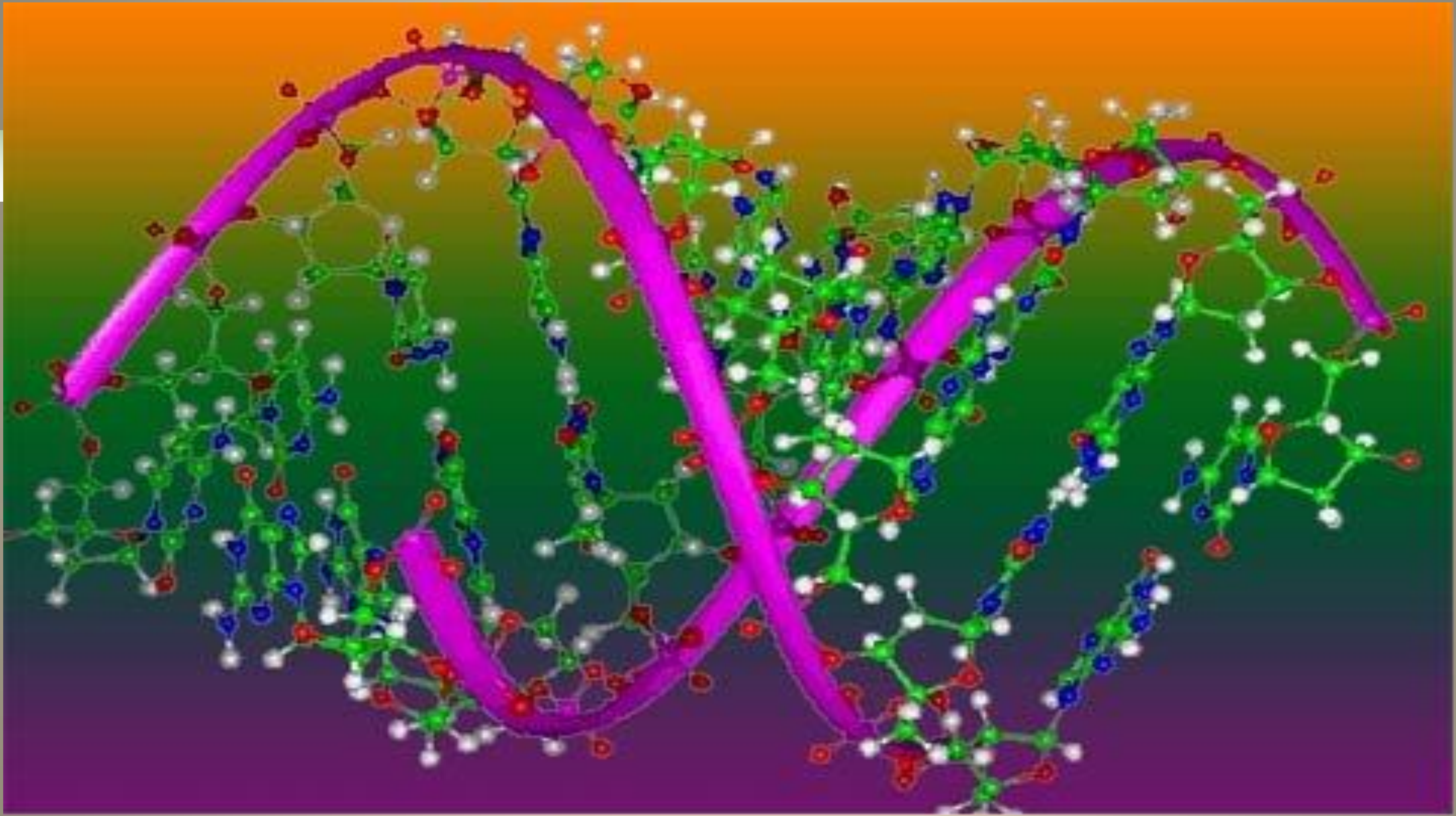


Lecture 5

- ***Implementation of genetic information: transcription, translation***

Key nucleus functions: storage and transmitting genetic information

- ***At the lecture, we consider the second function:***

implementation of hereditary information

And how is genetic information implemented??

- \- It is carried out in the process of transcription and translation

- ***Transcription*** **is a mechanism for transferring information from DNA to RNA, which ensures only part of the information encoded in DNA**

Translation **- the process of translating the genetic information stored in the nucleotide sequence of**

m-RNA in amino acid sequence

of polypeptide protein chain

RNA transcription

Transcription - the first stage of the hereditary information: Synthesis I-RNA (RNA of all kinds). ***Transcription*** unit - operon in prokaryotes, transcripton in eukaryotes; ***Matrix for transcription*** - one of DNA strands is kodogenic ***Principle of transcription -*** complementarity . ***Transcription product*** - all types of RNA:

Other types of RNAs

- **snRNAs - small nuclear RNAs**, function in a variety of nuclear processes, including the splicing of pre-mRNA
- **snoRNAs - small nucleolar RNAs**, used to process and chemically modify rRNAs
- **miRNAs - microRNAs**, regulate gene expression typically by blocking translation of selective mRNAs
- **siRNAs - small interfering RNAs**, turn off gene expression by directing degradation of selective mRNAs and the establishment of compact chromatin structures
- **Other noncoding RNAs** -function in diverse cell processes, including telomere synthesis, X-chromosome inactivation, and the transport of proteins into the ER

Types of RNAs

Three types of RNA are directly involved in protein synthesis:

1. ***mRNAs*** - messenger RNAs, code for proteins
2. ***rRNAs*** - ribosomal RNAs, form the basic structure of the **ribosome** and catalyze protein synthesis
3. ***tRNAs*** - transfer RNAs, central to protein synthesis as adaptors between mRNA and amino acids

Conditions for transcription

- ***1.presence of transkripton in DNA***

2. ***ribonucleotides***: nATF, nUTF, nTTF, nGTF

3.faktors of initiationA and B (initiate unwinding of the spiral in the DNA)

4.faktors of elongation (E, H, F) increase the activity of the RNA enzyme polymerase

5.protein factors of transcription (shl, CTF, B-protein), which help the RNA enzyme polymerase find promoter site of transkripton and joins enzyme

