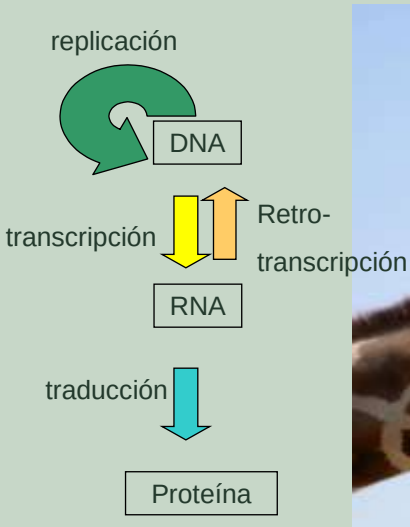
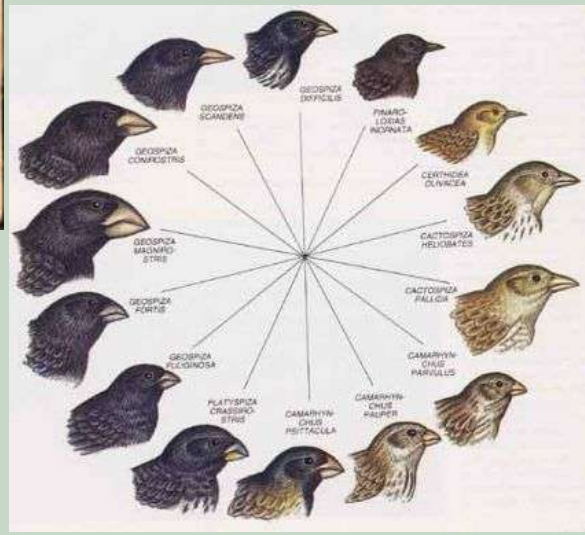
INTRODUCCION A LA BIOLOGIA CELULAR Y MOLECULAR

- Transcripción Genética -

El Dogma Central de la Biología Molecular

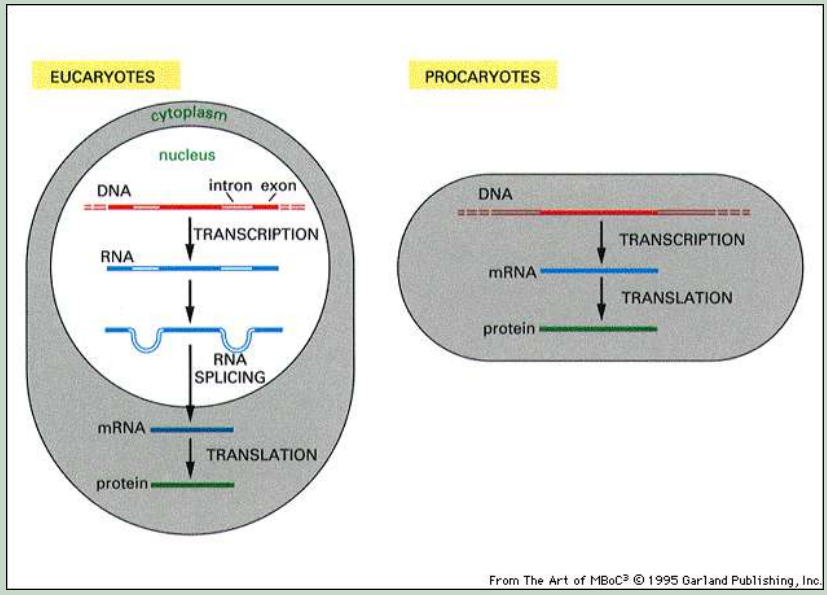




ARN

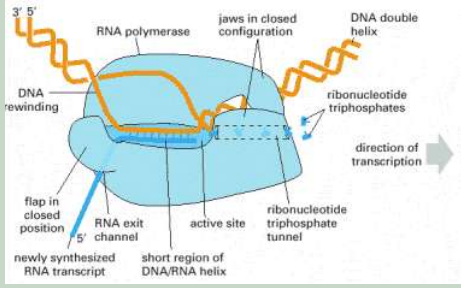
TYPE OF RNA	FUNCTION
mRNAs	messenger RNAs, code for proteins
rRNAs	ribosomal RNAs, form the basic structure of the ribosome and catalyze protein synthesis
tRNAs	transfer RNAs, central to protein synthesis as adaptors between mRNA and amino acids
snRNAs	small nuclear RNAs, function in a variety of nuclear processes, including the splicing of pre-mRNA
snoRNAs	small nucleolar RNAs, used to process and chemically modify rRNAs
Other noncoding RNAs	function in diverse cellular processes, including telomere synthesis, X-chromosome inactivation, and the transport of proteins into the ER

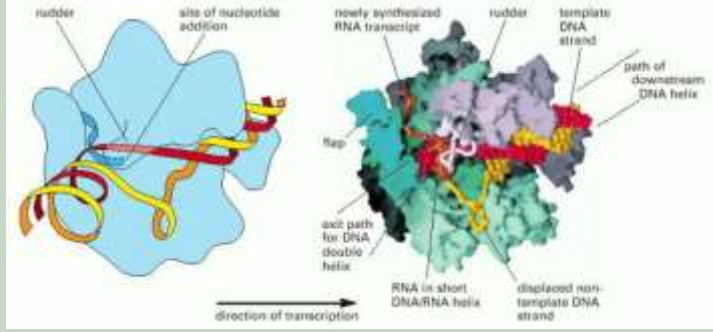
Eucariotas vs. Procariotas



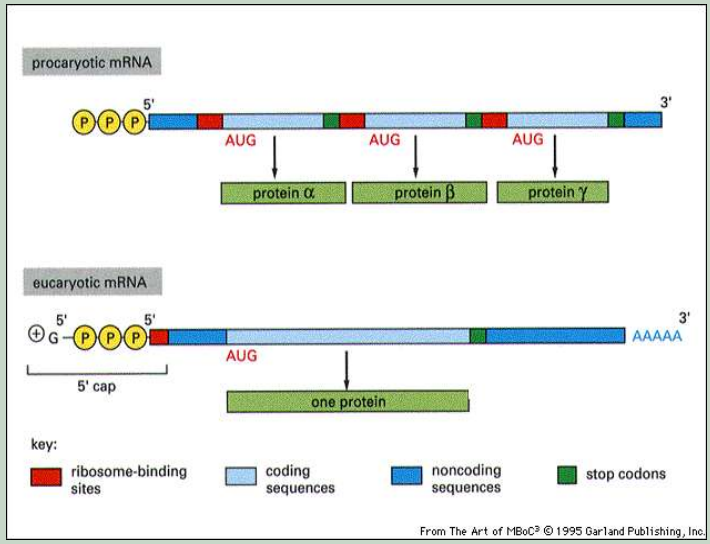
Genes

“Secuencia completa de ADN que está involucrada en la formación de una cadena polipeptidica o de un RNA funcional”

