Control of Gene Expression in Eukaryotic

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Eukaryotic cells have similar mechanisms for control of gene expression in prokaryotic, but they are more complex. Consider, for example, that prokaryotic cells of a given species are all the same, but most eukaryotes are multicellular organisms with many cell types, so control of gene expression is much more complicated.

Levels of Control of Gene Expression in Eukaryotes

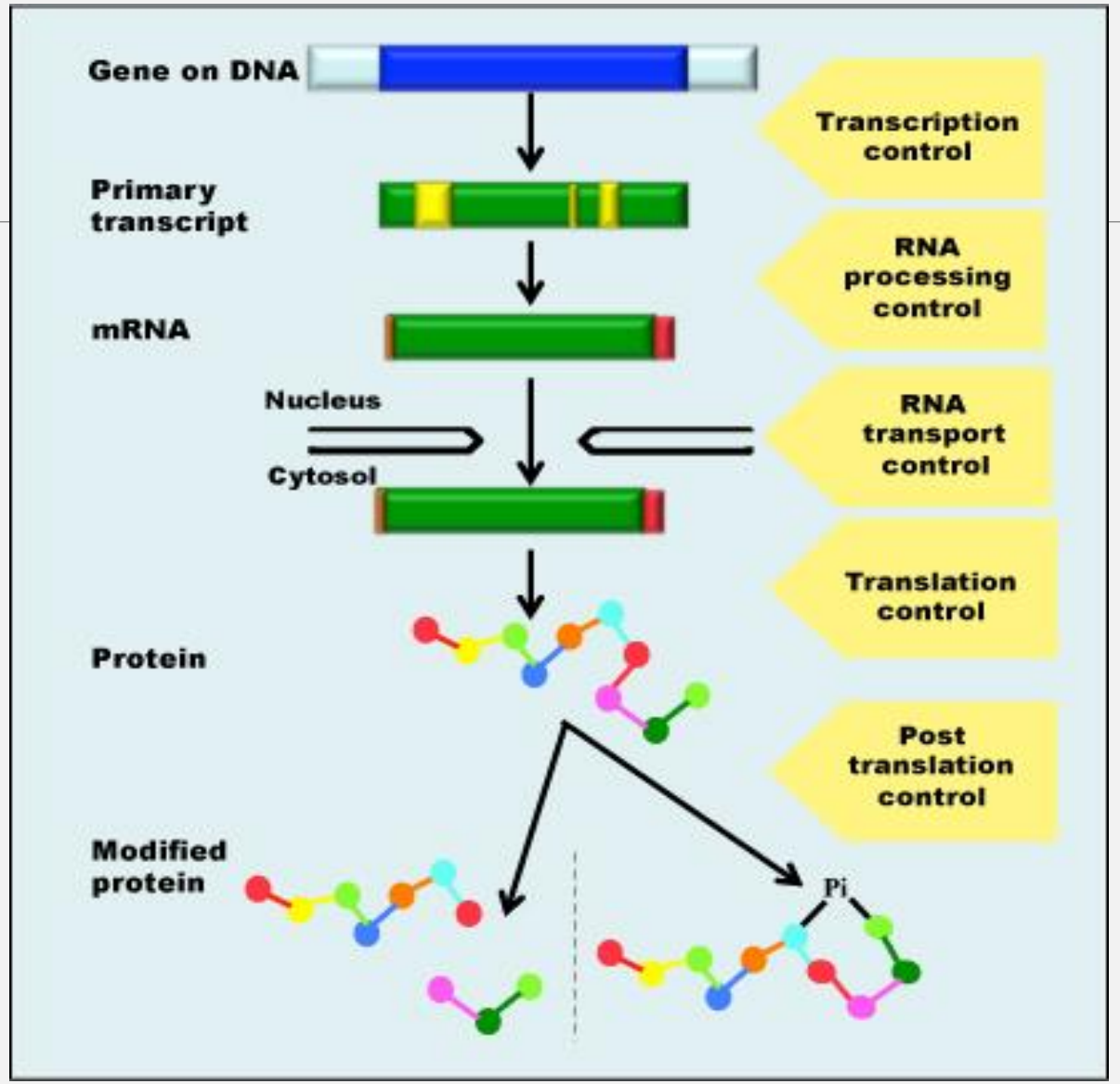
Transcriptional control

RNA processing control

RNA Transport control

mRNA translation control

mRNA degradation control


Gene on DNA
Primary transcript
mRNA
Nucleus
Cytosol
Protein
Modified protein
Pi
Transcription control
RNA processing control
RNA transport control
Translation control
Post translation control

