

Lecture Series 11

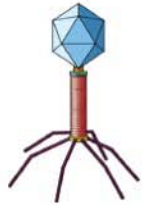
The Eukaryotic Genome and Its Expression

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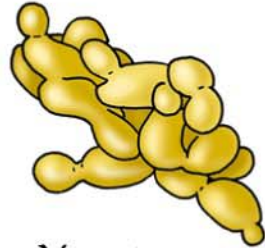
- A. The Eukaryotic Genome
- B. Repetitive Sequences (rem: teleomeres)
- C. The Structures of Protein-Coding Genes
- D. Transcriptional Control
- E. Posttranscriptional and Posttranslational Control

A. The Eukaryotic Genome

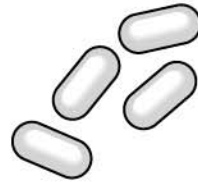
- Although eukaryotes have more DNA in their genomes than prokaryotes, in some cases there is NO apparent relationship between genome size and organism complexity.



Bacteriophage
10,000 bp
per cell



Yeast
24 million bp



E. coli
4 million bp



Caenorhabditis elegans
160 million bp per cell



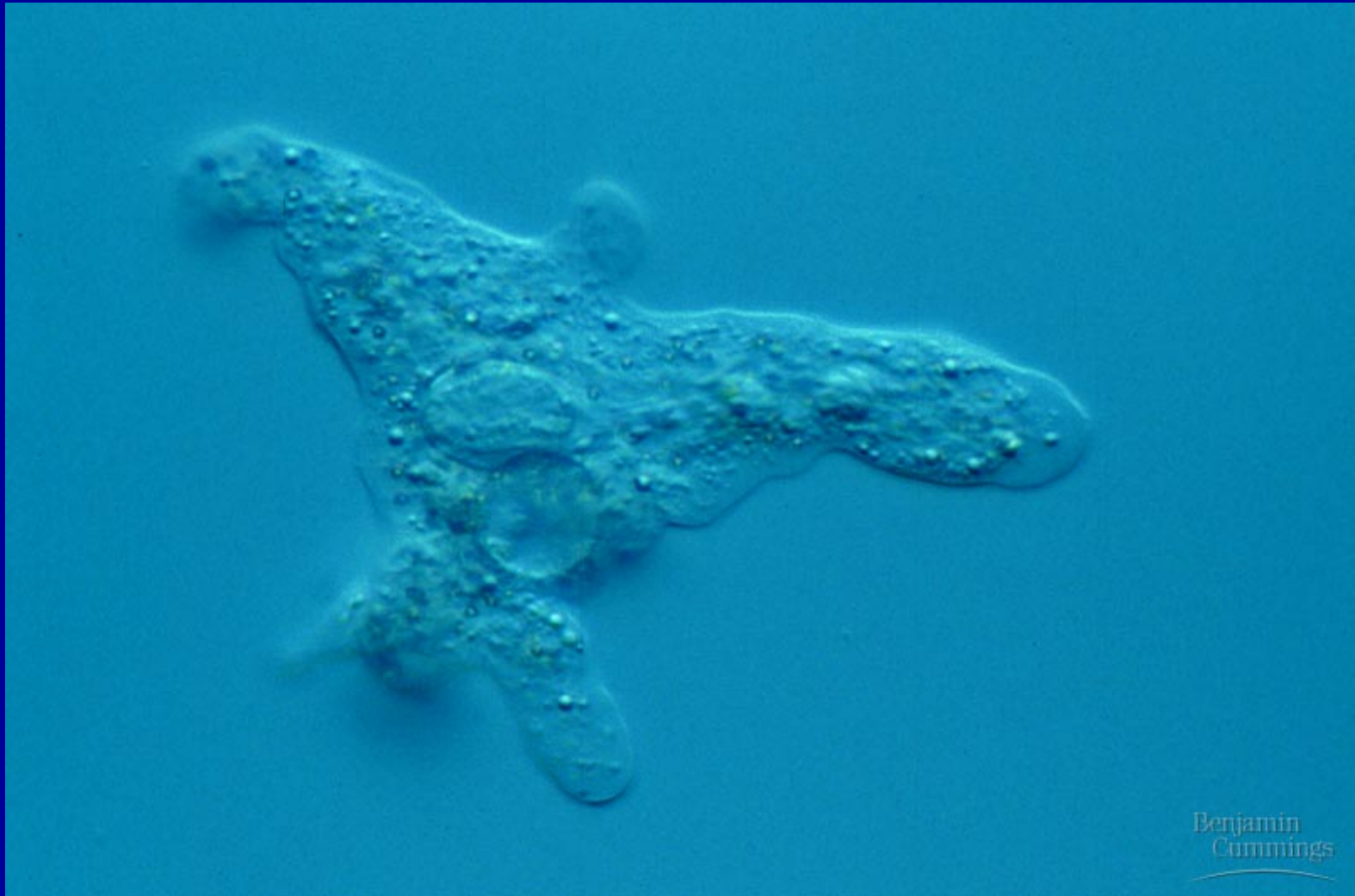
Fruit fly
330 million bp



Lily
106 billion bp



Human
6 billion bp
per cell



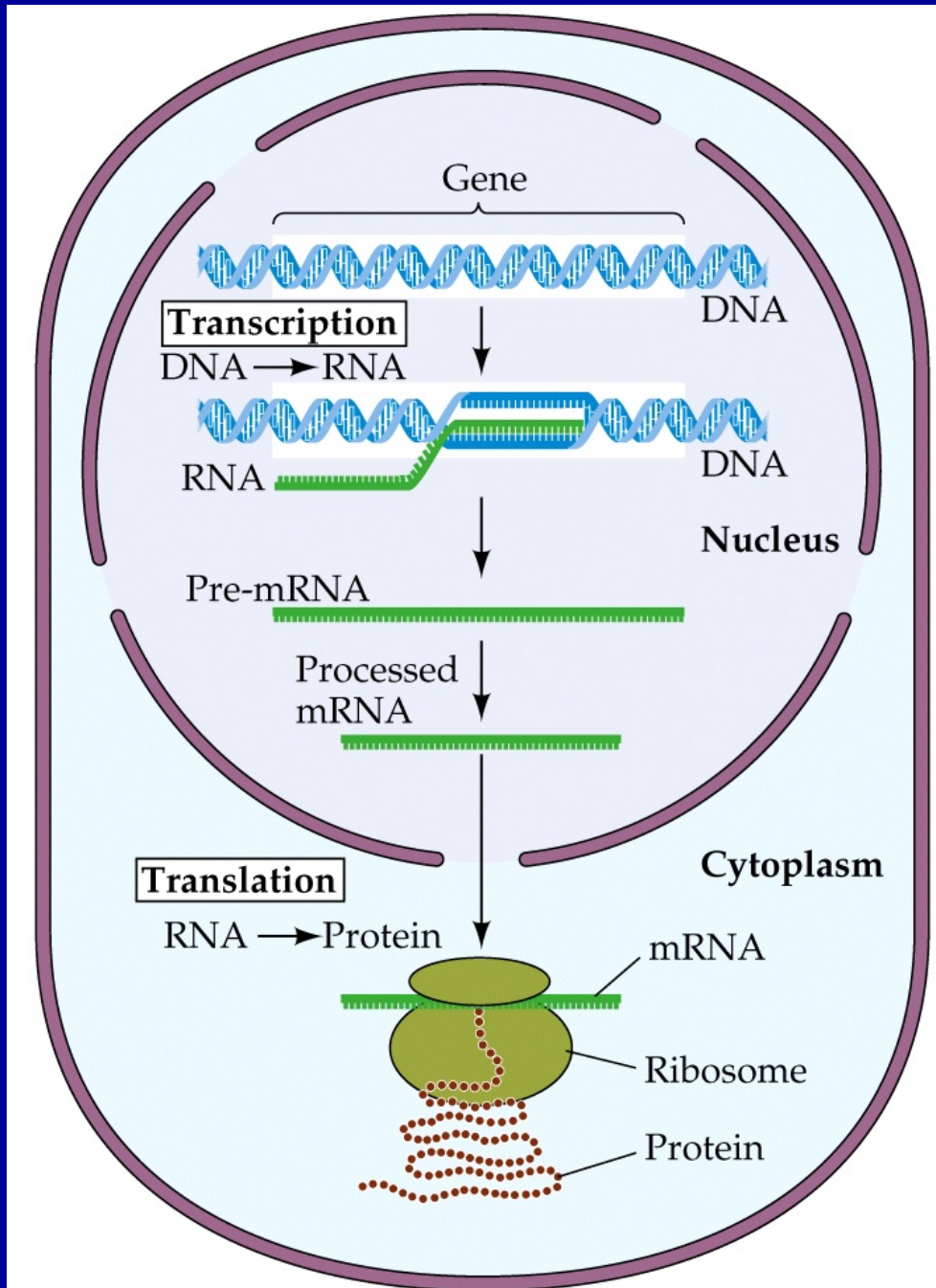
Amoeba dubia is the big winner at **670 Billion** base pairs per cell and an uncertain phylogeny!

14.1 *A Comparison of Prokaryotic and Eukaryotic Genes and Genomes*

CHARACTERISTIC	PROKARYOTES	EUKARYOTES
Genome size (base pairs)	10^4 – 10^7	10^8 – 10^{11}
Repeated sequences	Few	Many
Noncoding DNA within coding sequences	Rare	Common
Transcription and translation separated in cell	No	Yes
DNA segregated within a nucleus	No	Yes
DNA bound to proteins	Some	Extensive
Promoter	Yes	Yes
Enhancer/silencer	Rare	Common
Capping and tailing of mRNA	No	Yes
RNA splicing required	Rare	Common
Number of chromosomes in genome	One	Many

A. The Eukaryotic Genome

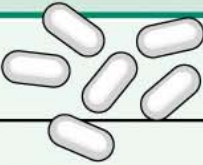
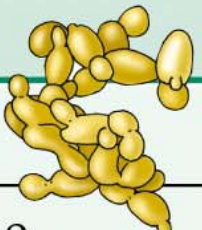
- Unlike prokaryotic DNA, eukaryotic DNA is separated from the cytoplasm by being contained within a nucleus. The initial mRNA transcript of the DNA may be modified before it is exported from the cytoplasm.