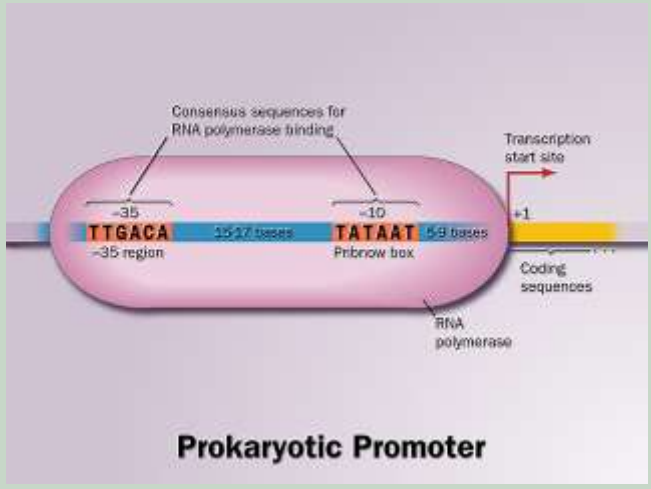

3′ 5′
RNA polymerase
jaws in closed configuration
DNA double helix
DNA rewinding
ribonucleotide triphosphates
direction of transcription
flap in closed position
RNA exit channel
active site
ribonucleotide triphosphate tunnel
5′
newly synthesized RNA transcript
short region of DNA/RNA helix


rudder
site of nucleotide addition
newly synthesized RNA transcript
rudder
template DNA strand
path of downstream DNA helix
flap
exit path for DNA double helix
RNA in short DNA/RNA helix
displaced non-template DNA strand
direction of transcription

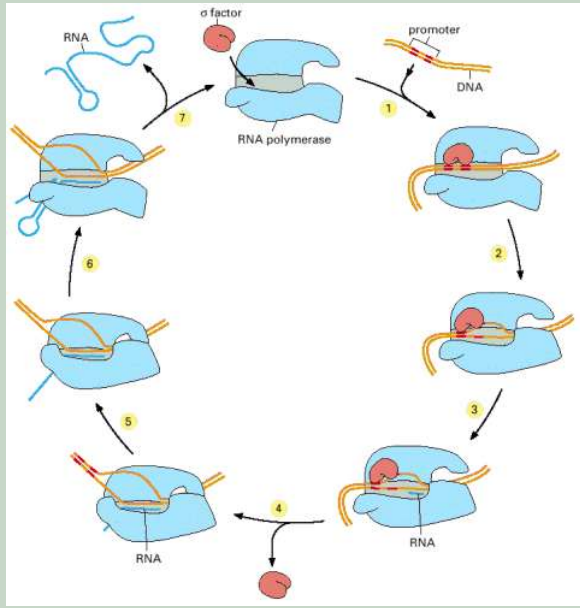
Genes



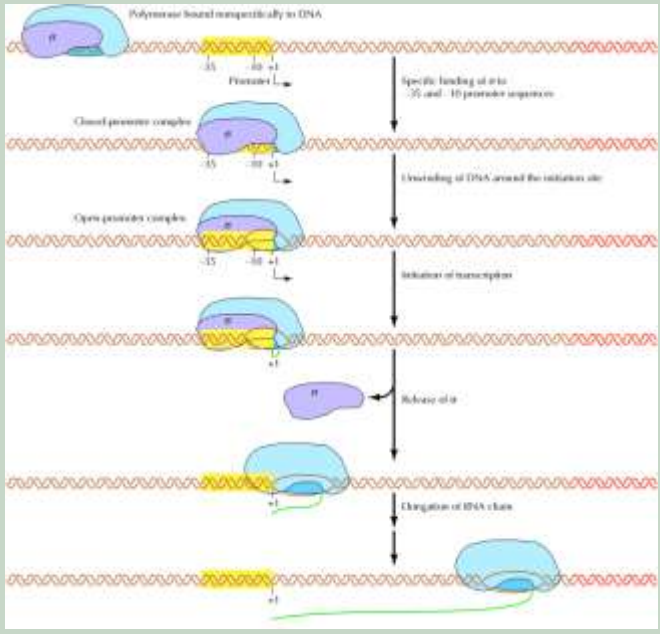
Promotor - PROCARIOTAS



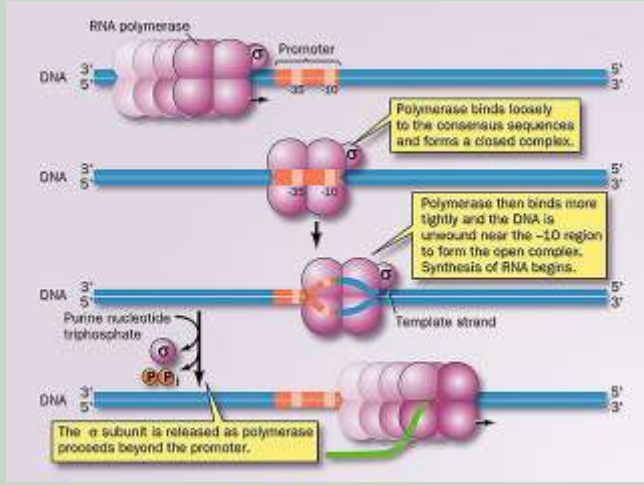
Ciclo de transcripción - PROCARIOTAS



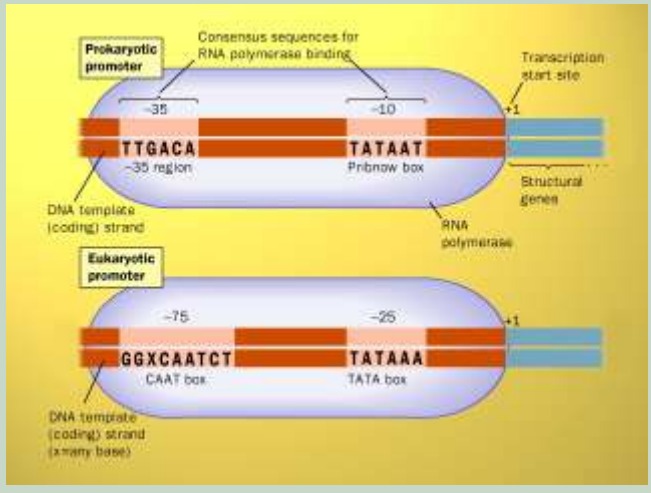
Comienzo de la transcripción- PROCARIOTAS