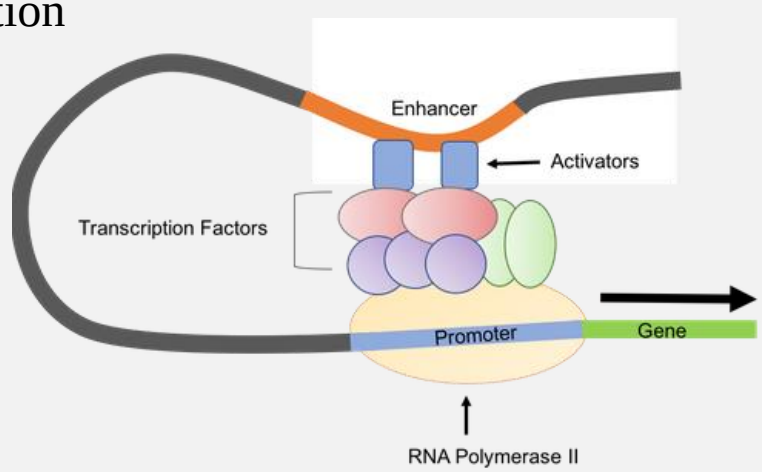
1- Transcriptional control

To start transcription, general transcription factors, such as TFIID, TFIIH, and others, must first bind to the TATA box and recruit RNA polymerase to that location.

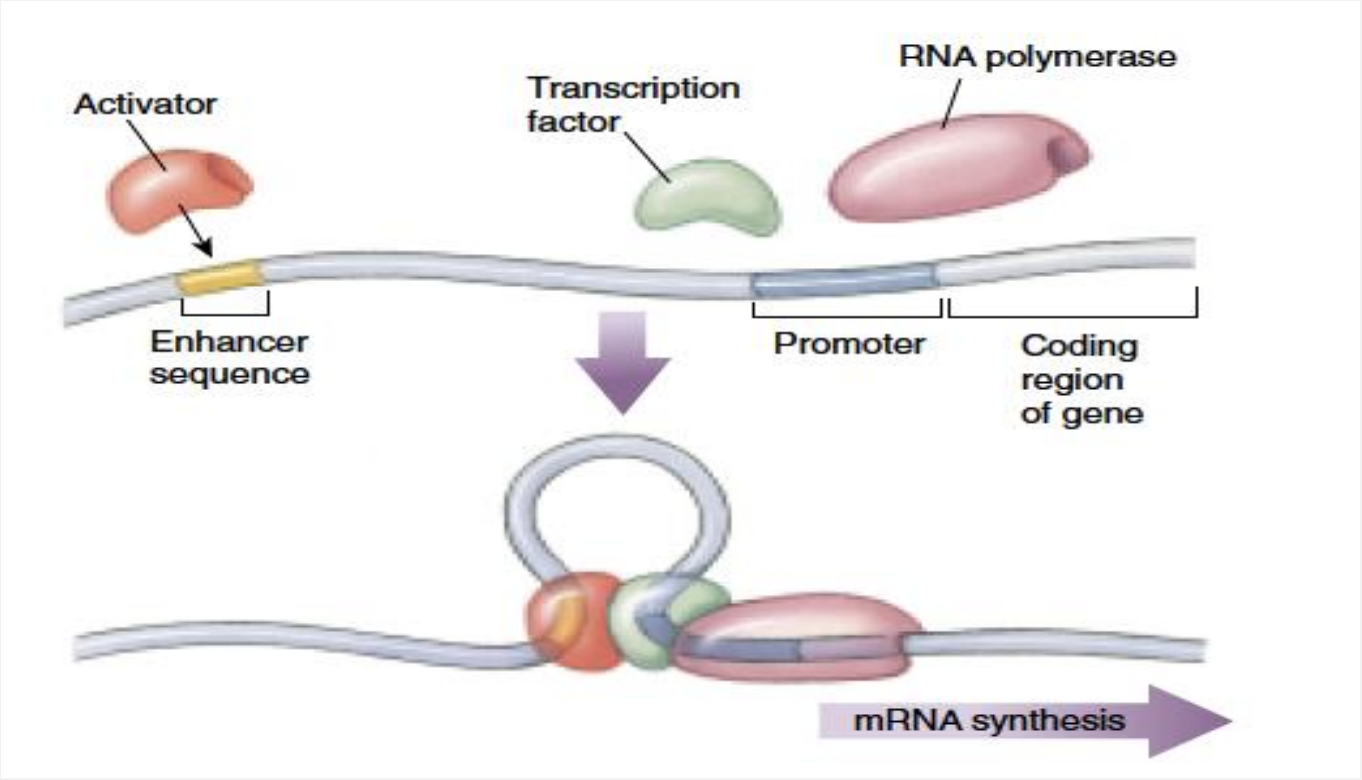
In addition to promoter sequences, enhancer regions help augment transcription. Enhancers can be upstream, downstream, within a gene itself, or on other chromosomes.