6. ***RNA enzyme polymerase***

***7.TATA factor*-**factor protein that joins RNA polymerase enzyme to promotion site of transkripton

8.DNK dependent RNA polymerase (I, II, III),

9.Ions of Mg and Mn

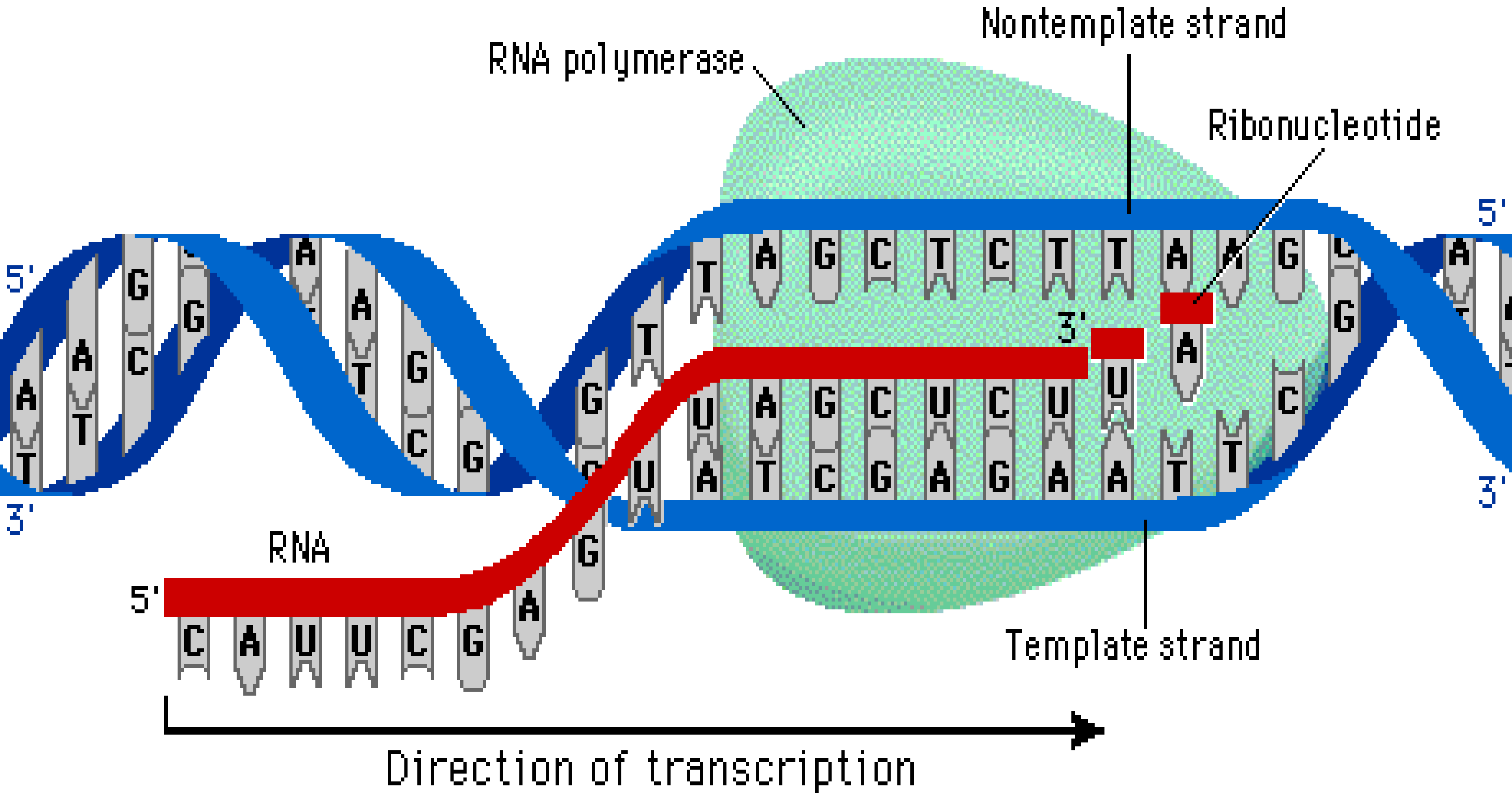
- **10.*ATF*,**

11.ferment ***poly A polymerase*** synthesizes a primary portion of mRNA 3 'end and forms a portion of polyadenylic tRNA

12.***Spliceosomes***-involved in the recognition of the boundaries between intron and exon, cut introns and join

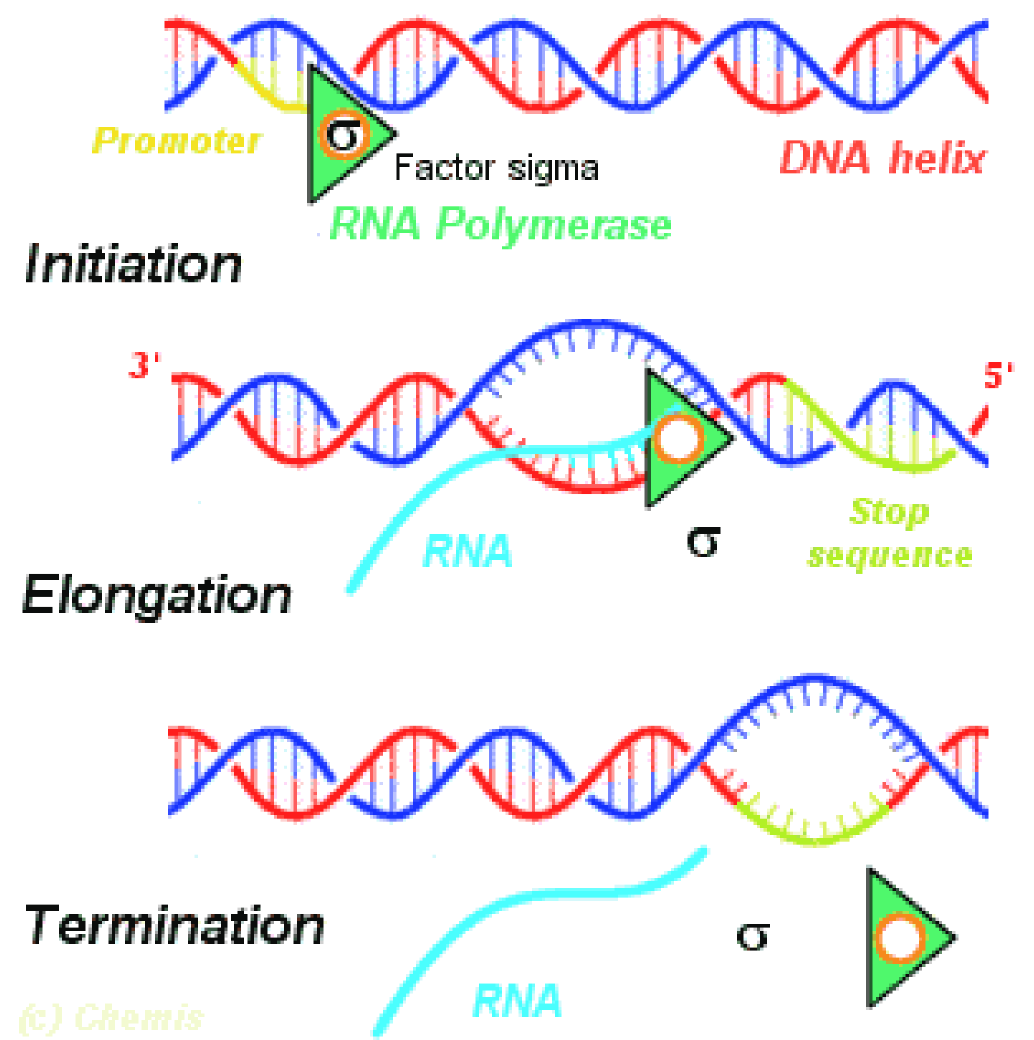
- exons

The process of transcription and stages of transcription:



Stages of transcription

- Transcription mechanism similar to the mechanism of replication DNA



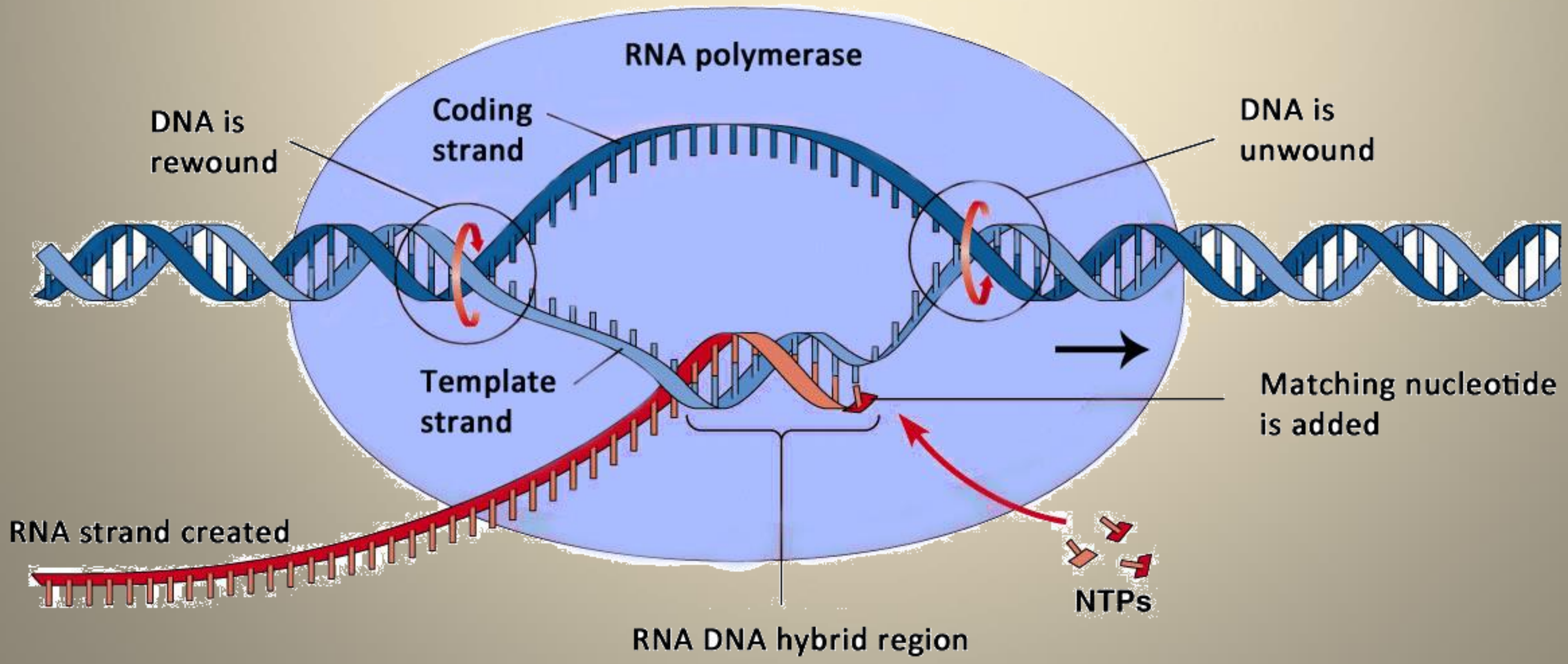
Transcription occurs in three stages:

- ***Initiation***
- ***Elongation***
- ***Termination***
- ***Modification (processing***

Sense and anti-sense strands of DNA

The template for transcription is only one strand of DNA. It is called ***template*** or ***antisense.***