Inicio de la transcripción - Procariotas



Promotores – Procariotas vs Eucariotas

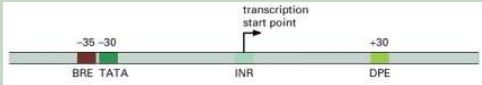


Polimerasas eucariotas

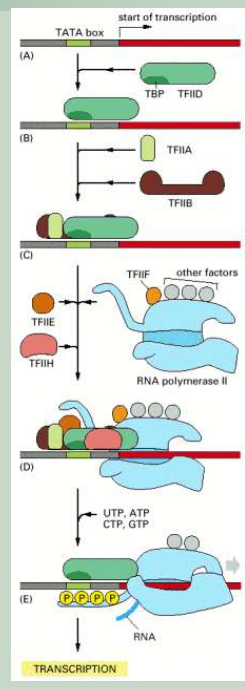
Eukaryotic RNA Polymerases

Type	Localization	Cellular transcripts
I	Nucleolus	18S, 5.8S, and 28S ribosomal RNAs (rRNA)
II	Nucleoplasm	mRNA precursors and small nuclear RNAs (snRNA)
III	Nucleoplasm	tRNAs and 5S rRNAs

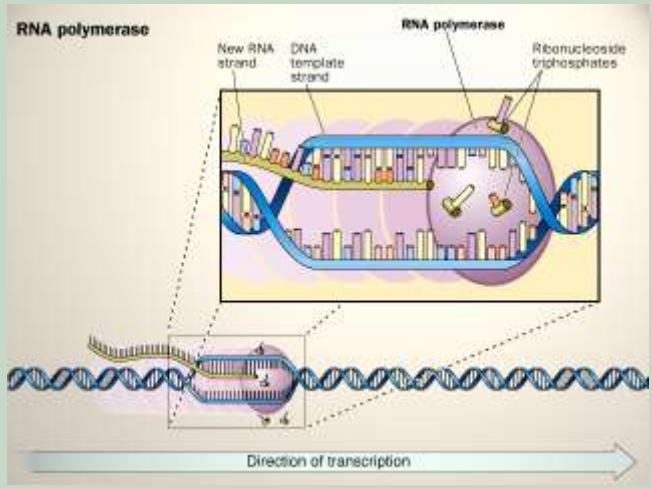
Inicio de la transcripción – ARNpol II (Eucariotas)

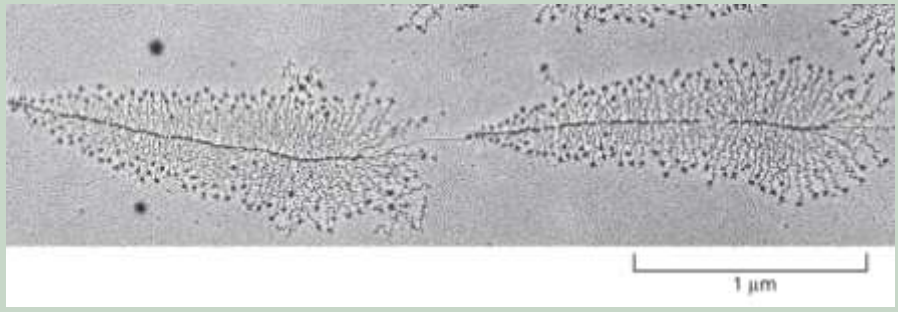


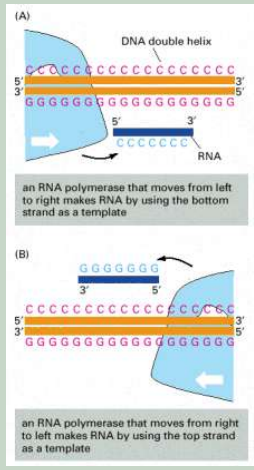
element	consensus sequence	general transcription factor
BRE	G/C G/C G/A C G C C	TFIIB
TATA	T A T A A/T A A/T	TBP
INR	C/T C/T A N T/A C/T C/T	TFIID
DPE	A/G G A/T C G T G	TFIID

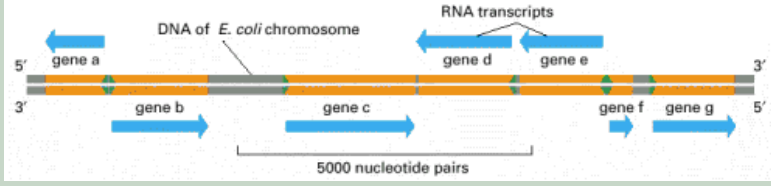


ARN Polimerasa





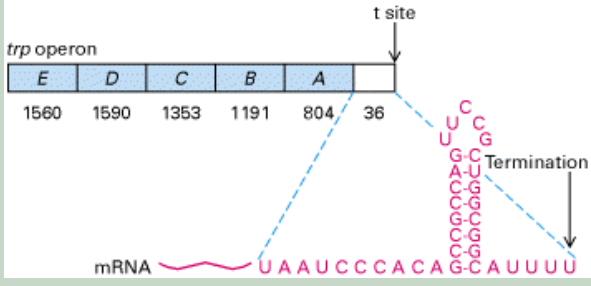




Fin de la transcripción

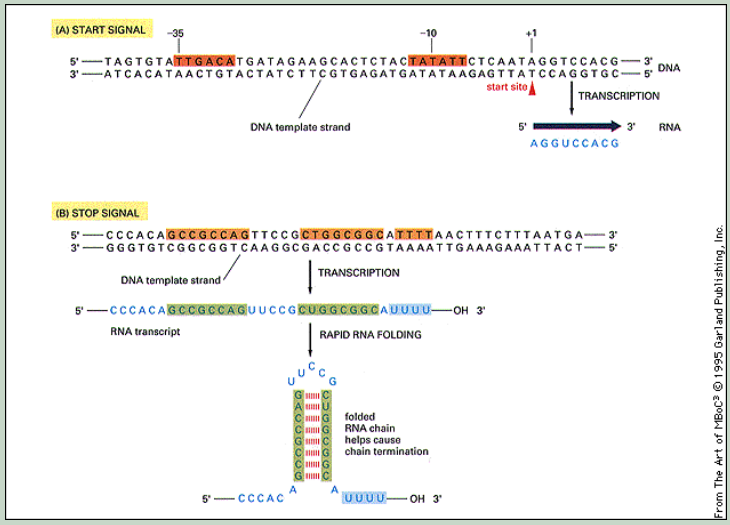
En procariontes se conocen dos sistemas de terminación de la transcripción que involucran a la misma RNA polimerasa, denominados: terminación Rho-independiente (la mayoría de los operones) y terminación Rho dependiente

Terminación Rho-independiente: Estas secuencias de terminación poseen dos características típicas, una serie de residuos U en el RNA transcripto, y, antes de estos, una región autocomplementaria rica en GC.

