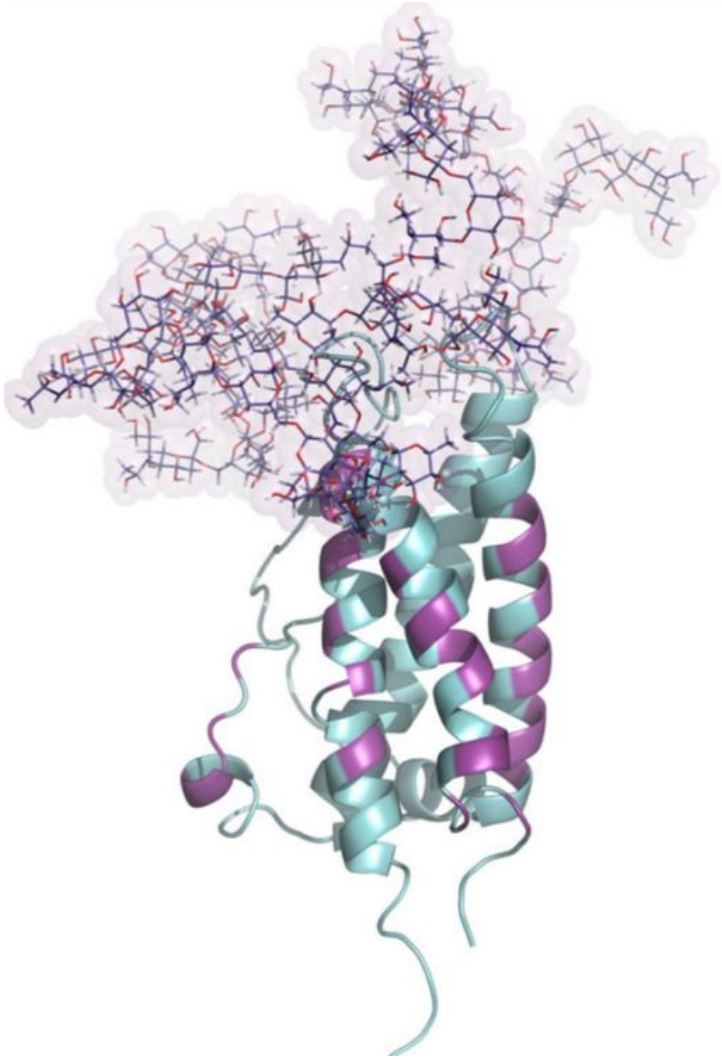
- Addition of a phosphate group (PO_4^{2-})
- Catalyzed by **kinases**
- Occurs on serine, threonine, or tyrosine residues
- Plays central role in signal transduction pathways
- Regulates enzyme activity, cell signaling, and the cell cycle
- Reversible modification **(phospatases)**



https://doi.org/10.1002/minf.201600010

Glycosylation

- Attachment of sugar molecules to proteins
- Catalyzed by **glycosyltransferases**
- **N-linked:** Sugars attached to asparagine (via nitrogen)
- **O-linked:** Sugars attached to serine or threonine (via oxygen)
- Important for protein folding, stability of egzoproteins, membrane proteins, and cell-cell interactions
- Glycosylated proteins, such as antibodies, can exhibit varying **immunological** properties depending on the structure of their sugar chains.



Erythropoietin structure. The oligosaccharide chains are responsible for 40% of its molecular weight.

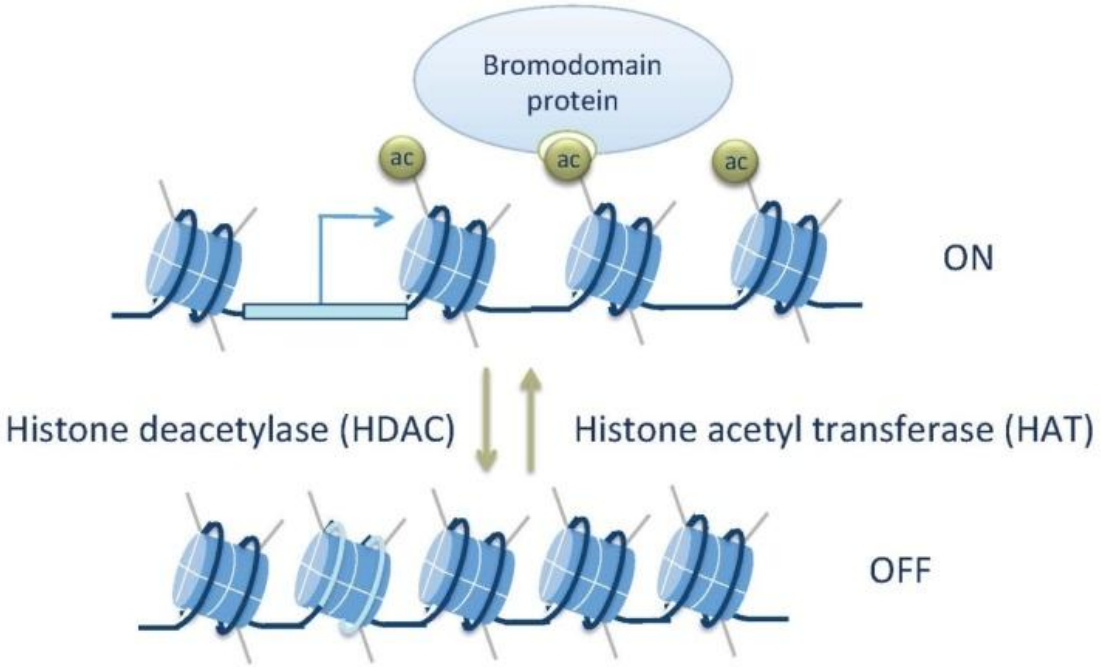
DOI: 10.4103/1673-5374.215240

Acetylation

- Addition of an acetyl group (CH_3CO) to lysine residues
- Catalyzed by **acetyltransferases**
- **Deacetylases** remove acetyl group – reversible mechanism
- Affects protein stability, interactions, and gene expression