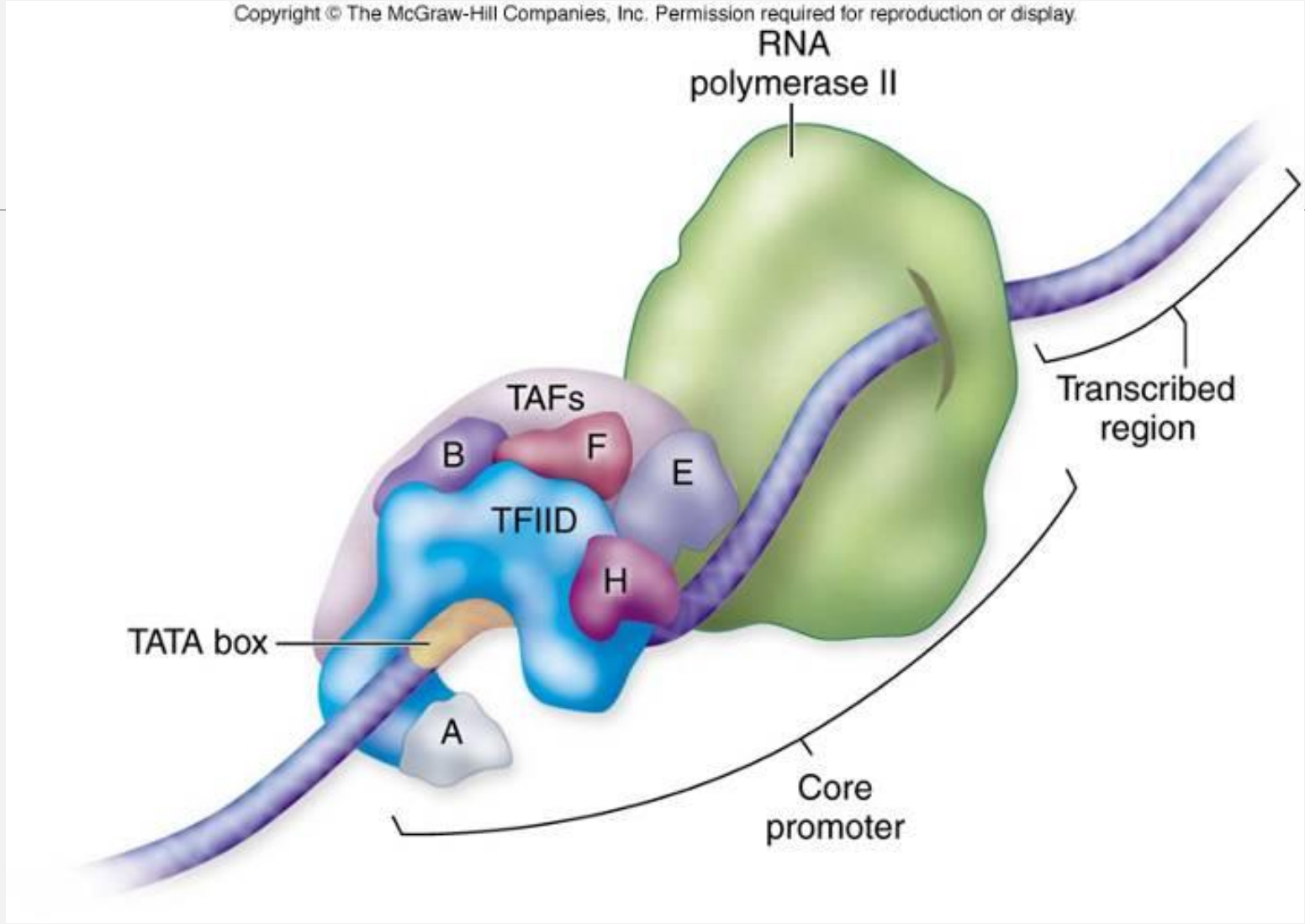
Transcription factors bind to enhancer regions to increase or prevent transcription

Enhancers are DNA sequences to which specific transcription factors (activators) bind to increase the rate of transcription.



