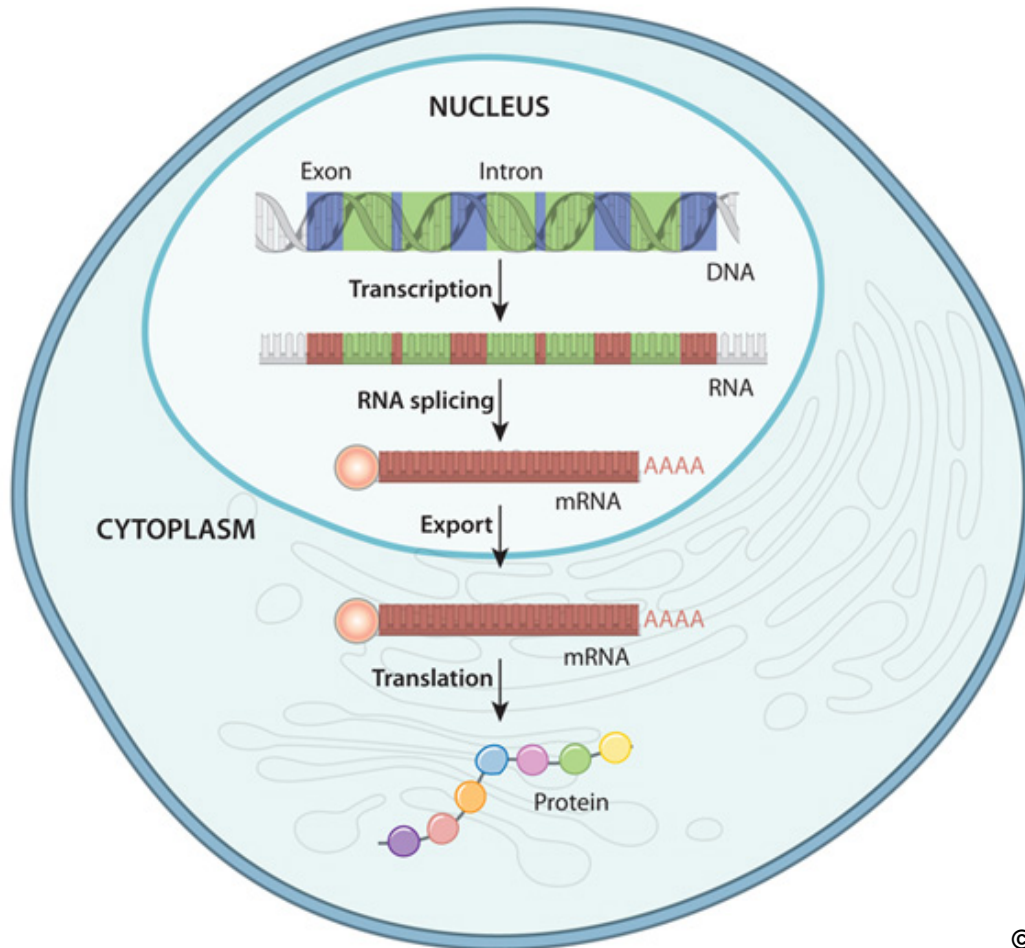
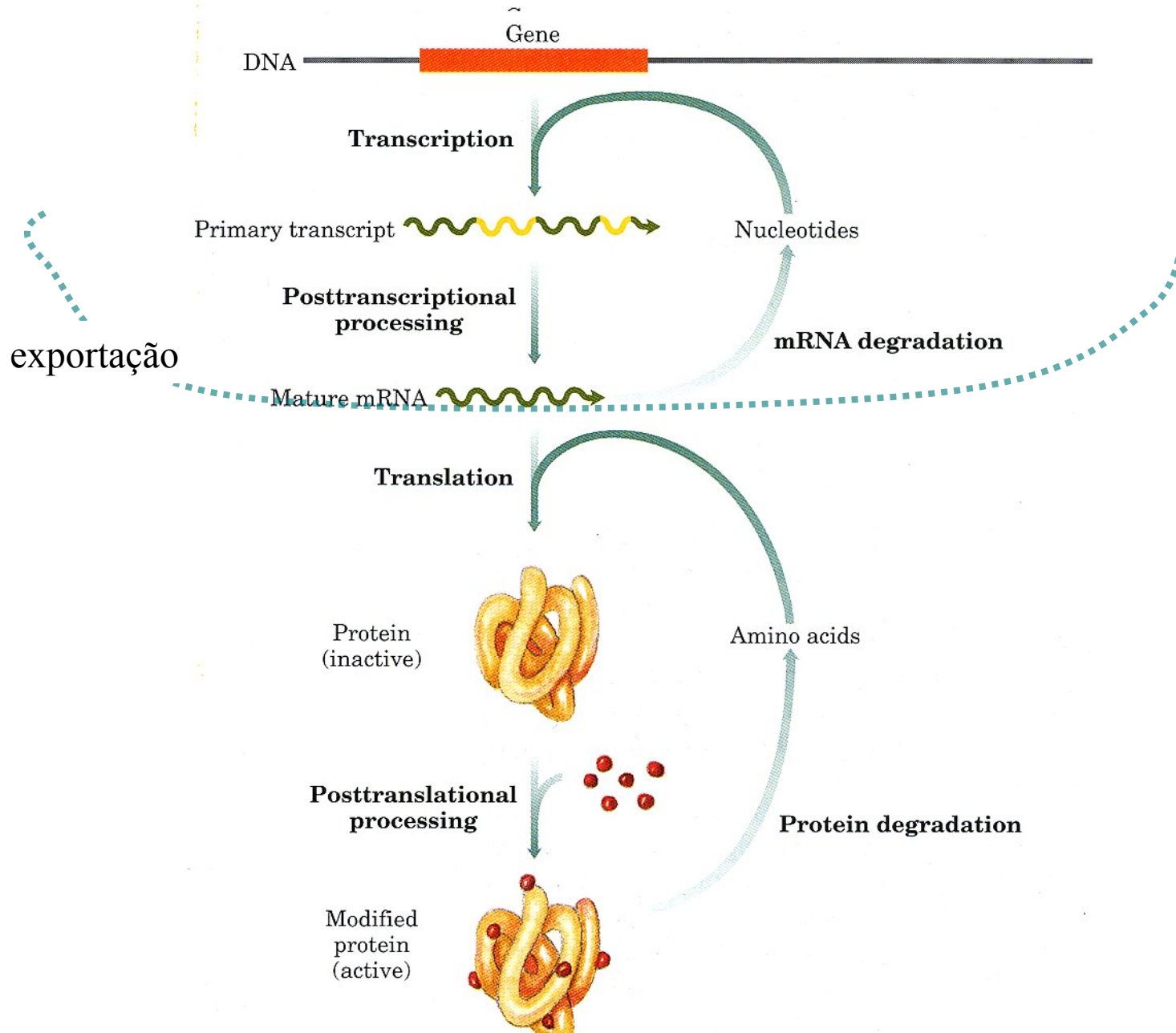


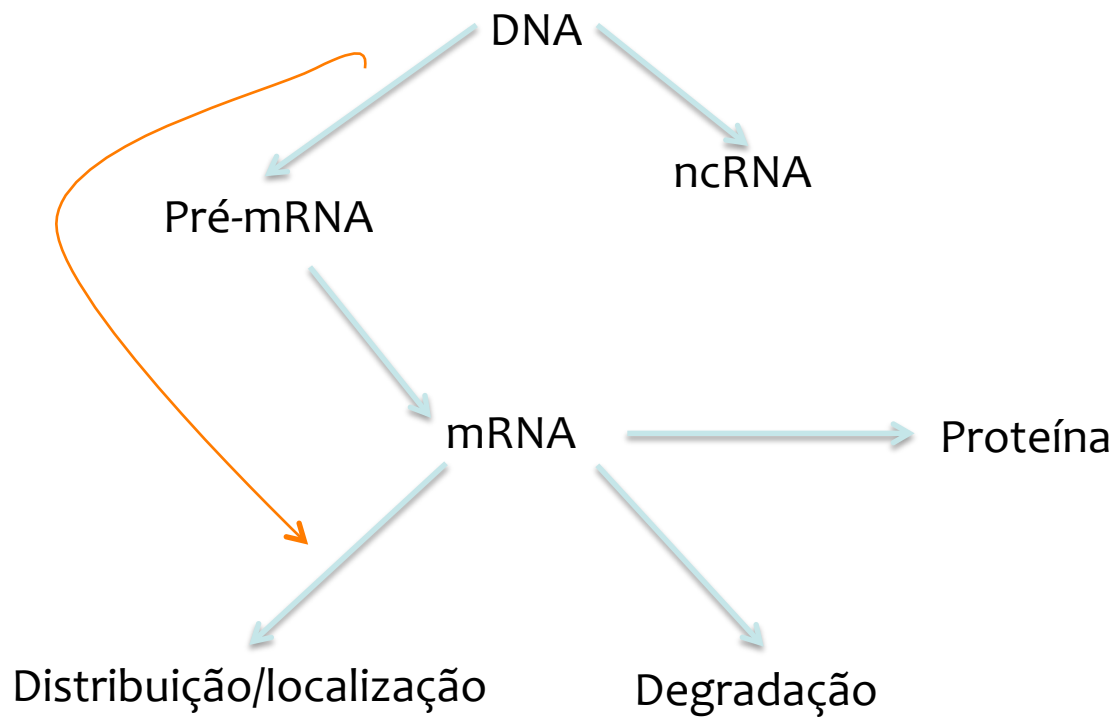
Regulação da Expressão Gênica



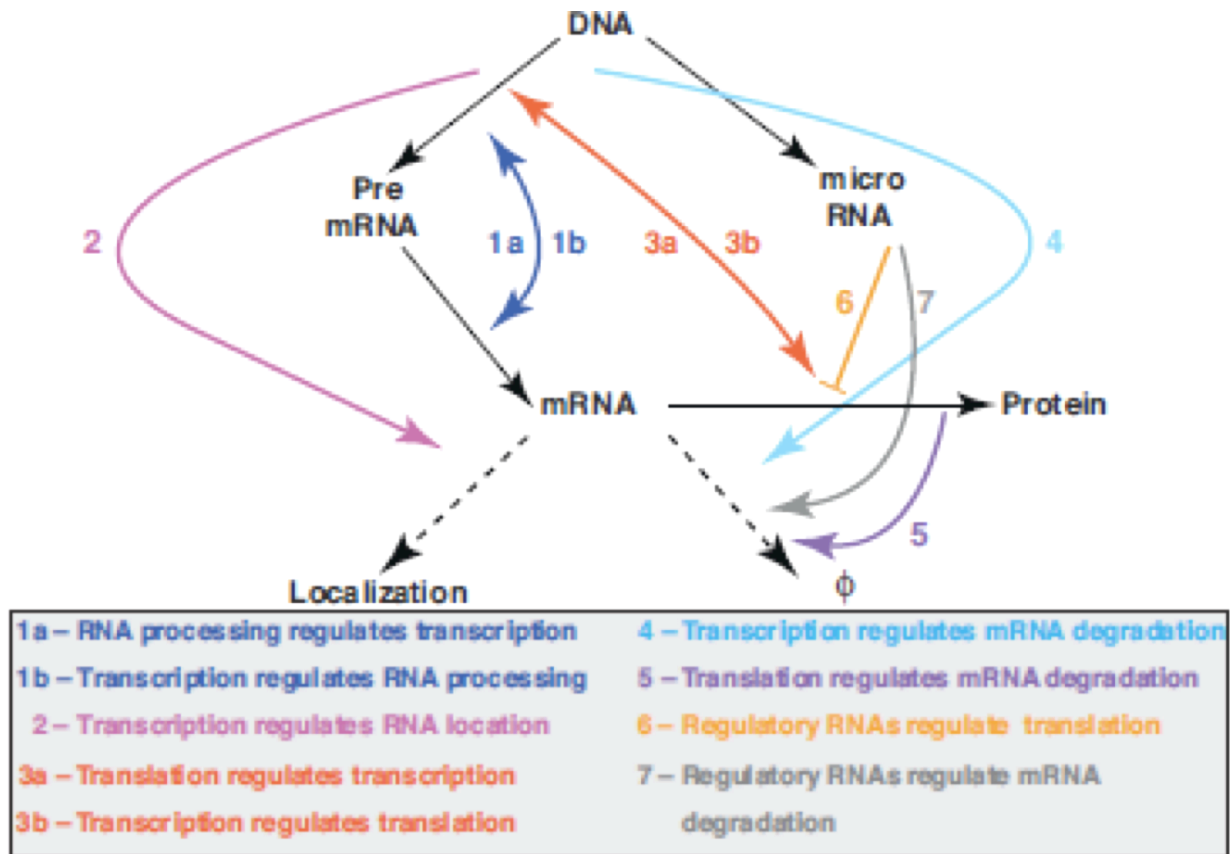
Transcrição: controle de expressão de genes



