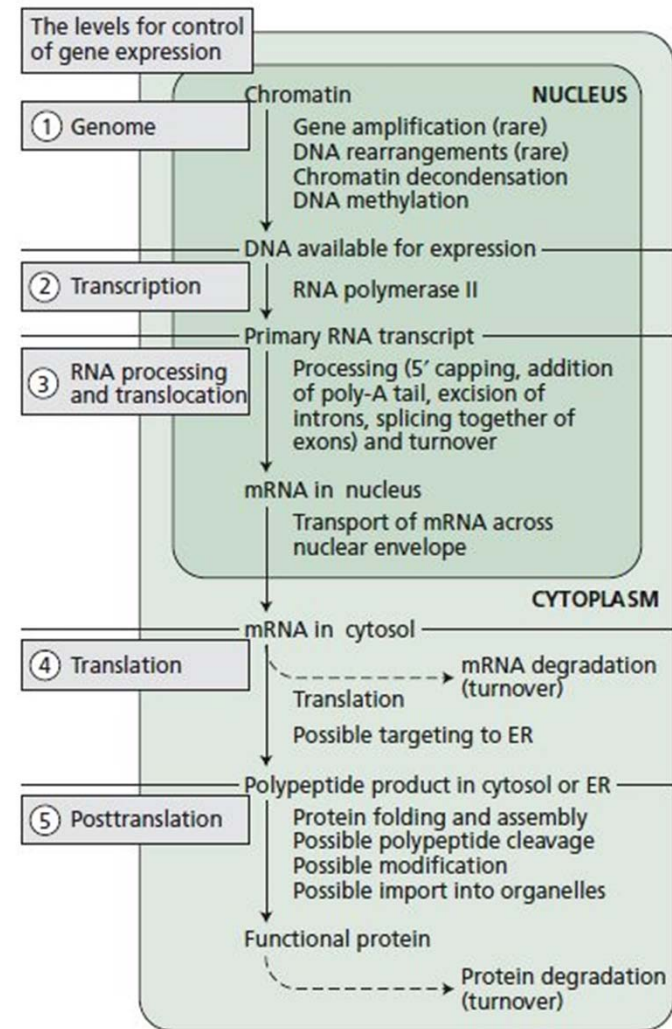


Gene Expression & regulation

Eukaryotic gene expression regulation takes place at different levels



Gene Expression & regulation

Examples of posttranscriptional regulation:

1- Expression of SSU5B in *Lemna gibba* (duckweed) roots:



The same mRNA species is regulated differentially depending on the type of tissue

One of the proteins of the small subunit of RuBisCO protein is called *SSU5B*. It is expressed in both roots and leaves of the aquatic plant duckweed at the same level. However, its mRNA content in roots is lower compared to frond (leaf) tissues. So the roots have lower content of photosynthetically active RuBisCO, and hence lower photosynthetic activity. The regulation of *SSU5B* is through controlling the **turnover** of its pre-mRNA in the nucleus. The root tissues have higher turnover (degradation) of *SSU5B* as compared to the leaf tissues.



Gene Expression & regulation

2- Expression of PvPRP in bean tissues under function infection

Bean leaves express the proline rich protein PvPRP1 in the cell walls

Upon fungal infection the mRNA encoding the PvPRP protein is rapidly degraded.

Gene Expression & regulation

Codon usage bias

Codon bias affects the translatability of mRNA

There are **64 different codons** (**61 codons** encoding for amino acids plus 3 stop codons) but only **20 different translated amino acids** → each amino acid has more than one code

If an mRNA message contains a large number of triplet codons that are rare for cells in a certain tissue, a small number of charged tRNAs available for those codons will slow translation.