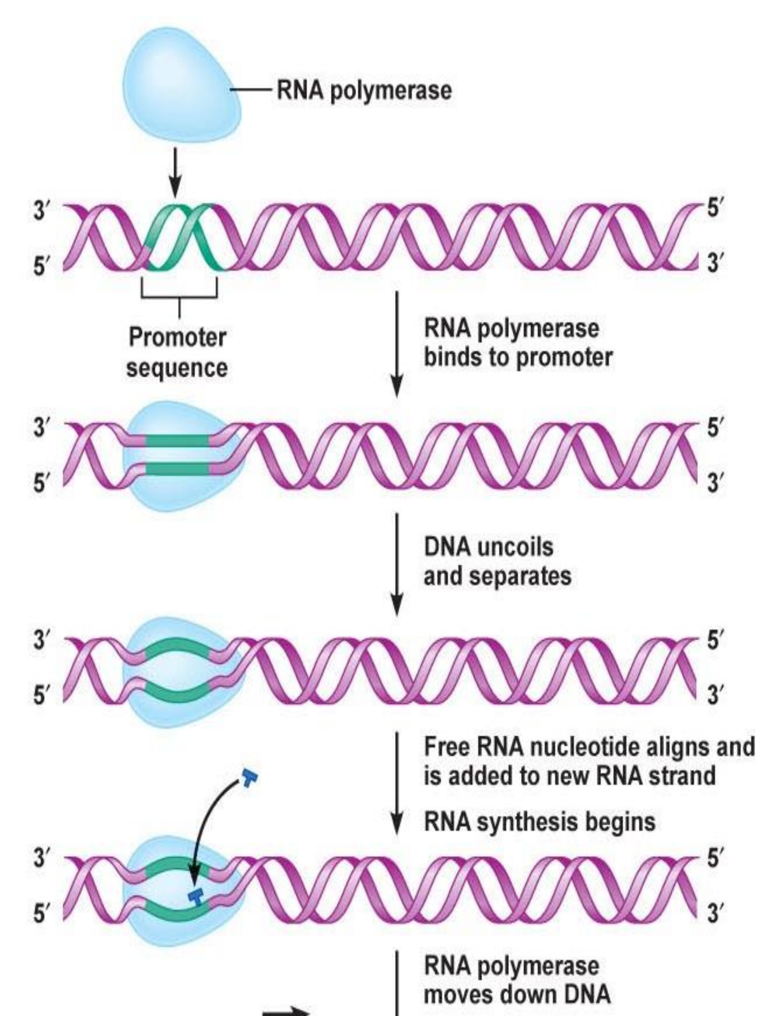
The second chain which is not involved in the transcription called ***coding*** or ***sense,*** since ***its nucleotide sequence corresponds to the nucleotide sequence of RNA synthesized***



Distinguish between the sense and anti-sense strands of DNA

- the ***sense strand*** is the ***coding strand*** and has the same base sequence as mRNA, with uracil instead of thymine
- the ***anti-sense strand is transcribed*** and has the same base sequence as tRNA, with uracil instead of thymine

1. ***Initiation*** - the process begins with the initiating codon of the promoter to which RNA polymerase joins

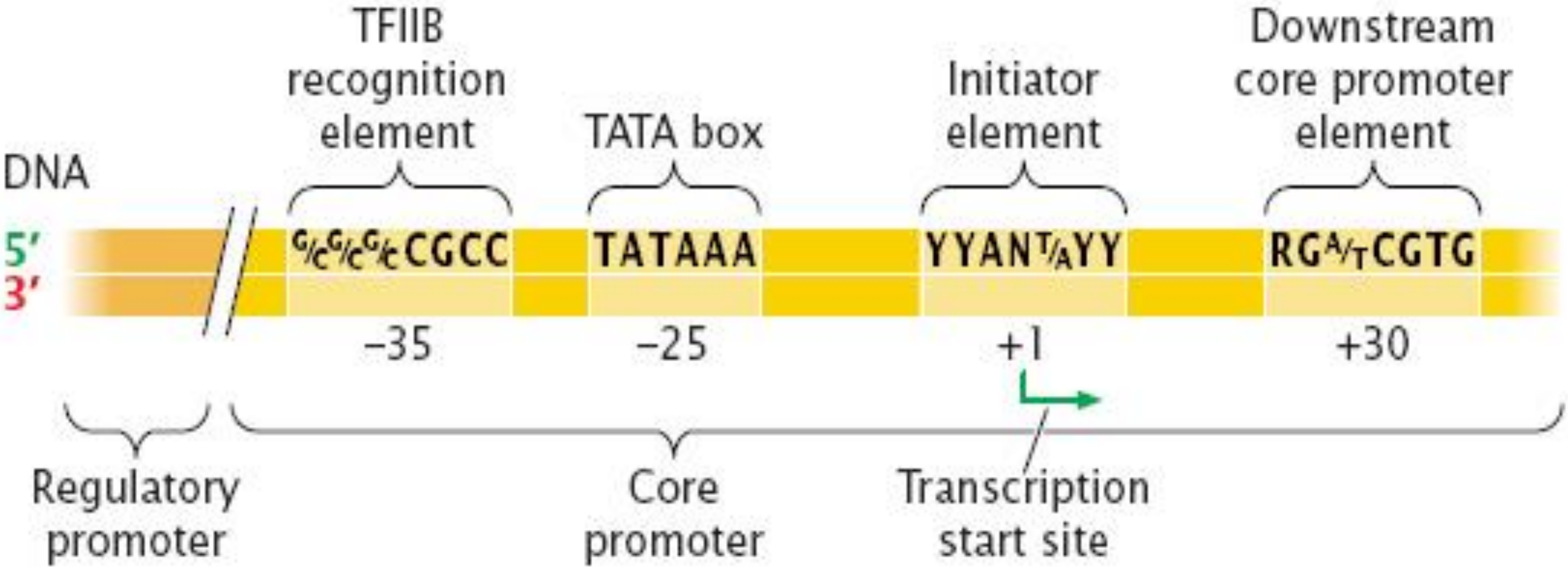


Initiation : The first step in transcription is ***initiation,*** when the ***RNA pol*** binds to the DNA upstream (5′) of the gene at a specialized sequence called a ***promoter.***

RNA polymerase unwinds and unzips DNA double strand, attaches to ***promoter region*** of gene, which marks the beginning point for transcription

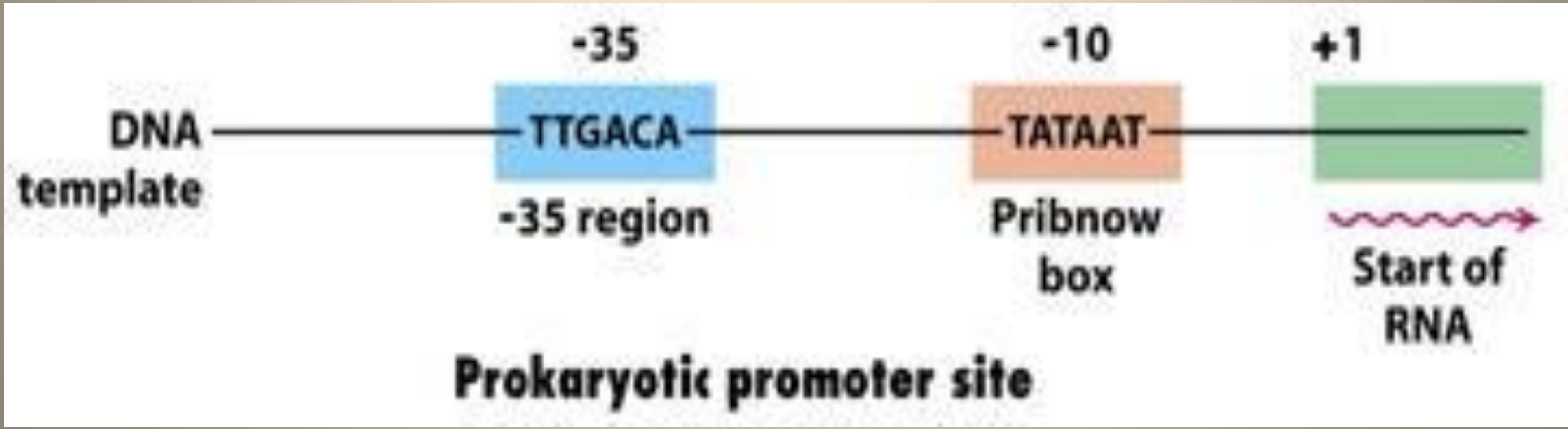
Promoter

- In bacteria, promoters are usually composed of three sequence elements, whereas in eukaryotes, there are as many as seven elements.