HISTONE ACETYLATION

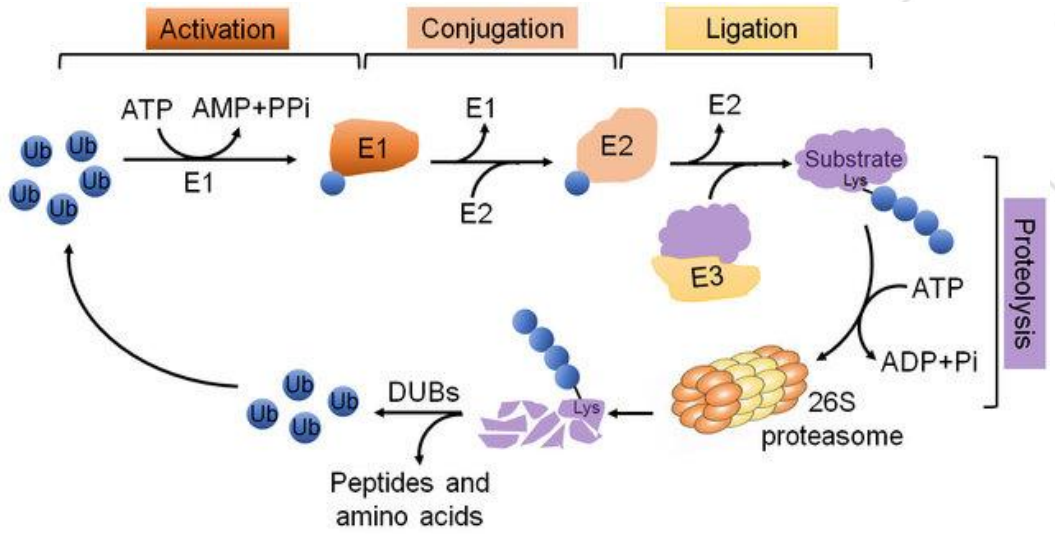
Gene expression regulation: Histone acetylation reduces the positive charge of histones, decreasing their affinity for negatively charged DNA. This loosens DNA packaging, allowing for increased accessibility of genes for transcription.



https://www.su.se/english/research/research-projects/transcription-coregulators-and-histone-acetylation?open-collapse-boxes=research-project-publications

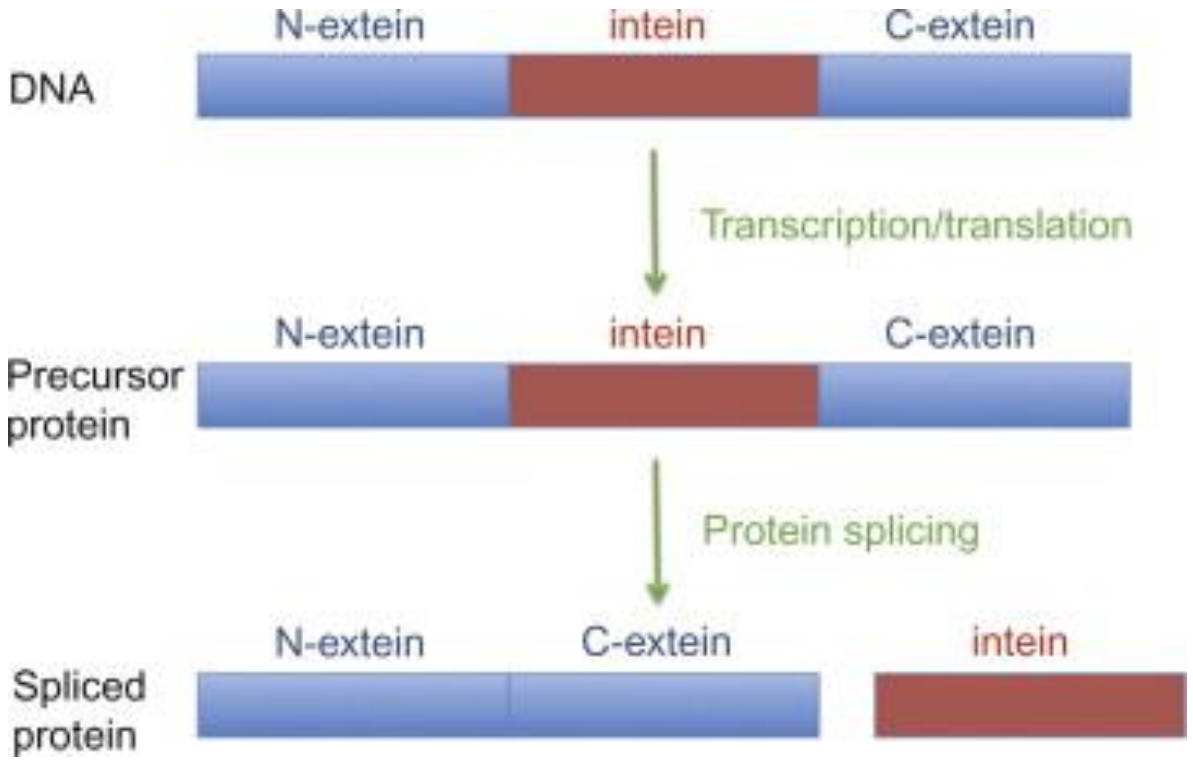
Ubiquitination

- Addition of small protein - ubiquitin - to a target protein (lysine, cysteinę, serine and threonine residues)
- Multistep enzyme cascade (**E1, E2, E3)**
- **Quality Control**: tags proteins for degradation via the proteasome
- Controls protein levels and regulates cell cycle and stress response



DOI: 10.3390/ijms22115754

PROTEIN SPLICING



Neil D. Rawlings, Guy Salvesen, Handbook of Proteolytic Enzymes (Third Edition), Academic Press,2013,ISBN 9780123822192,

More and more examples

quiz

- 10 questions

VIBE PROJECT

Virtual Biomedical and STEM/STEAM Education

2021-1-HU01-KA220-HED-000032251

Funded by the European Union

Funded by the European Union. Views and opinions expressed are however those of the author(s) only and do not necessarily reflect those of the European Union or the European Education and Culture Executive Agency (EACEA). Neither the European Union nor EACEA can be held responsible for them.