Codon usage bias: refers to differences in the frequency of occurrence of synonymous codons in coding DNA

Codon usage bias fine tunes gene expression

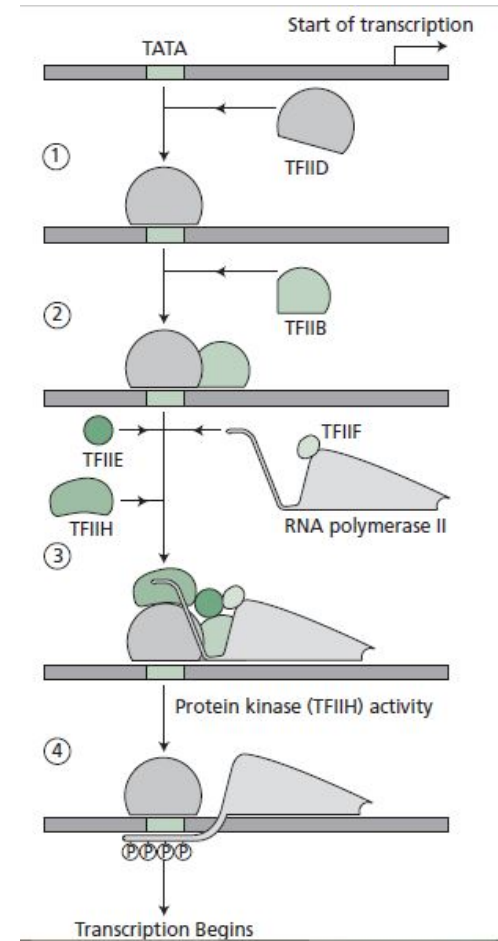
		Second nucleotide							
		U	C	A	G				
U	UUU	Phe	UCU	Ser	UAU	Tyr	UGU	Cys	U
	UUC		UCC		UAC		UGC		C
	UUA	Leu	UCA		UAA	STOP	UGA	STOP	A
	UUG		UCG		UAG	STOP	UGG	Trp	G
C	CUU		CCU		CAU	His	CGU		U
	CUC	Leu	CCC	Pro	CAC		CGC	Arg	C
	CUA		CCA		CAA	Gln	CGA		A
	CUG		CCG		CAG		CGG		G
A	AUU	Ile	ACU		AAU	Asn	AGU	Ser	U
	AUC		ACC	Thr	AAC		AGC		C
	AUA		ACA		AAA	Lys	AGA	Arg	A
	AUG	Met	ACG		AAG		AGG		G
G	GUU		GCU		GAU	Asp	GGU		U
	GUC	Val	GCC	Ala	GAC		GGC		C
	GUA		GCA		GAA	Glu	GGA	Gly	A
	GUG		GCG		GAG		GGG		G

Gene Expression & regulation

Most of gene expression regulation is through regulating transcription

Differences in transcription between prokaryotes and eukaryotes:

- 1- Types of RNA polymerases
- 2- Accessory proteins of RNA polymerase
- 3- The complexity of promoters



Gene Expression & regulation

Structure of promoters in eukaryotes

Core promoter (minimal promoter)

- Upstream to the gene
- 100 bp length
- Contain elements called “Proximal promoter sequences”

1- TATA box: at -25 position - binds transcription initiation complex

2- CAAT box: at -80 position - binds regulatory proteins (TFs)

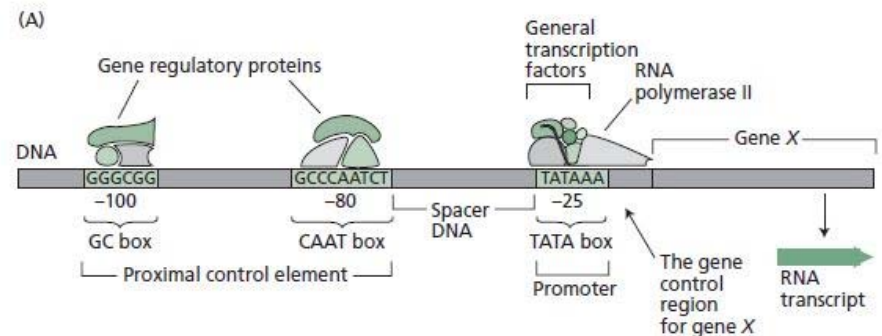
3- GC box at -100 position: binds regulatory proteins