Prokaryotic promoter

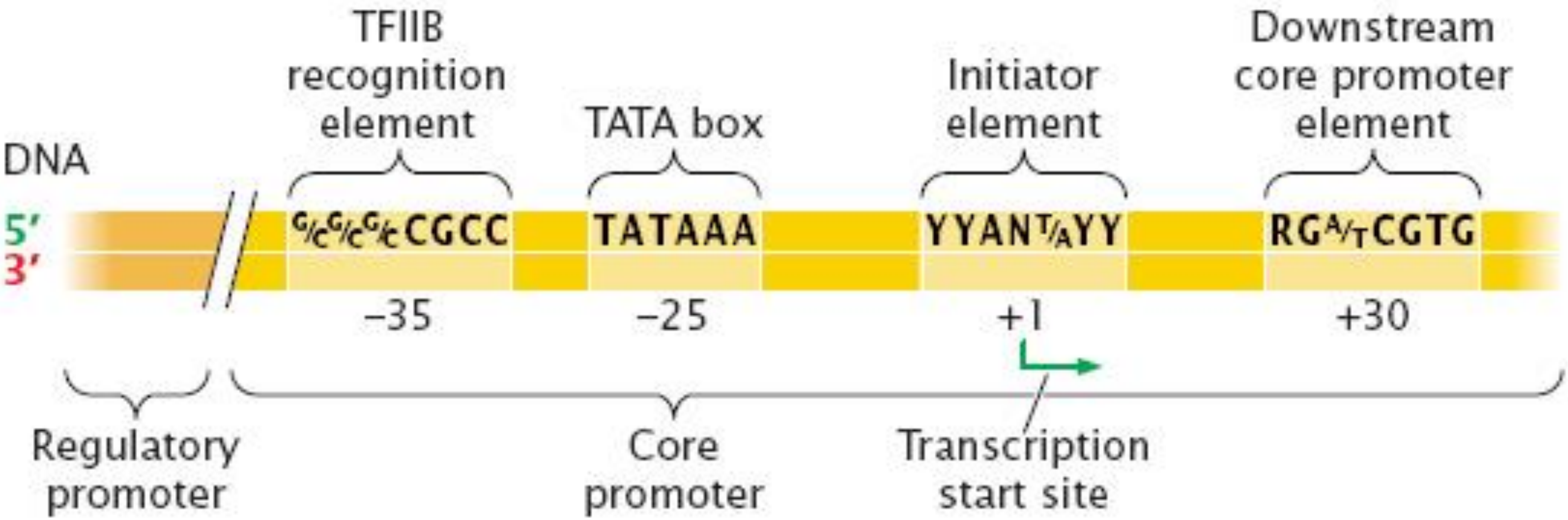
- In prokaryotes, most genes have a sequence called the ***Pribnow box***, with the consensus sequence TATAAT positioned about ***ten base pairs*** away from the site that serves as the location of transcription initiation.
- Many genes also have the consensus sequence TTGCCA at a position ***35 bases upstream*** of the start site, and some have what is called an ***upstream element***, which is an A-T rich region 40 to 60 nucleotides upstream that enhances the rate of transcription



Prokaryotic promoter site

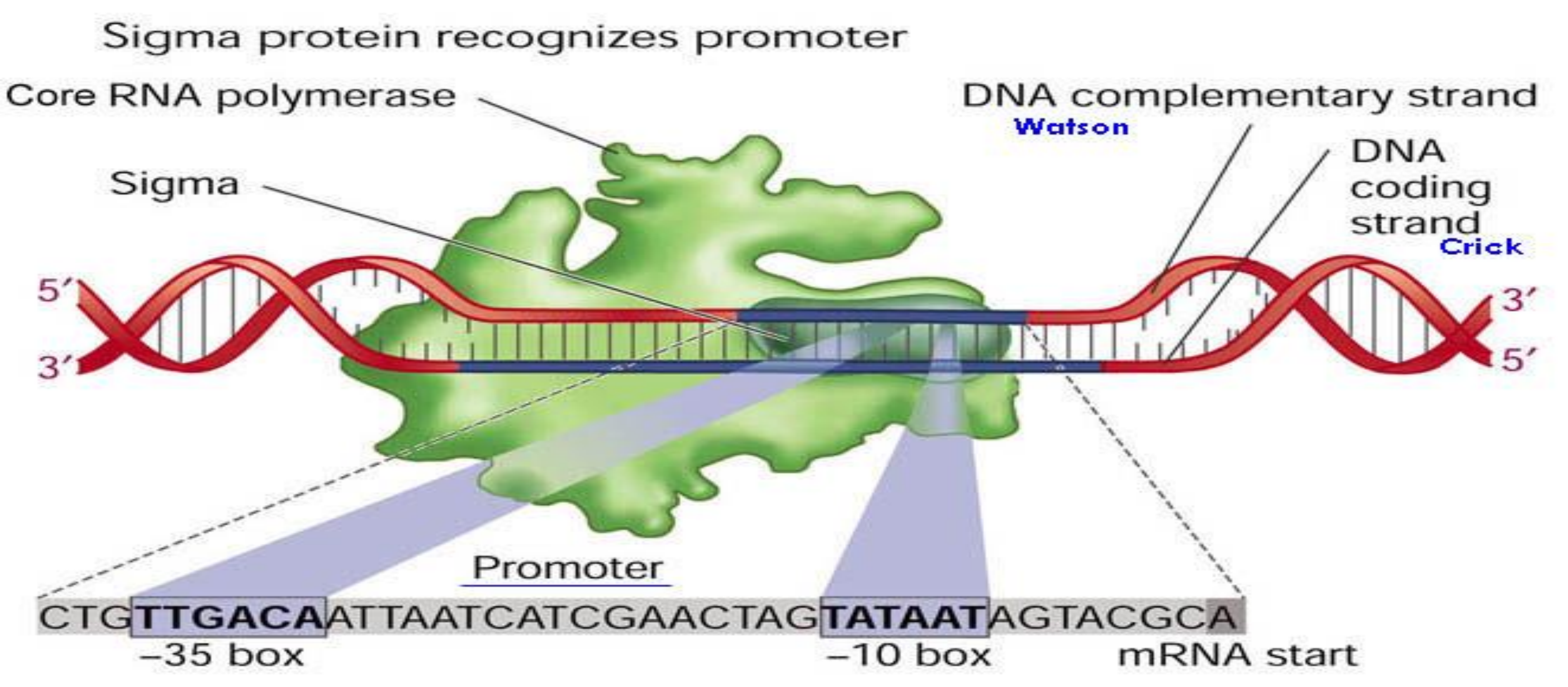
Eukaryotic promoters

- In eukaryotes, the "core" promoter for a gene transcribed by pol II is most often found immediately upstream (5′) of the start site of the gene. Most pol II genes have a ***TATA box*** (consensus sequence TATTAA) 25 to 35 bases **upstream** of the initiation site, which affects the transcription rate and determines location of the start site.



RNA polymerase is an enzyme complex

- Because eukaryotic DNA is tightly packaged as chromatin, transcription also requires a number of specialized proteins ***(transcription factors or cofactors***) that help make the coding strand accessible.
- The most important - the ***sigma factor***, **TFIID** cofactors each and each performs its role in the process of translation



Types of RNA polymerase

There are three different types of ***RNA polymerase*** in eukaryotic cells (bacteria have only one):

RNA pol I **-** transcribes the genes that encode most of the ***ribosomal RNAs*** (rRNAs)

RNA pol II - transcribes the ***messenger RNAs***

RNA pol III - transcribes the genes ***transfer RNAs, one small rRNA***, other small regulatory RNA molecules.

Types of RNA polymerase

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2. ***Elongation*** is the principle of complementarity to the 5'-/ to the 3 'end and there is the construction of pro -precursor RNA- on the DNA matrix

3.Process of termination of RNA synthesis comes to a stop codon (UAA, UAG, UGA).