Os destinos dos transcritos

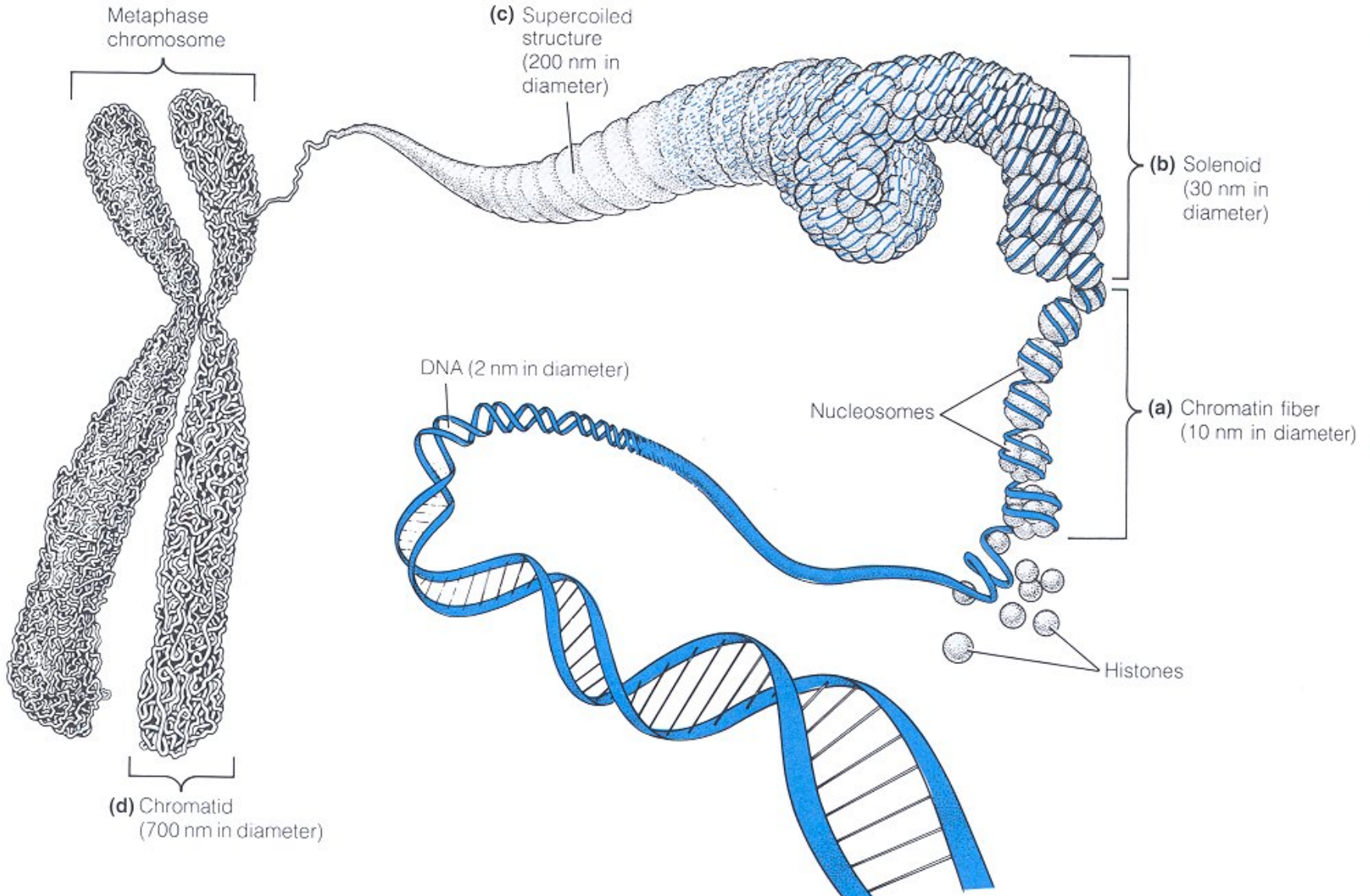


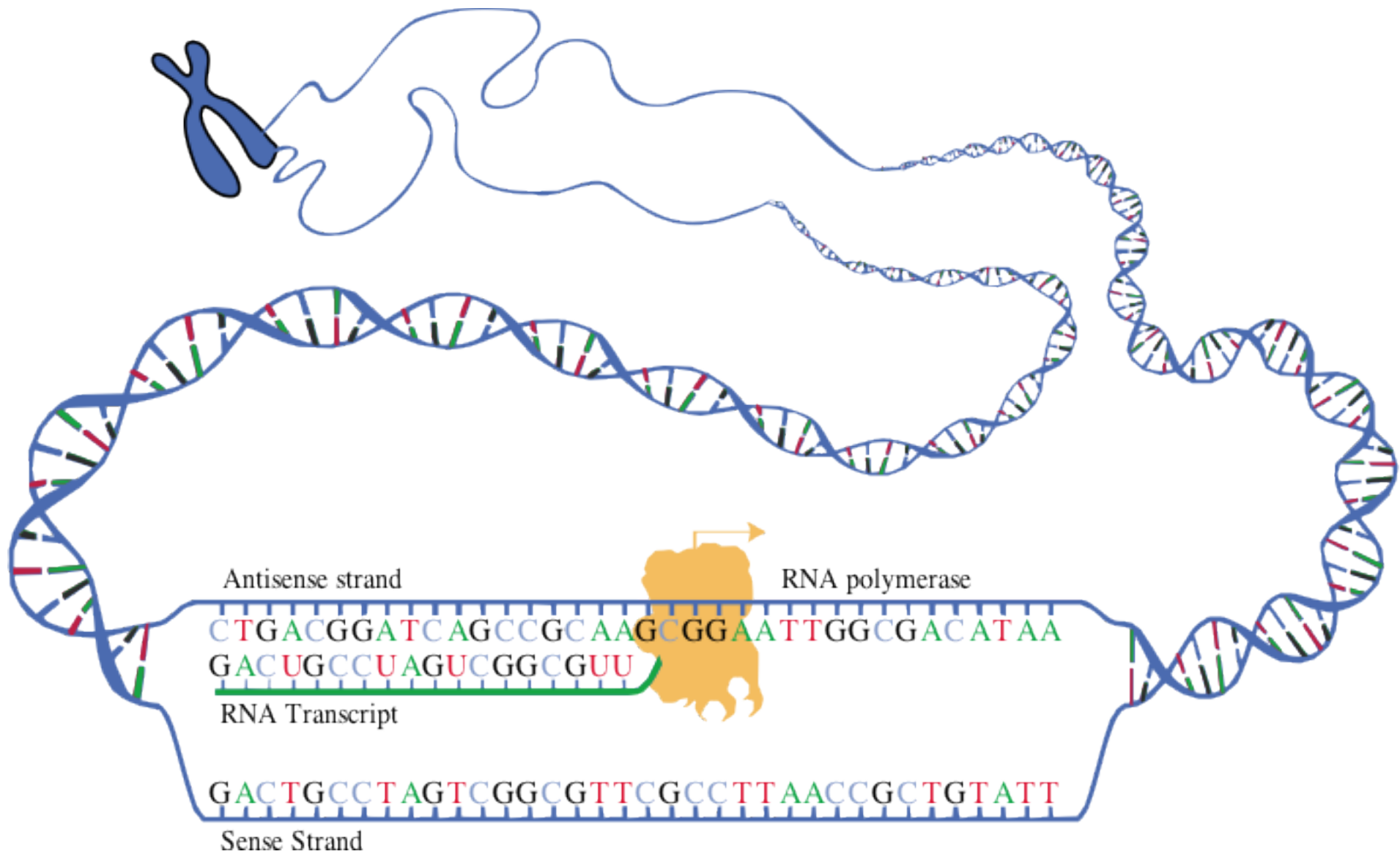
Acoplamento e redes de controle



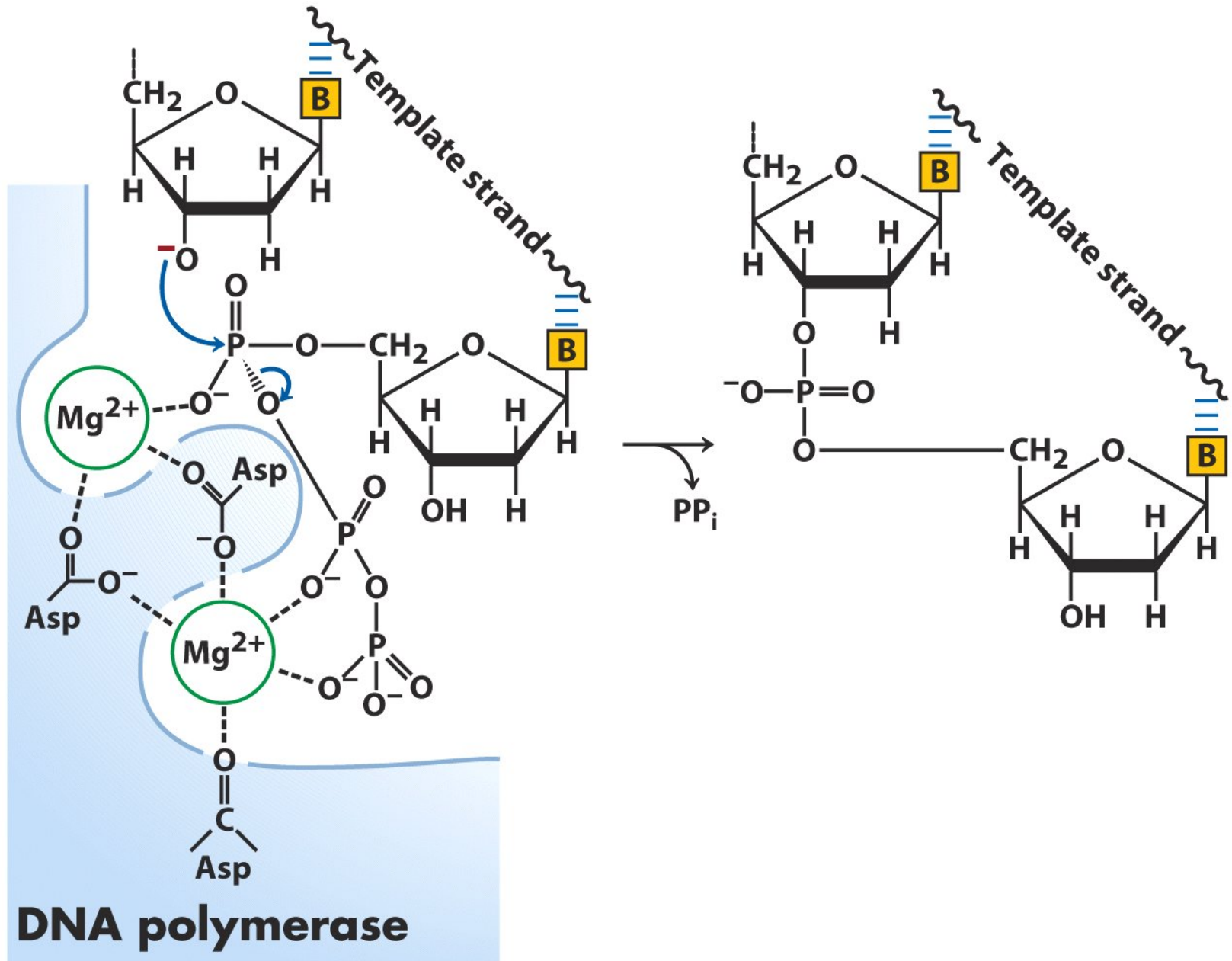
TRENDS in Genetics

Cromatina & Transcrição

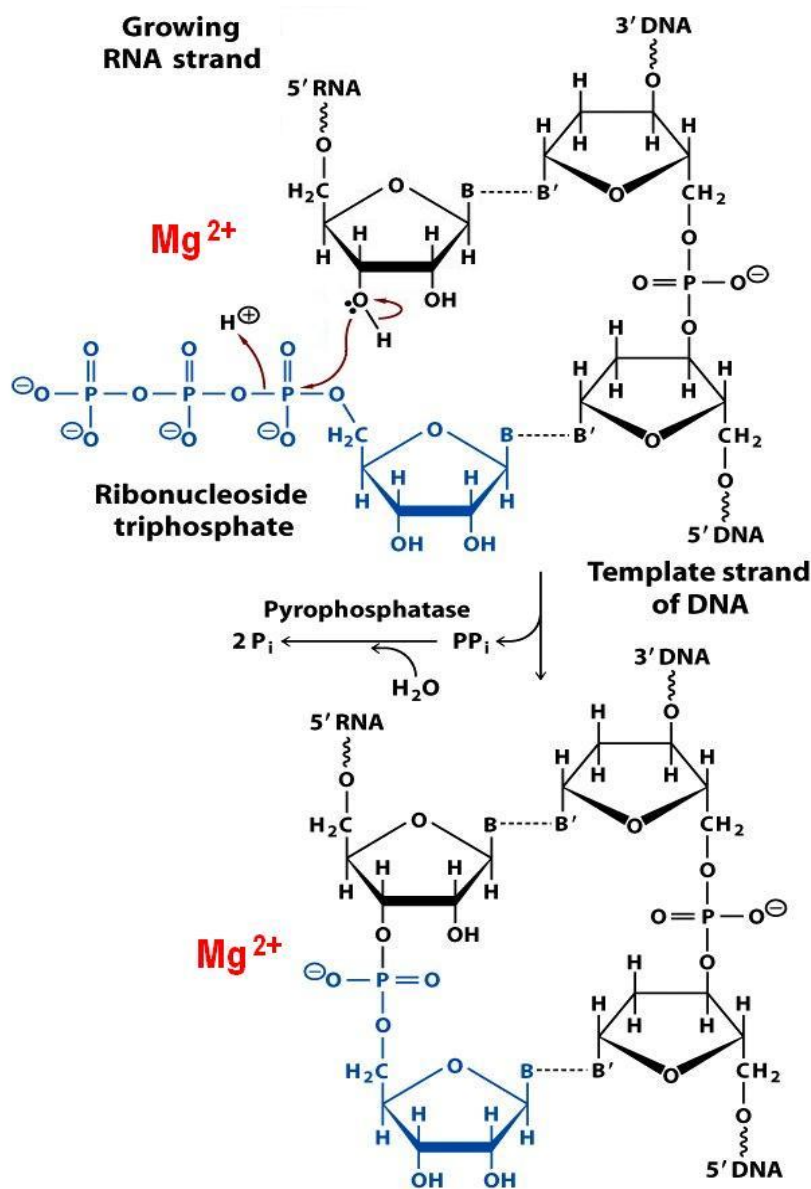




Síntese do polímero: ligações fosfodiéster

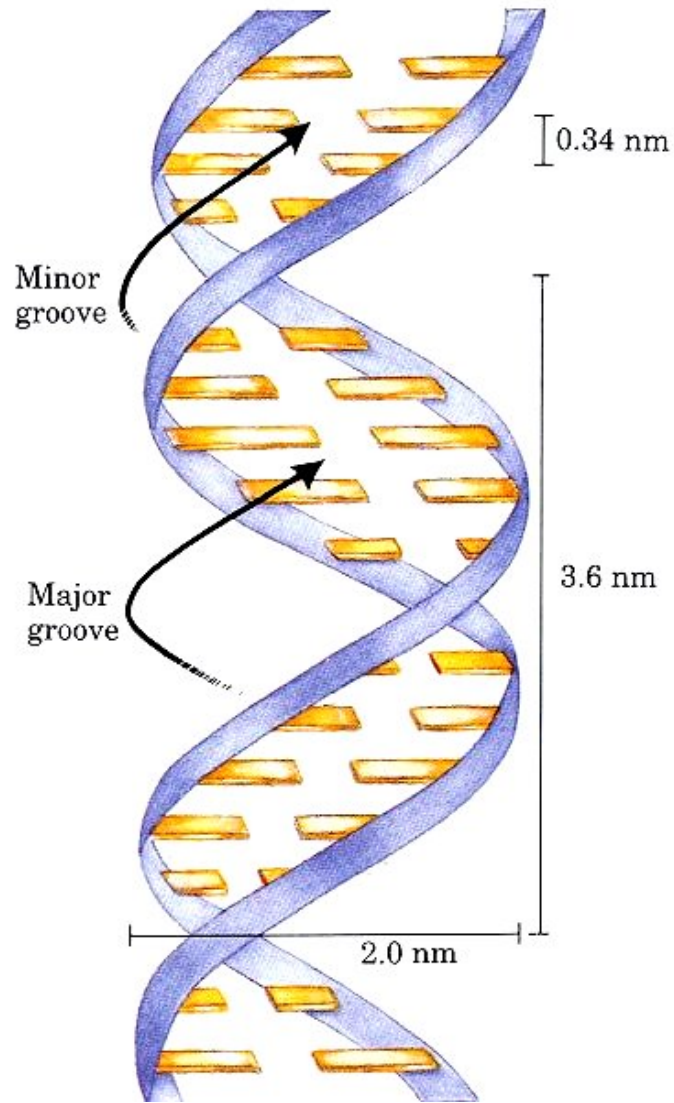


O que é Transcrição?