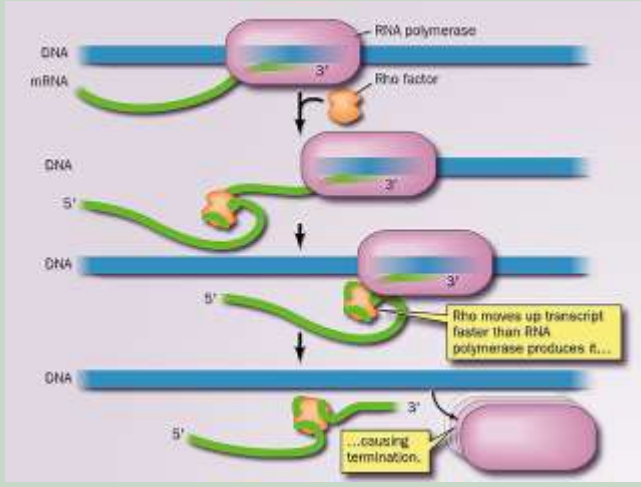


Esta estructura tallo-asa obliga a hacer una pausa a la RNA polimerasa. Además los pares de bases entre los residuos U en el extremo 3´ de la hebra de RNA naciente y los residuos de A en la hebra de DNA plantilla son muy inestables en comparación con otros tipos de apareamientos de Watson-Crick

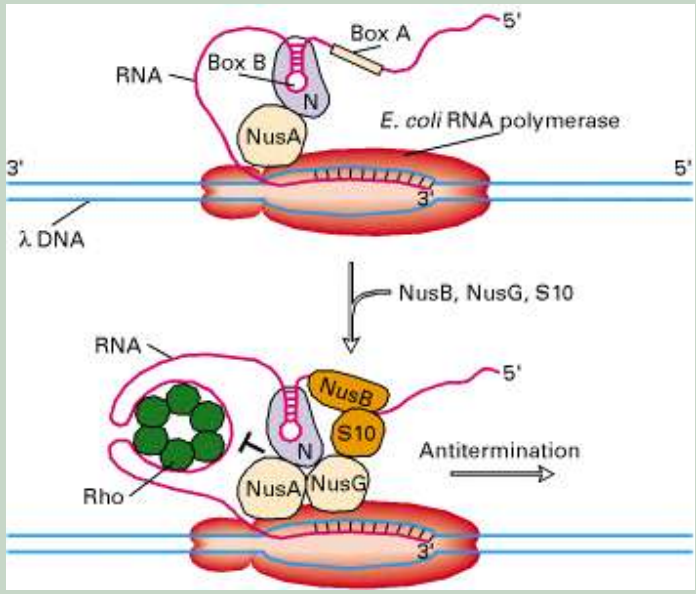
Fin de la transcripción Rho independiente



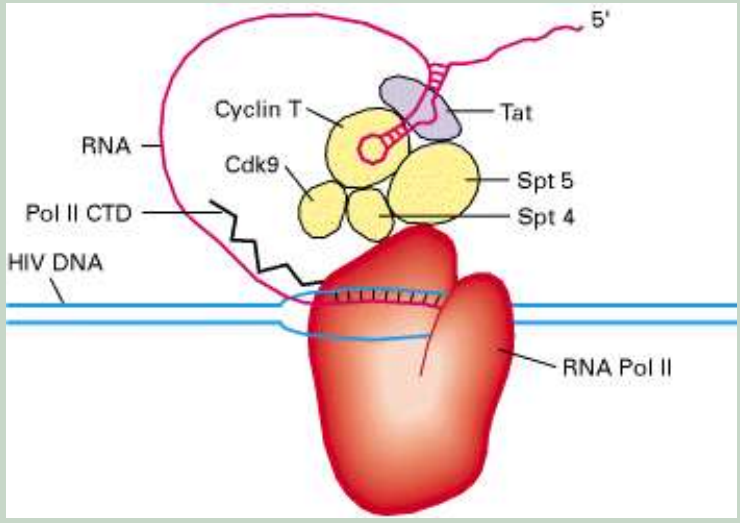
Fin de la transcripción RHO dependiente - PROCARIOTAS



Fin de la transcripción RHO dependiente - PROCARIOTAS

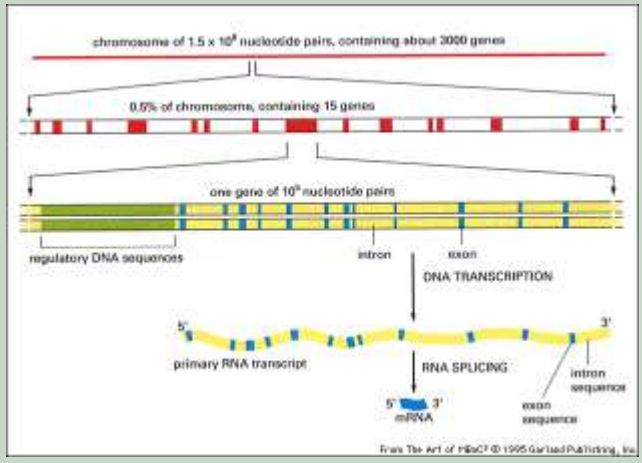


Fin de la transcripción – HIV RNA pol II

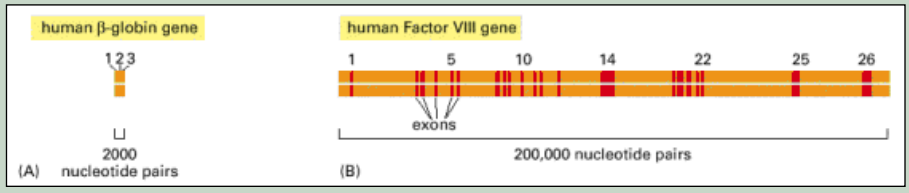


Complejo de antiterminación compuesto por la proteína Tat de HIV y varias proteínas celulares eucariontes. El elemento TAR en el transcripto de HIV contiene secuencias reconocidas por la TAT y la proteína celular ciclina. La ciclina T, activa y contribuye a ubicar la Cdk9, una quinasa, cerca de su sustrato, el CTD de la RNA polimerasa II, el cual es hiperfosforilado por esta quinasa.