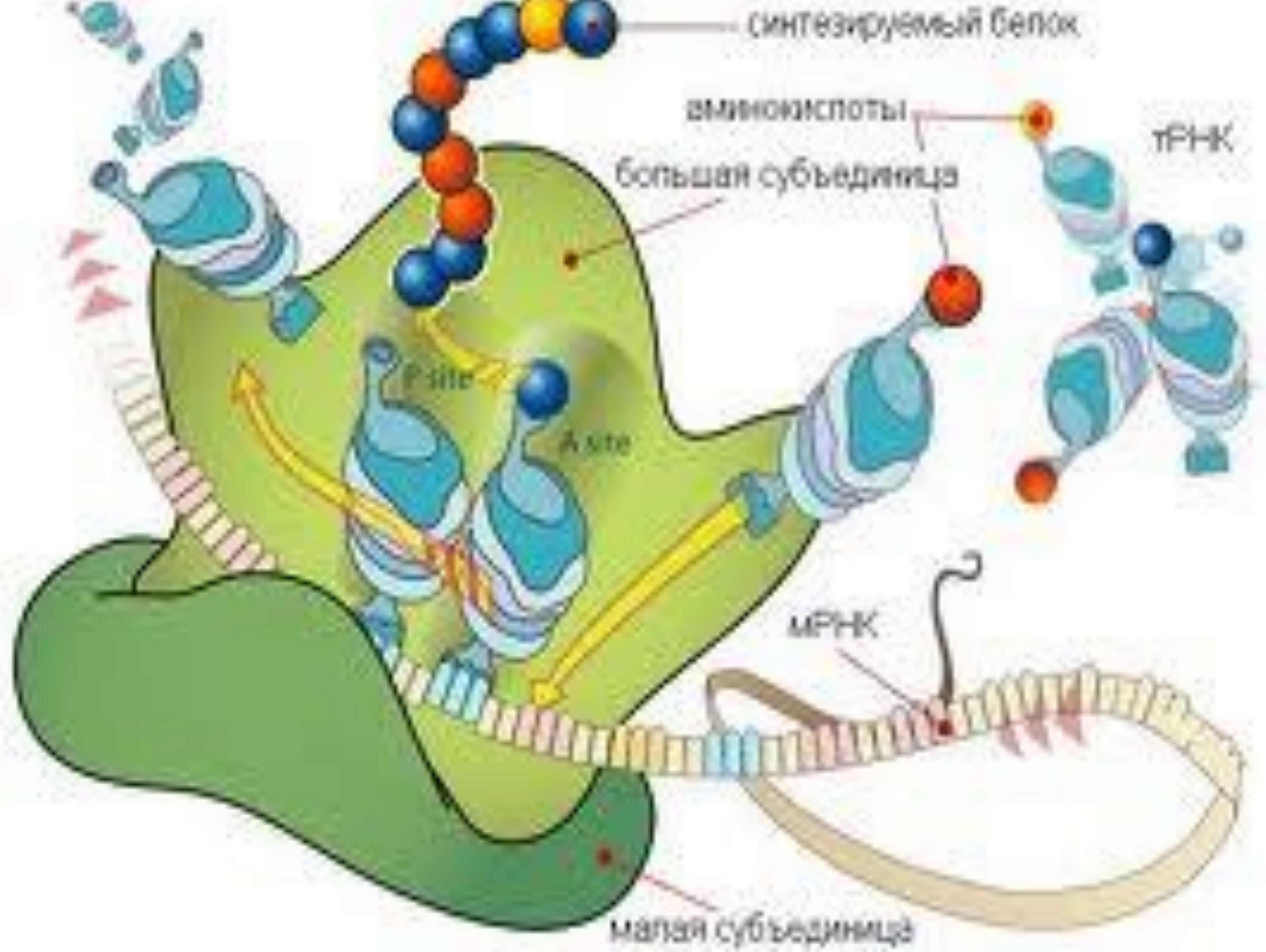
The result is a pro-RNA.

And last

4. Modification (processing)

- 4. **Modification (processing)** - a process of maturation of pro – RNA to i-RNA, which occurs in 3 stages:
  a). **capping the 5'-end**, which consists in joining to this end of the mRNA a so called cap (cap-structure, which is formed by GTP nucleotides)
  b).**polyadenilisation 3'-addition of poly A** nucleotides as well for storing information on the terminal end
  v**).splicing** – cuting introns from mRNA and exons connection through a phosphodiester bond the result is a messenger RNA and its transport from the nucleus to the cytoplasm through the nuclear pores.

Translation (Protein synthesis)


синтезируемый белок
аминокислоты
тРНК
большая субъединица
P site
A site
мРНК
малая субъединица

Translation

(Protein synthesis)

- ***Translation*** is the process of transferring of genetic information stored in the nucleotide sequence of the mRNA in the amino acid sequence

of the polypeptide chain: from mRNA to aminoacid. As a result protein is synthesized. Protein biosynthesis is an important process in nature

***Stages of protein synthesis*:**

1.cytosolic
2.ribosomal

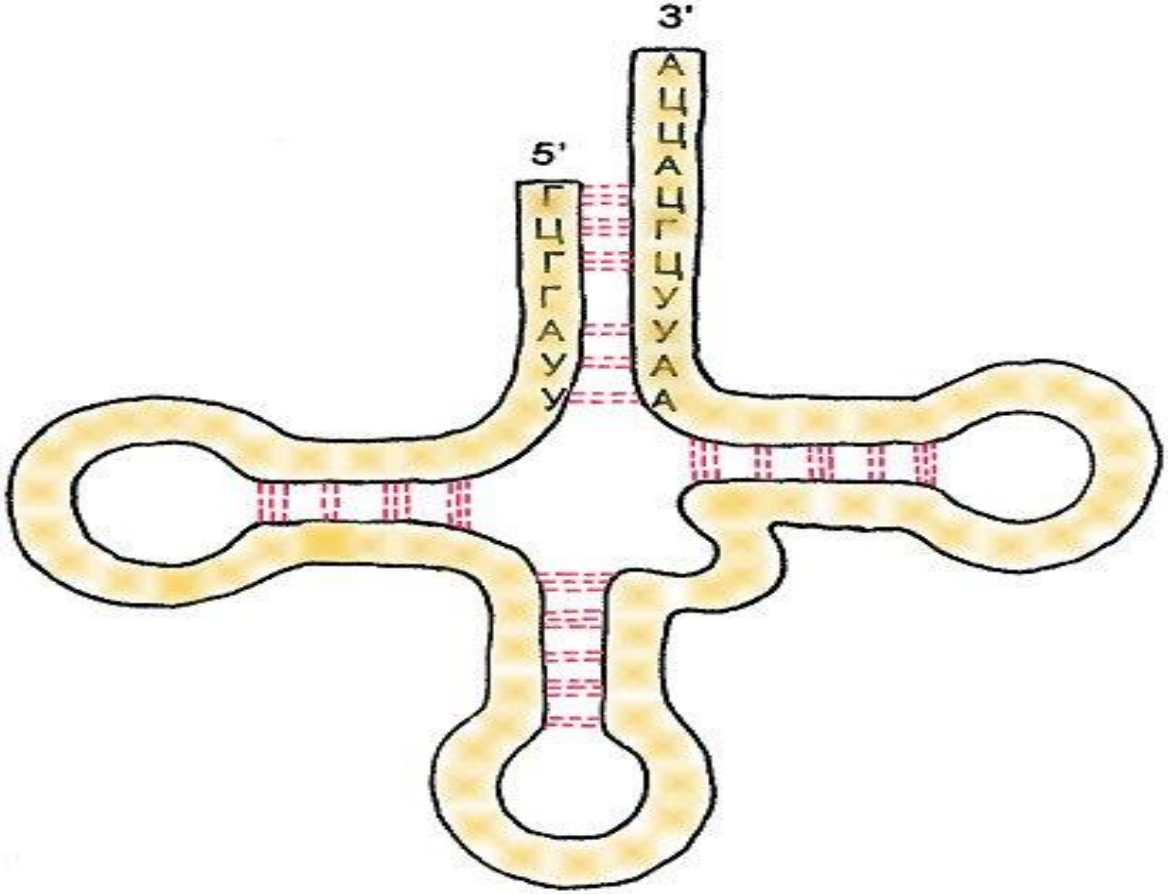
Conditions required for translation

- Matrix for ***translation*** : messenger RNA (mRNA)

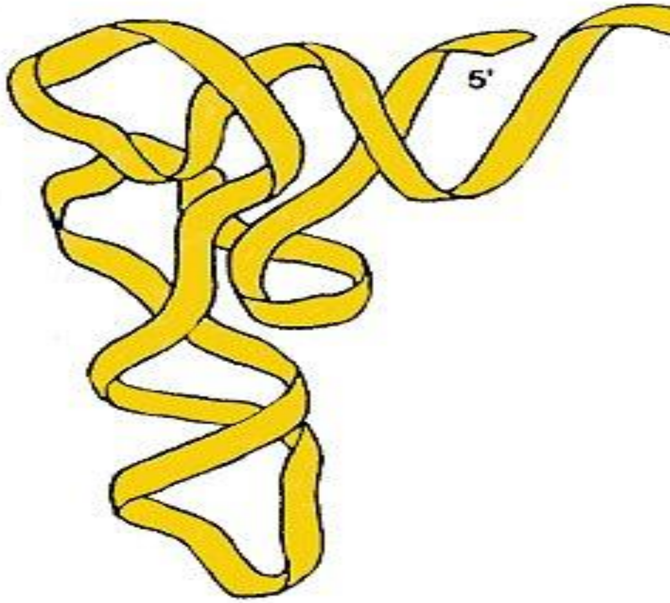
2.Principle of translation: **complementarity**

3.Product of translation: ***primary polypeptide***

Transport RNA



Структура молекулы тРНК с водородными связями, похожая на клеверный лист. Первичная последовательность указана только для части молекулы



Третичная структура

Translation conditions:

Activity of tRNA:

in D - loop of tRNA (acceptor branch) - work enzymes aminoacyl-tRNA synthetase, they activate amino acids and load them into tRNA. Each synthetase (minimum 20) recognizes only its amino acid and puts it on its tRNA;

in the T-loop of tRNA enzymes work to ensure joing to the ribosomal subunit of tRNA

2.Ribosomyes- the center for reading genetic information. It consists of two subunits : small and large .

On the ribosome synthesized protein interacts with tRNA and mRNA. The ribosome is involved in the formation of peptide bonds between amino acid residues .

In the center of the ribosome has 2 centres:

_**aminoacyl** - (center of recognition amino acids) and

- **peptidyl** (center of joining amino acids to the peptide chain) .

