RAMA UNIVERSITY

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FACULTY OF ENGINEERING &TECHNOLOGY

DEPARTMENT OF BIOTECHNOLOGY

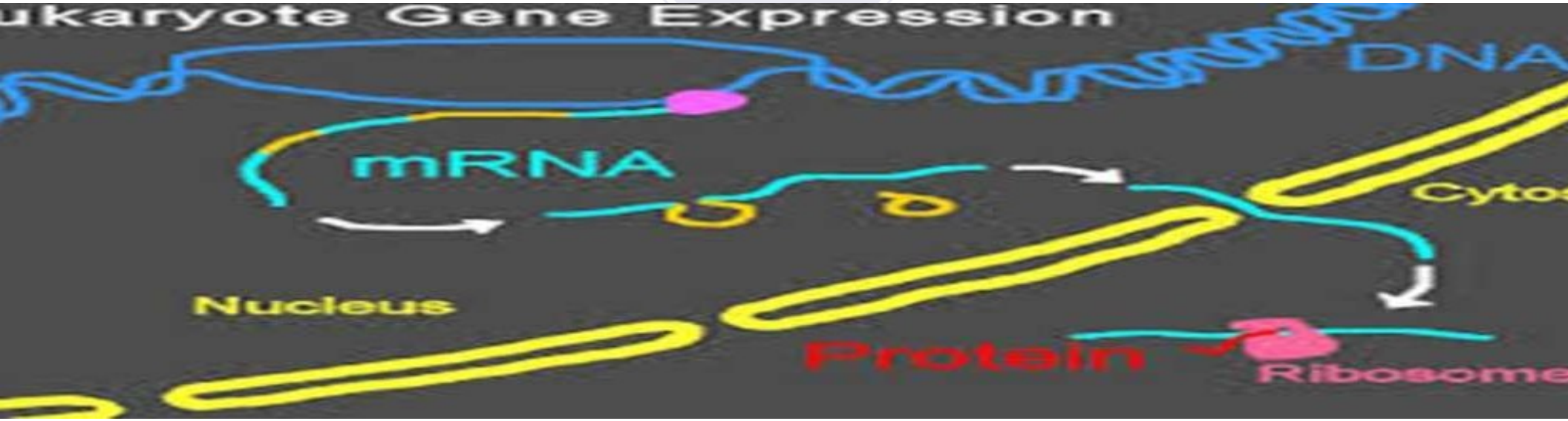
karyotic gen Regulation

Eukaryotic cells have a much larger genome Eukaryotes have much greater cell specialization

Thus eukaryotic cells contain an enormous amount of DNA that does not program the synthesis of RNA or protein