A. The Eukaryotic Genome

- The genome of the single-celled budding yeast contains genes for the same metabolic machinery as bacteria, as well as genes for protein targeting in the cell.

14.2 Comparison of the Genomes of *E. coli* and Yeast

	<i>E. COLI</i>		YEAST	
Genome length (base pairs)	4,640,000		12,068,000	
Number of proteins	4,300		6,200	
Proteins with roles in:				
Metabolism	650		650	
Energy production/storage	240		175	
Membrane transporters	280		250	
DNA replication/repair/ recombination	120		175	
Transcription	230		400	
Translation	180		350	
Protein targeting/secretion	35		430	
Cell structure	180		250	

A. The Eukaryotic Genome

- The genome of the multicellular roundworm *Caenorhabditis elegans* contains genes required for intercellular interactions.
- The genome of the fruit fly has fewer genes than that of the roundworm. Many of its sequences are homologs of sequences on roundworm and mammalian genes.

14.3

C. elegans Genes Essential to Multicellularity

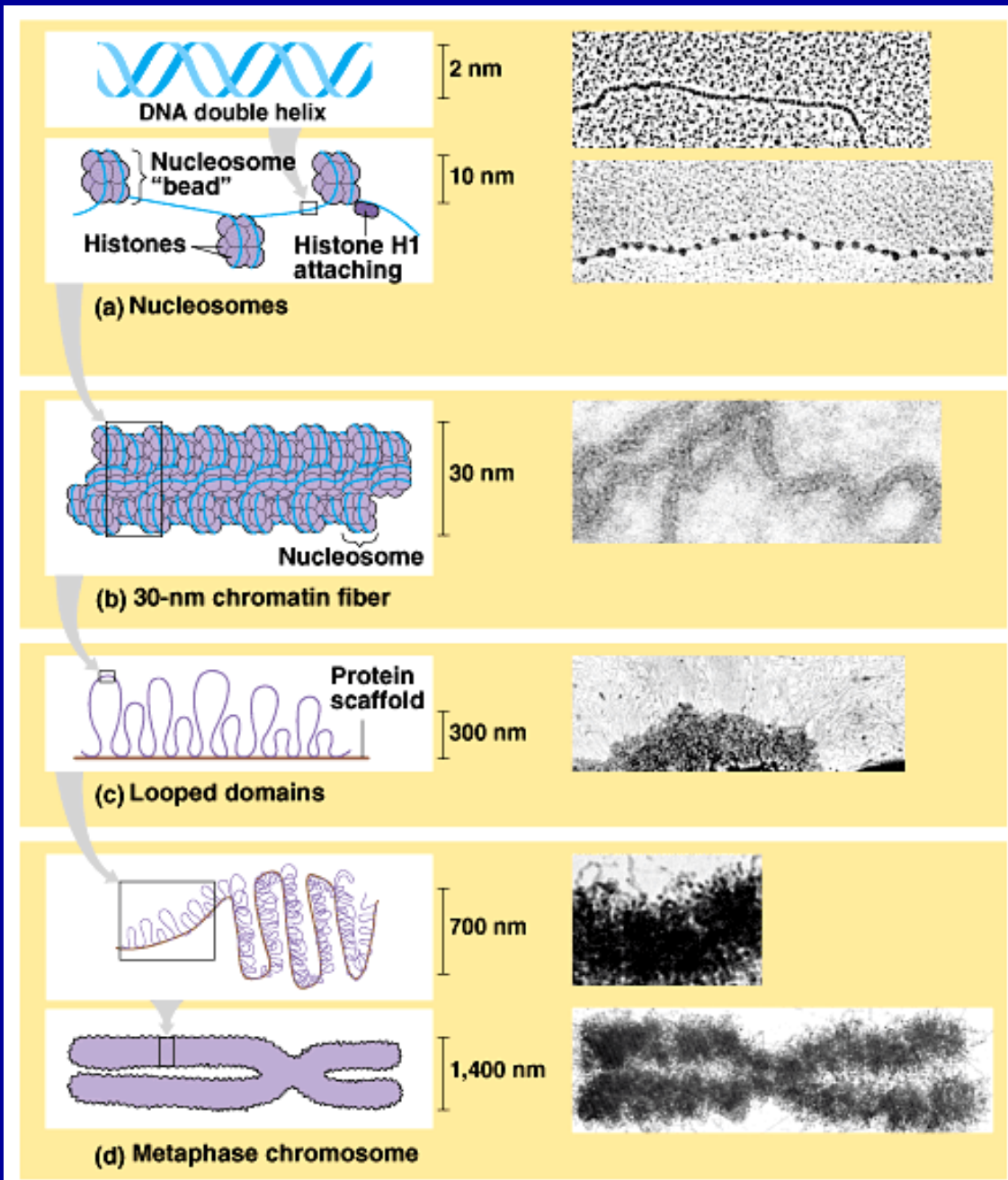
FUNCTION	PROTEIN/DOMAIN	GENES
Transcription control	Zinc finger; homeobox	540
RNA processing	RNA binding domains	100
Nerve impulse transmission	Gated ion channels	80
Tissue formation	Collagens	170
Cell interactions	Extracellular domains; glycotransferases	330
Cell-cell signaling	G protein-linked receptors; protein kinases; protein phosphatases	1,290



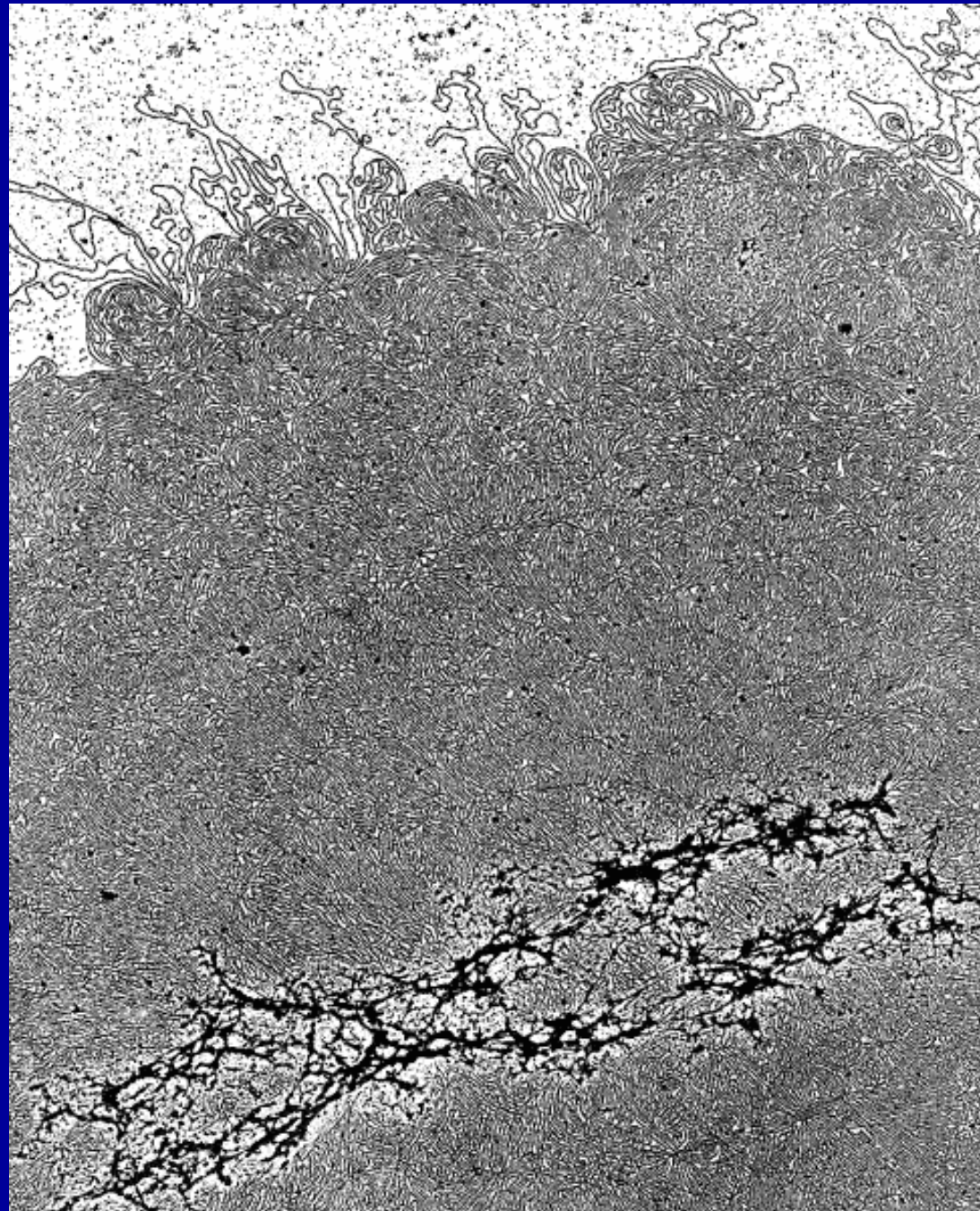
Chromatin in a developing salamander ovum