PÉCSI TUDOMÁNYEGYETEM
UNIVERSITY OF PÉCS

U.PORTO

Politechnika Śląska

DEX innovation centre

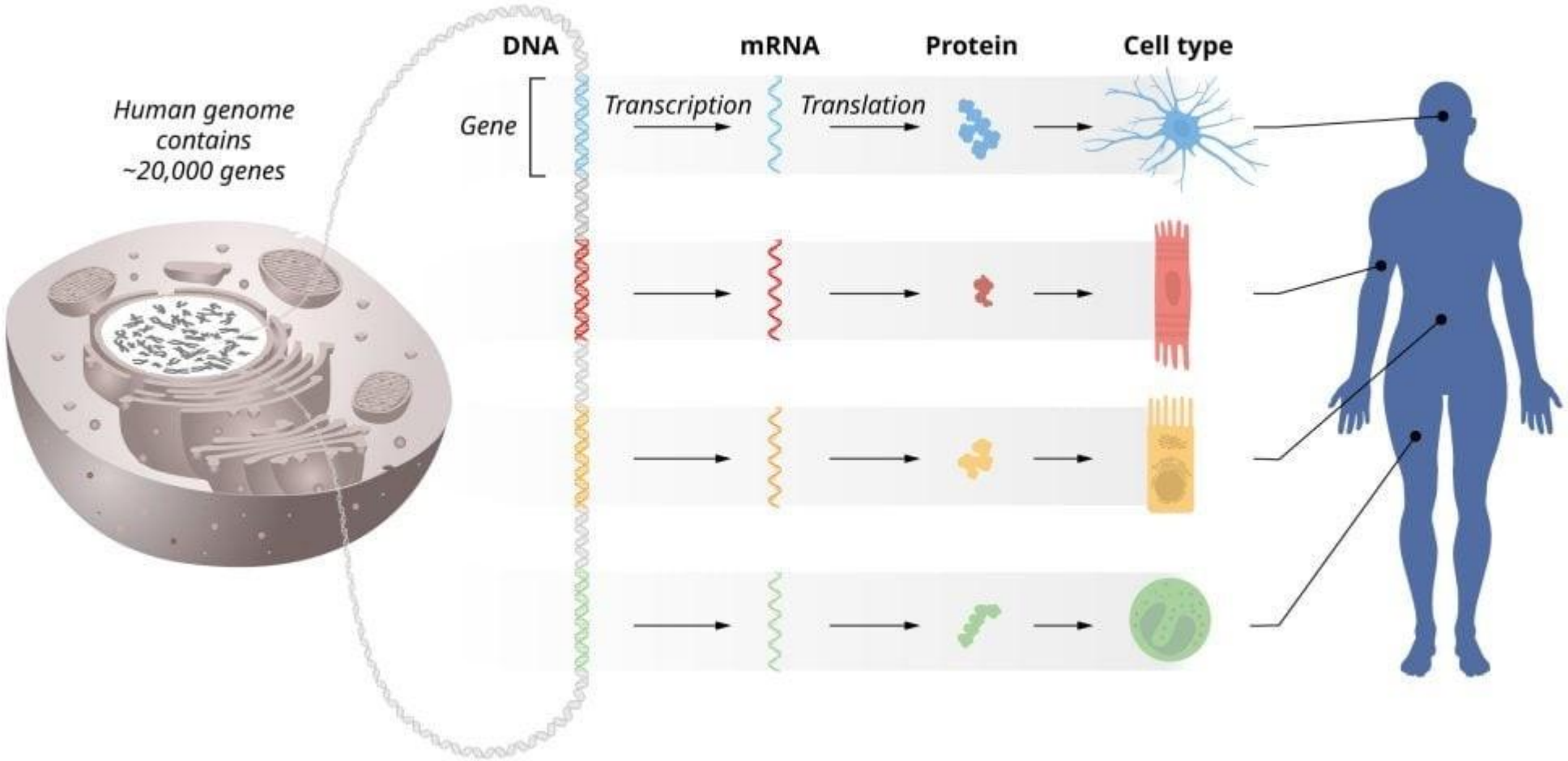
VIBE PROJECT

FROM CELL GENOME TO PROTEOME

3.6. Regulation of Gene Expression

EXPLORING THE MYSTERIES OF LIFE: AN INTRODUCTION TO CELL BIOLOGY

Regulation of Gene Expression



The Nobel Committee for Physiology or Medicine. Ill. Mattias Karlén

Regulation of Gene Expression:

- Ensures proper gene expression in the right cells and at the right time
- Allows cellular differentiation, organ formation, and tissue specialization
- Enables adaptation to environmental changes (e.g., stress, nutrient availability)

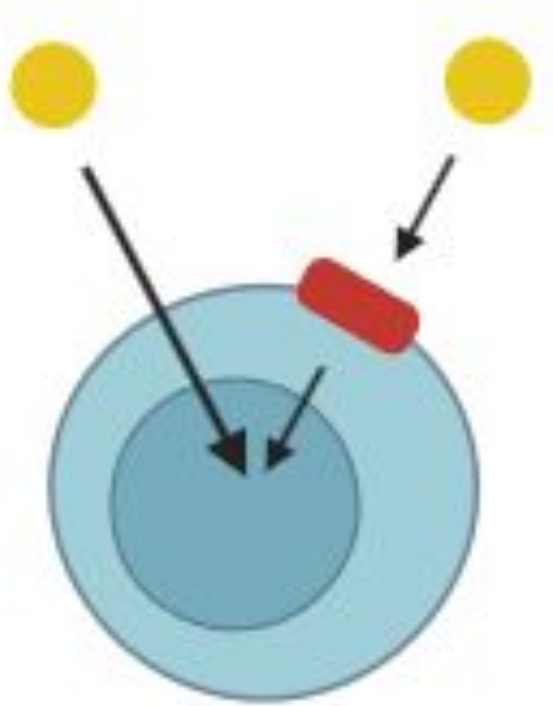
Key Triggers of Regulatory Pathways

- **Hormones:** Chemical messengers like insulin, estrogen, and cortisol bind to receptors, activating signal transduction pathways that regulate gene expression.
- **Growth Factors:** Proteins such as epidermal growth factor (EGF) activate pathways that control cell division, differentiation, and survival.
- **Environmental Signals:** Changes in temperature, light, or oxygen levels can trigger stress response pathways (e.g., heat shock proteins or hypoxia-inducible factors).
- **Nutrients:** Availability of nutrients like glucose, amino acids, or lipids can regulate genes involved in metabolism and energy production.
- **Cellular Stress:** Factors like DNA damage, oxidative stress, or viral infection can activate DNA repair genes and other protective mechanisms.