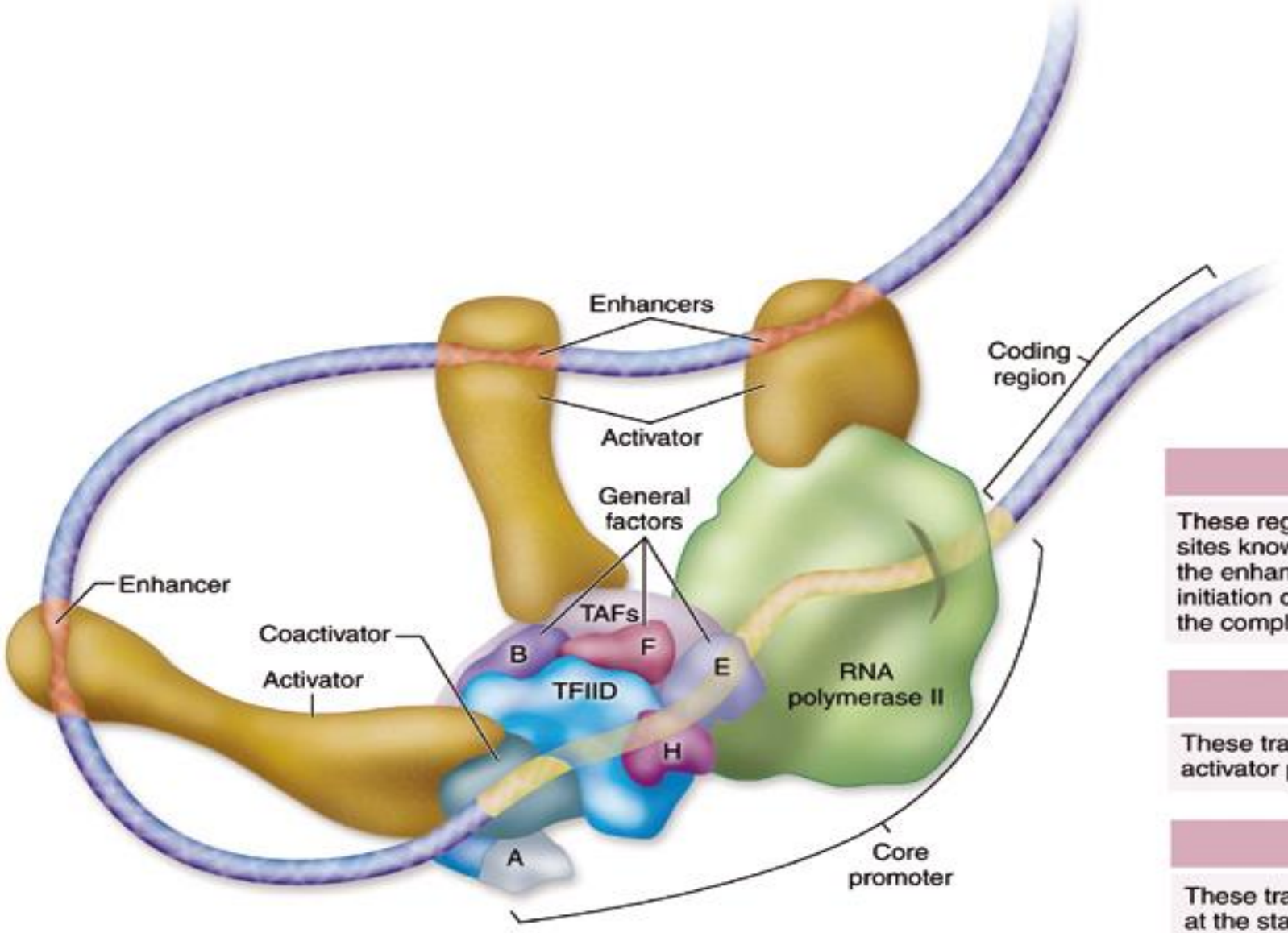
How enhancers work. The enhancer site is located far away from the gene being regulated. Binding of an activator (red) to the enhancer allows the activator to interact with the transcription factors (green) associated with RNA polymerase, activating transcription.