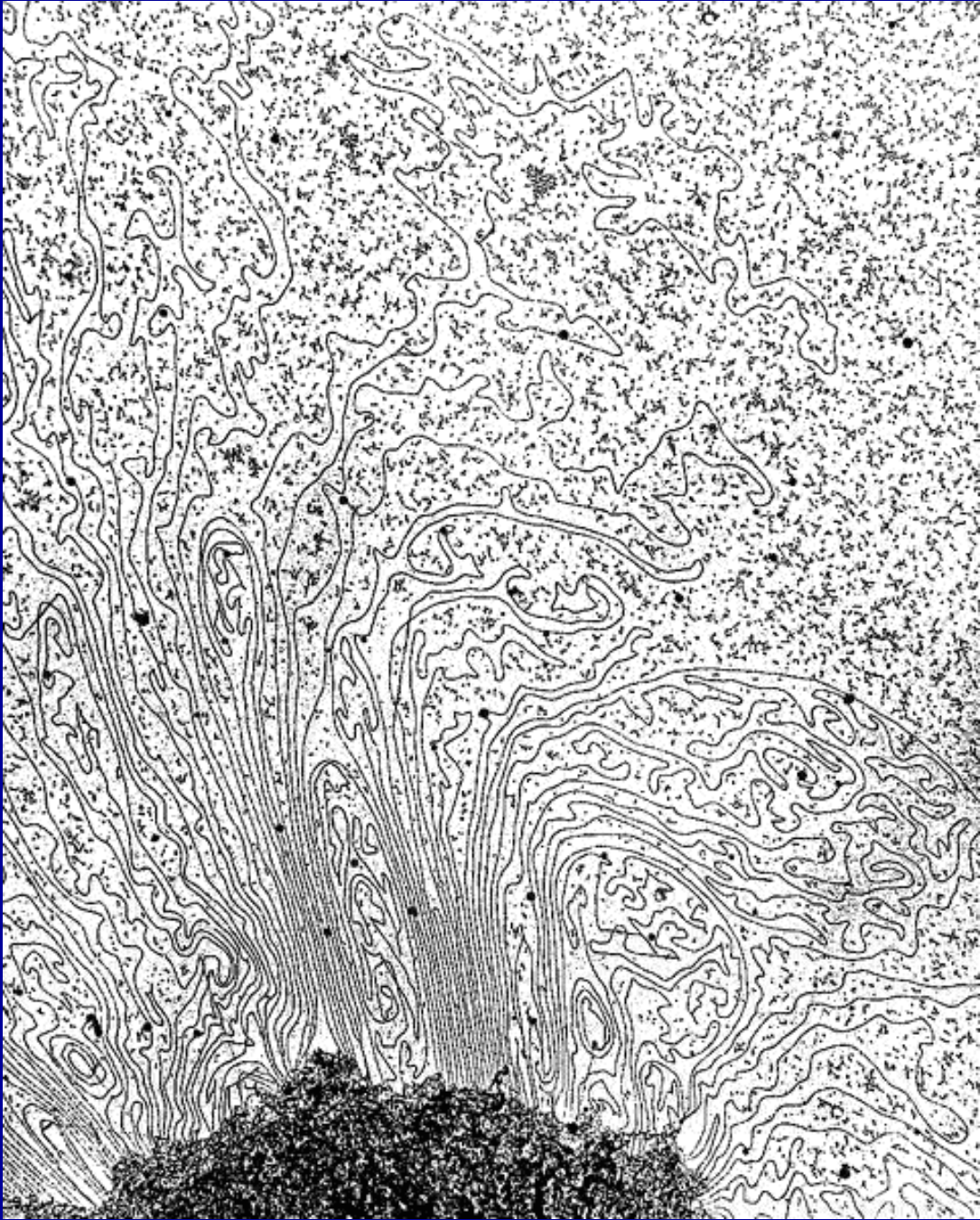
Levels of chromatin packing



Chromatin



Chromatin, detail



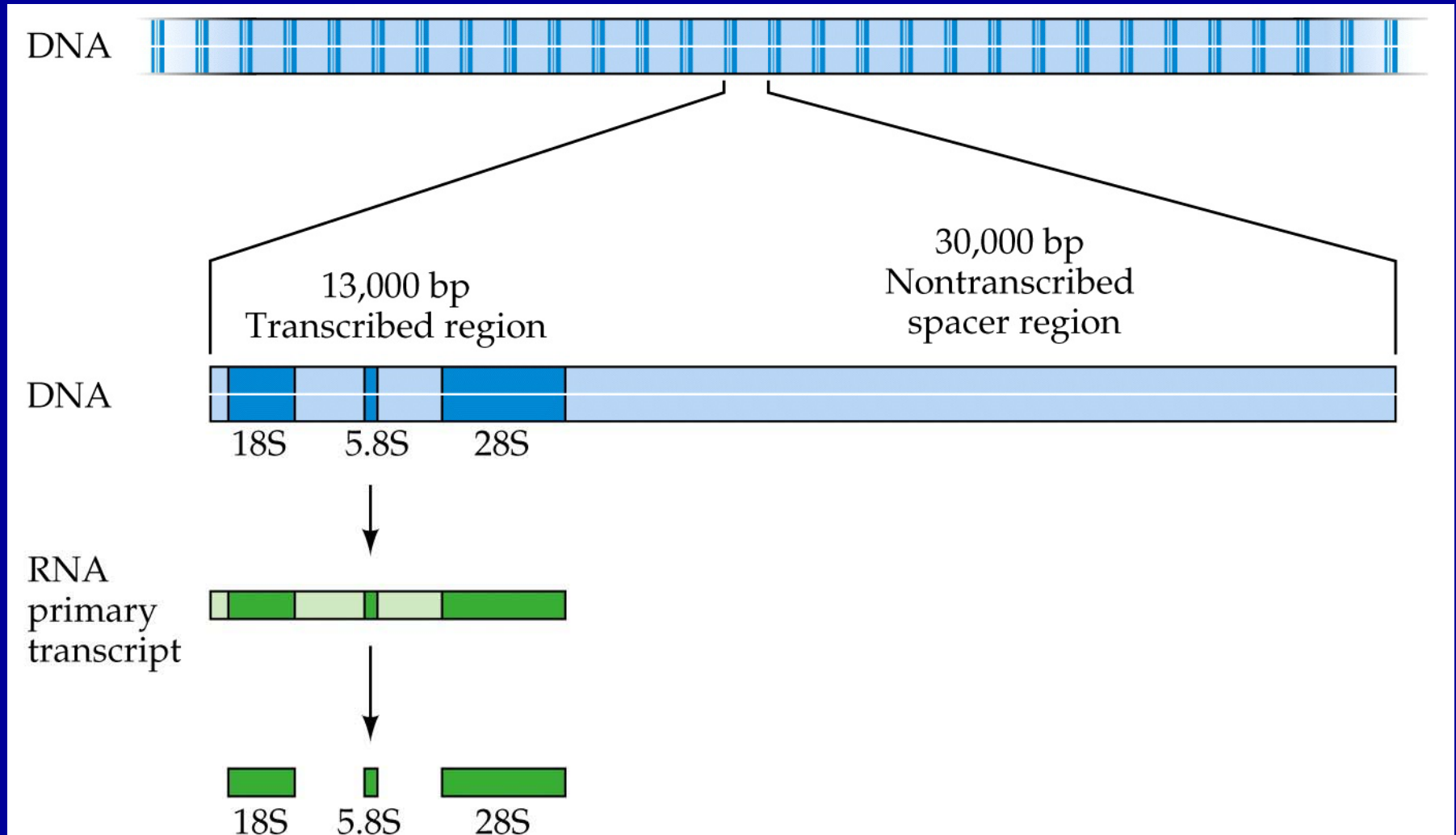
B. Repetitive Sequences

- Highly repetitive DNA is present in up to millions of copies of short sequences. It is not transcribed. Its role is unknown.
- Rem: Some moderately repetitive DNA sequences, such as telomeric DNA is found at the ends of chromosomes.

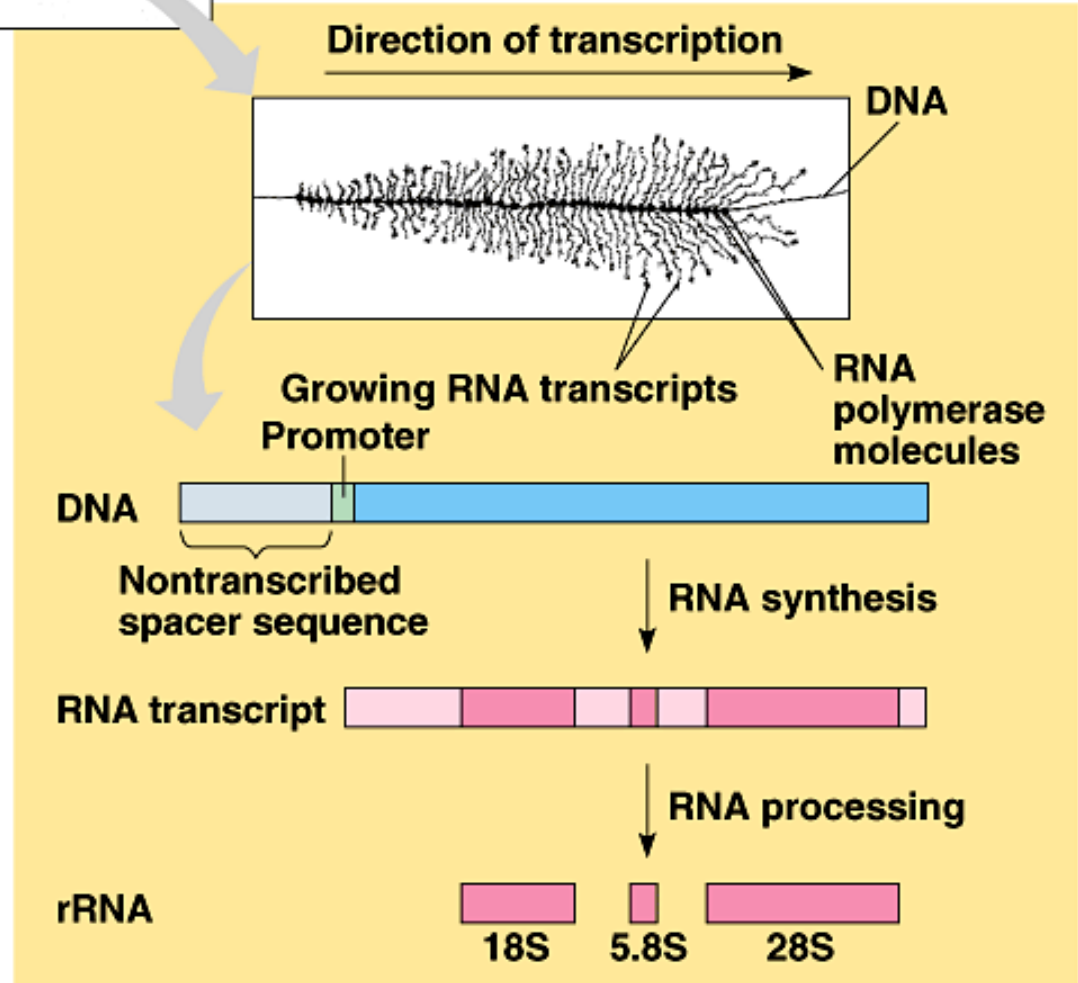
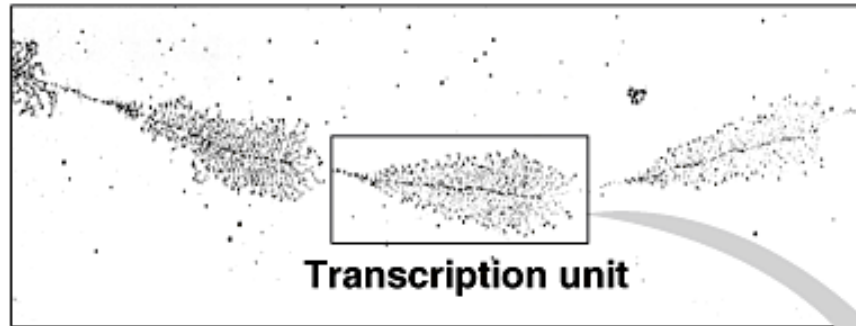
B. Repetitive Sequences

- Some moderately repetitive DNA sequences, such as those coding for ribosomal RNA's, are transcribed.
- Three rRNAs result, two go to the large subunit and one goes to the small subunit.