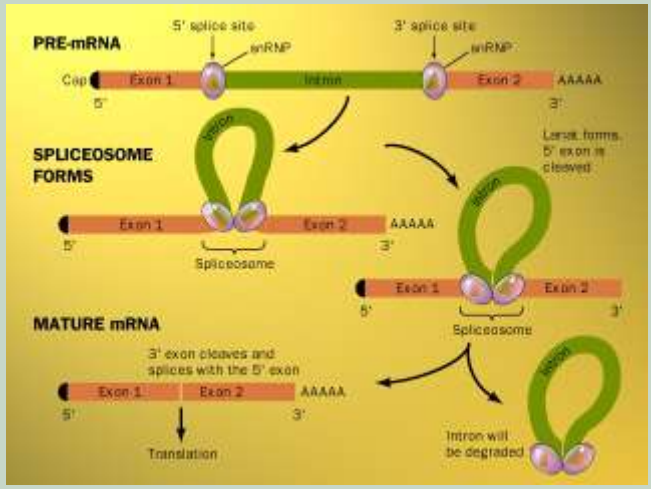
Intrones y exones



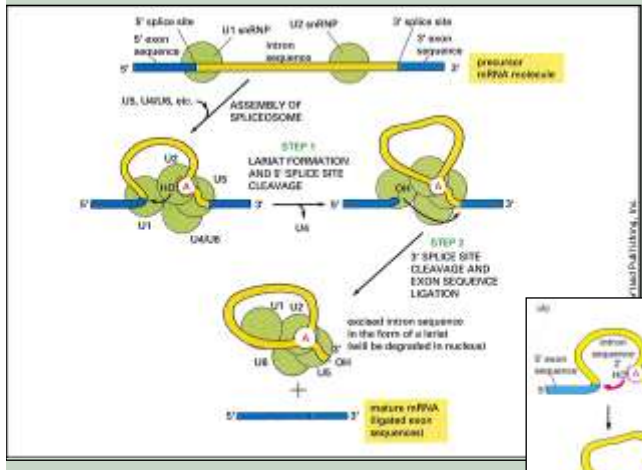
Intrones y exones

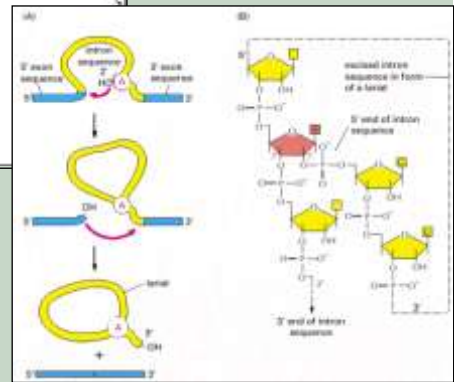


Splicing

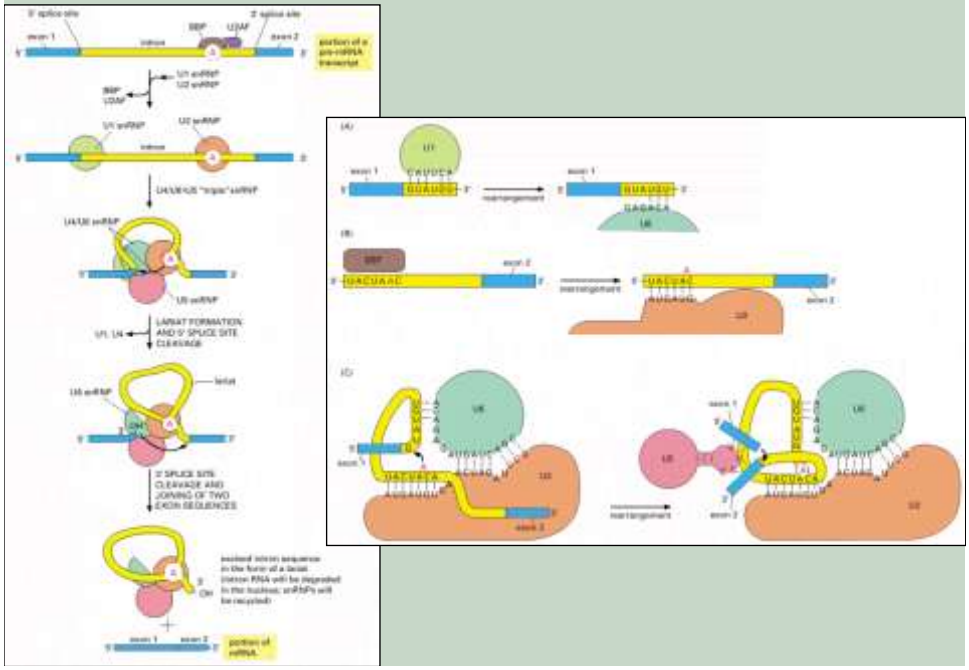


Splicing

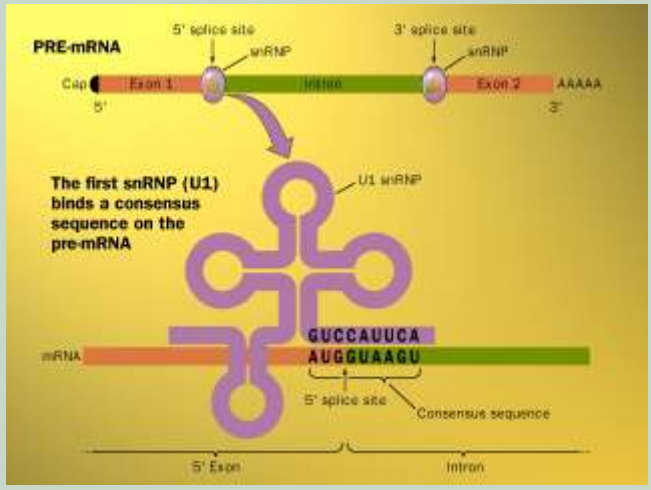




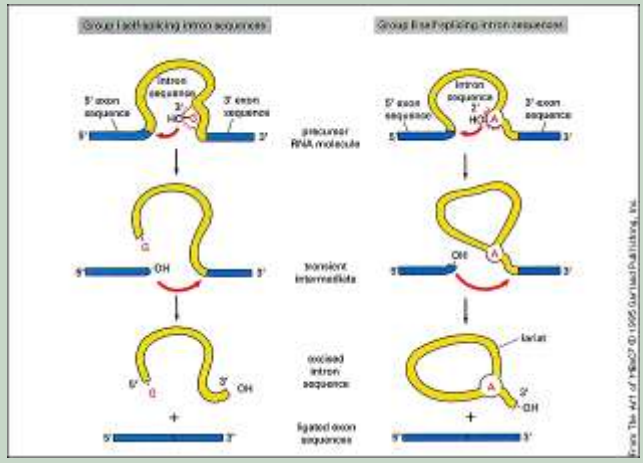
Intrones de tipo III



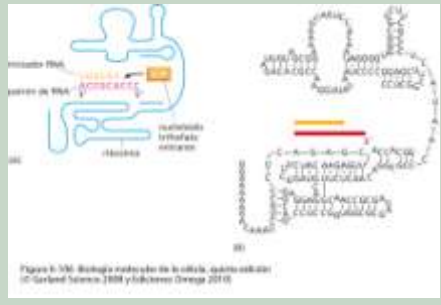
Splicing

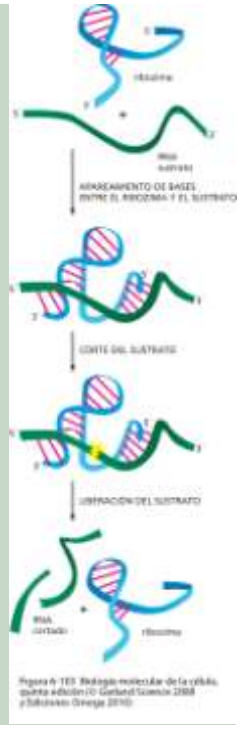

PRE-mRNA
5' splice site
snRNP
3' splice site
snRNP
Cap
Exon 1
Intron
Exon 2
AAAAA
5'
3'
The first snRNP (U1) binds a consensus sequence on the pre-mRNA
U1 snRNP
GUCCAUUCA
mRNA
AUGGUAAGU
5' splice site
Consensus sequence
5' Exon
Intron