3.Aminoacids build blocks of proteins

4. ATF energy

Cytosolic protein biosynthesis stage : At this stage, the recognition , selection of amino acids and their joining to the tRNA

Stages of protein biosynthesis:

cytosolic stage

ribosomal stage

- **Cytosolic stage** : At this stage, the recognition , selection of amino acids and their joining to the tRNA and amino acid activation and its transfer to the tRNA .

Ribosomal stage : At this stage, the assembly of the polypeptide chain on ribosomes in accordance with the genetic code .

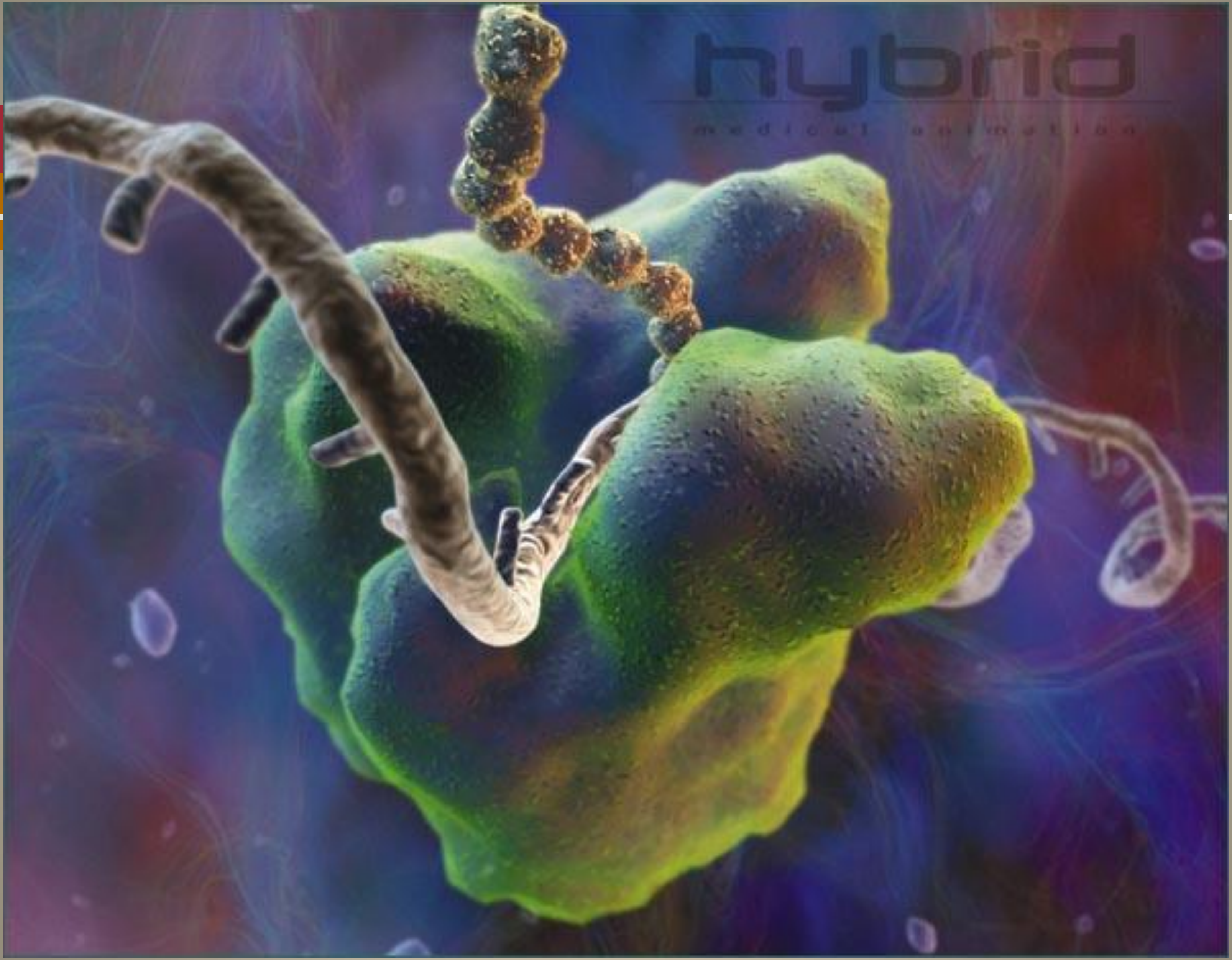
Stops of **ribosomal stages:initiation** - initiation complex assembly ,

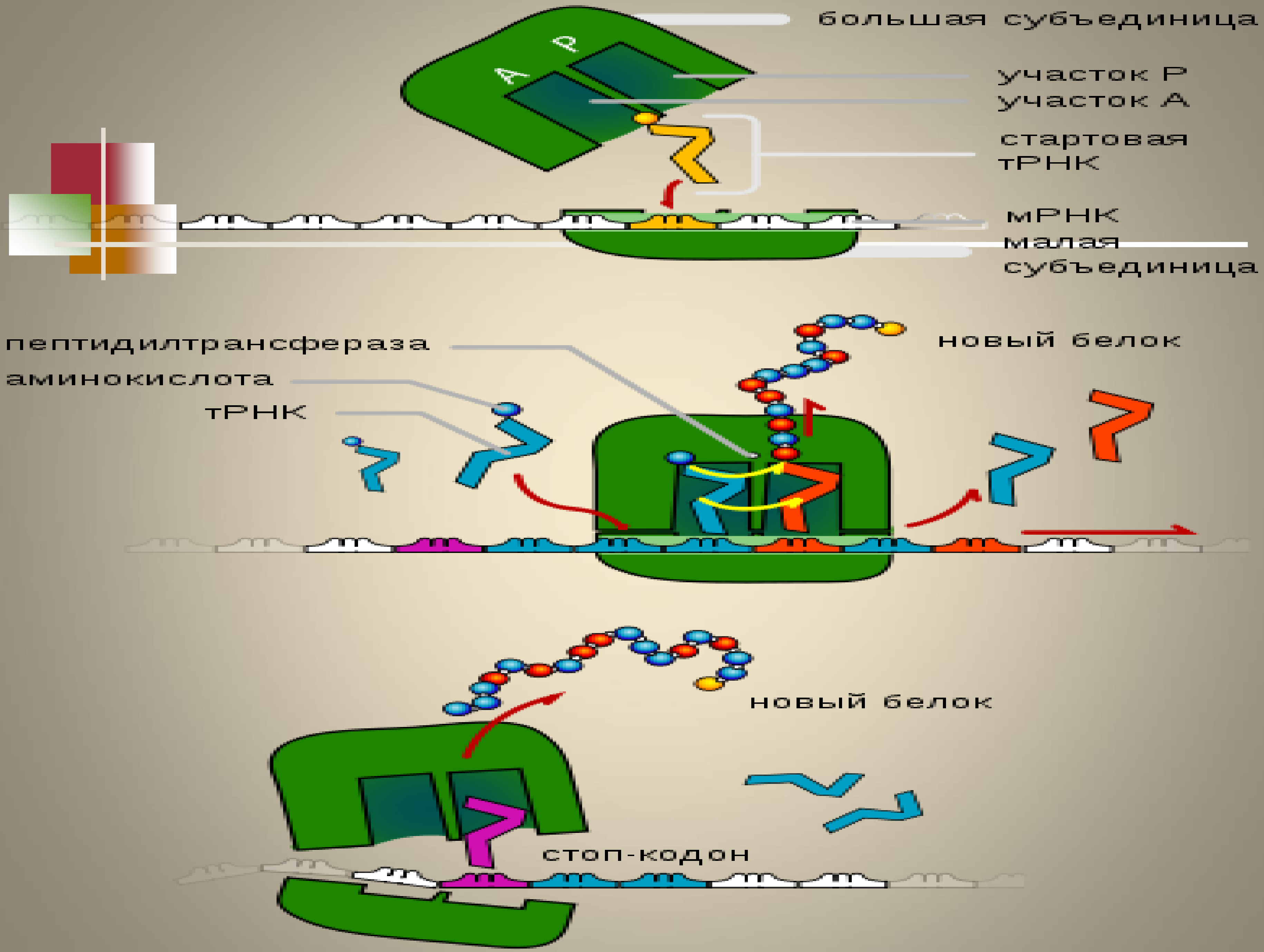
elongation - the formation of the first dipeptide , polypeptide chain capacity , moving of mRNA

termination - the completion of construction of the primary structure of the future protein, exit of the polypeptide from ribosomes .