Moderately repetitive DNA sequences

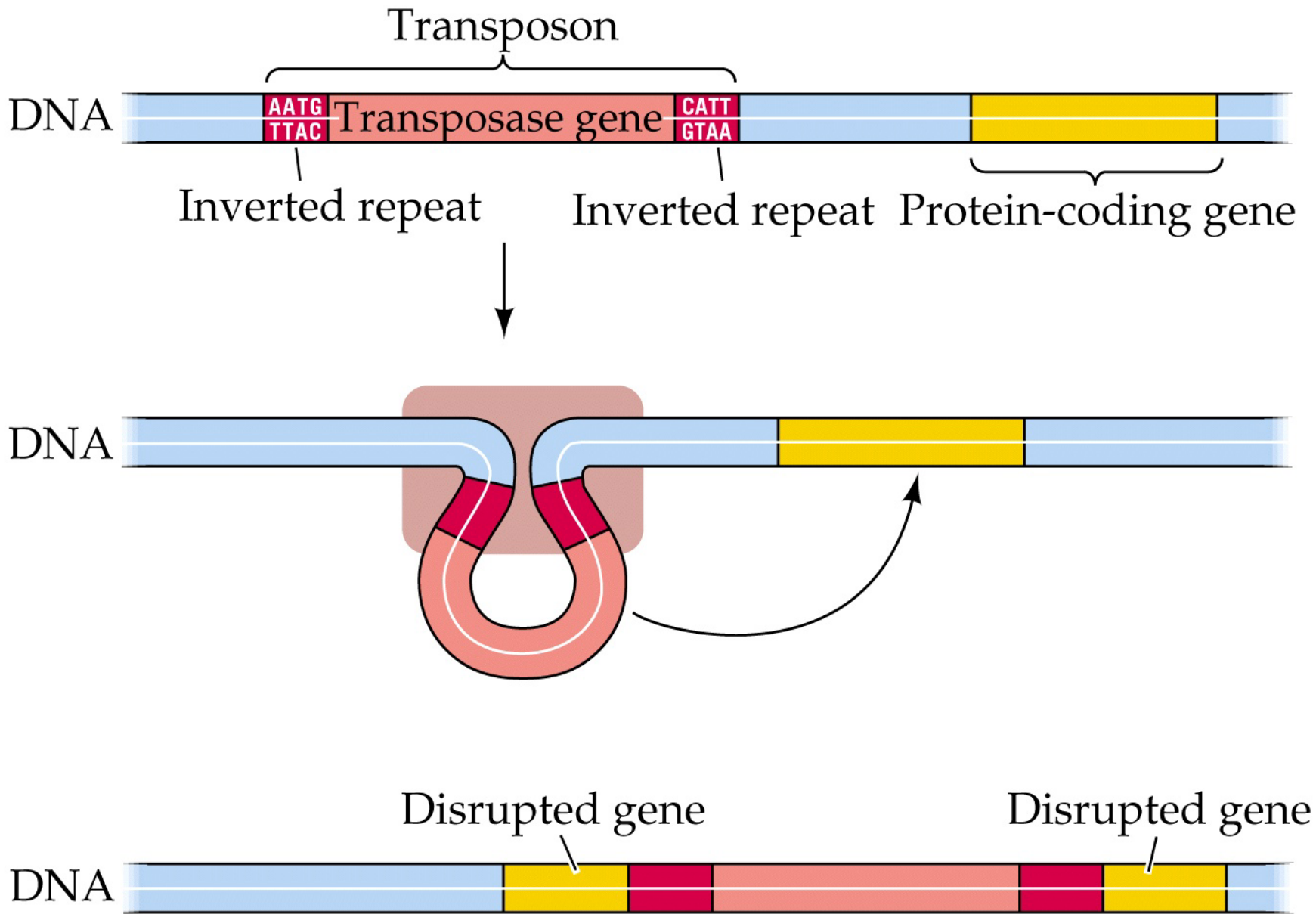


Part of a family of identical genes for ribosomal RNA



B. Repetitive Sequences

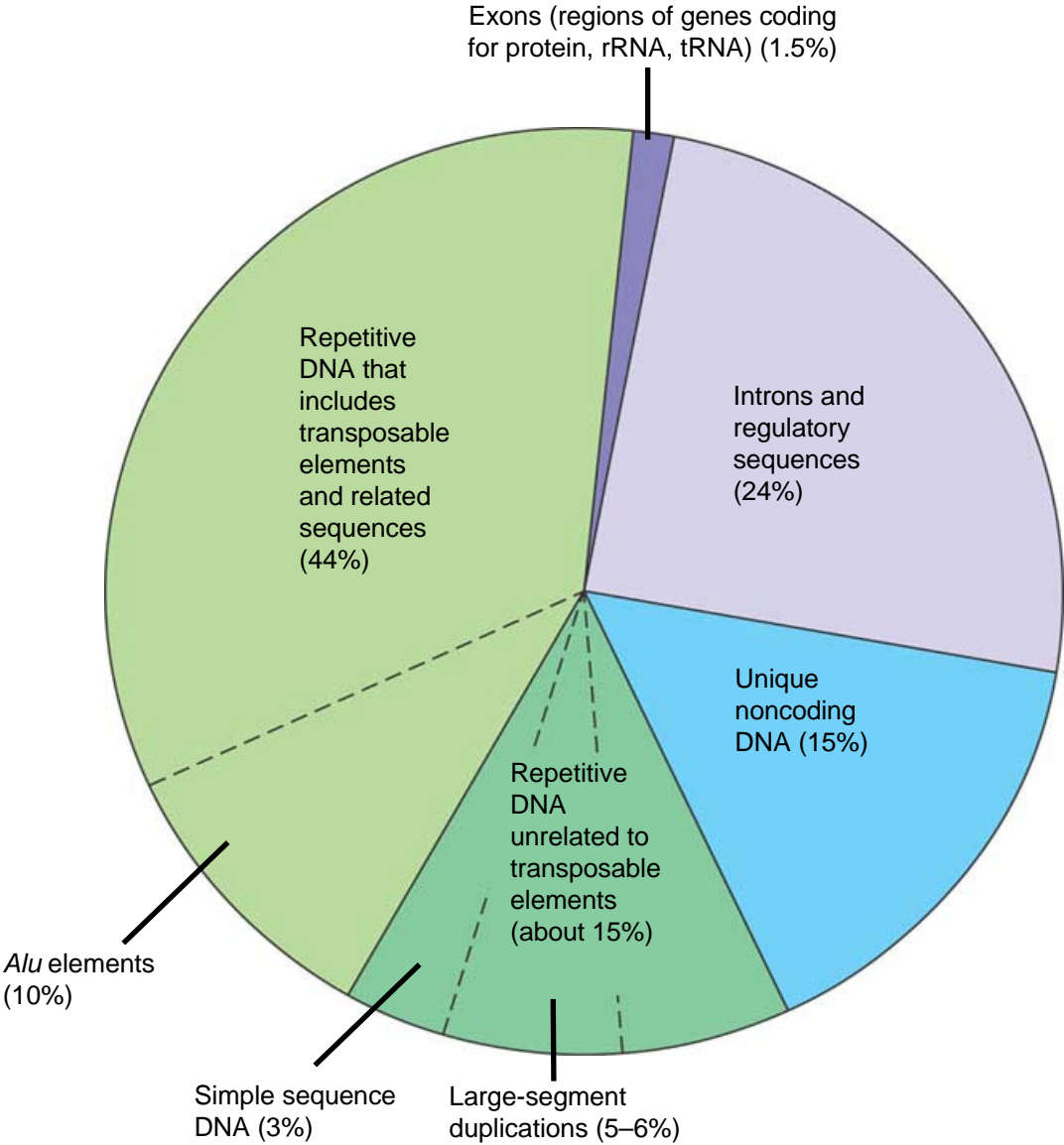
- Some moderately repetitive DNA sequences are transposable, or able to move about the genome. These are known as Transposons.