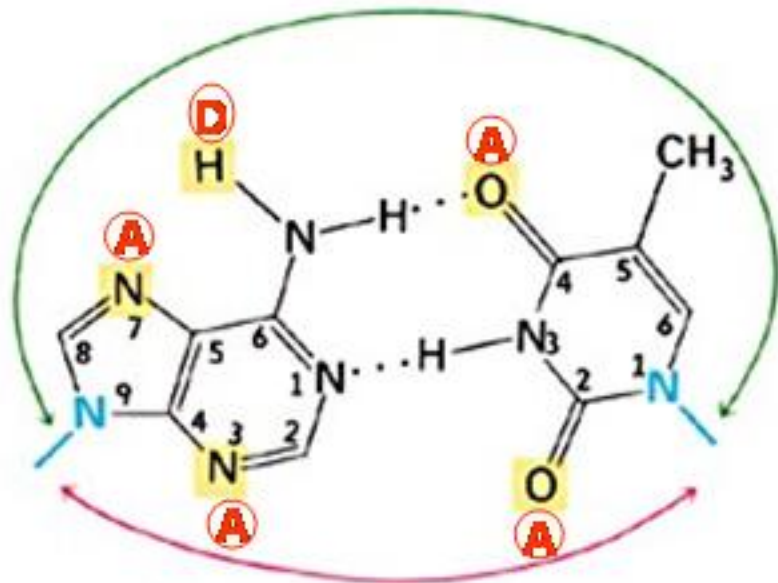
- Dependente de DNA
- Reação enzimática (RNA polimerase)
- Independente de *primer*
- 5' → 3'
- NTPs: ATP, GTP, CTP e UTP

A dupla hélice



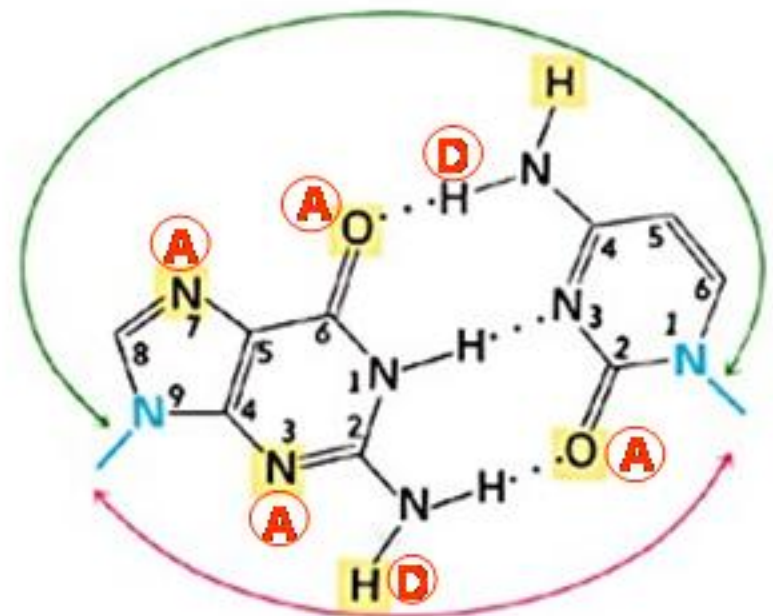
Base pairs: H-bonding properties

Major groove



Minor groove
Adenine : Thymine
A:T

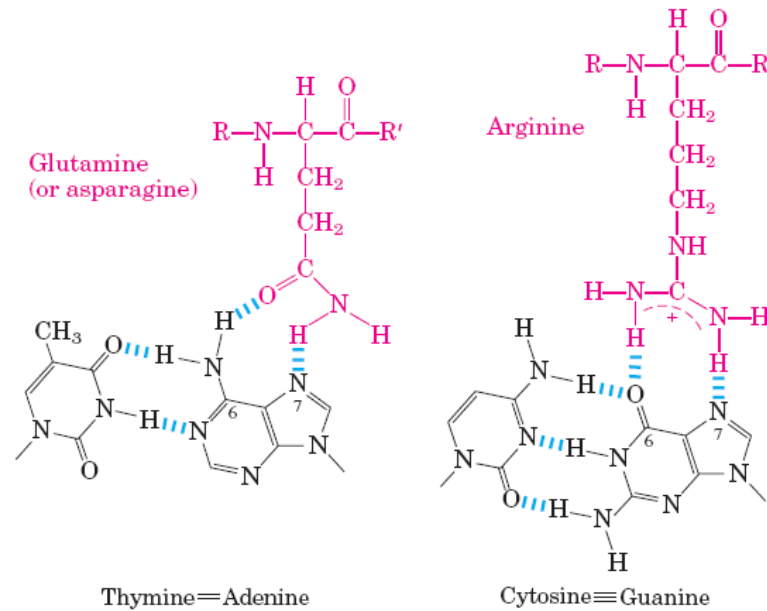
Major groove



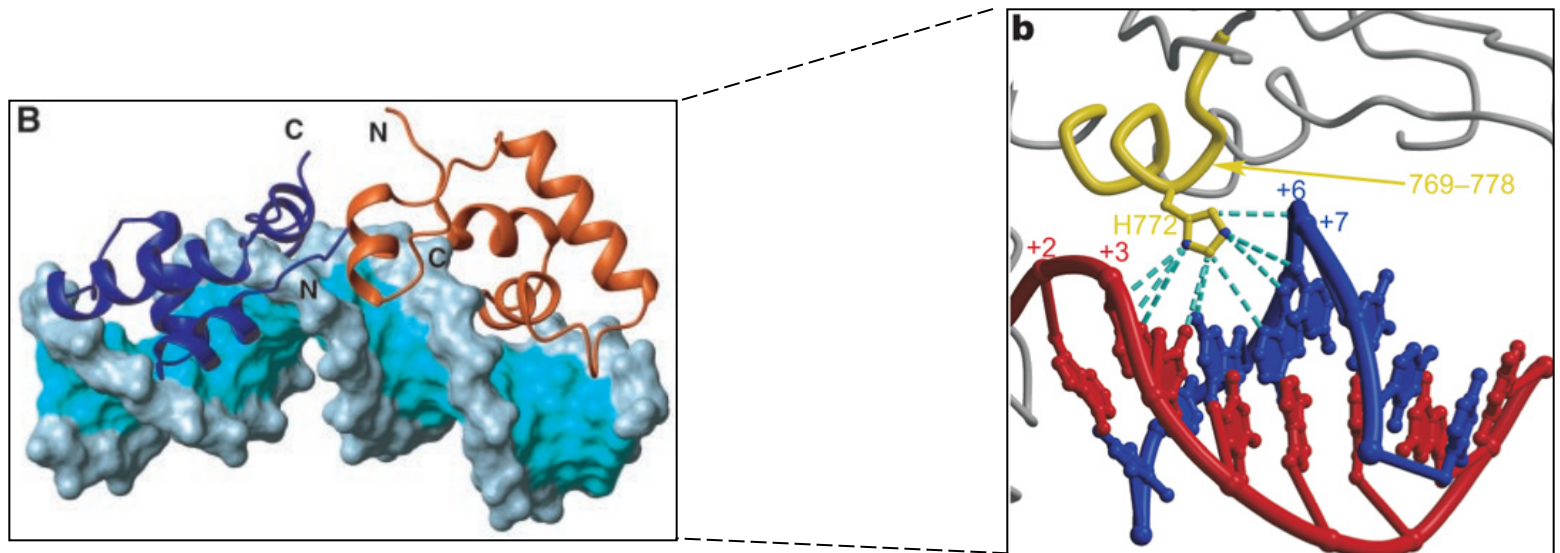
Minor groove
Guanine : Cytosine
G:C

Bases are H-donors (D) or acceptors (A)

Início da Transcrição: Interação DNA-Proteína

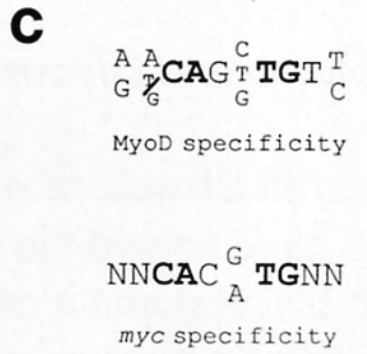
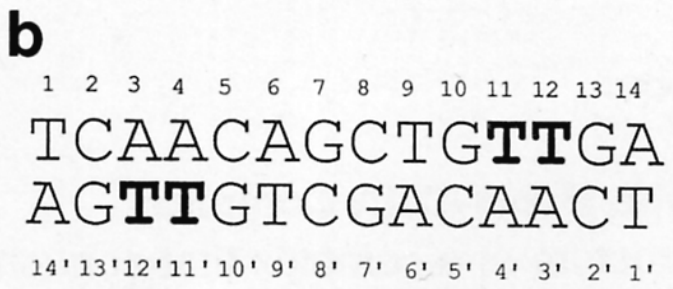
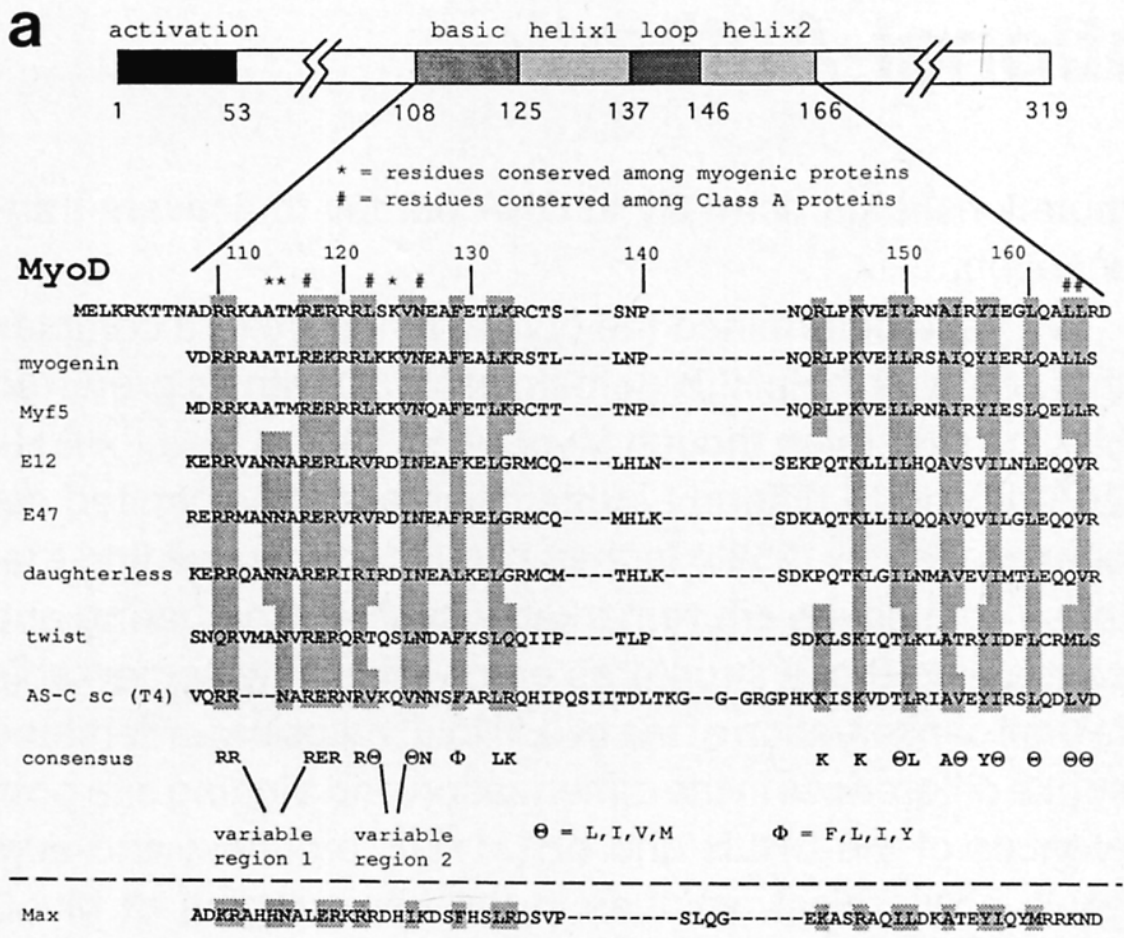