- ***Cytosolic protein biosynthesis stage***: at this stage, the recognition, selection of amino acids and their joining to the tRNA (in the cytoplasm) take place

ribosomal stage



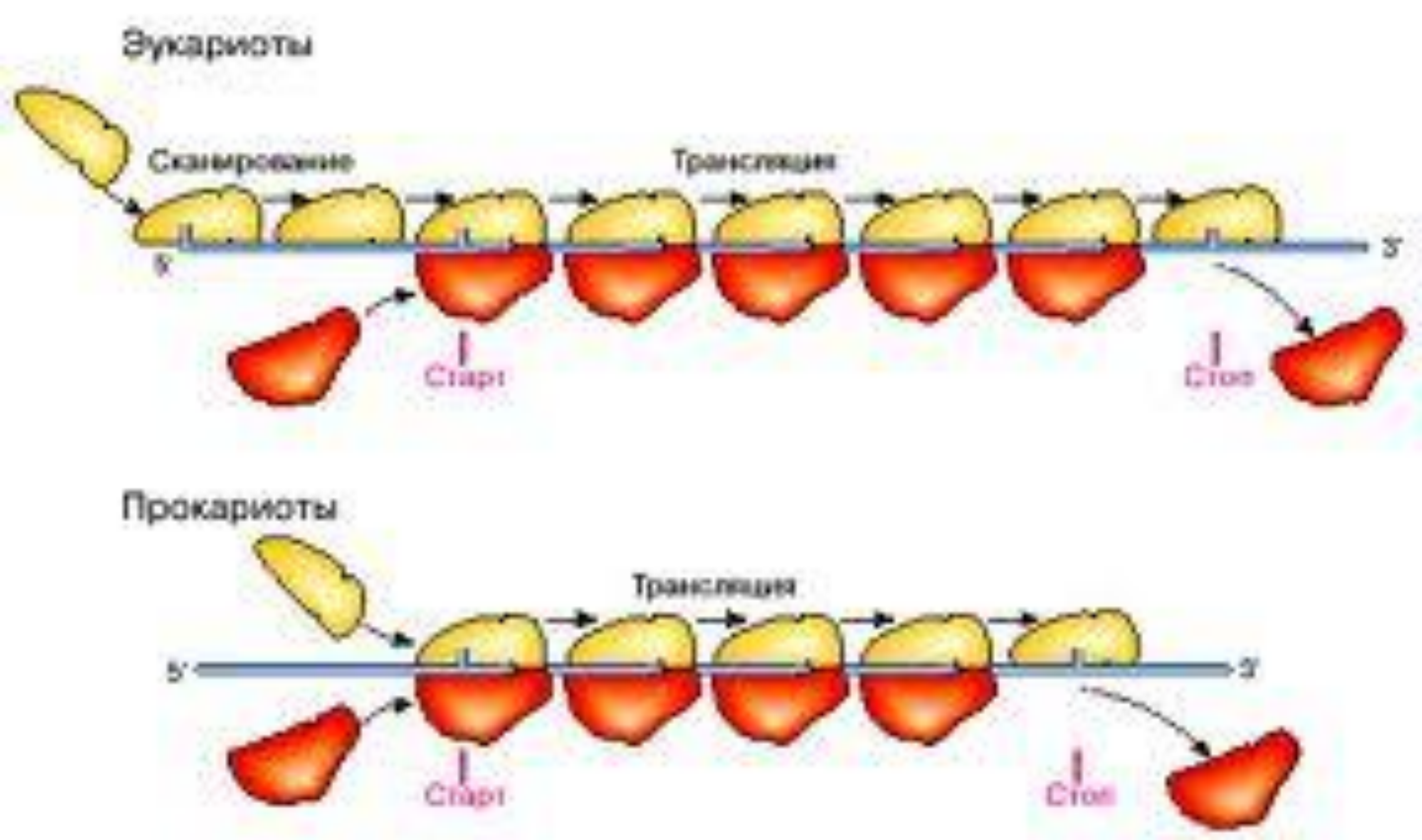

большая субъединица
A
P
участок P
участок A
стартовая тРНК
мРНК
малая субъединица
пептидилтрансфераза
аминокислота
тРНК
новый белок
новый белок
стоп-кодон

- ***Characterization of ribosomal stage***

1. ***Initiation.*** To the site of m-RNA with **initiation codon AUG** joins first tRNA with aminoacid -methionine, which is the primer. When forming part of the initiation complex there is an joining of two subunits of ribosomes. As a result, by the end of the initiation **AK-methionine** in the ribosomal **peptidyl is located - and in aminoacyl - next t-RNA with the corresponding aminoacid** Ribosome makes a "step" on one triplet.

- 2. ***Elongation, elongation of protein*** molecules, this step is the principle of the triplet genetic code and nonoverlappiry continuity. Peptidyl and aminoacyl sites of ribosomes are very close, so between the two amino acids the peptide bond is formed by the action of peptidyl transferase.

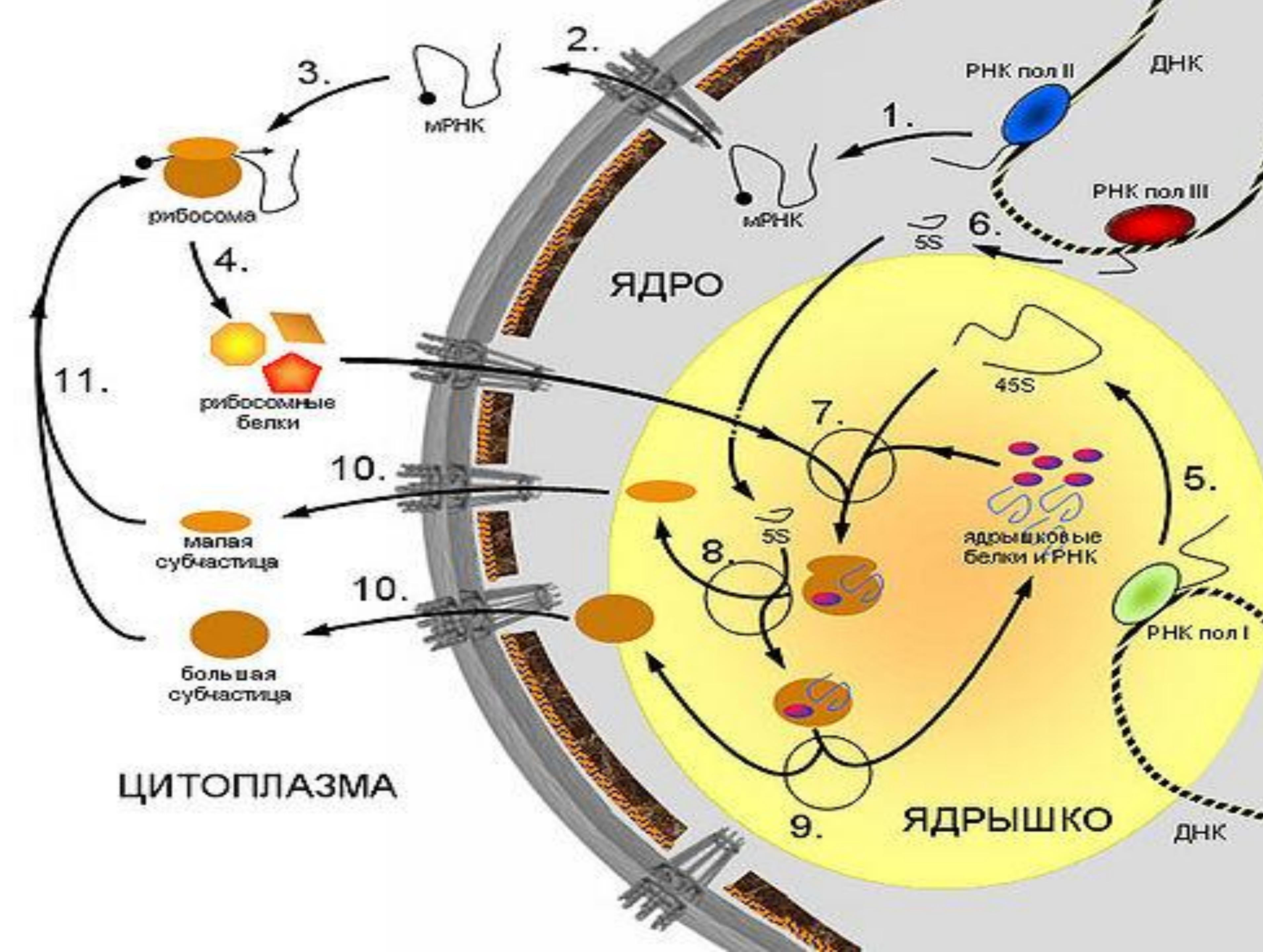
polyribosomes



- ***3. Termination:*** elongation process goes to the ***termination codon (UAA, UAG, UGA)***, which is included in the acceptor site of the ribosome, after which the connection-of RNA and ribosome is lost and ribosome splits into two subunits

4. *Posttranslation changes - option) - modification*

The primary protein passes through cytoplasmic reticulum into the apparatus Golgi, where modification takes place (protein acquires secondary structure).