Transposons in corn

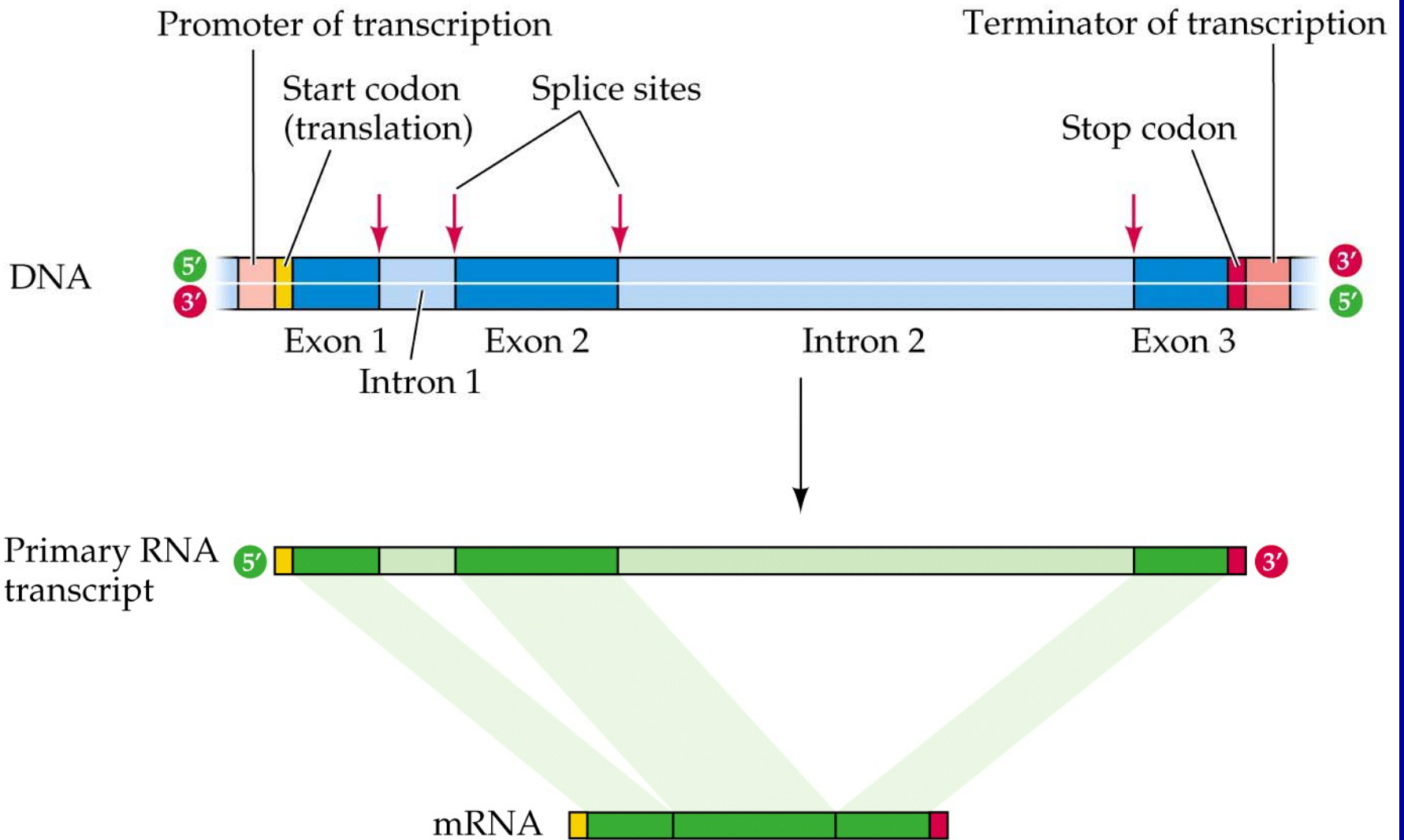


Types of DNA sequences in the human genome



C. The Structures of Protein-Coding Genes

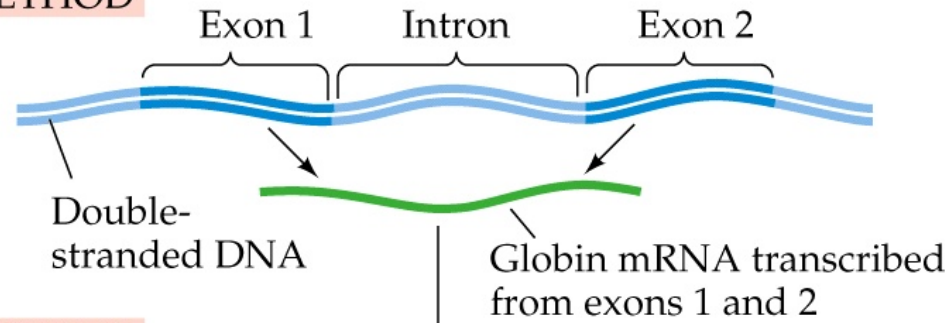
- A typical protein-coding gene has noncoding internal sequences (introns) as well as flanking sequences that are involved in the machinery of transcription and translation in addition to its exons or coding regions.
- These are usually single copy genes.



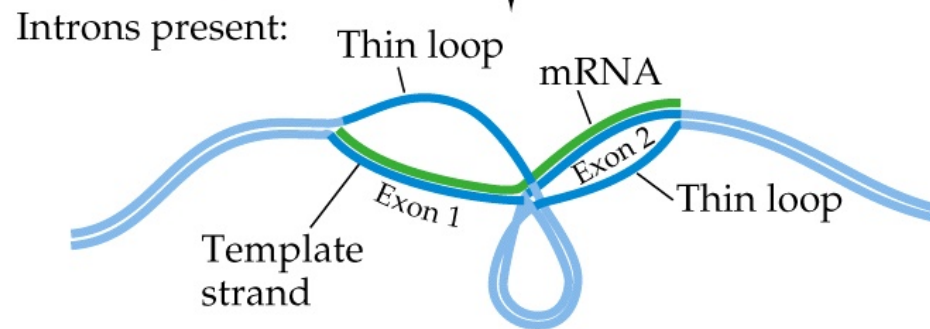
EXPERIMENT

Question: Are there regions within the coding sequence of a gene that do not end up in its mRNA?

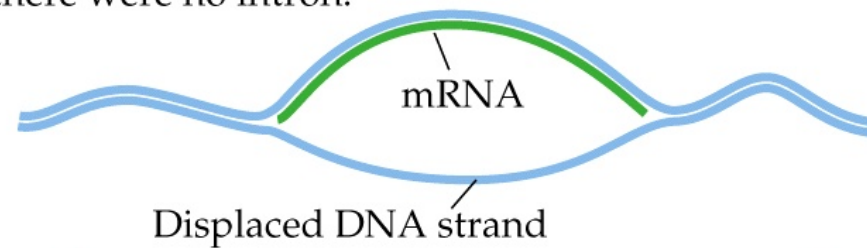
METHOD



RESULTS



If there were no intron:



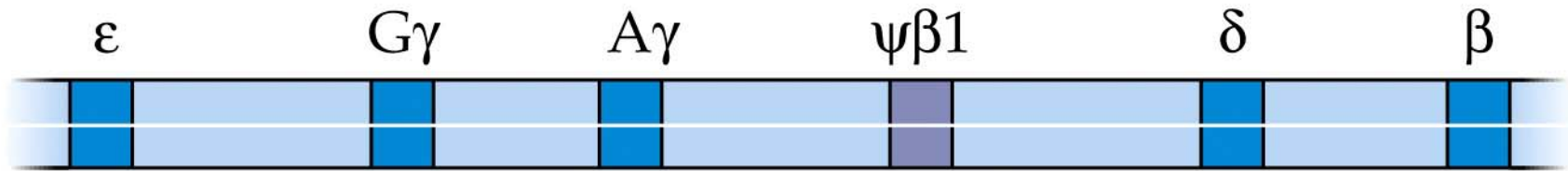
Conclusion: The final mRNA does not contain noncoding internal regions in a gene in DNA.

C. The Structures of Protein-Coding Genes

- Some eukaryotic genes form families of related genes that have similar sequences and code for similar proteins. These related proteins may be made at different times and in different tissues.
- Some sequences in gene families are pseudogenes, which code for nonfunctional mRNA's or proteins.