Mediator and Coactivator

- **Coactivators** and **mediators** are also required for the function of transcription factors.
  - coactivators and mediators bind to transcription factors and bind to other parts of the transcription apparatus



Activators

These regulatory proteins bind to DNA at distant sites known as enhancers. When DNA folds so that the enhancer is brought into proximity with the initiation complex, the activator proteins interact with the complex to increase the rate of transcription.

Coactivators

These transcription factors transmit signals from activator proteins to the general factors.

General Factors

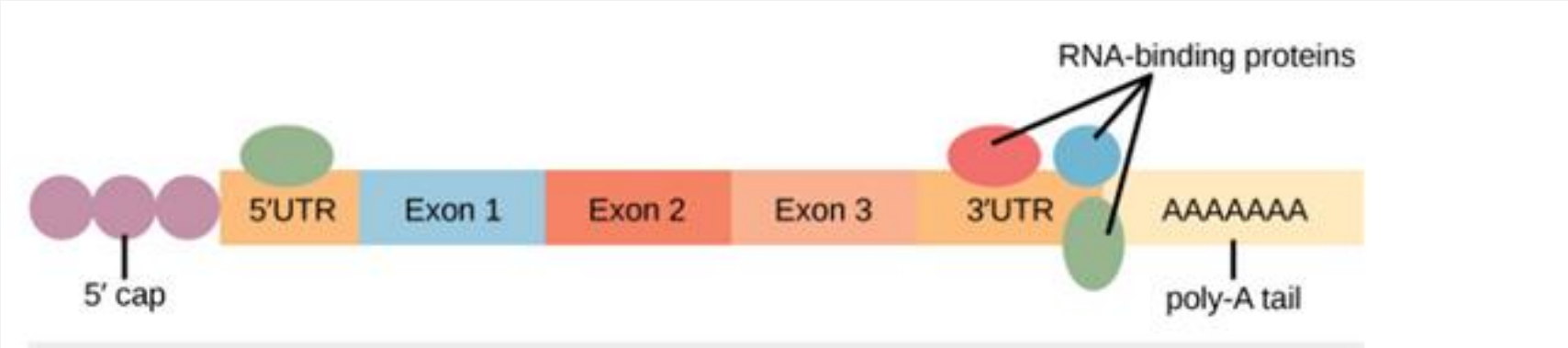
These transcription factors position RNA polymerase at the start of a protein-coding sequence and then release the polymerase to initiate transcription.

2- RNA processing control

1- Before the mRNA leaves the nucleus, it is given two protective “caps” that prevent the end of the strand from degrading during its journey.

The 5′ cap, which is placed on the 5′ end of the mRNA, is usually composed of a methylated guanosine triphosphate molecule (GTP).

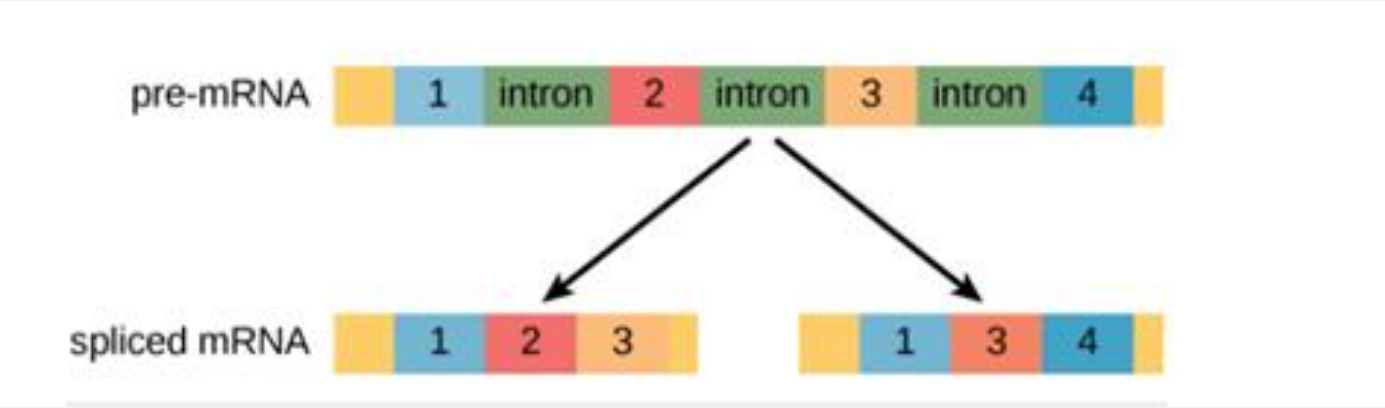
The poly-A tail, which is attached to the 3′ end, is usually composed of a series of adenine nucleotides.