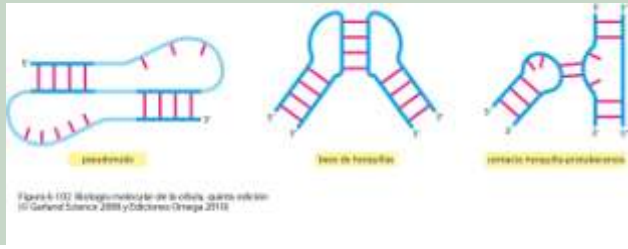
Autosplicing – RNA catalitico



Intrones de tipo I y II







Splicing alternativo

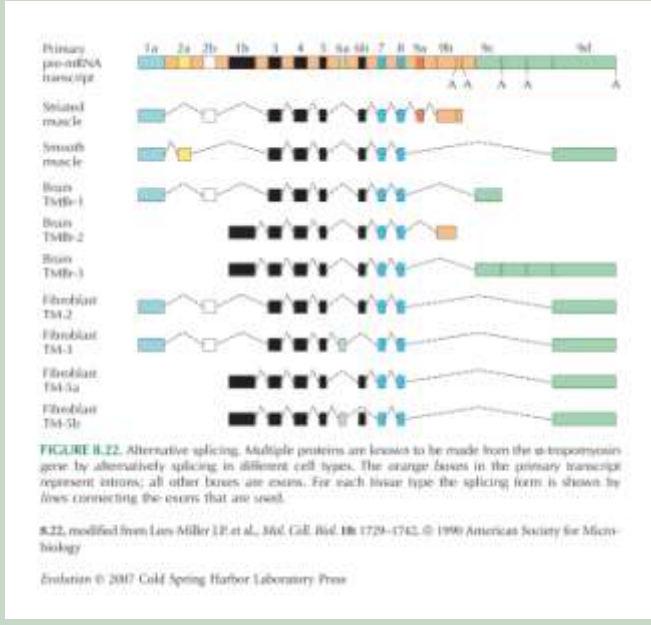


FIGURE 8.22. Alternative splicing. Multiple proteins are known to be made from the α-tropomyosin gene by alternatively splicing in different cell types. The orange boxes in the primary transcript represent introns; all other boxes are exons. For each tissue type the splicing form is shown by lines connecting the exons that are used.

8.22, modified from Lees-Miller J.P. et al., *Mol. Cell. Biol.* **10**: 1729–1742, © 1990 American Society for Microbiology

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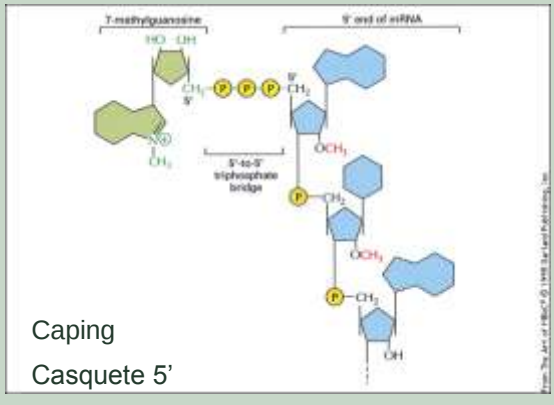
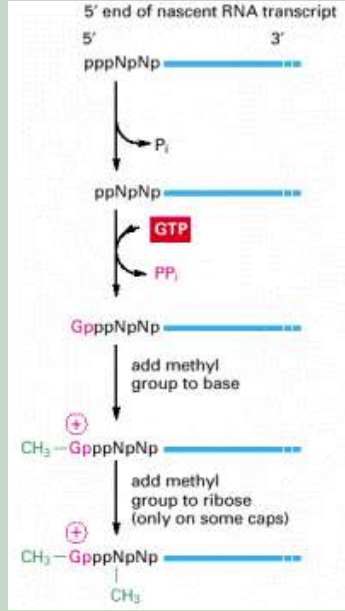
Maduración del transcripto primario. CAP

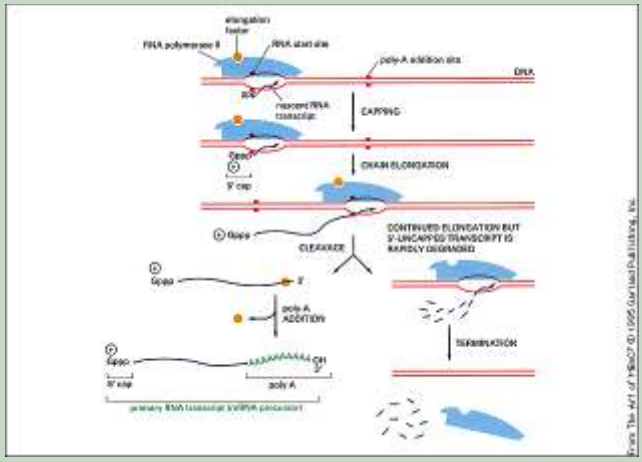


Caping

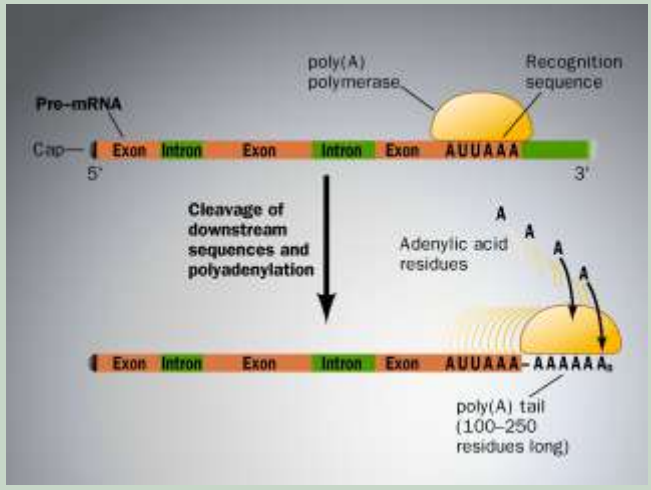
Casquete 5’