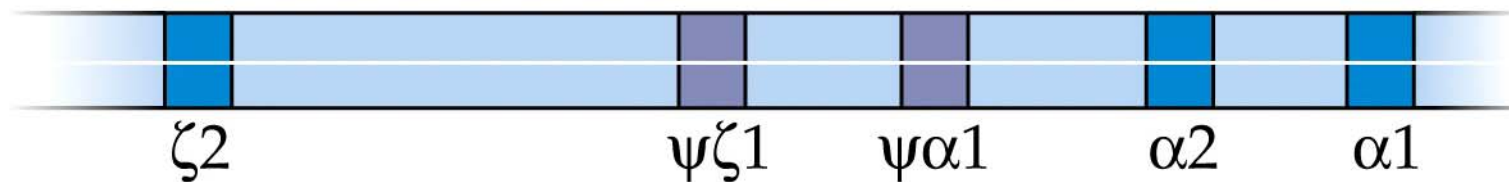
Gene Families

β -Globin
gene cluster



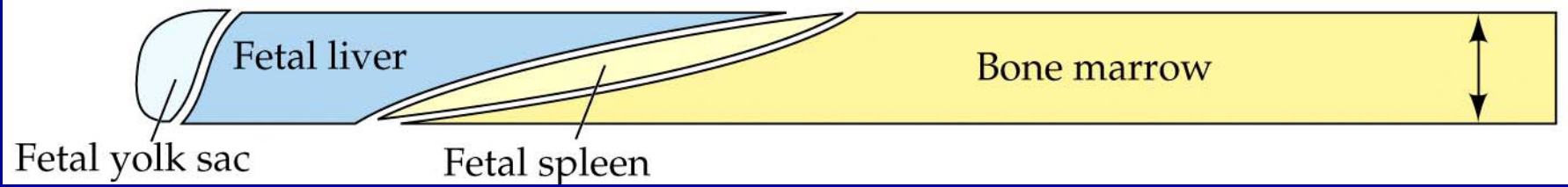
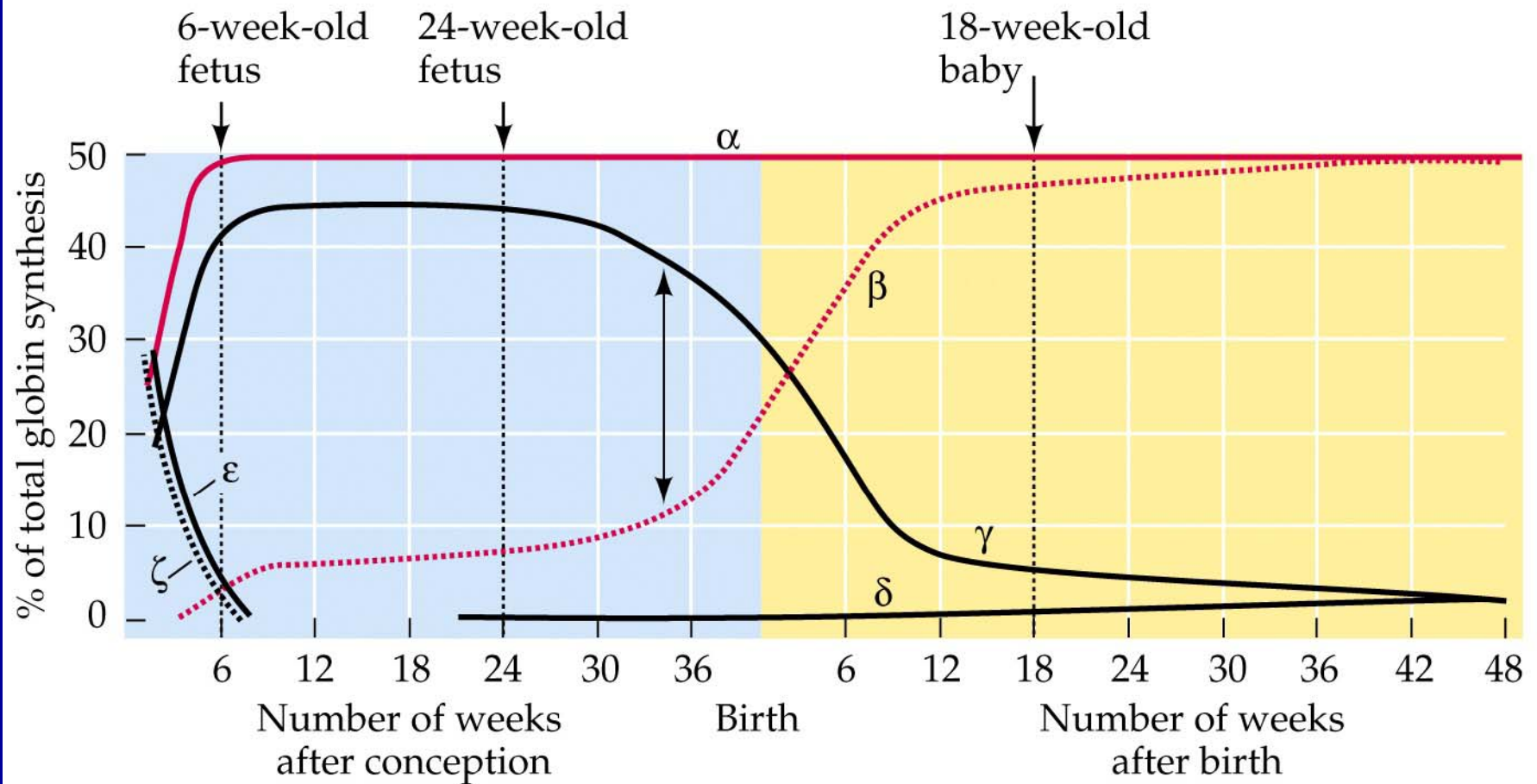
Pseudogenes

α -Globin
gene cluster

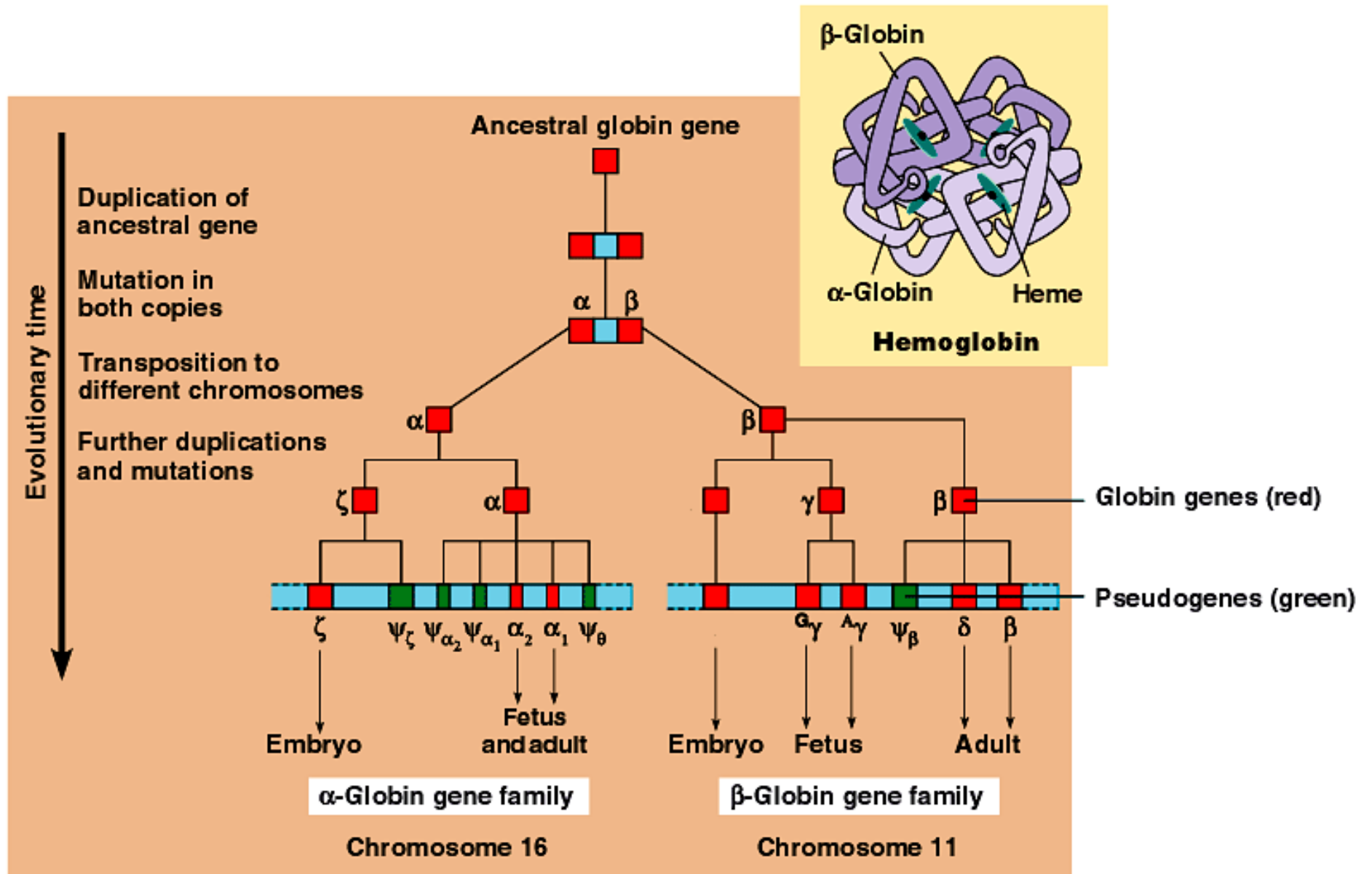


C. The Structures of Protein-Coding Genes

- Differential expression of different genes in the β -globin family ensures important physiological changes during human development.



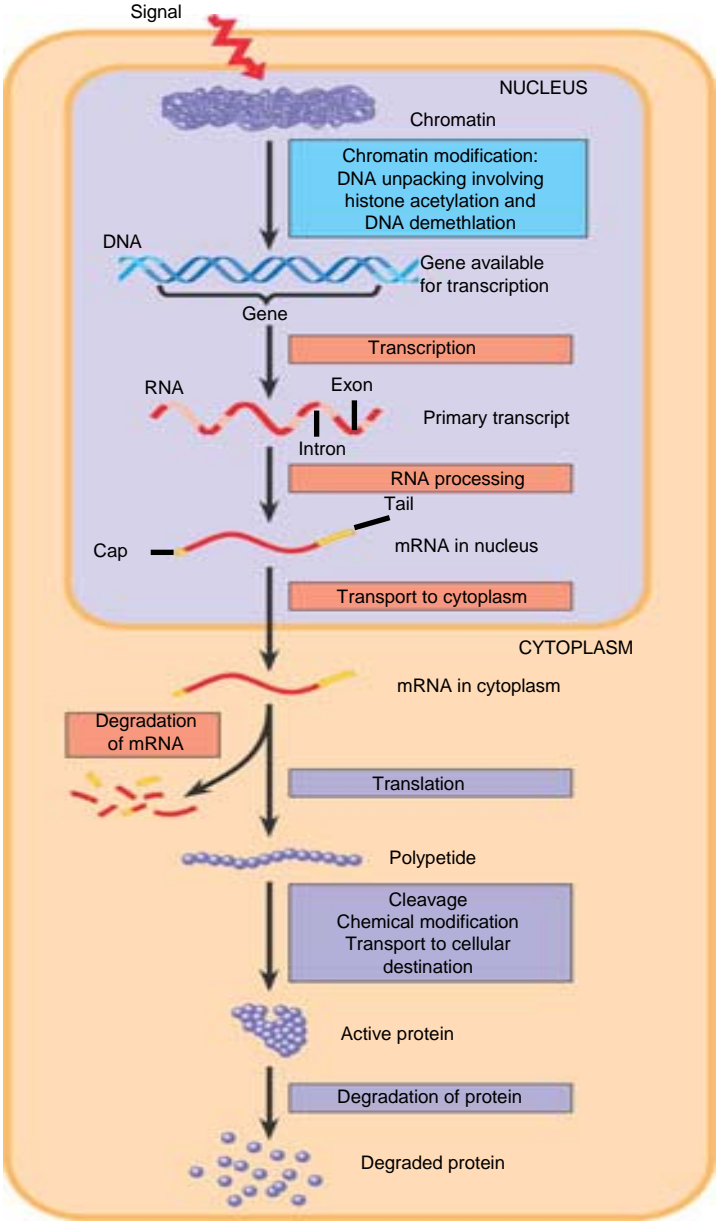
The evolution of human α -globin and β -globin gene families



D. Transcriptional Control

- Eukaryotic gene expression can be controlled at the transcriptional, posttranscriptional, translational, and posttranslational levels.