Maquinaria de transcrição: Interação DNA-Proteína

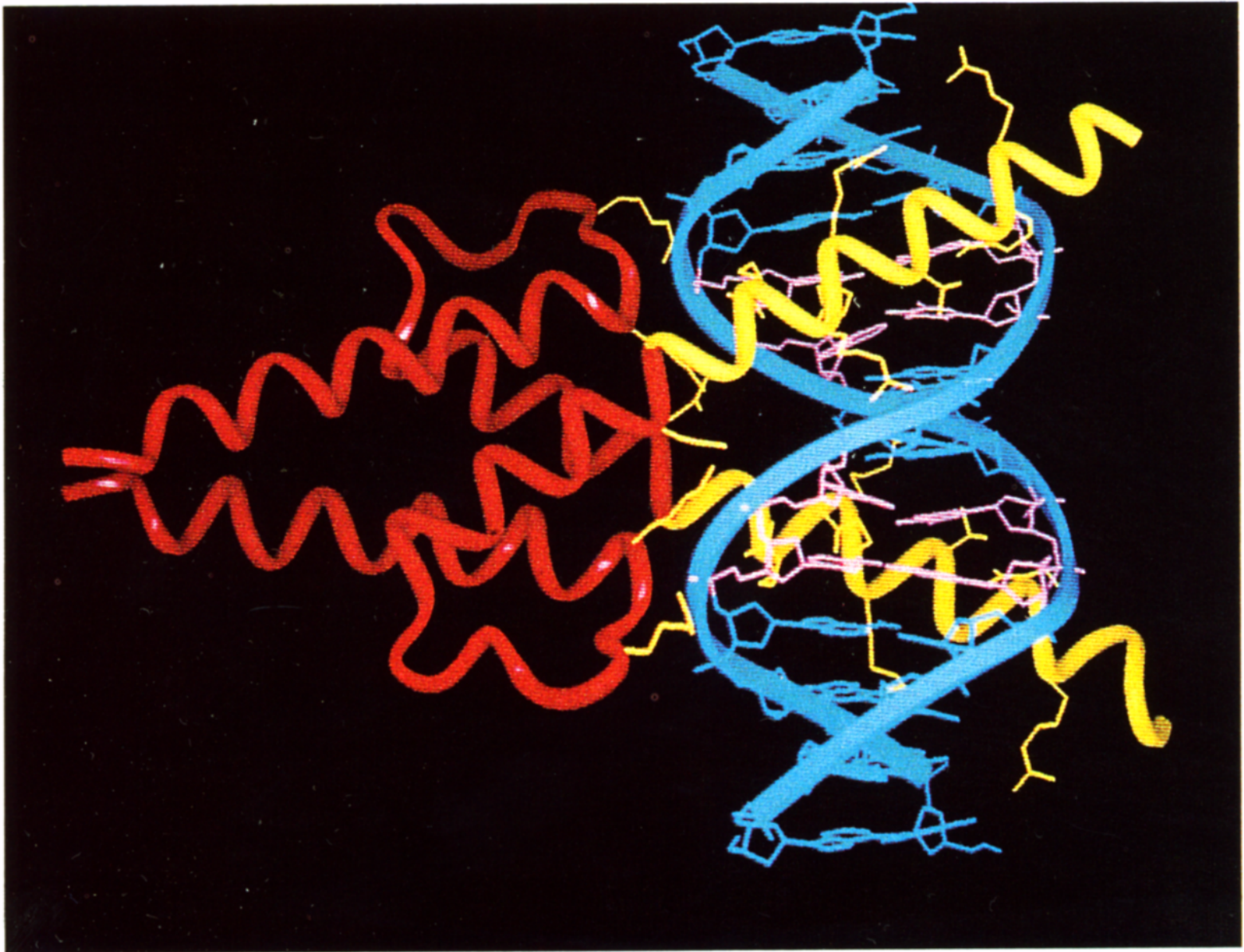


TFs: Domínios, estruturas e interações

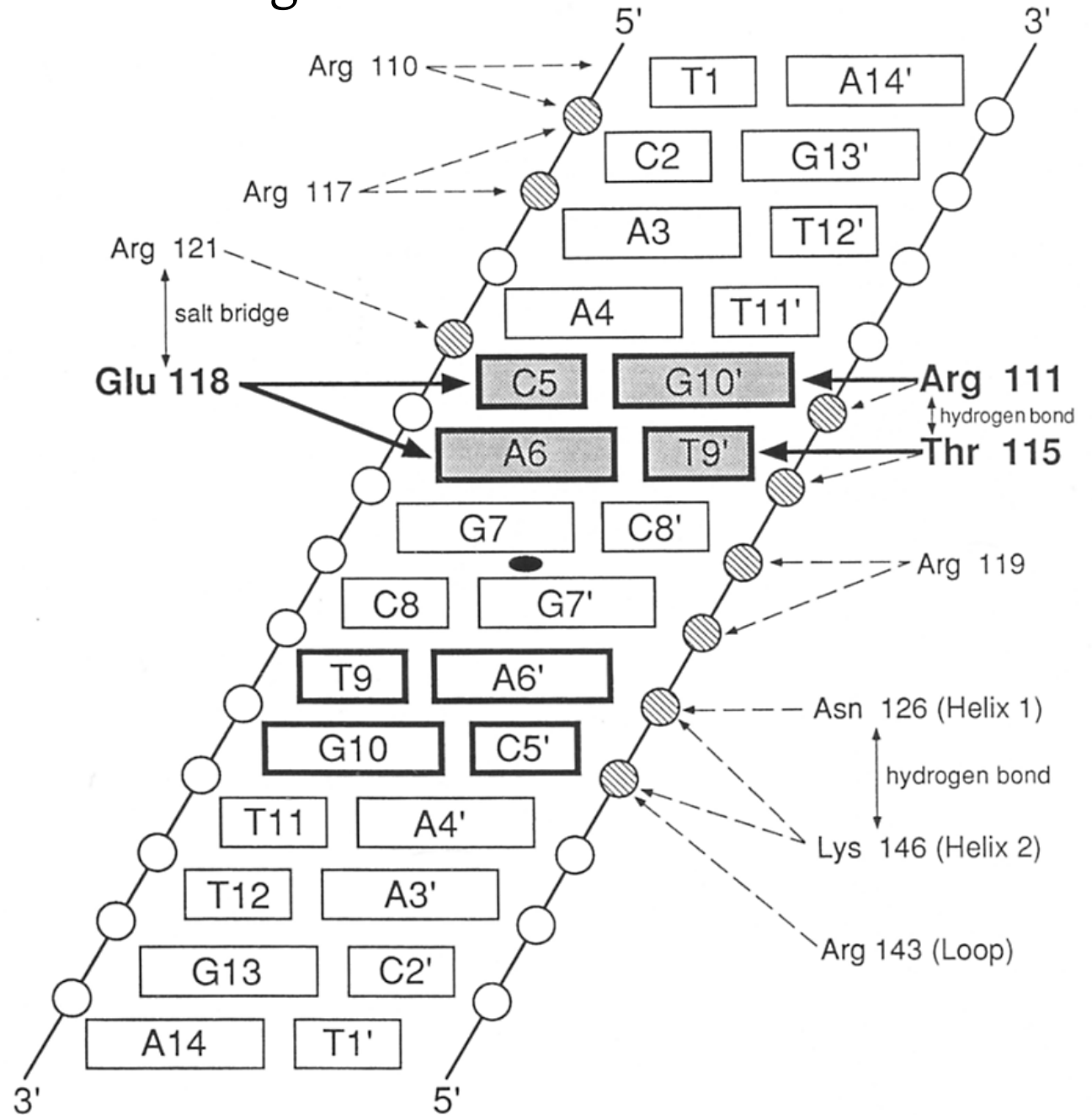
MyoD HLH domain & DNA fragment



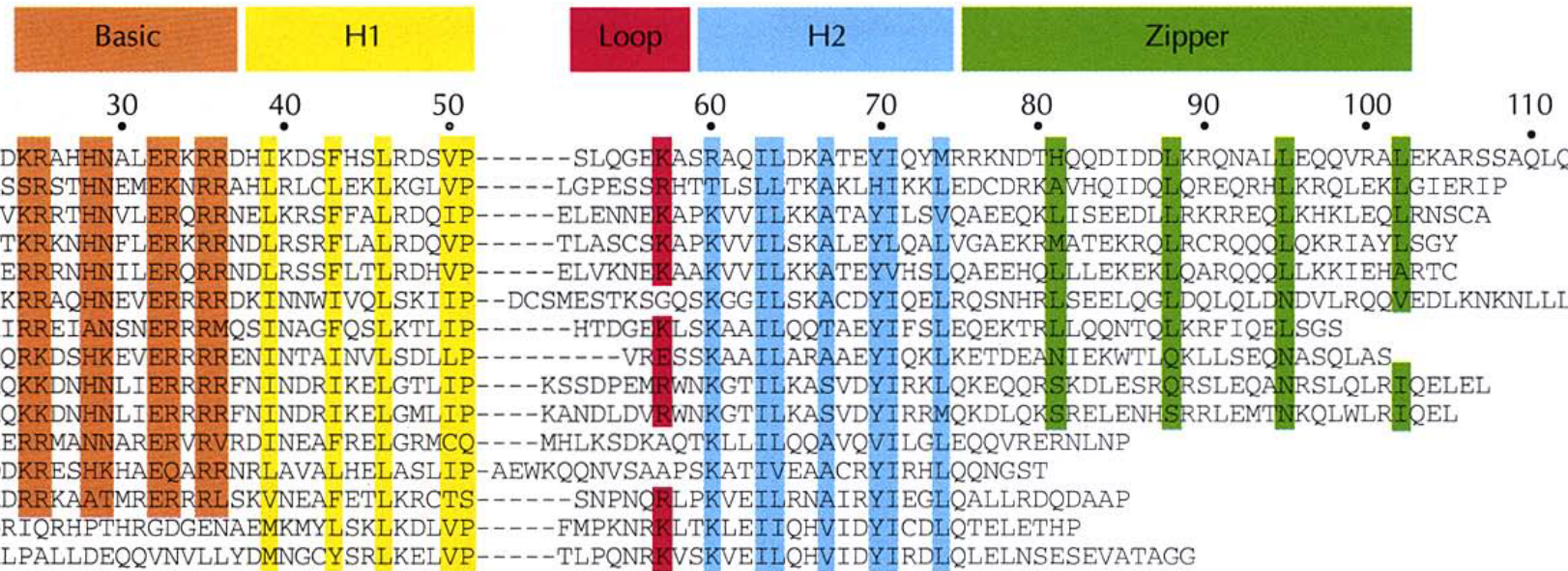
MyoD HLH domain & DNA fragment



MyoD HLH domain & DNA fragment

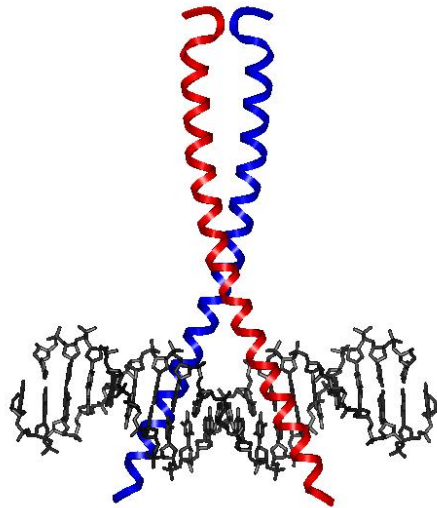


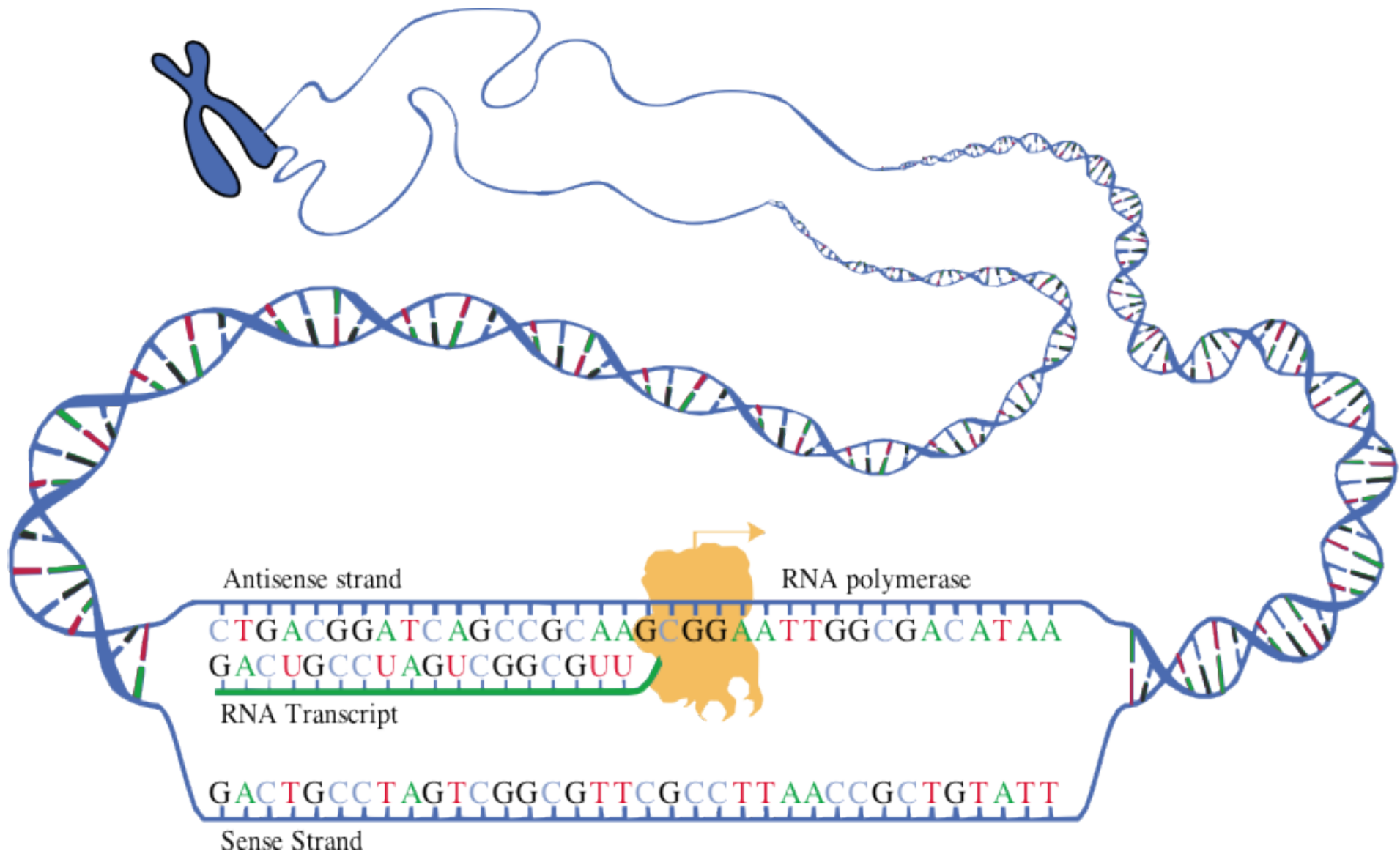
Início da Transcrição: Interação DNA-Proteína