Direct vs. Indirect Action of Triggers

DIRECT

- Signaling molecule is transported across the cell mebrane



INDIRECT

- Signaling molecule is binding to a cell surgace receptor, which transmits the signal into the cell

Created in https://BioRender.com

Duration of Genome Activity Changes

Short-term

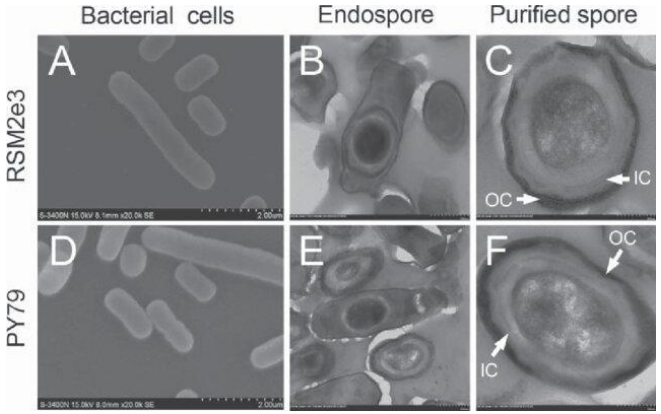
- Continuous proteome remodelling
- Cell adaptation to environmental changes

Long-term

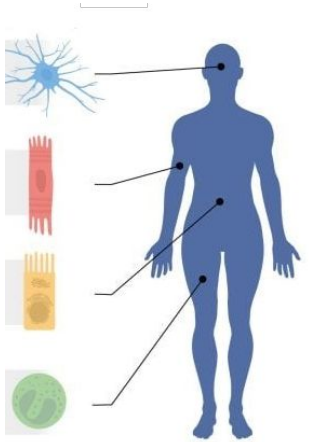
- Long-term proteome specialization
- Cell differentiation

Permanent

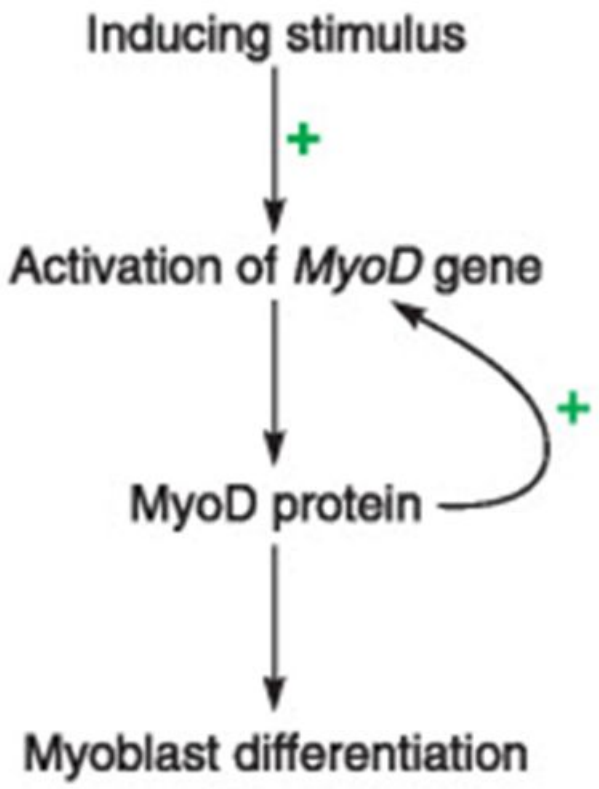
- Permanent proteome specialization
- Cell differentiation