Stages in gene expression that can be regulated in eukaryotic cells



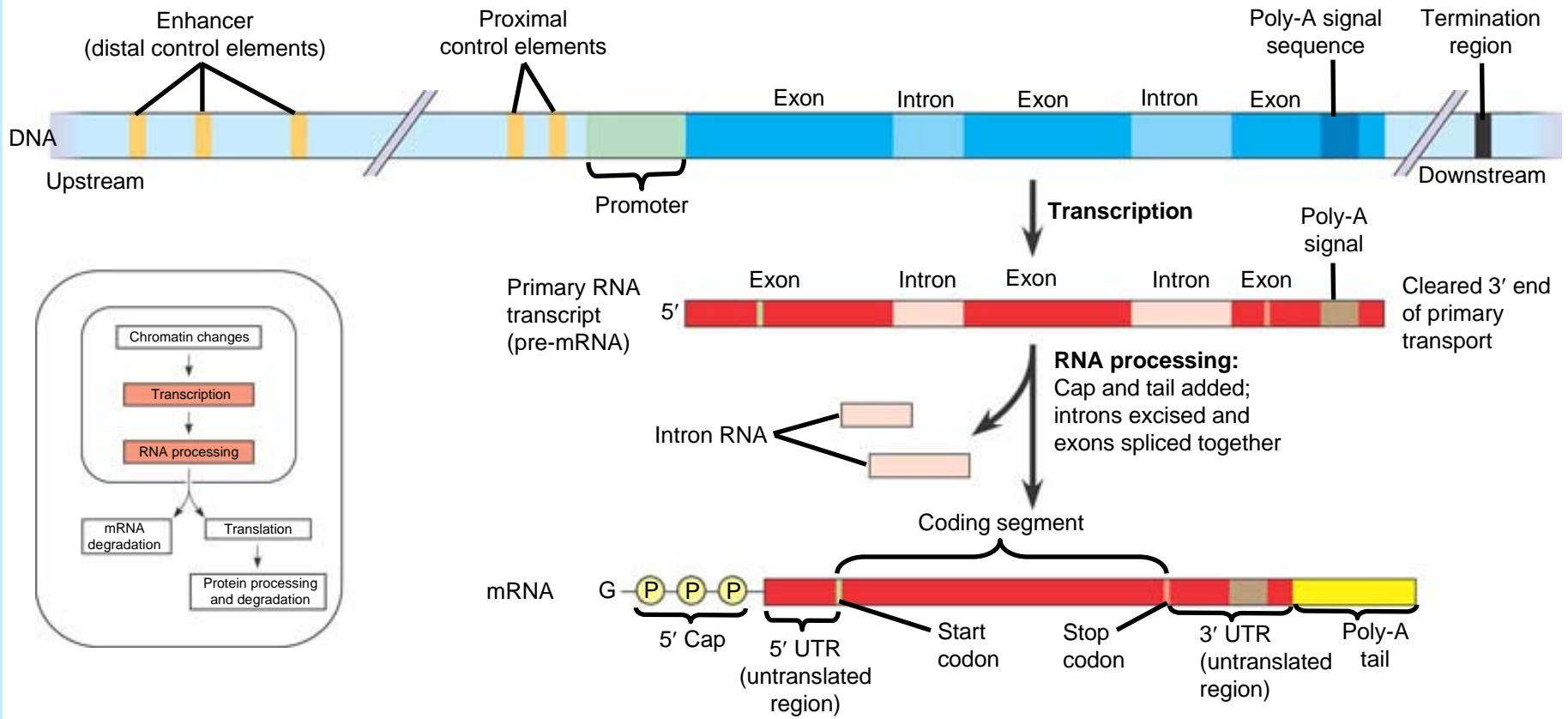
D. Transcriptional Control

- The major method of control of eukaryotic gene expression is selective transcription, which results from specific proteins binding to regulatory regions on DNA.

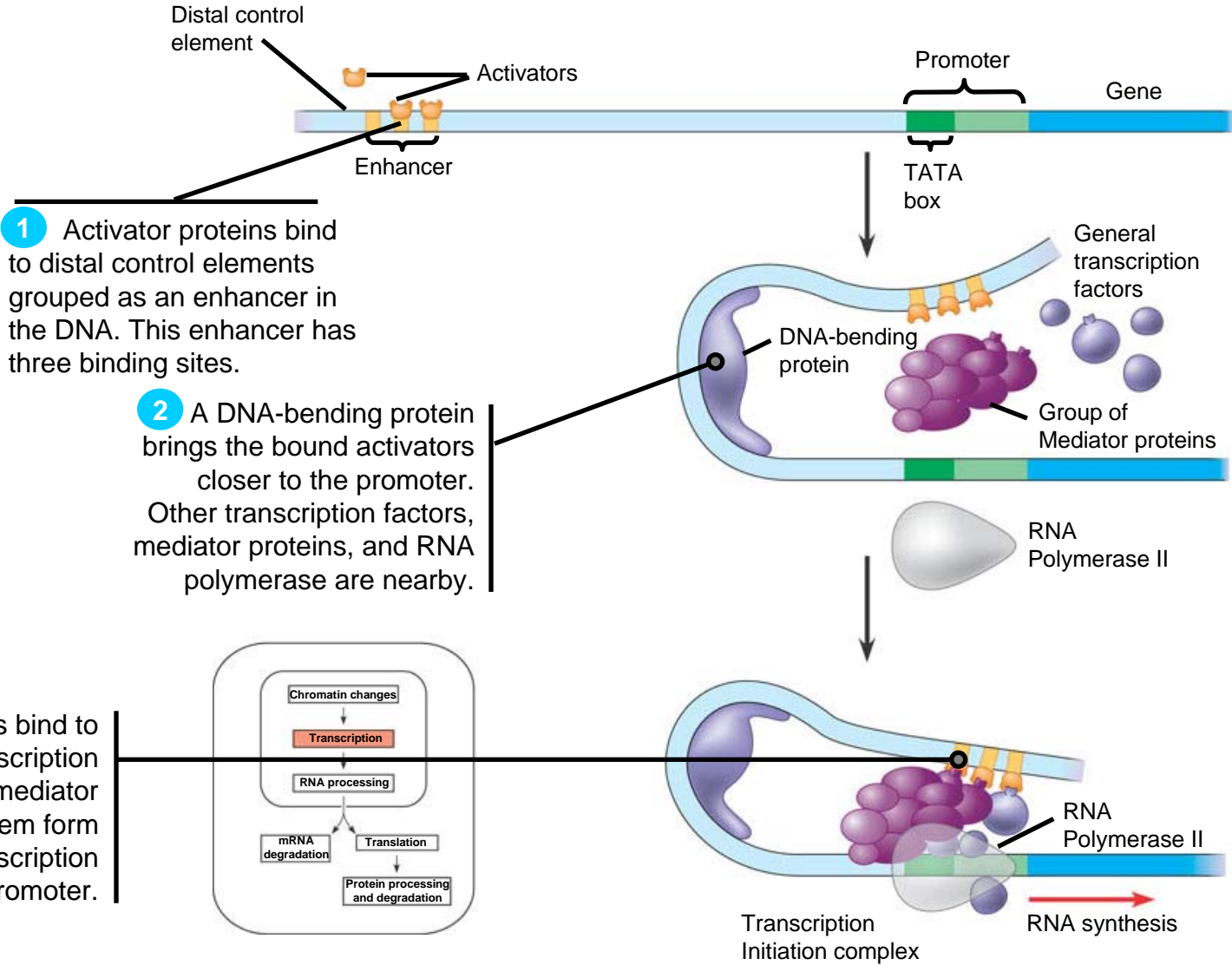
D. Transcriptional Control

- A series of transcription factors must bind to the promoter before RNA polymerase can bind.
- Whether RNA polymerase will initiate transcription also depends on the binding of regulatory proteins, activator proteins, and repressor proteins.

A eukaryotic gene and its transcript



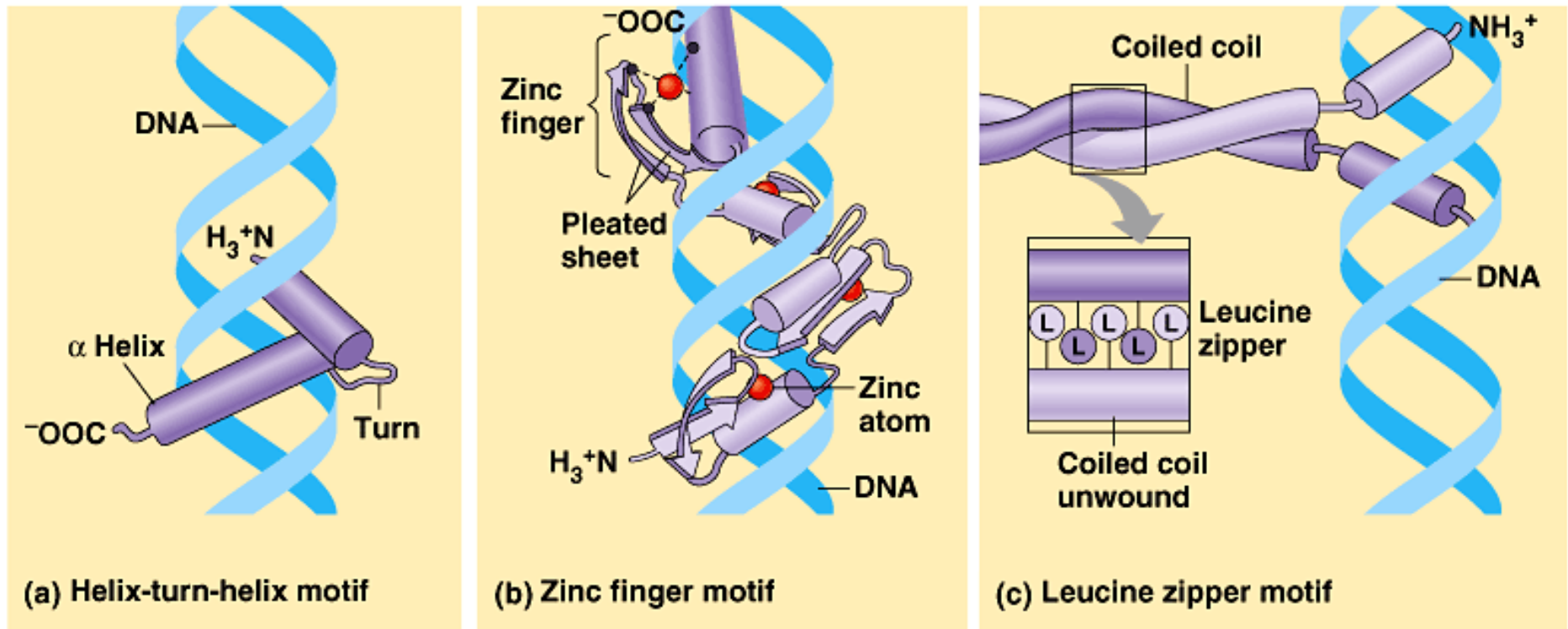
A model for the action of enhancers and transcription activators



D. Transcriptional Control

- The DNA-binding domains of most DNA-binding proteins have one of four structural motifs: helix-turn-helix, zinc finger, leucine zipper, or helix-loop-helix.