Início da Transcrição: Interação DNA-Proteína

Leucine Zipper:
GCN4



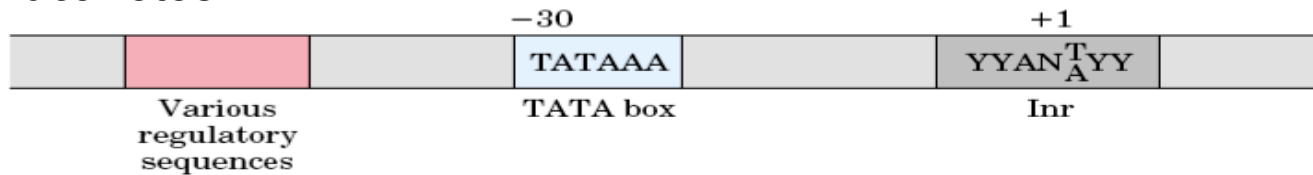


Início da Transcrição Depende de Promotores

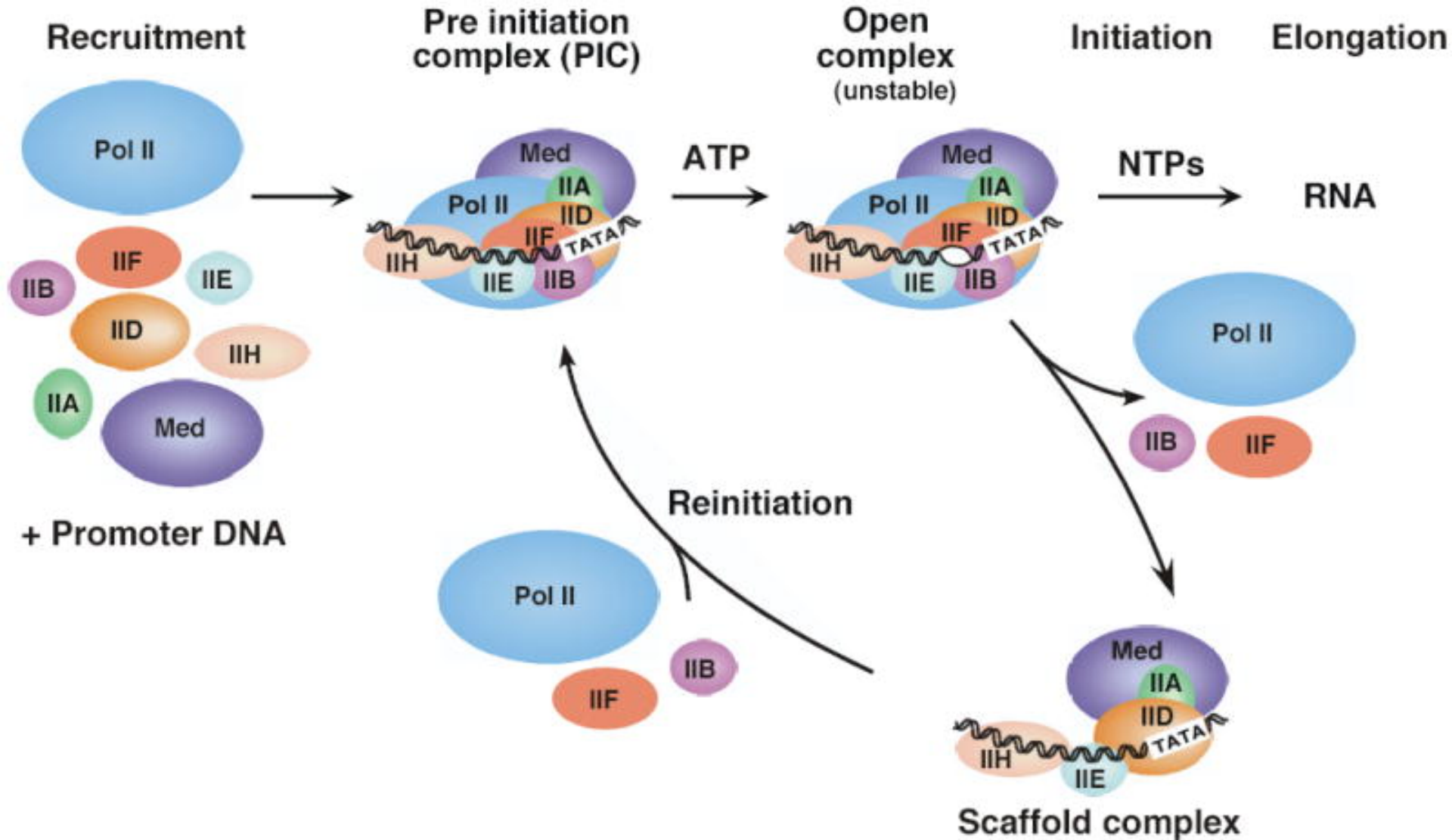
Procaríotos



Eucariotos



Iniciação e reiniciação da Transcrição



Da complexidade de interações de um fator de transcrição

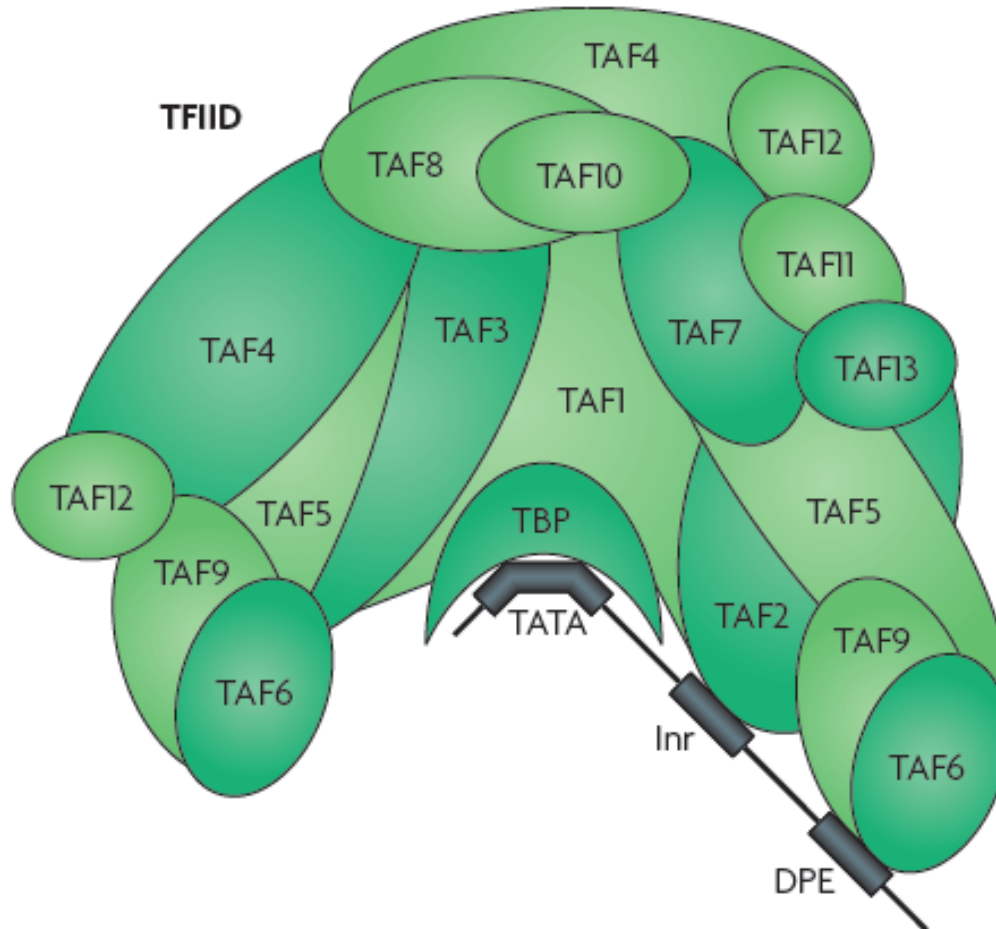
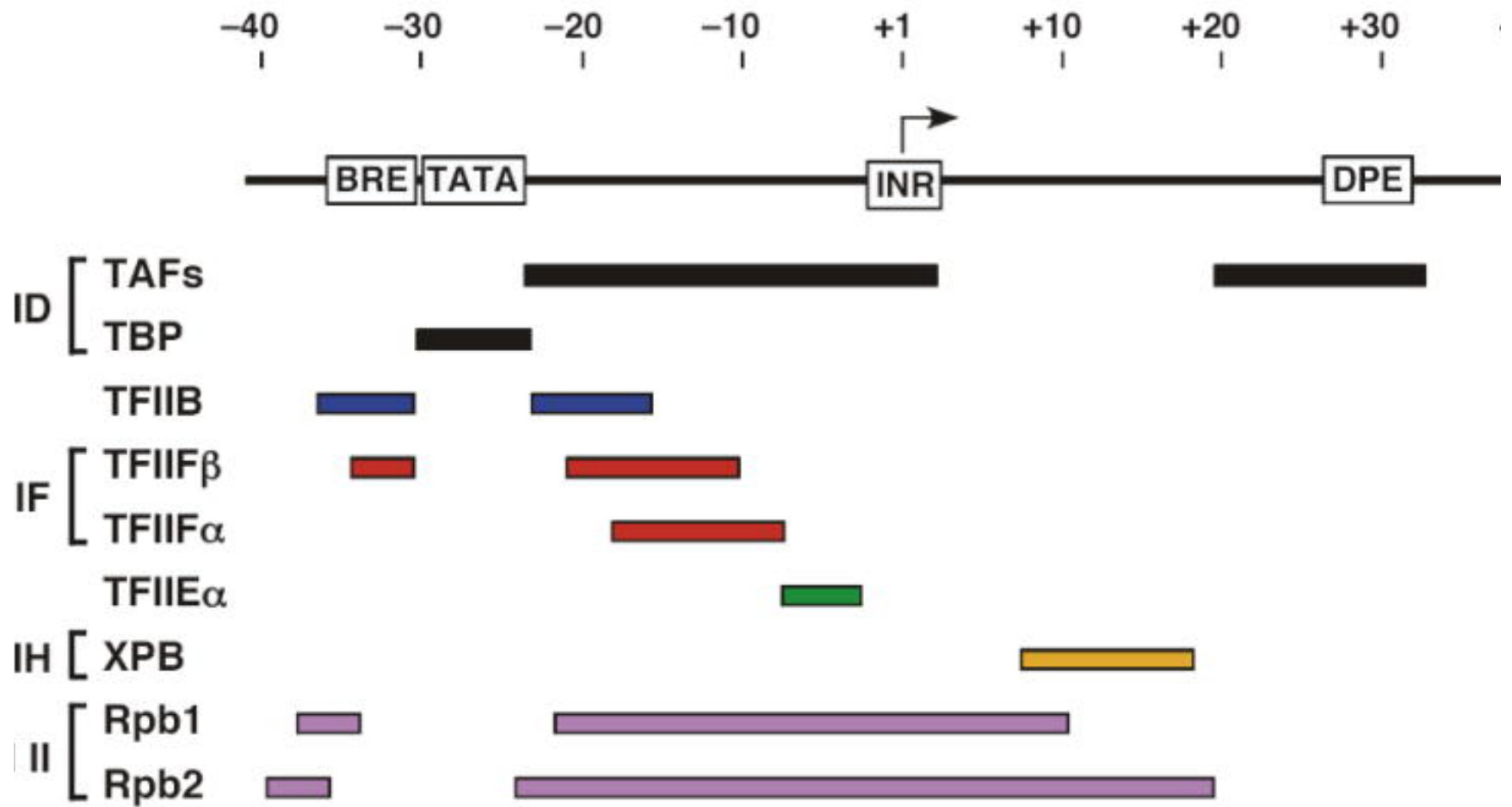
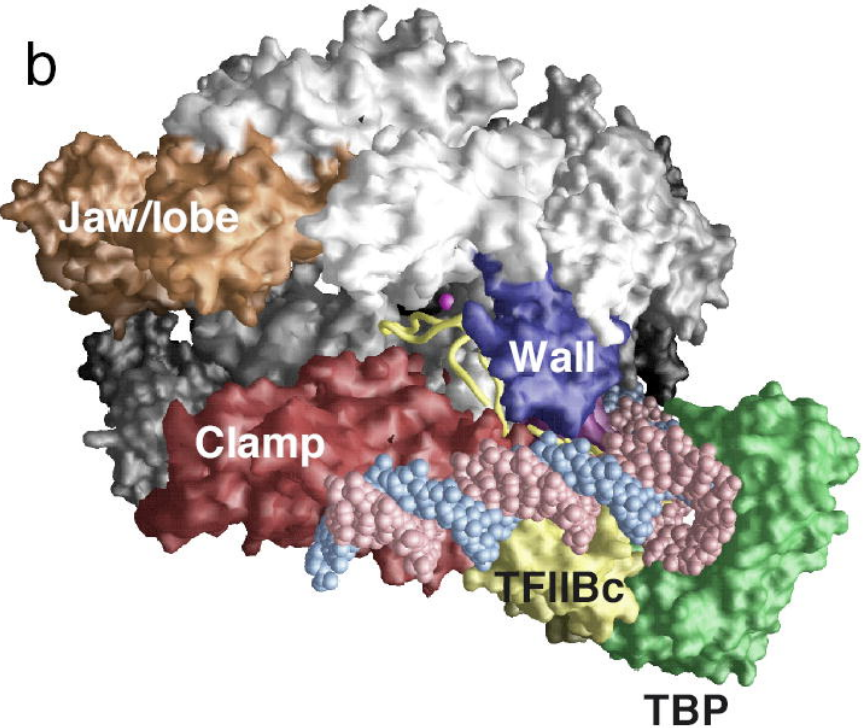
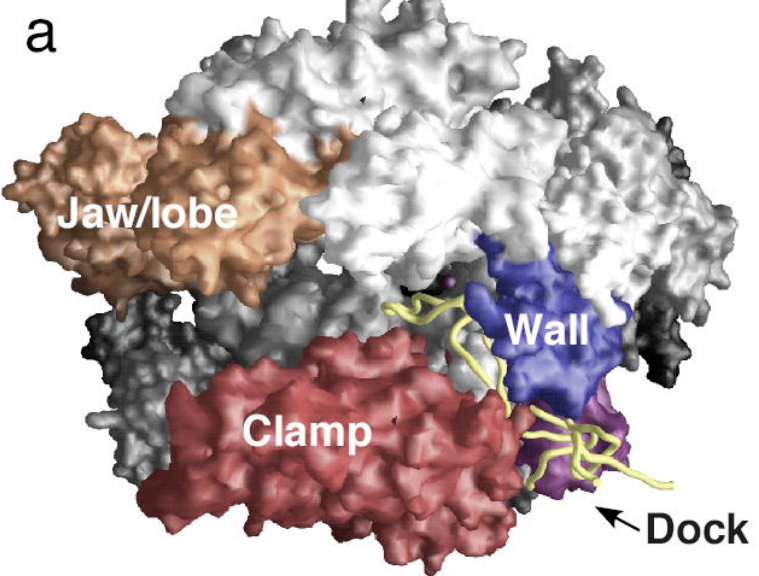