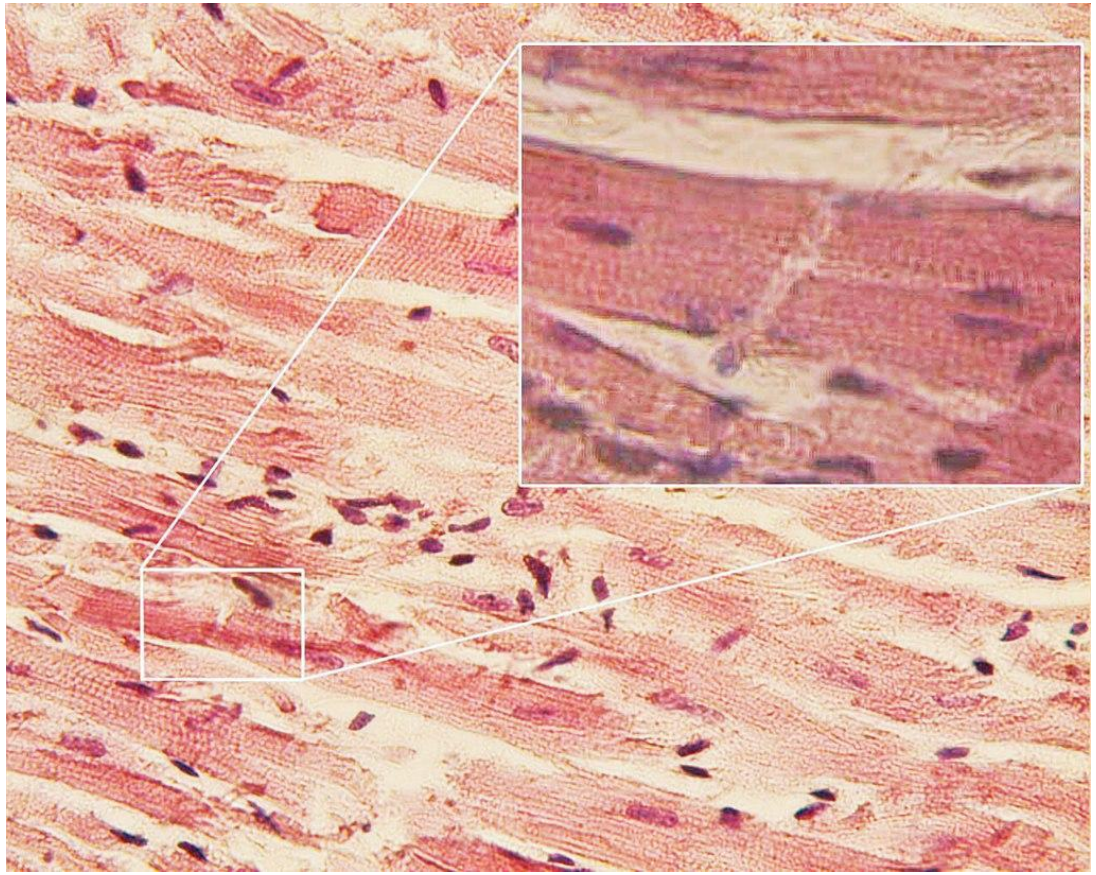


DOI: 10.4161/hv.36122



Feedback loop mechanism

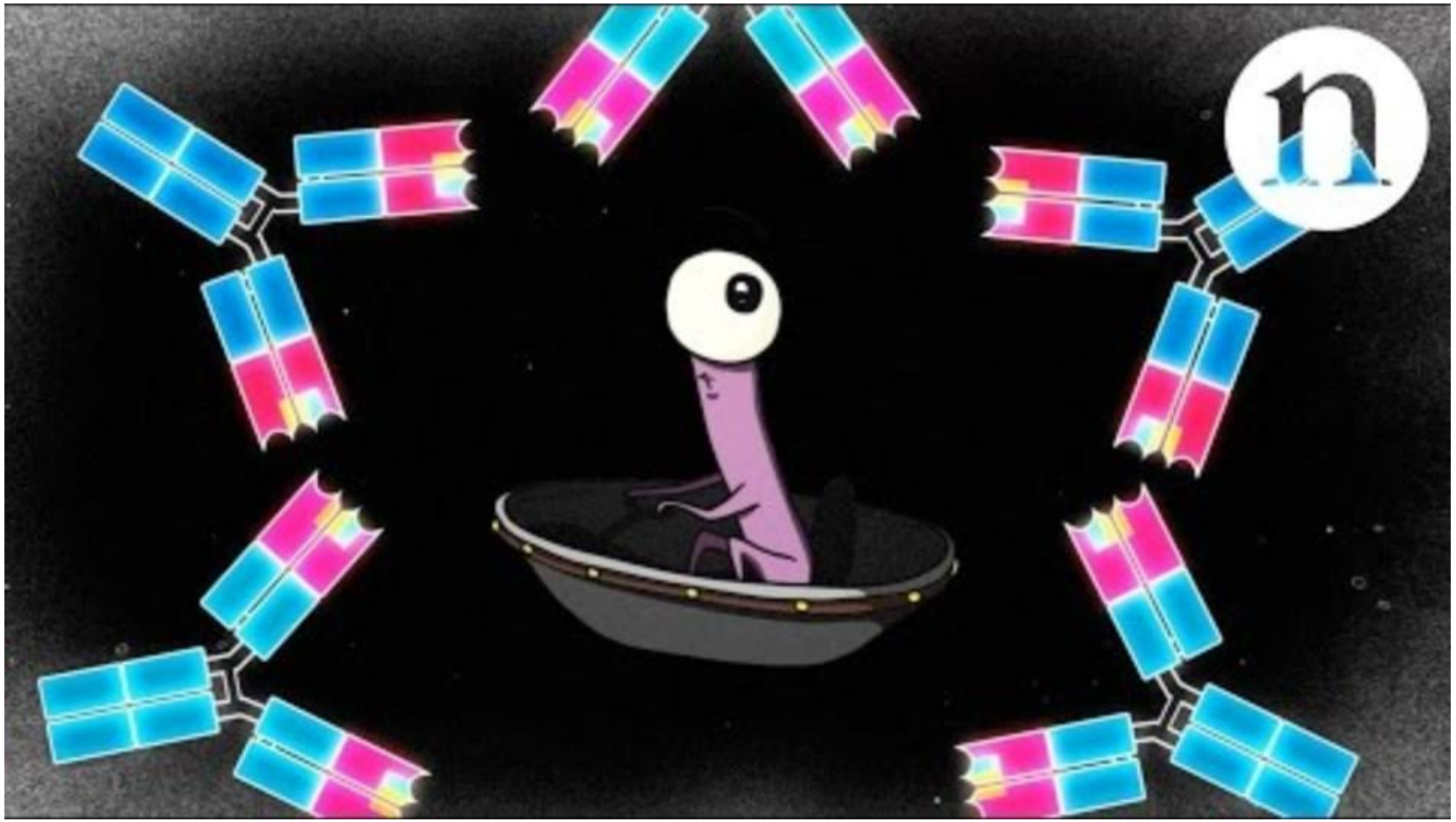




Levels of Gene Regulation

1. **Genome Rearrangements:** Lead to permament changes in the genetic material
2. **Transcriptional Level**: Control of when and how much RNA is synthesized
3. **Post-transcriptional Level:** Modifications to the mRNA transcript and influence its stability, localization, and translation efficiency
4. **Translational Level:** Regulation of mRNA translation into protein
5. **Post-translational Level:** Modifications to proteins after they are made, affecting their activity or stability. These levels provide a range of control mechanisms that allow precise regulation of gene expression