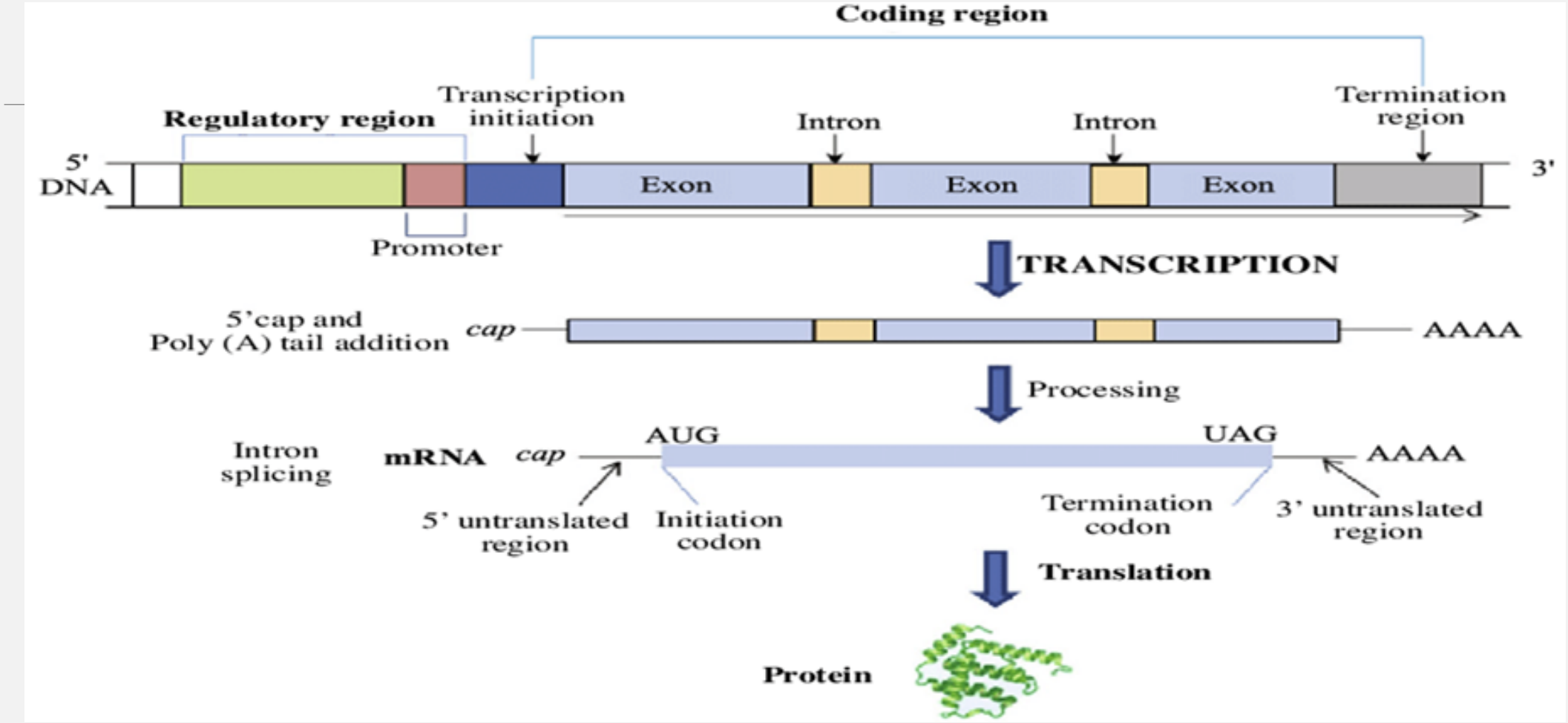


2- RNA is transcribed, but must be processed into a mature form before translation can begin. This processing after an RNA molecule has been transcribed, but before it is translated into a protein, is called post-transcriptional modification.