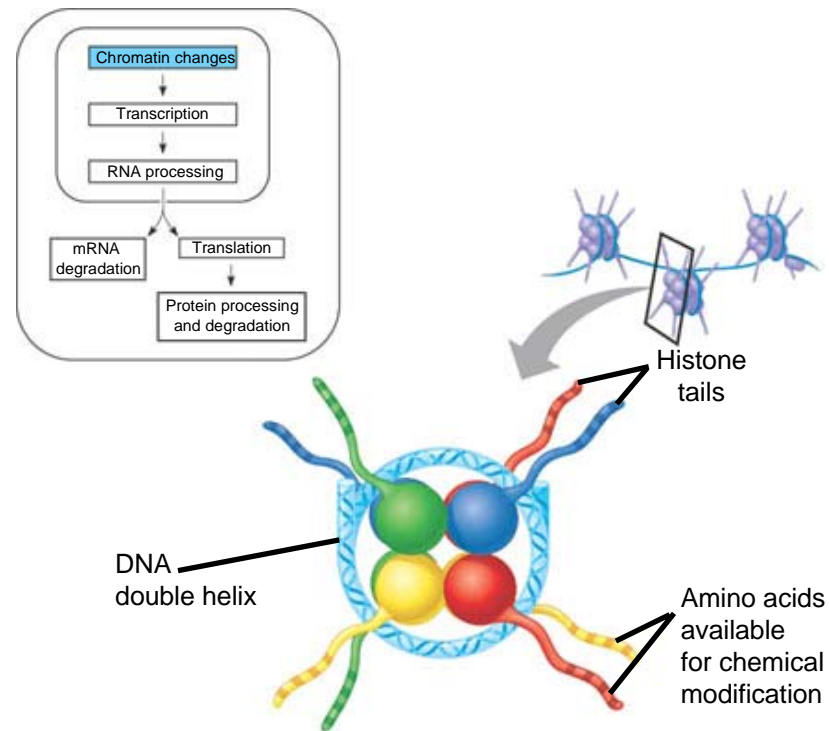
Three of the major types of DNA-binding domains in transcription factors



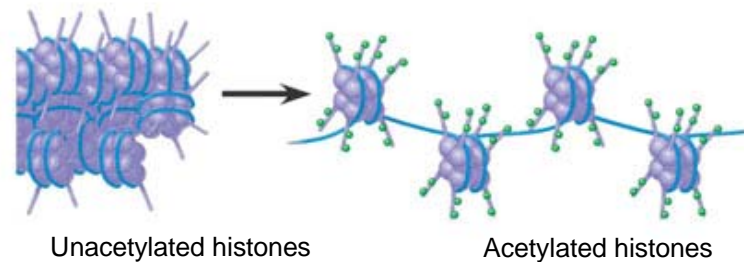
D. Transcriptional Control

- Acetylation of histone tails promotes loose chromatin structure that permits transcription to more readily occur.

A simple model of histone tails and the effect of histone acetylation



(a) Histone tails protrude outward from a nucleosome

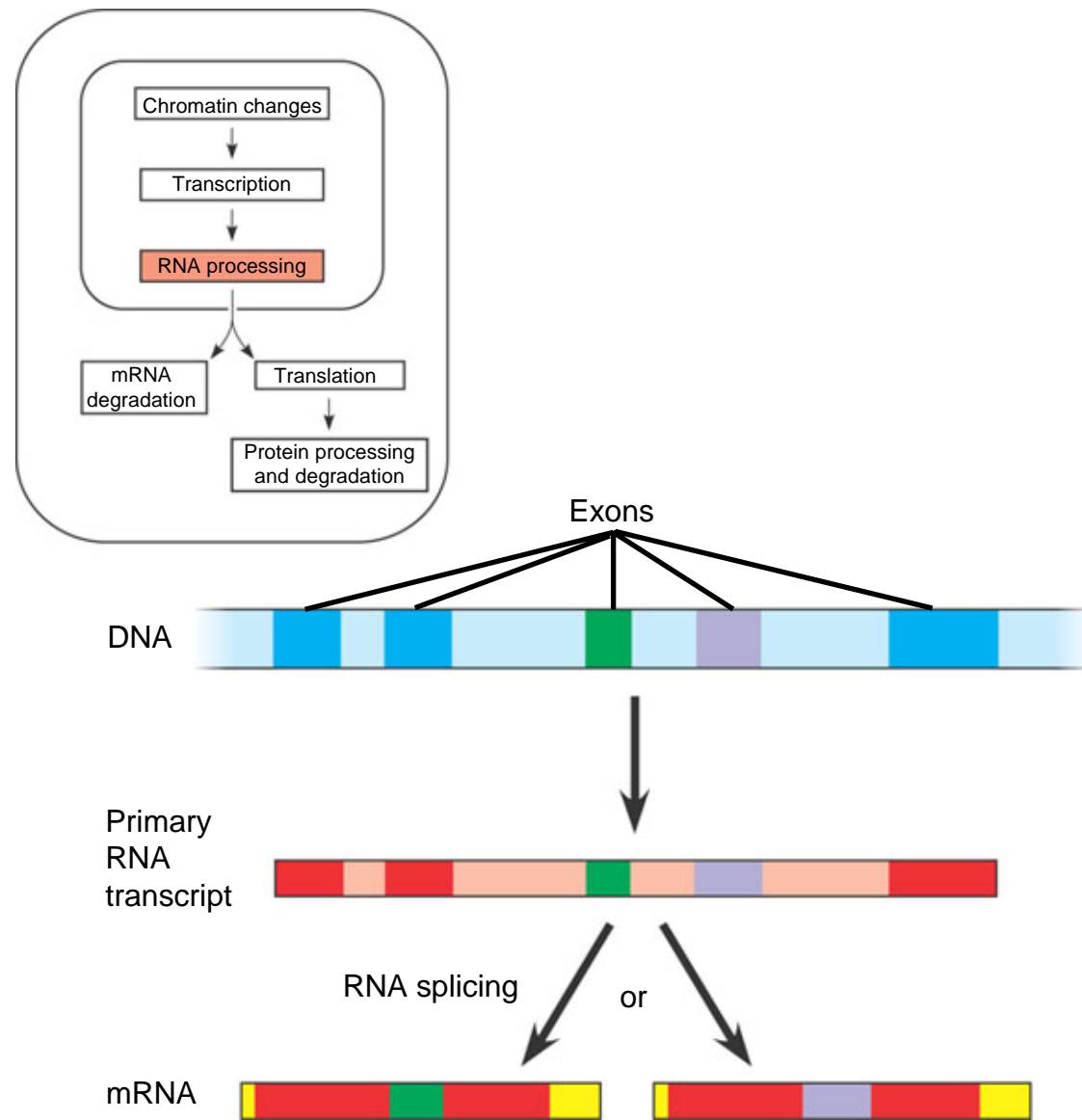


(b) Acetylation of histone tails promotes loose chromatin structure that permits transcription

E. Posttranscriptional Control

- Because eukaryotic genes have several exons, alternative mRNAs can be generated from the same RNA transcript.
- This alternate splicing can be used to produce different proteins.
- The stability of mRNA in the cytoplasm can be regulated by the binding of proteins.

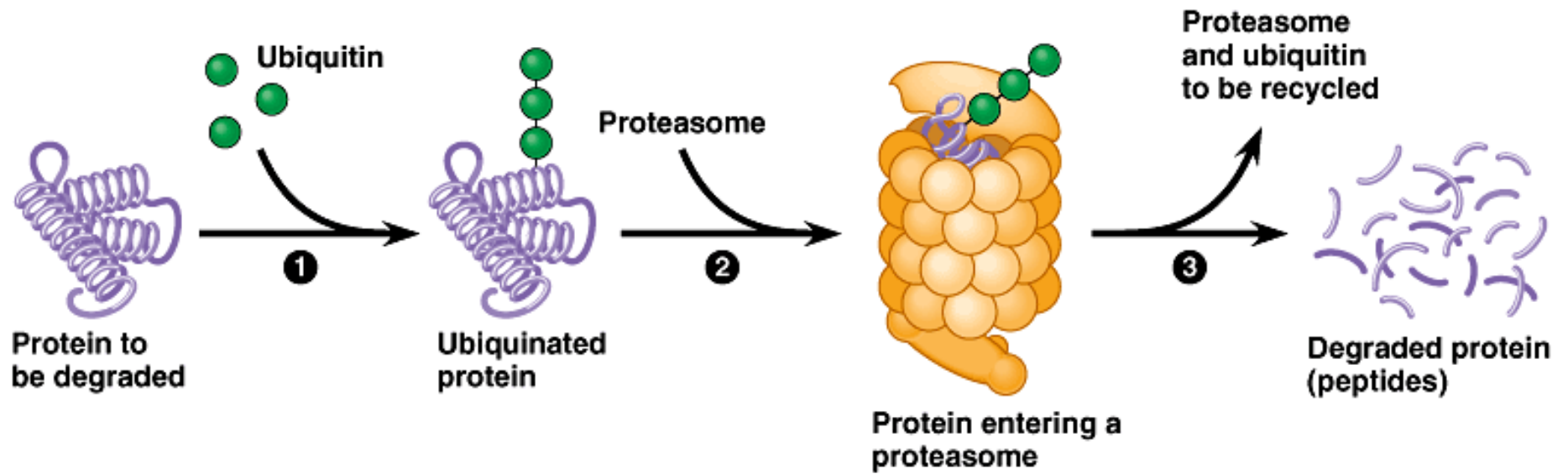
Alternative RNA splicing



E. Posttranslational Control

- Proteasomes degrade proteins targeted for breakdown.

Degradation of a protein by a proteasome



Proteasomes