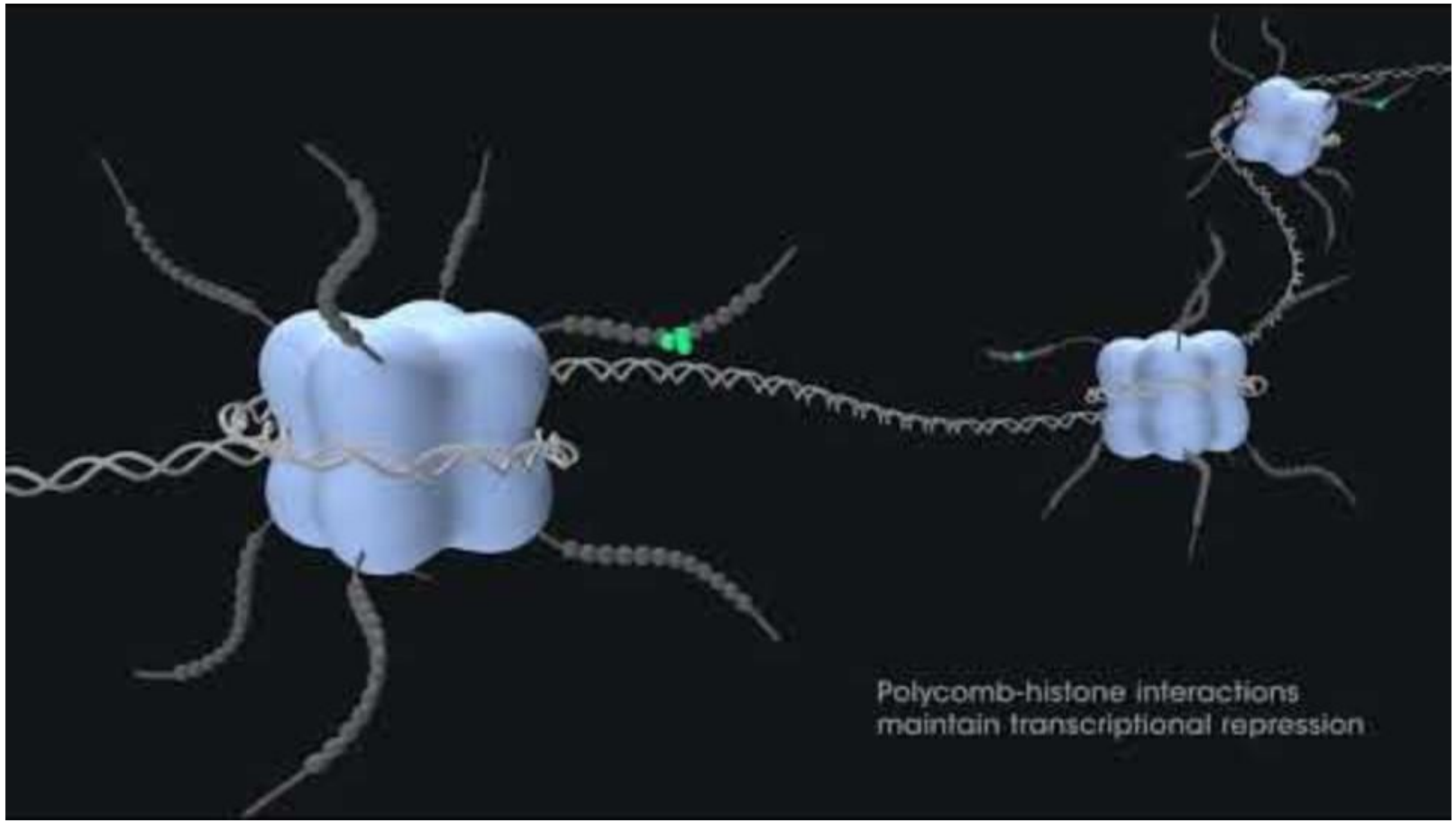
Genome Rearrangmenets – Antibody Diversity