RNA splicing, the first stage of post-transcriptional control

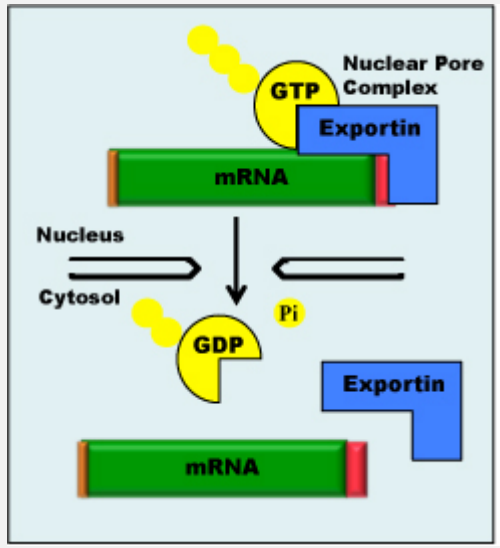
In eukaryotic cells, the RNA transcript often contains regions, called introns, that are removed prior to translation. The regions of RNA that code for protein are called exons . After an RNA molecule has been transcribed, but prior to its departure from the nucleus to be translated, the RNA is processed and the introns are removed by splicing.




Coding region
Transcription initiation
Regulatory region
Intron
Intron
Termination region
5'
DNA
Exon
Exon
Exon
3'
Promoter
TRANSCRIPTION
5'cap and
Poly (A) tail addition
cap
AAAA
Processing
Intron
splicing
mRNA
cap
AUG
UAG
AAAA
5' untranslated
region
Initiation
codon
Termination
codon
3' untranslated
region
Translation
Protein

3- Transport control

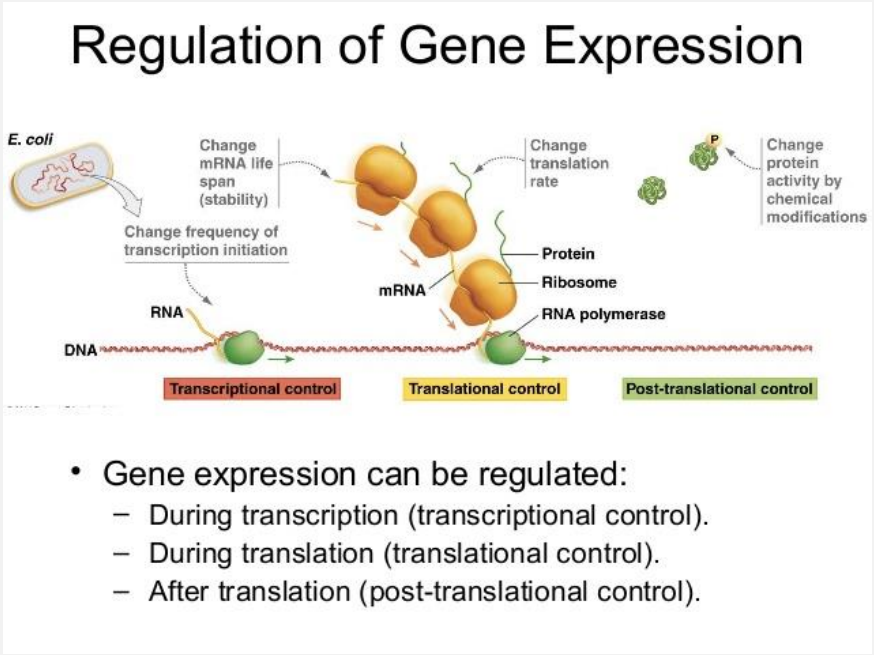
Gene expression requires the movement of mRNA molecules from the nucleus to the cytoplasm. The export process is controlled by Nuclear Pore Complexes (NPCs), The Nuclear Pore Complex binds with a guanosine triphosphate (GTP) molecule that is hydrolyzed by a GTPase molecule into GDP. The energy released by cleaving the phosphate bond is used to shuttle the mRNA through the nuclear pore. Once through the pore the Nuclear Pore Complex dissociates and the GDP molecule returns to the nucleus leaving the mRNA in the cytoplasm