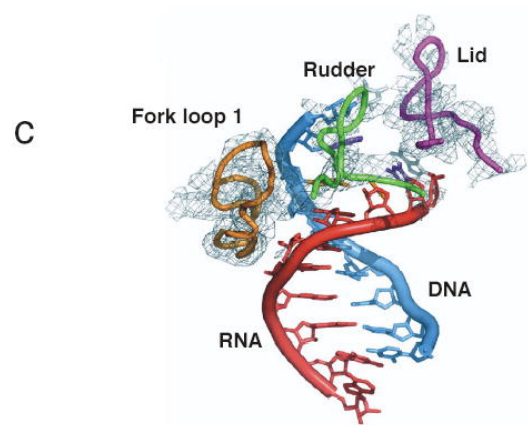
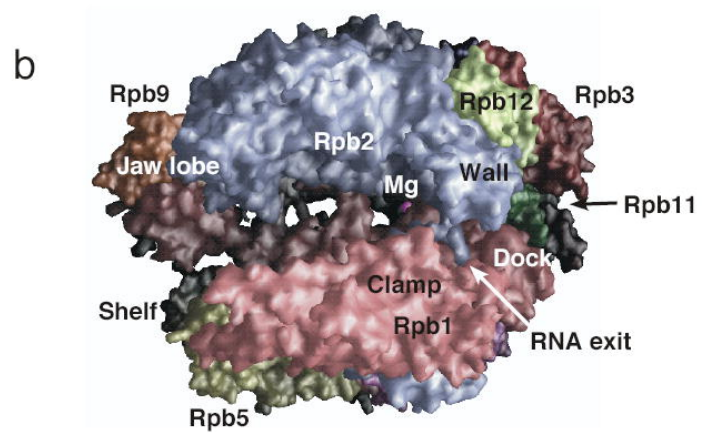
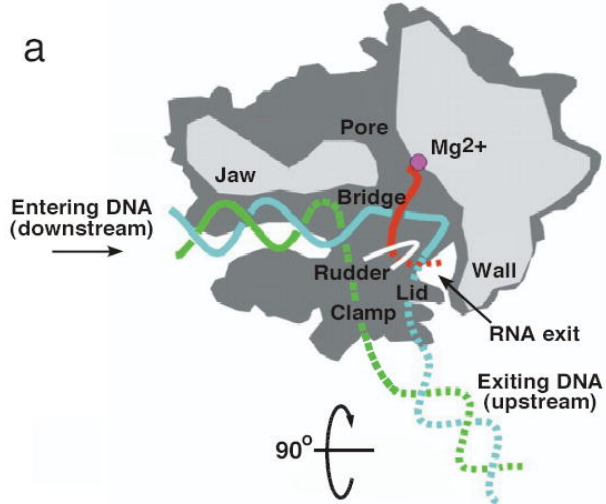
Figure 1 | **Core promoter recognition by TFIID.**



RNA polimerase II



RNA polimerase II & Complexo de alongação

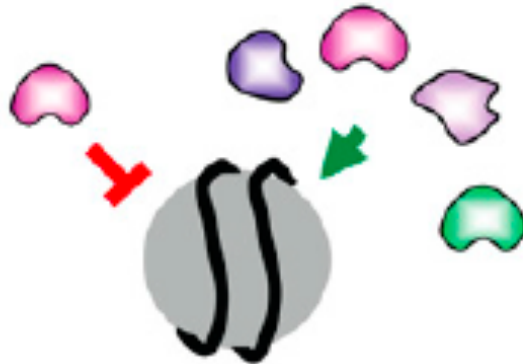


Pioneer transcription factors

- Eventos iniciais na cromatina: Pioneer TFs ligam-se primeiro
- Podem ser determinantes de destino celular
- Permitem respostas mais rápidas
- Diferentes associações = destinos celulares diversos
 - Perspectivas de reprogramação celular

Pioneer Transcription Factors

Most transcription factors



- 1 - cooperativity allows nucleosome/chromatin binding
- 2 - simultaneous binding with other factors

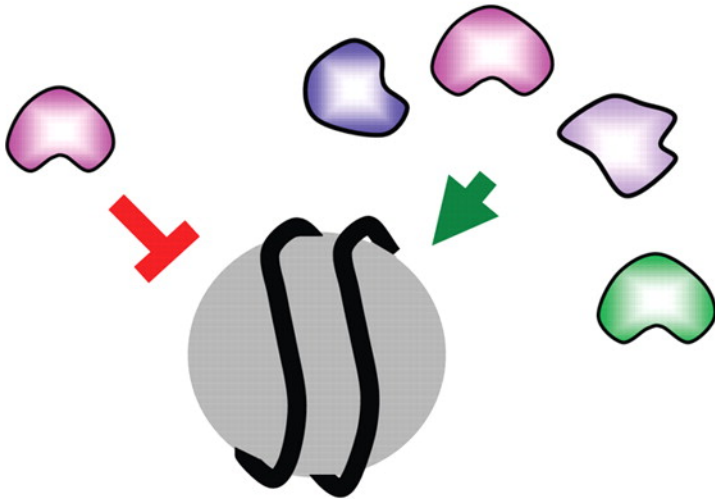
Pioneer transcription factors



- 1 - independent nucleosome/chromatin binding
- 2 - precedes other factors binding

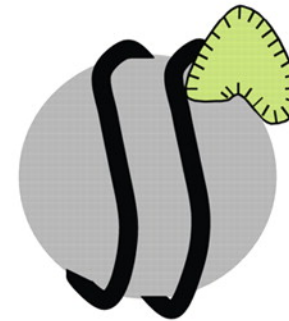
Properties that distinguish pioneer factors from other transcription factors.

Most transcription factors



- 1- cooperativity allows nucleosome/chromatin binding
- 2 - simultaneous binding with other factors

Pioneer transcription factors



- 1 - independent nucleosome/chromatin binding
- 2 - precedes other factors binding

Zaret K S , Carroll J S Genes Dev. 2011;25:2227-2241

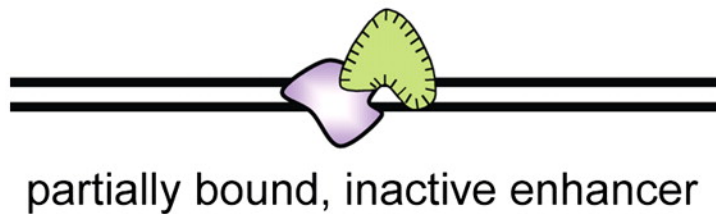


Passive and active roles for pioneer factors in endowing transcriptional competence.

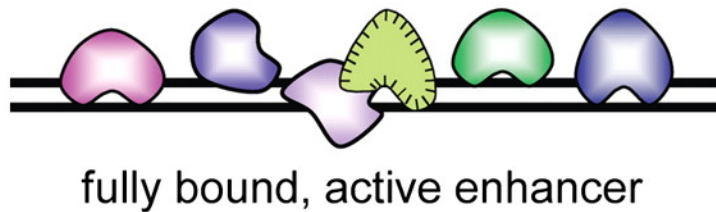
Pioneer factors:

Passive role:

prior binding speeds
inductive responses

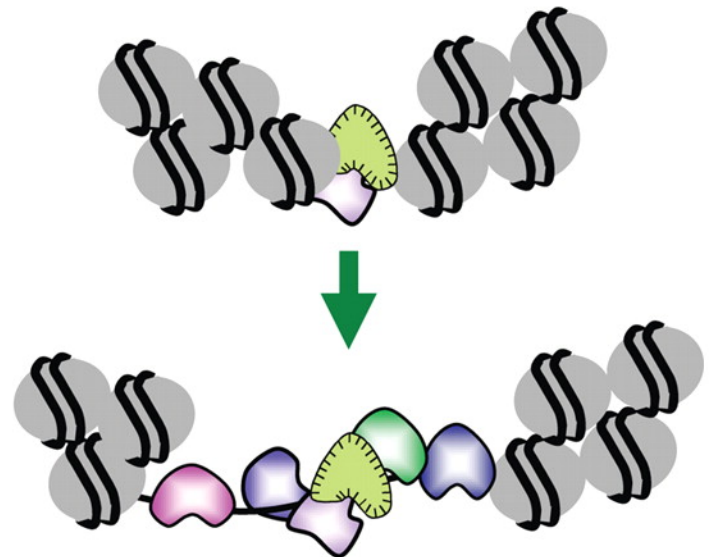


↓ *induction*



Active roles:

opening chromatin,
enable other factors to bind



Zaret K S , Carroll J S Genes Dev. 2011;25:2227-2241

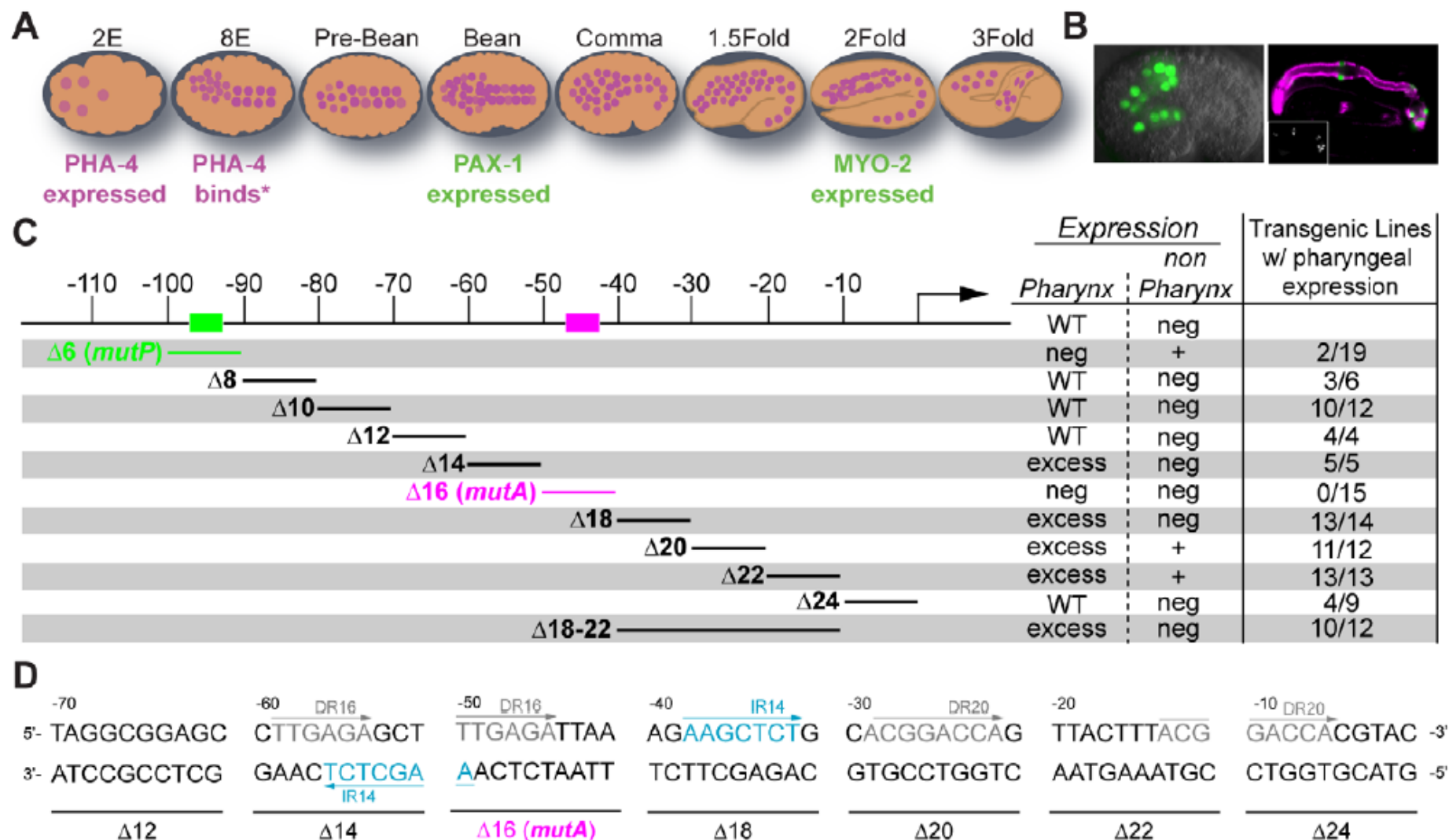


Dynamic Chromatin Organization during Foregut Development Mediated by the Organ Selector Gene PHA-4/FoxA