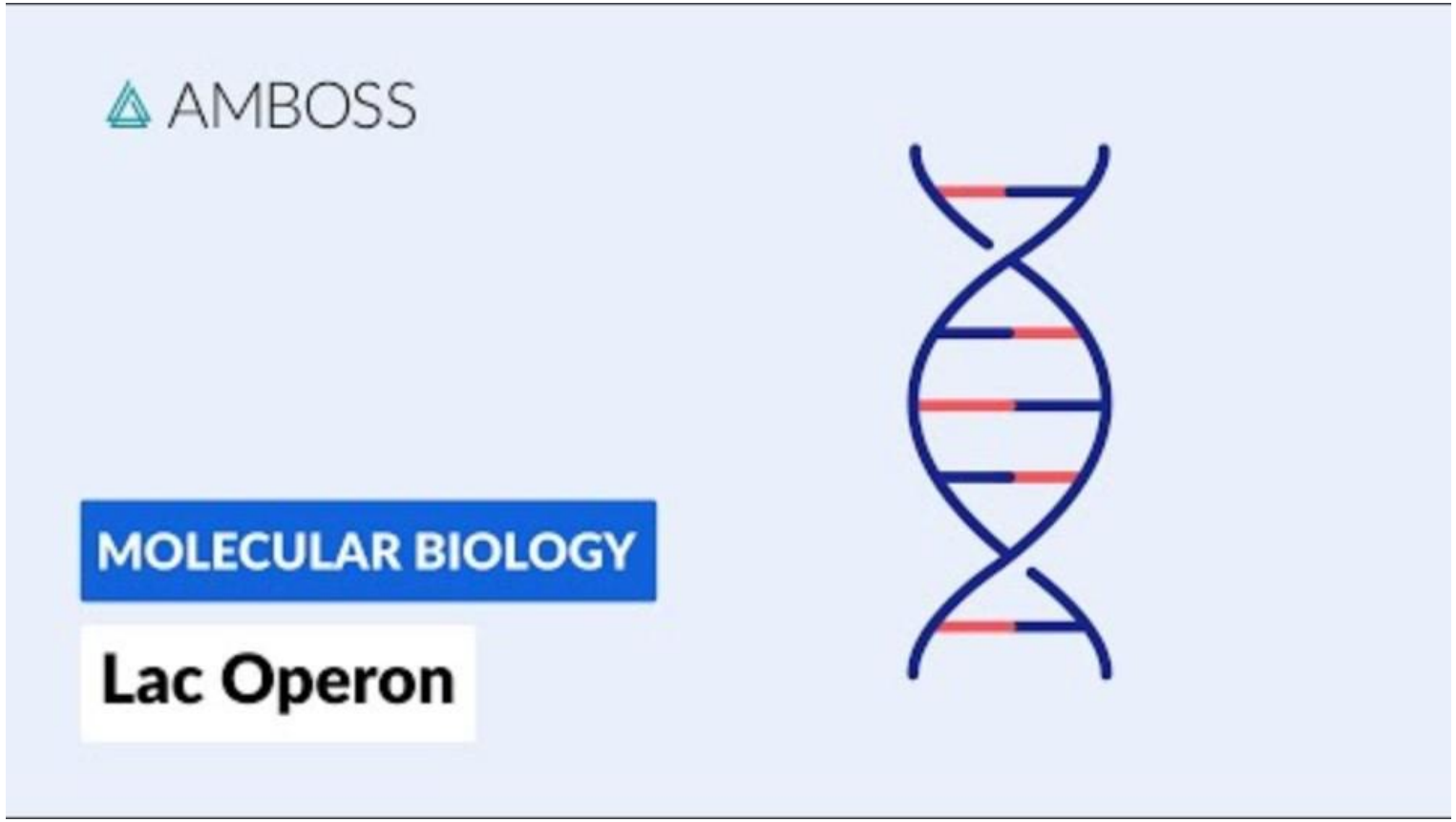
Level: Transcription

STAGE	EXAMPLE OF REGULATION
Gene availability	**Epigenetics (Eukaryota)**: Changes in gene expression without altering DNA sequence. •**DNA Acetylation**: Increases gene expression by loosening chromatin structure. •**DNA Methylation**: Represses gene expression by adding methyl groups to DNA.
	Histone modifications affect chromatin structure and determine which genes are accessible
Transcription initiation	Efficient initiation is influenced by activators, repressors and other control systems •**Transcription Factors**: Proteins that regulate gene expression by binding to DNA. •**Enhancers**: DNA sequences that increase transcription by interacting with transcription factors.