2.
3.
мРНК
РНК пол II
ДНК
1.
рибосома
мРНК
РНК пол III
6.
5S
4.
ЯДРО
45S
11.
рибосомные белки
7.
10.
5.
малая субчастица
5S
8.
ядрышковые белки и РНК
10.
РНК пол I
большая субчастица
ЦИТОПЛАЗМА
9.
ЯДРЫШКО
ДНК

- ***Structure of transcripton***

Operon - polycistronic model

1.Spasor plot **(SSR)**

2.promoter

3.operator

4.Structural unit: S1, S2, S3

terminator

Restriction site (SSR)

Structure:

Polidromic DNA segment separating transkriptons forms a so-called "hairpin" in the DNA. Consists of inverted nucleotides (guanine and cytosine more)

Function: Separation of transkriptons

The promoter(P)

- The sequence of nucleotides in the DNA, providing recognition and joining of RNA polymerase

  Or-acceptor band - it begins with the synthesis of messenger RNA and a special protein repressor or inducer interacts with it. Transcription depends on this process

The promoter(P)

- .**CAAT block** - active site consisting of 70-80-100 pins of nucleonides and ends CAAT

  Function: RNA polymerase recognition

- **TATA block** (**Hognessa block**) - consists of 30 pairs of nucleotide sequences enriched with adenine and thymine

  Function-joining of RNA polymerase

Transcription initiation site

- TAC - which when translated will fit aminoacid- methionine (TAC DNA)
- Point of initiation, the starting point

The operator (O)

- -Information DNA segments carry information about the structure-functional-related proteins, regulatory proteins

Structural($S_1S_2S_3$…..)

- ***exons*** – information areas carry data about the structure of the protein
- ***introns*** – njn- informatory portions do not carry information about the structure of the protein
- DSS splice donor site - sequence of nucleotides separating introns and exons.

By their borders introns are spliced and exons are joined .

- DNA triplets corresponding to stop codons and RNA stop translation

Terminator (T)

- The nucleotide sequence of poly-A, where growth of RNA chain stops (termination point)

genetic code

- Transcription process occurs on the program of the genetic code

genetic code

Genetic Code - a system of recording information on DNA molecules, which is reflected in the nucleotide sequence defining the order of the amino acids in the protein molecules. Table of the genetic code built for mRNA.

Properties of the genetic code

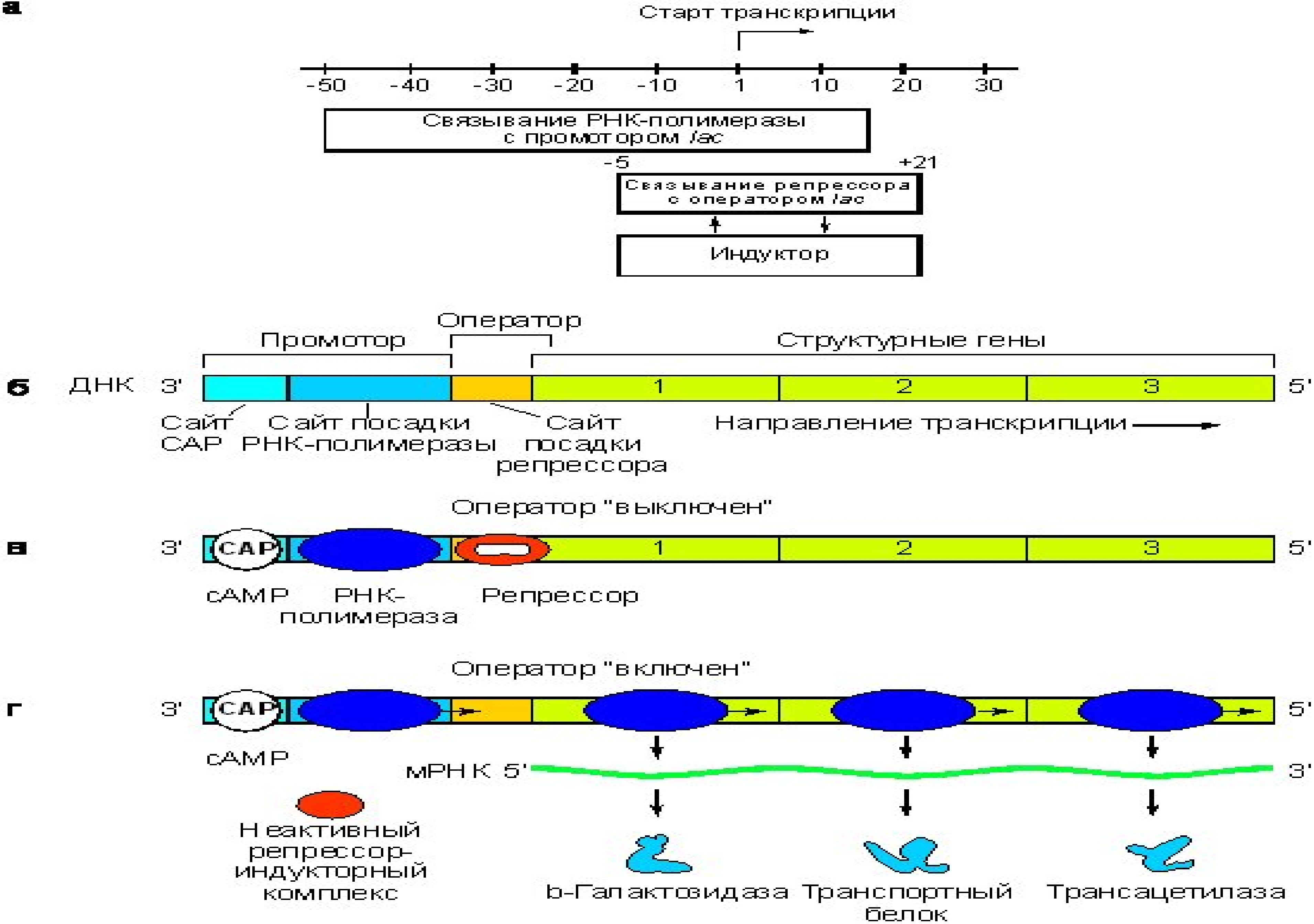
- *1*.***Triplet***. a triplet or codon is a seguence of 3 nucleotides that encode one aminoacid
- ***2.Universal property***. All organisms on the earth have the same triplets encoding the same amino acid.

- 3. ***Degeneracy (redundancy***). Each amino acid is encoded by more than one codon. The exception is the amino acid methionine and tryptophan. Each of them is encoded by only one triplet. ***To encode 20 amino acids a combination of 61 nucleotides is used***. AUG triplet coding methionine, is known as the start. So begins the synthesis of protein.

Three codons (UAA, UAG, UGA) carry information about the termination of proteinsynthesis.

They are called termination triplets.

- 4. ***Unambiguity.*** Each triplet encodes only one amino acid.
- 5. ***Colinearity*** – matching amino acid sequences in protein molecule with the sequence of m-RNA triplets
- 6. Nonoverlapping one nucleotide is not a part of two adjacent triplets.
- 7. ***Continuity*** codons follow each other.



а

Старт транскрипции

-50 -40 -30 -20 -10 1 10 20 30

Связывание РНК-полимеразы с промотором *lac*

-5 +21

Связывание репрессора с оператором *lac*

Индуктор

б

Оператор

Промотор

Структурные гены

ДНК 3' 1 2 3 5'

Сайт CAP

Сайт посадки РНК-полимеразы

Сайт посадки репрессора

Направление транскрипции

в

Оператор "выключен"

3' CAP 1 2 3 5'

cAMP

РНК-полимераза

Репрессор

г

Оператор "включен"

3' CAP 5'

cAMP

мРНК 5' 3'

Неактивный репрессор-индукторный комплекс

b-Галактозидаза

Транспортный белок

Трансацетилаза

genome organization

- 1.” Loop"domains"
- 2.Insulatory DNA segments
- 3.Klaster genes
- 4. Gene tandem
- 5.Amplification
- 6.TATA block, CAAT block promo
- 7.Enhancers, insulators ,silencers

Human Genome

The entire mass of DNA in haploid cells - called the genome.

Structure and function of the genome is studied by special science - genomics.

The purpose of the international program "Human Genome" is to sequenced genome, to determine the nucleotide sequence of all genes.

Fine structure of the gene

Cistron - basic unit of function , which determines the sequence of amino acids in a particular protein. Cistron - is synonymous with gene.

Recon is an elementary unit of recombination in crossing over . It is a pair of nucleotides.

Mouton basic unit of genetic variability , that is cistron minimum unit that can mutate . It corresponds to 1 pair of nucleotides in the DNA.

Transkripton transcription unit in eukaryotic model representing monocistronic gene.

Operon transcription unit in prokaryot representing a polycistronic gene model .

DNA segments (cistrons), which contain information about a group of functionally related structural proteins and the regulatory zone which controls the transcription of the protein (gene - operator) .


Валерий Александров. Тобольск.

Happy New Year

- Good luck in your studies!
- I wish to find a lot of friends in RUSSIA!
- Do not be afraid of our winter-there are only 2 months left and spring will come, and then summer!
- It will be warm ,and even hot!
- You will remember RUSSIAN new year with snow and fir trees!,
- Skis, skates and sleighs !