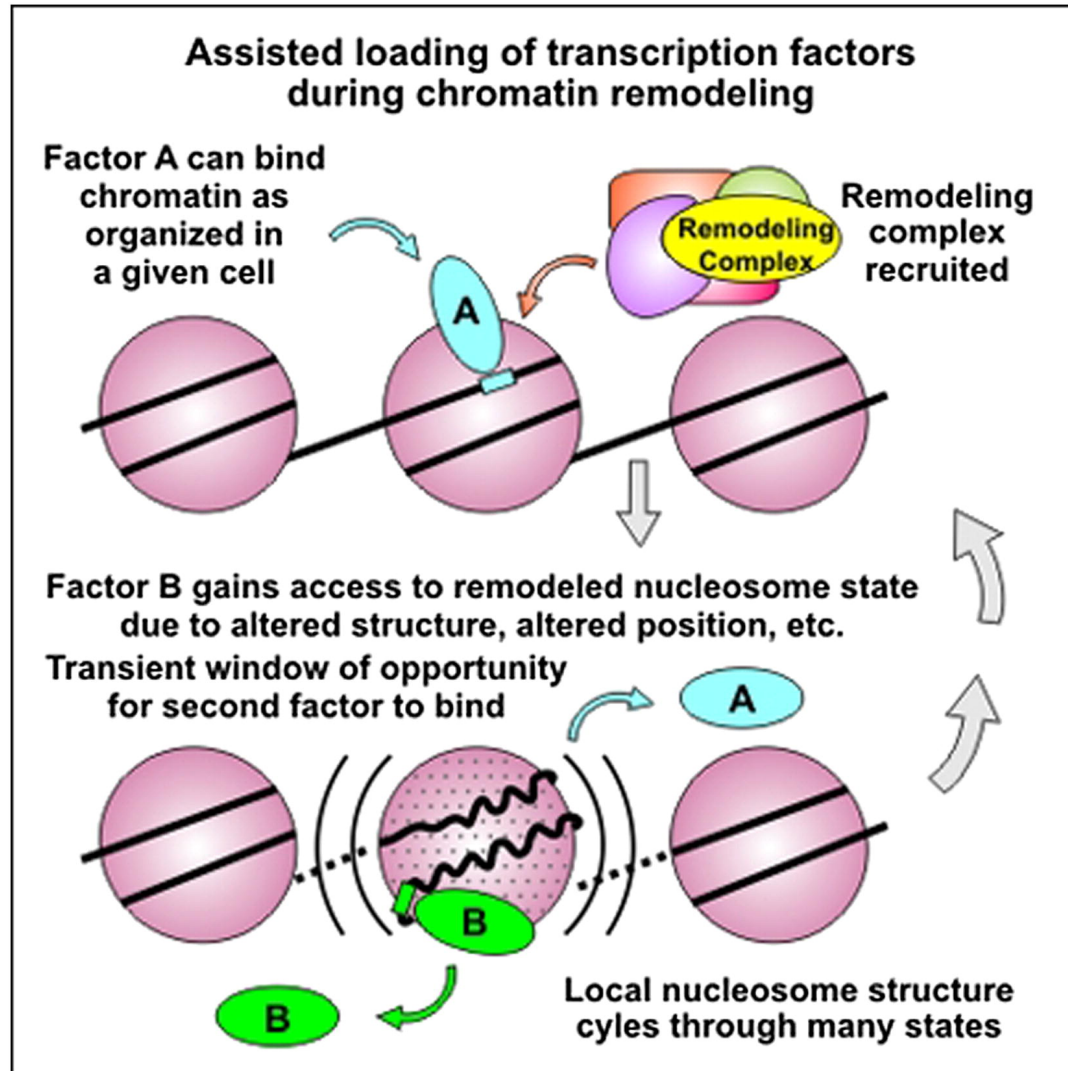
Tala H. I. Fakhouri, Jeff Stevenson^{1a}, Andrew D. Chisholm^{1b}, Susan E. Mango*

Selector genes govern the fates of groups of cells related to each other by virtue of their cell type, position or affiliation to an organ [1]. Genomic methods have revealed that selector genes directly control hundreds, even thousands, of target genes, which define the characteristics of a particular cell type [2–6]. For example, the

Figure 1. Scanning mutagenesis of the *pax-1* promoter. (A) A cartoon depicting the pattern of PHA-4 expression during different stages of embryogenesis. Embryonic events that occur at specific developmental stages are annotated.

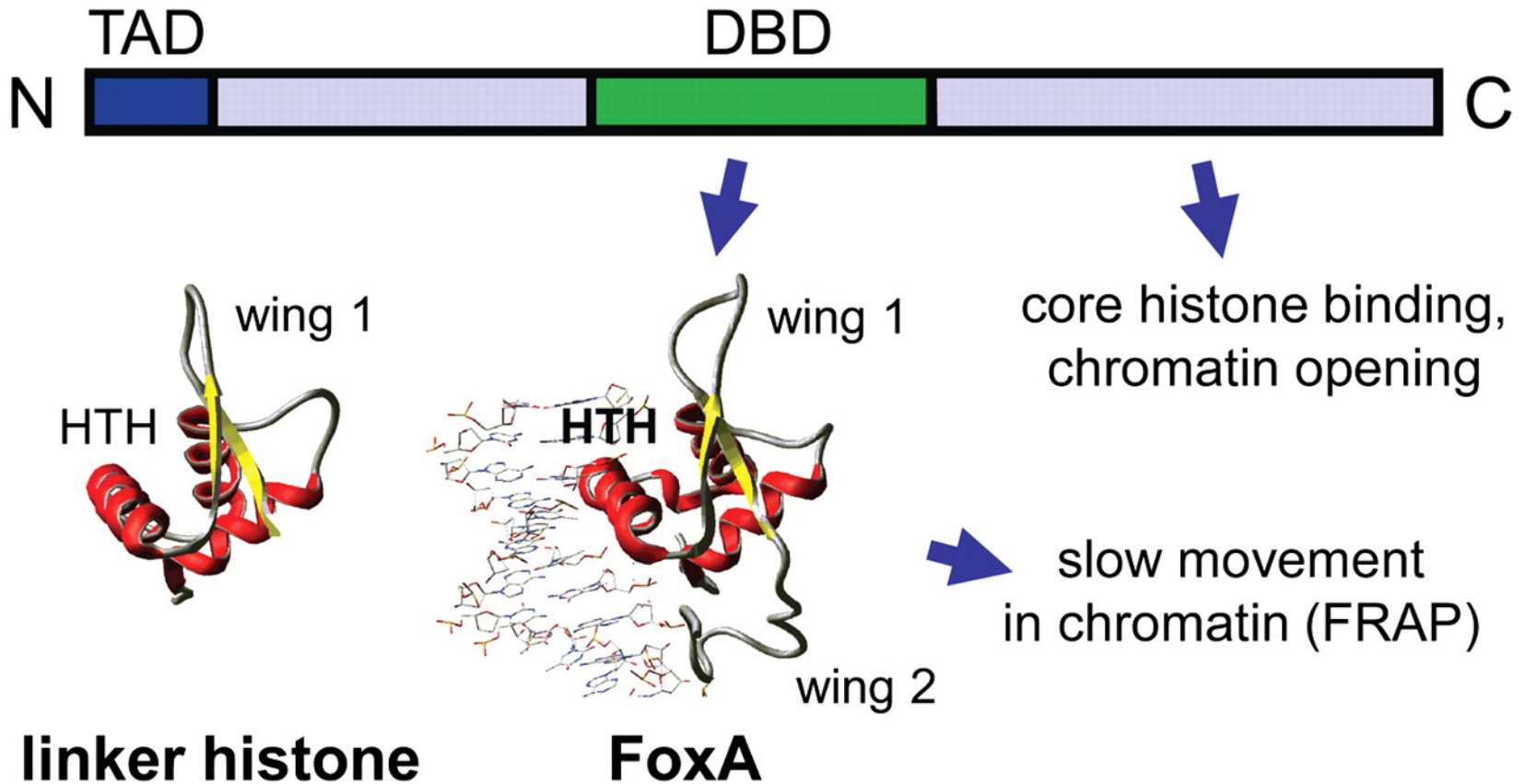


Pioneer TFs: access of target sites on nucleosomes



FoxA factors possess features of linker histones and conventional transcription factors.

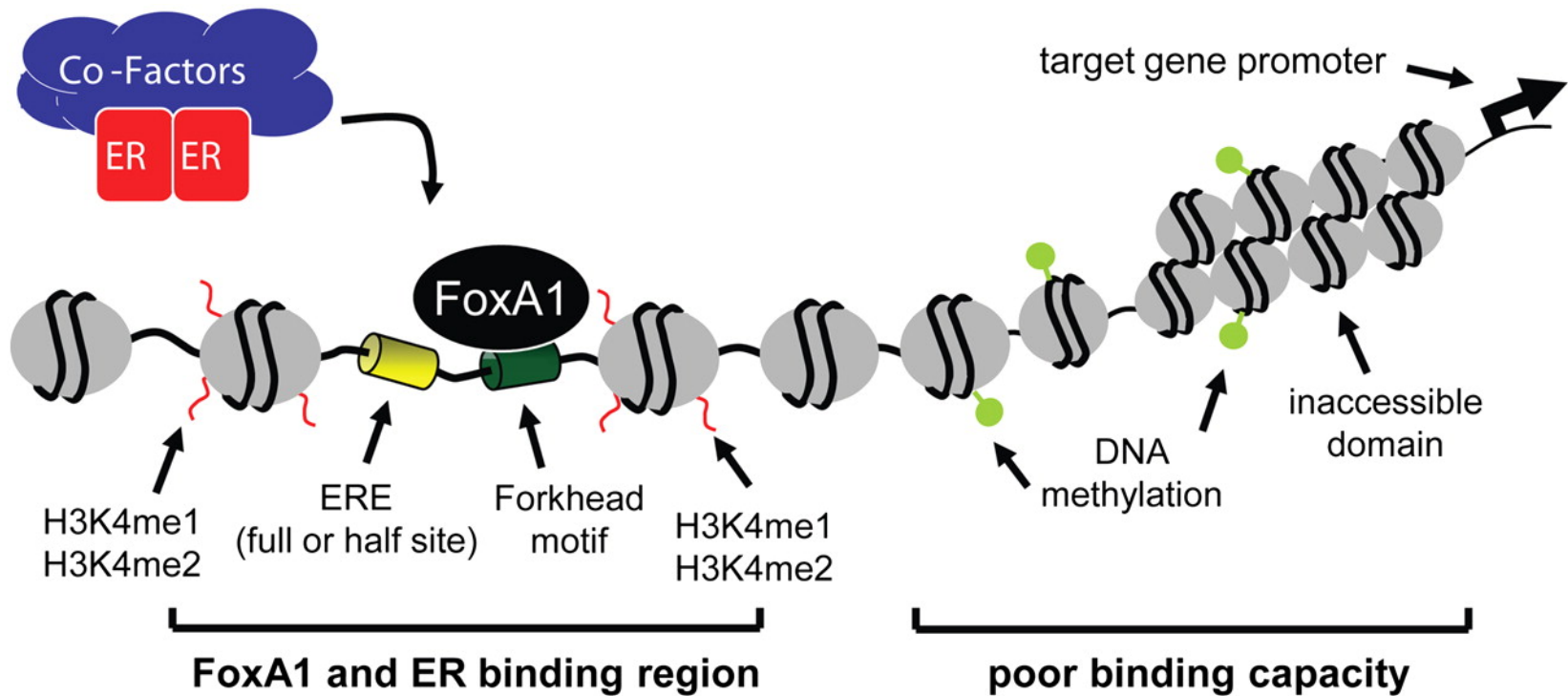
FoxA domain structure:



Zaret K S , Carroll J S Genes Dev. 2011;25:2227-2241

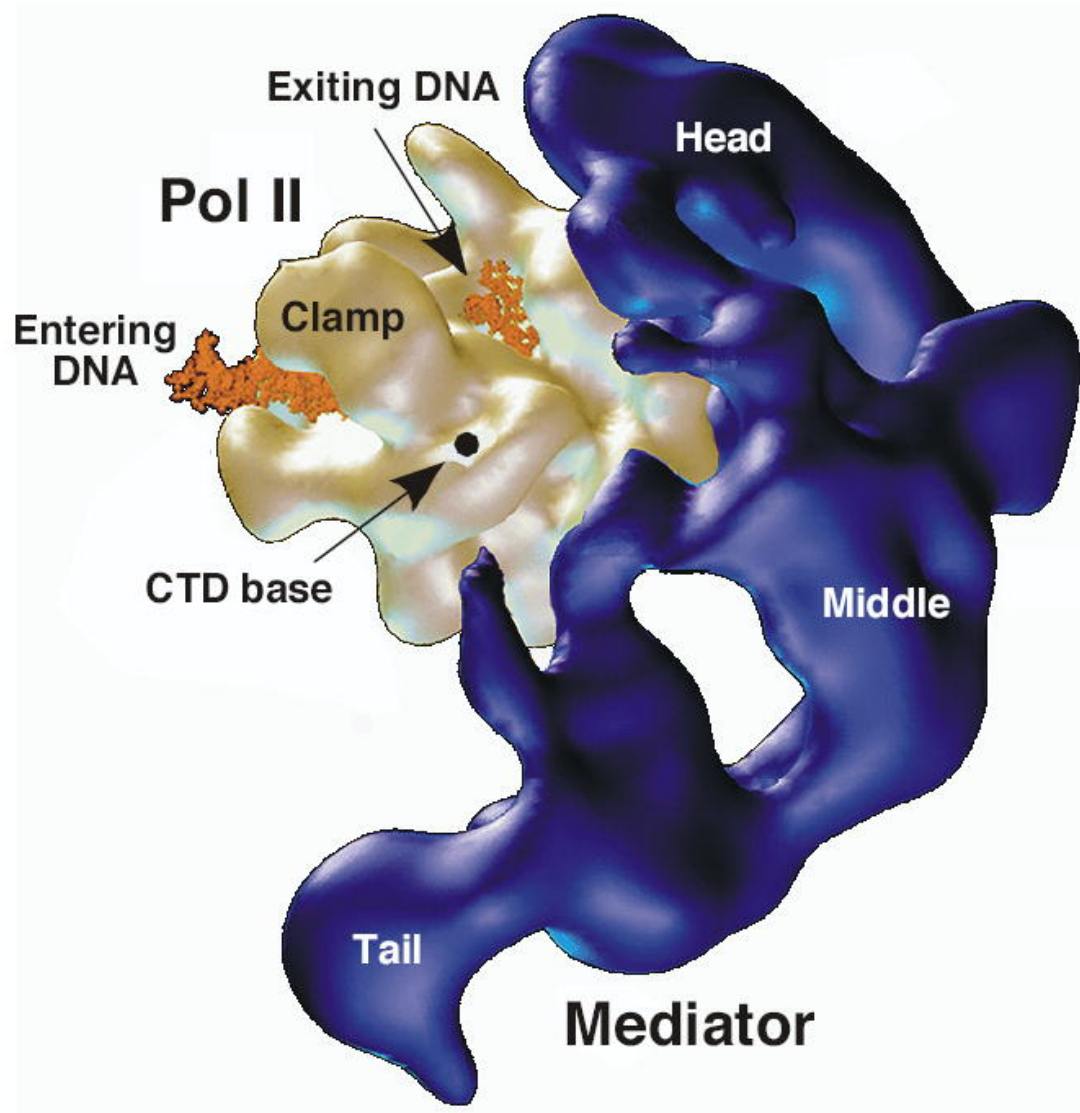


Optimal chromatin features for FoxA1 binding to chromatin in breast cancer cells.



Zaret K S , Carroll J S Genes Dev. 2011;25:2227-2241





The coherent Mediator

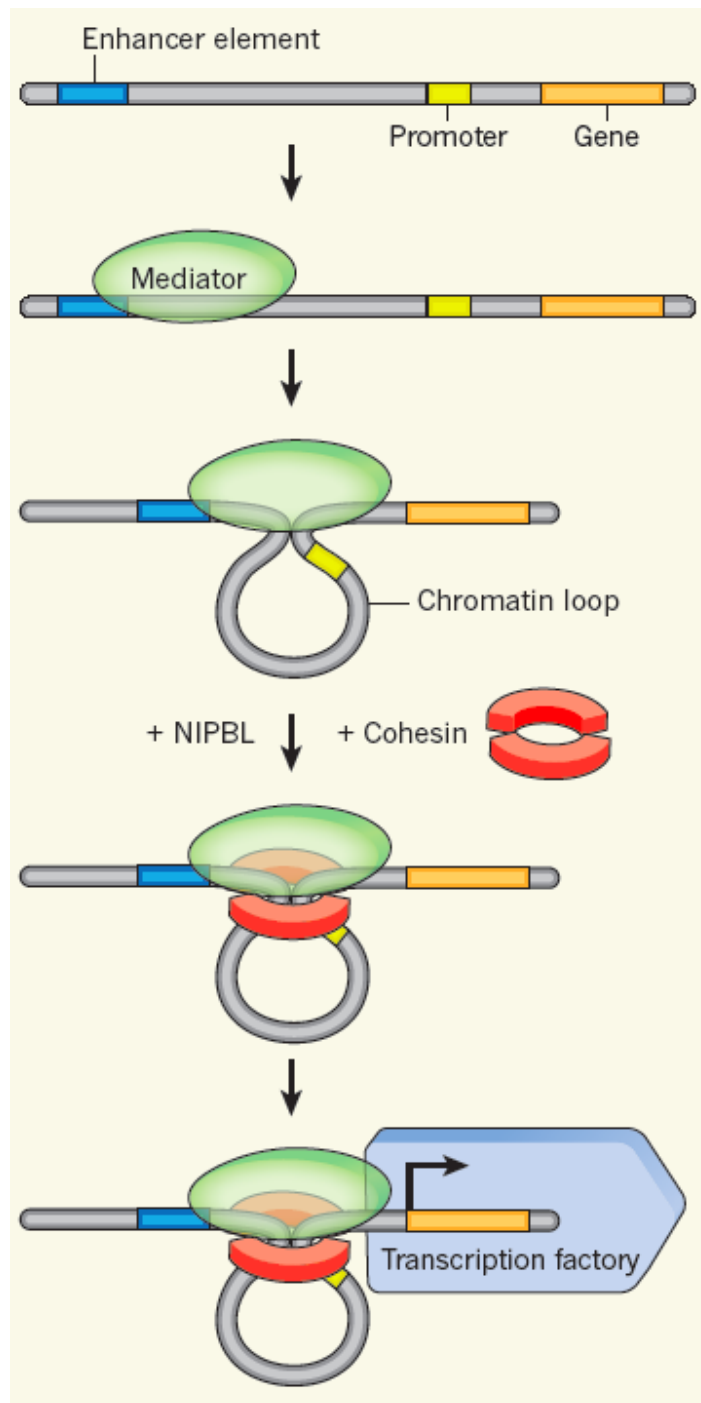
Enhancer sequences increase gene transcription with the help of a co-activator complex, the Mediator. Another protein complex — cohesin — seems to work with Mediator to bring together enhancers and promoters. [SEE ARTICLE P. 430](#)

ROLF OHLSSON

The coherent Mediator

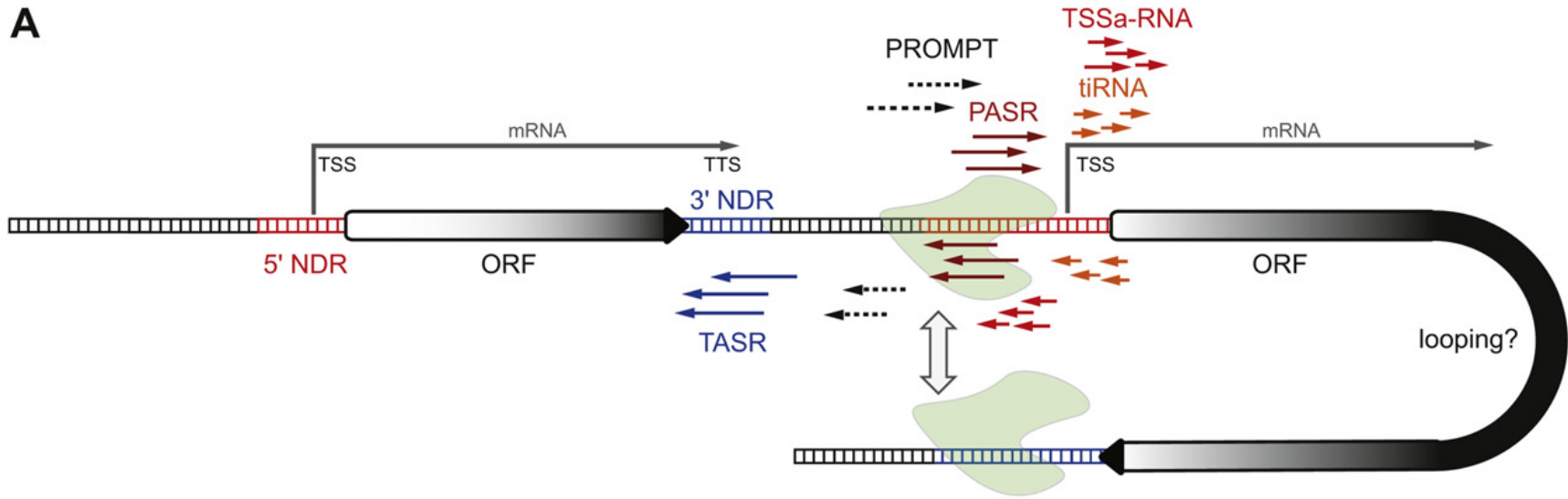
do this? A paper² in this issue describes the discovery that the Mediator complex recruits another protein complex, cohesin, to provide coherence between enhancer and promoter sequences (Kagey *et al.*, page 430).

The coherent Mediator

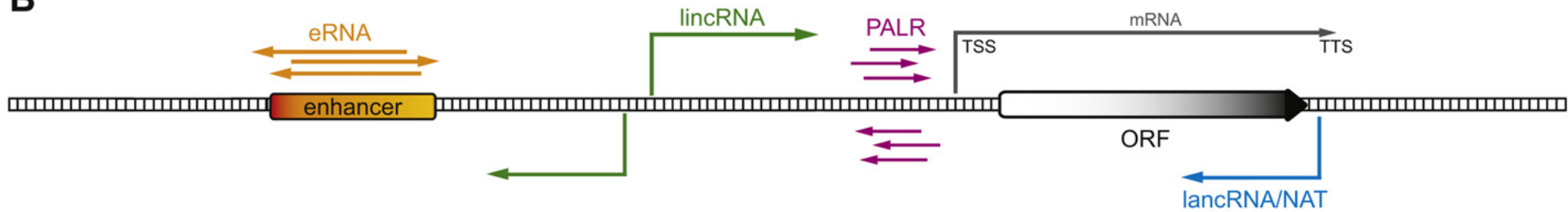


ncRNAs diversos & controle de expressão

A



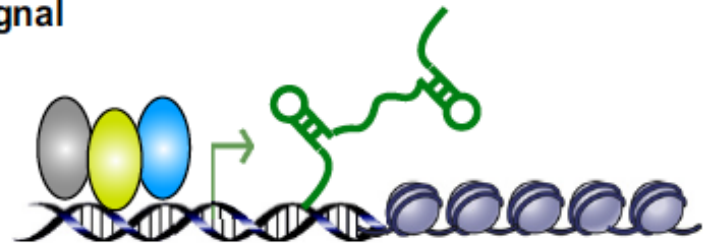
B



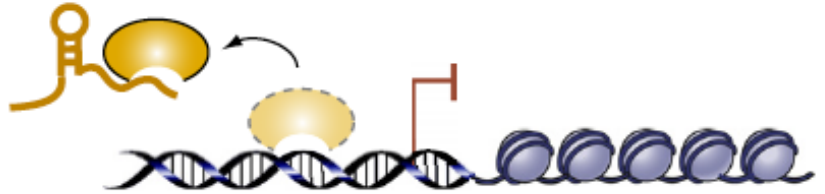
TSS transcription start site
TTS transcription termination site
DNA
RNAPII
stable RNA
unstable RNA

lncRNA mecanismos diversos: Controle de expressão

I. Signal



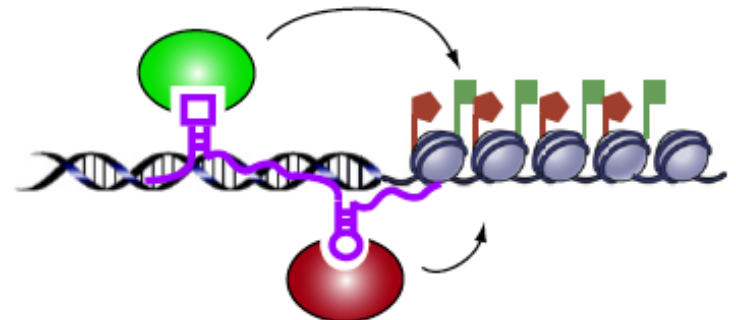
II. Decoy



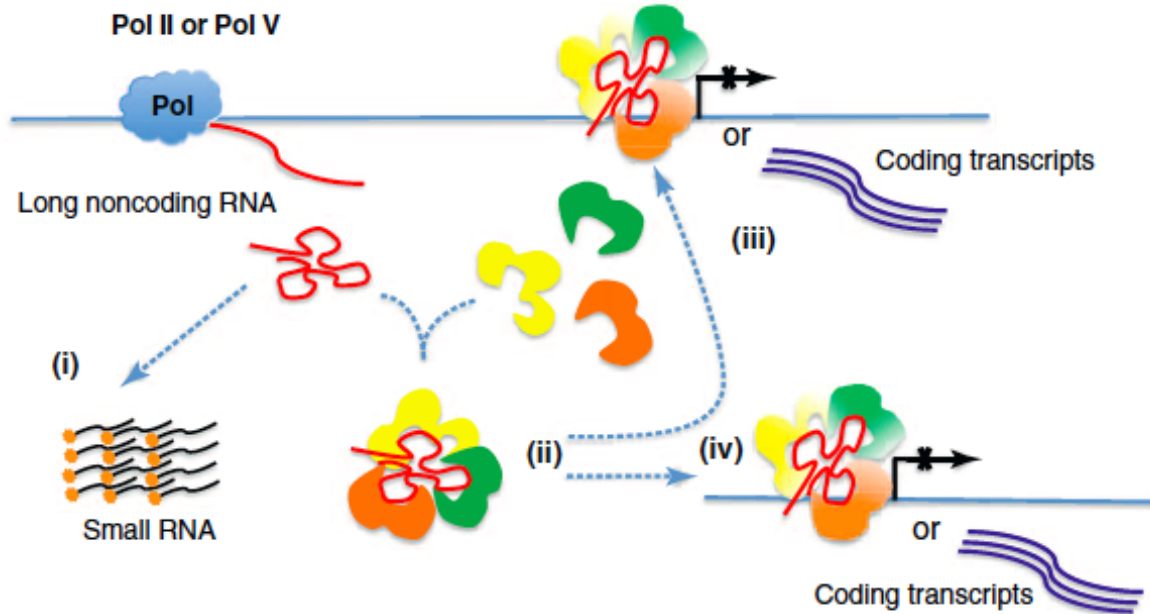
III. Guide



IV. Scaffold



ncRNAs diversos & controle de expressão



O RNA como molécula regulatória