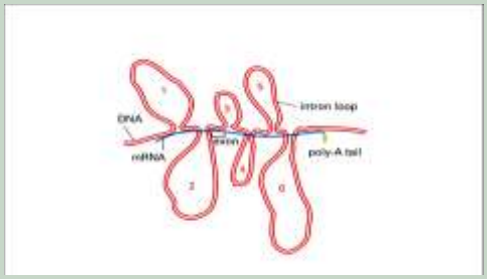
ARNm

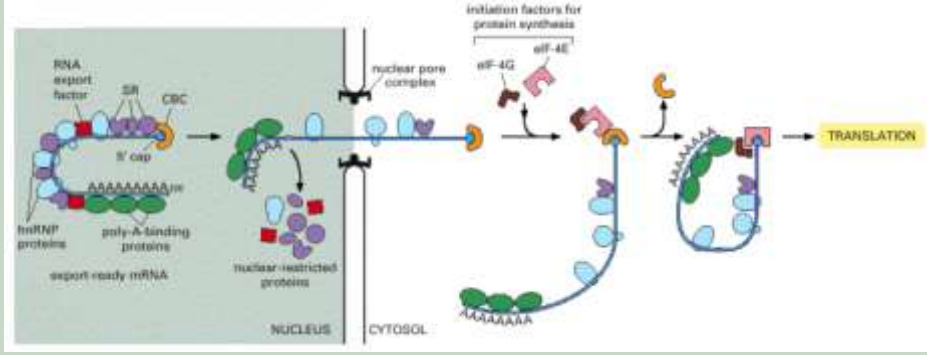


Poliadenilación

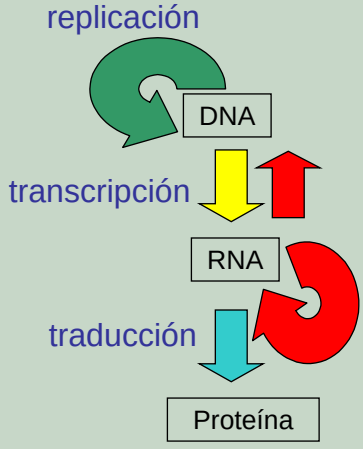


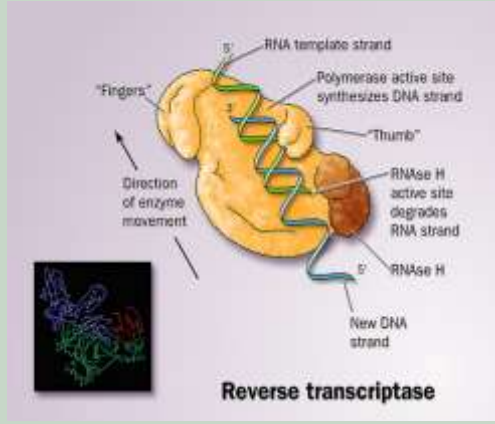
DNA vs. mRNA maduro



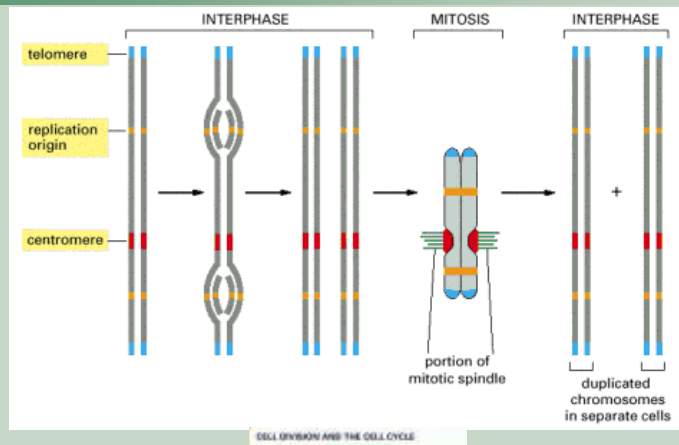


Retrotranscripción y replicación de RNA

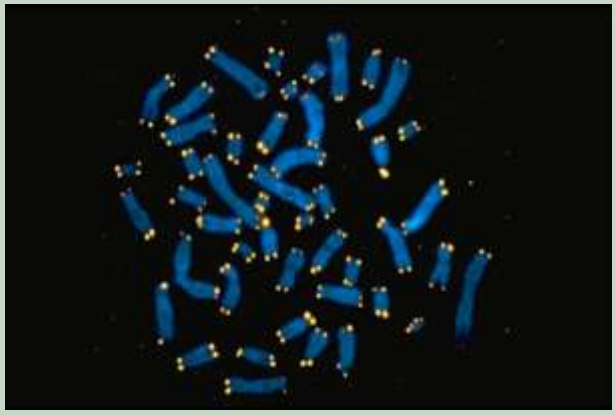


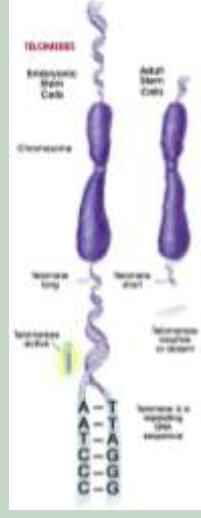


ADN



Cromosomas y Telómeros

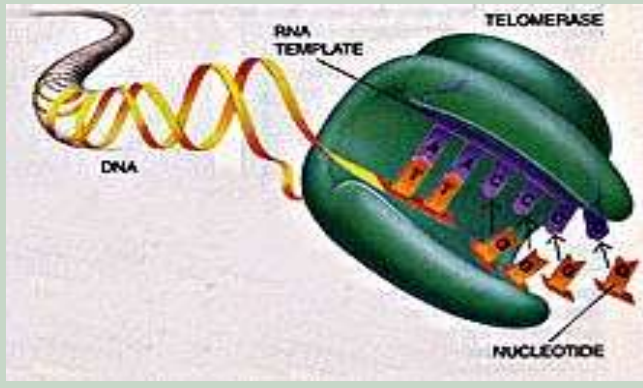




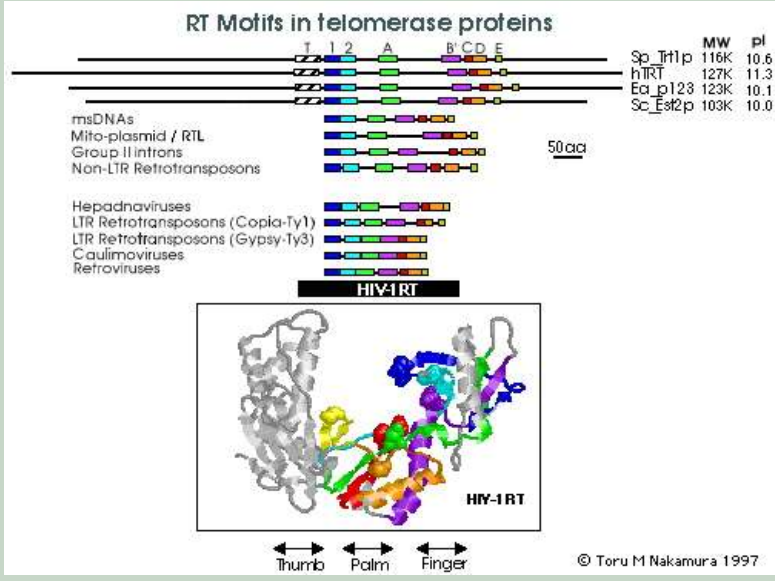
TELOMERASA

Es la enzima responsable de la replicación del ADN telomérico. Es una ribonucleoproteína, que contiene el templado de ARN con el que se impide la perdida de secuencias que se produciría normalmente en cada división celular.