Cis-acting elements: DNA sequences

Trans-acting factors: proteins that bind to the cis-acting elements

Regulatory sequences

- Located within 1000 upstream of gene
- They are called distal regulatory elements
- Positively acting TFs that bind to these sequences are activators
- Negatively acting TFs that bind to these sequences are repressors
- The sequences involved in gene regulation by hormones and signals are response elements



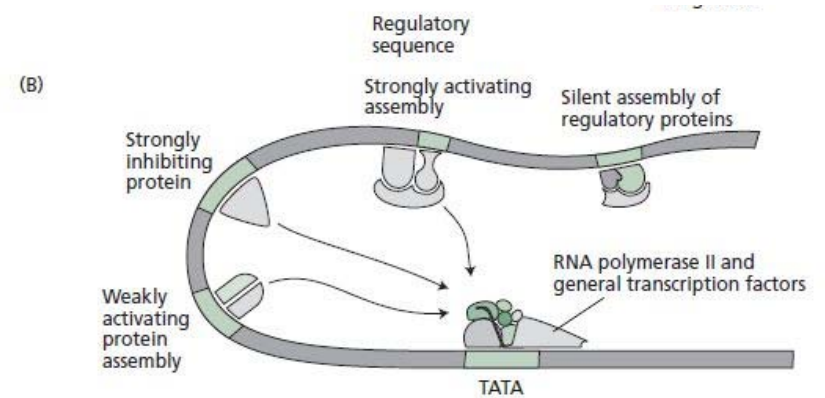
Gene Expression & regulation

Outside promoter at thousands of bases away from transcription start site there are other regulatory sequences:

Can be located upstream or downstream tens of thousands of bases from their target sequence

Positive regulatory sequences are called enhancers

Negative regulatory sequences are called silencers





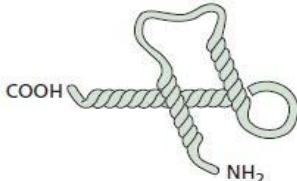


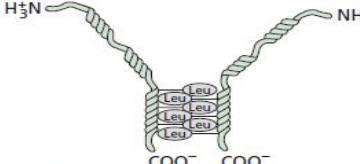
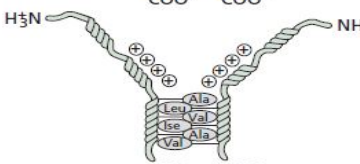
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Transcription factors usually have 3 domains:

- 1- DNA binding domain: it can bind specific sequence(s) of DNA
- 2- Transcription activation domain
- 3- ligand-binding domain

Gene Expression & regulation

Table 14.1
DNA-Binding Motifs

Name	Examples of proteins	Key structural features	Illustration
Helix-turn-helix	Transcription factors that regulate genes in anthocyanin biosynthesis pathway	Two α helices separated by a turn in the polypeptide chain; function as dimers	
Zinc finger	COP1 in <i>Arabidopsis</i>	Various structures in which zinc plays an important structural role; bind to DNA either as monomers or as dimers	
Helix-loop-helix	GT element-binding protein of phytochrome-regulated genes	A short α helix connected by a loop to a longer α helix; function as dimers	
Leucine zipper	Fos and Jun	An α helix of about 35 amino acids containing leucine at every seventh position; dimerization occurs along the hydrophobic surface	
Basic zipper (bZip)	Opaque 2 protein in maize, G box factors of phytochrome-regulated genes, transcription factors that bind ABA response elements	Variation of the leucine zipper motif in which other hydrophobic amino acids substitute for leucine and the DNA-binding domain contains amino acids	



Main differences in transcription between prokaryotes and eukaryotes:

Prokaryotes	Eukaryotes
Transcription is coupled to translation	Transcription is separated from translation
No mRNA processing	Extensive mRNA processing (capping, tailing, intron splicing, alternative splicing)
Simple promotor structure	Core promotor + regulatory sequences
No transcription factors	Transcription factors are involved
Polycistronic mRNA	No polycistronic mRNA
Genes arranged in operons	No gene arrangement in operons