Changes in chromatin structure

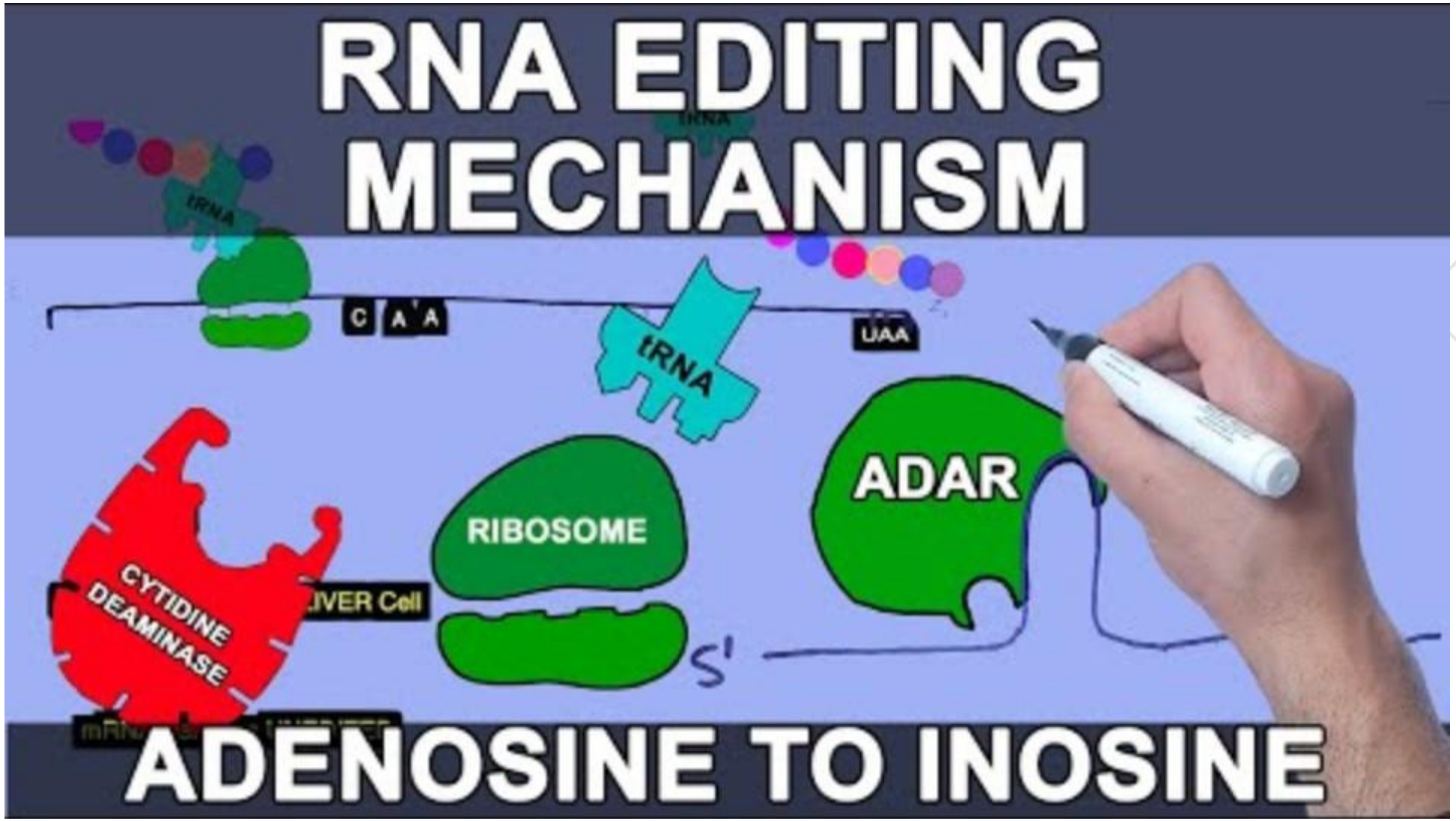


Level Gene Regulation in Prokaryotes: The Lac Operon



Level: Post-transcriptional

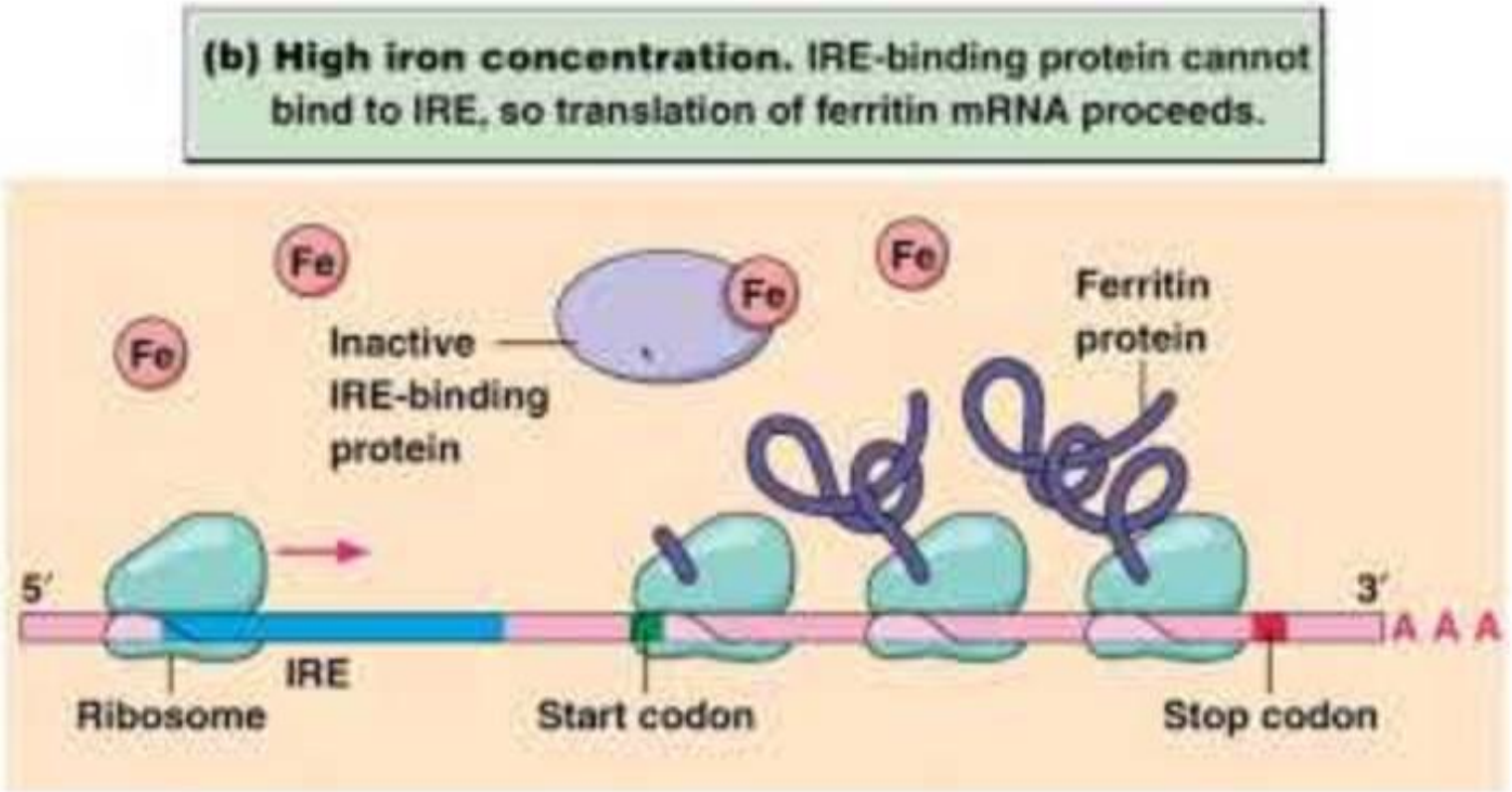
STAGE	EXAMPLE OF REGULATION
mRNA editing	**5’ Capping process + Polyadenylation** Regulating protein synthesis through poly(A) tail elongation to activate dormant maternal mRNAs during oogenesis and early development 
	RNA editing of apolipoprotein B mRNA leads to liver- and intestine-specific forms of this protein


RNA EDITING MECHANISM
tRNA
C A A
tRNA
UAA
ADAR
RIBOSOME
CYTIDINE DEAMINASE
LIVER Cell
5'
ADENOSINE TO INOSINE

Level: Translational and Post-Translational

STAGE	EXAMPLE OF REGULATION
Translation initiation	In some eukaryotes, iron controls the search for the initiation codon by ribosomes in the ferritin mRNA
Protein synthesis	Frameshifting allows translation of the two subunits of DNA polymerase III from the *E. coli dnaX* gene
Post-translational modifications	Alternative cleavage of polyproteins leads to the formation of tissue-specific protein products
	Many proteins involved in signal transduction are activated by phosphorylation

high Iron —> translation



QUIZ

VIBE PROJECT

Virtual Biomedical and STEM/STEAM Education

2021-1-HU01-KA220-HED-000032251

Funded by the European Union

Funded by the European Union. Views and opinions expressed are however those of the author(s) only and do not necessarily reflect those of the European Union or the European Education and Culture Executive Agency (EACEA). Neither the European Union nor EACEA can be held responsible for them.

PÉCSI TUDOMÁNYEGYETEM
UNIVERSITY OF PÉCS

U.PORTO

Politechnika Śląska

DEX innovation centre