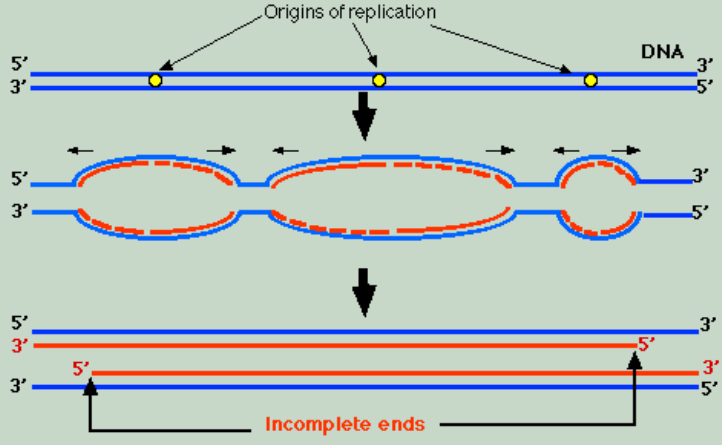
TELOMERASA

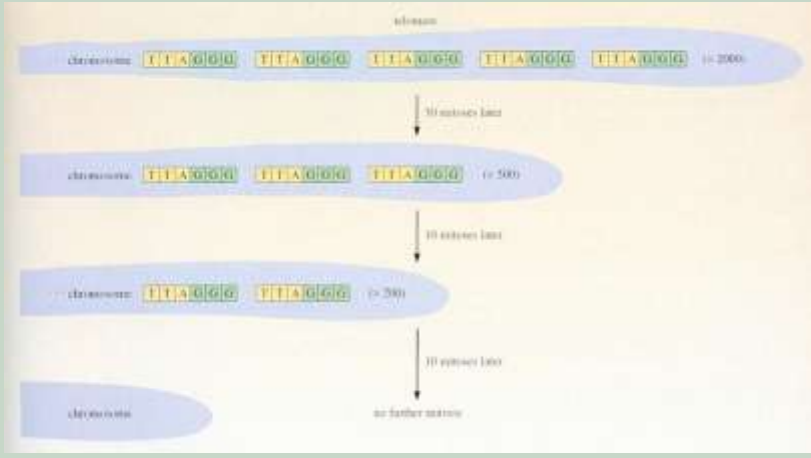


HOMOLOGIA DE LA TELOMERASA



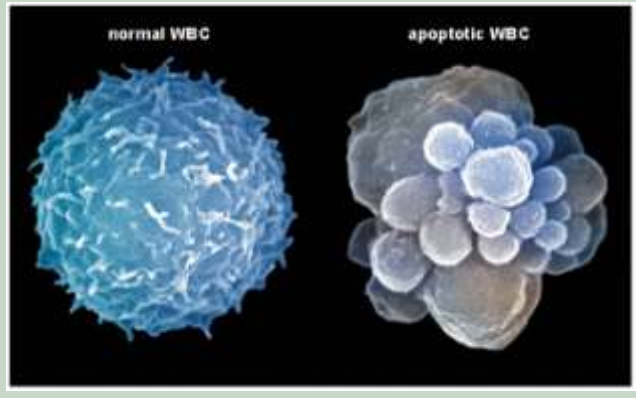
Acortamiento telomérico

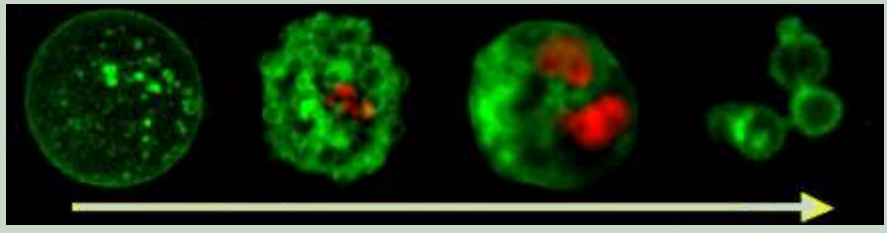




Senescencia Replicativa

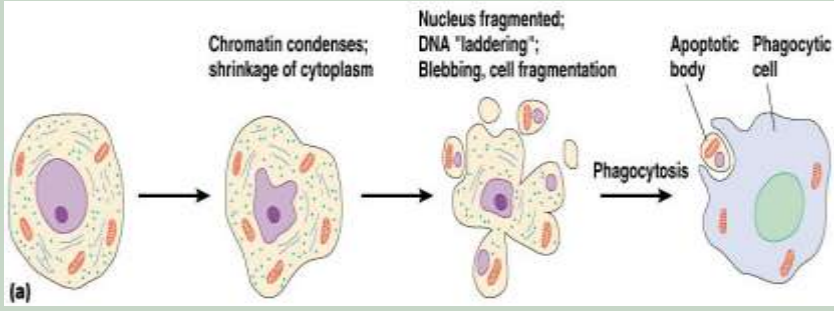
Apoptosis





APOPTOSIS VS. NECROSIS

- ACHICAMIENTO CELULAR
- CONDENSACIÓN DE LA CROMATINA
- FRAGMENTACION DEL ADN
- VACUOLIZACION CITOPLASMÁTICA
- LISIS CELULAR



Research article

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Potential involvement of oxidative stress in cartilage senescence and development of osteoarthritis: oxidative stress induces chondrocyte telomere instability and downregulation of chondrocyte function

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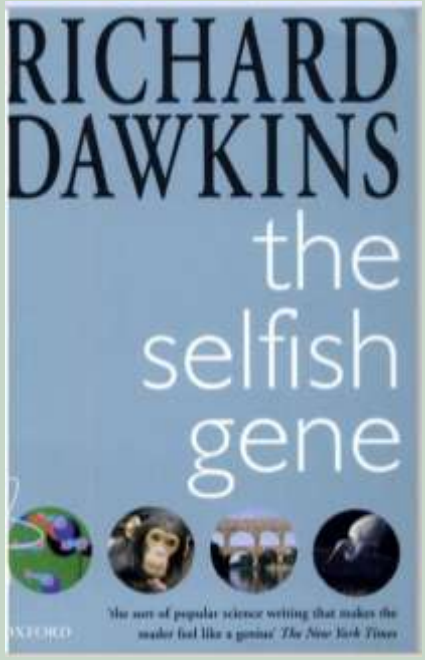
Progeria



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