4- Post- Translation control

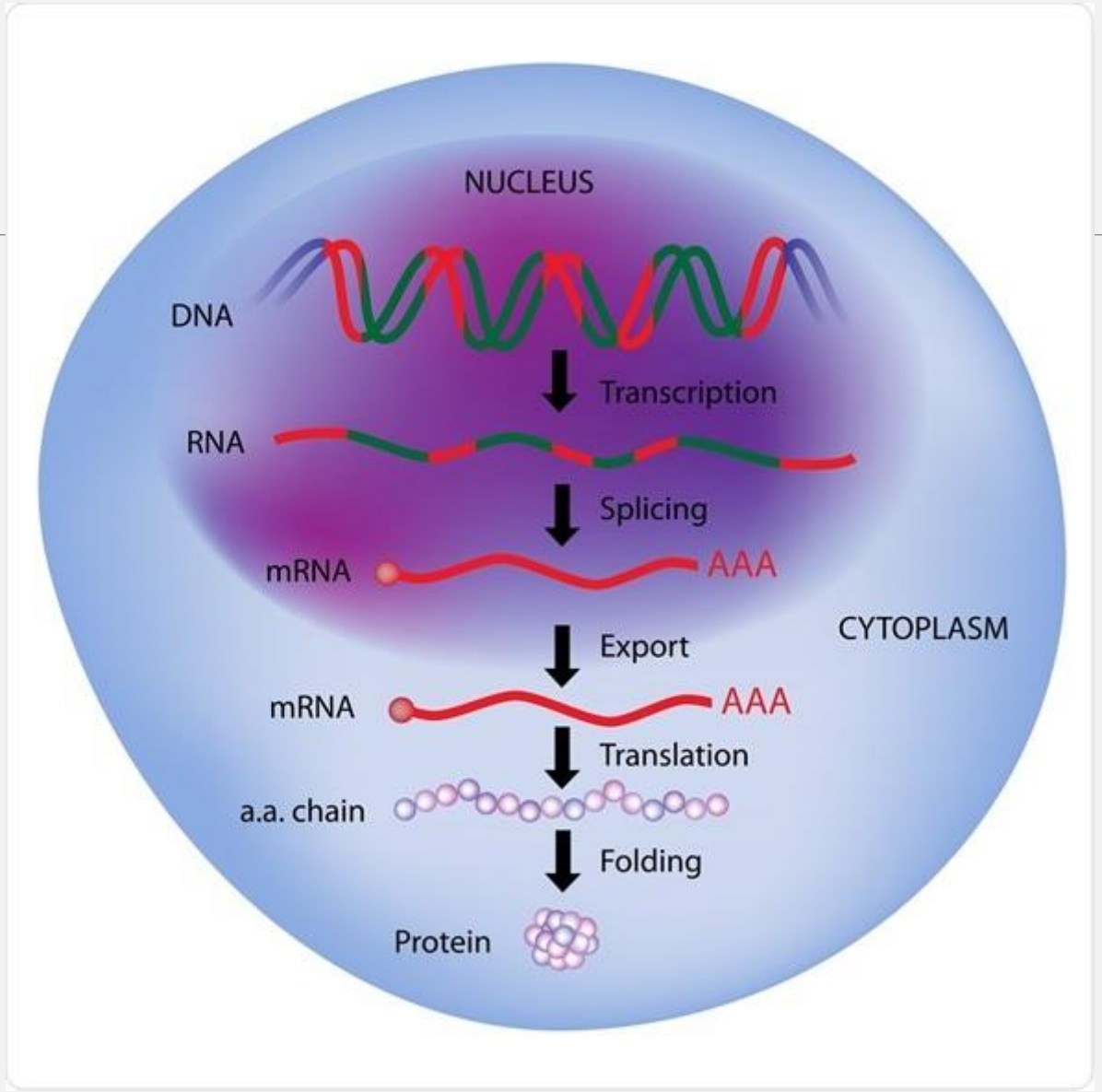
Three major mechanisms for post-translational modification are:

- Cleaving the protein (removing amino acids)
- Adding chemical groups to the protein
- Combining the protein with one or more other proteins



5- mRNA degradation control

Once the RNA is transported to the cytoplasm, the length of time that the RNA resides there can be controlled. Each RNA molecule has a defined lifespan and decays at a specific rate. This rate of decay can influence how much protein is in the cell. If the decay rate is increased, the RNA will not exist in the cytoplasm as long, shortening the time for translation to occur. Conversely, if the rate of decay is decreased, the RNA molecule will reside in the cytoplasm longer and more protein can be translated. This rate of decay is referred to as the RNA stability.


NUCLEUS
DNA
Transcription
RNA
Splicing
mRNA
AAA
CYTOPLASM
Export
mRNA
AAA
Translation
a.a. chain
Folding
Protein