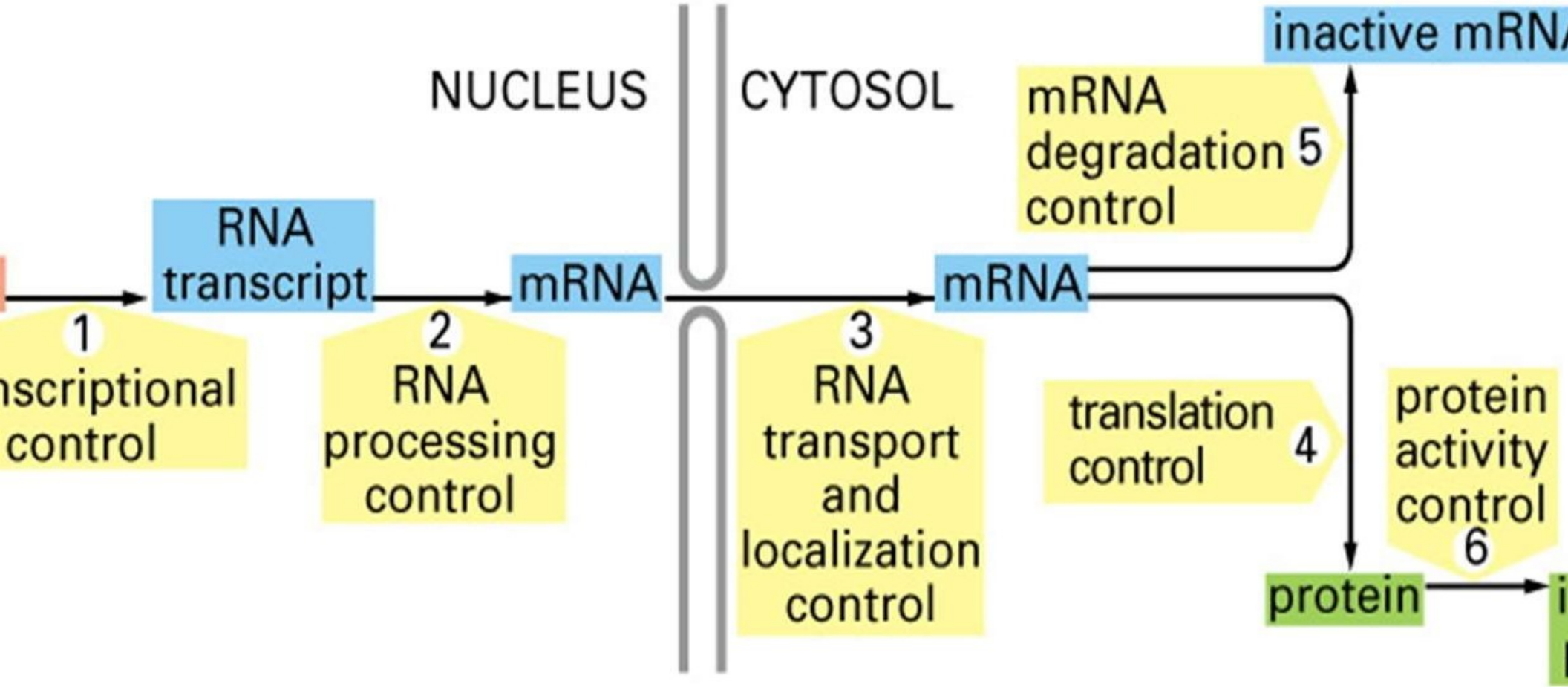
This requires complex organization

In eukaryotes expression of gene into proteins can be controlled at various locations



of Eukaryotic gene Regulation

Transcriptional control. 2.RNAprocessing control.
RNA transport & localisation control
Translation control.
mRNAdegradation control. 6.Protein activator control.


NUCLEUS
CYTOSOL
inactive mRNA
mRNA degradation control
5
RNA transcript
mRNA
mRNA
1
nscriptional control
2
RNA processing control
3
RNA transport and localization control
translation control
4
protein activity control
6
protein

vo forms of chromatin

chromatin – A lesser coiled transcriptionally active region which can
easily accessed by the RNA polymerases.

eterochromatin – A highly condensed transcriptionally inactive region. The genes in
gion cannot be accessed by the RNA polymerases for active transcription.

biquitination:

itination of H2A – Transcriptional inactivation Ubiquitination of H2B -
criptional activation

Mechanisms affects the chromatin Structure:

- Histone modifications – These modifications make a region of gene either transcriptionally active or inactive.

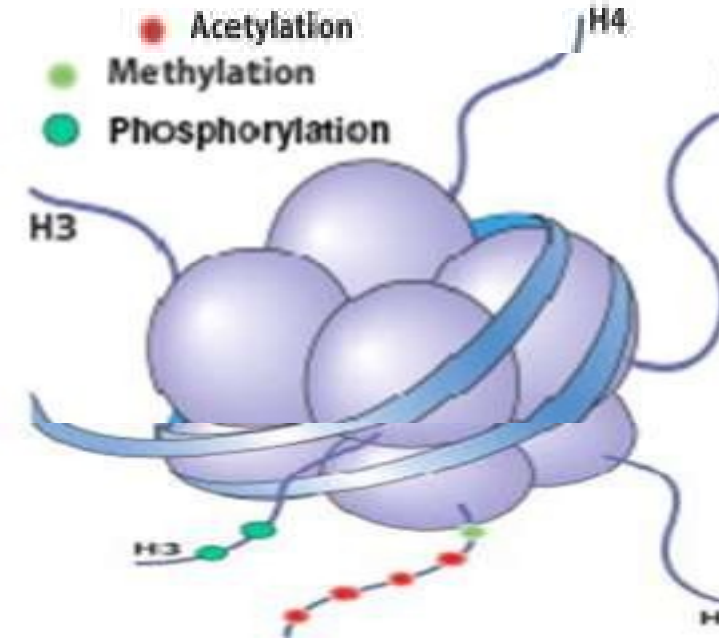
  Acetylation

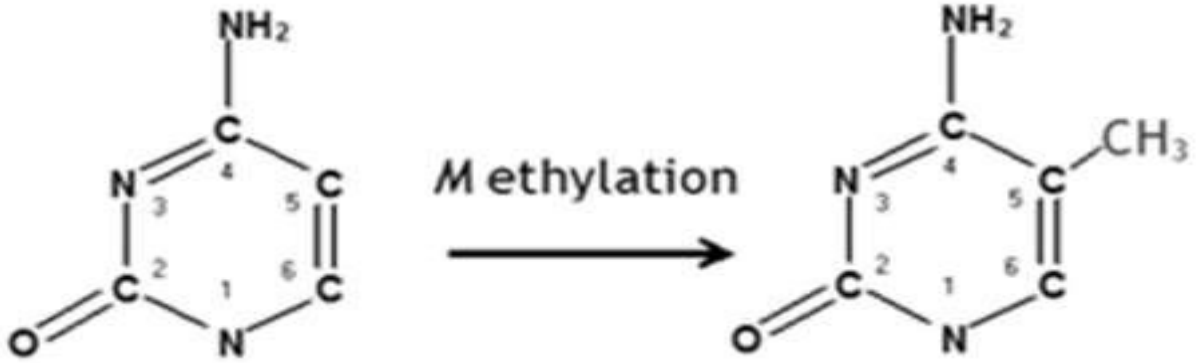
- ↑Acetylation ----↓ Condensation of DNA ----- ↑ Transcription of genes in that region Ubiquitination

Ubiquitination of H2A – Transcriptional inactivation Ubiquitination of H2B - Transcriptional activation

ethylation

methylation:is the addition or removal of a methyl
p predominantely where cytosine bases occur
ecutively.
s occur consecutively.
methylation:is the addition or removal of a methyl
p predominantely where cytosine bases occur
ecutively.
s occur consecutively. Methylation occurs
often in symmetrical CG sequences.



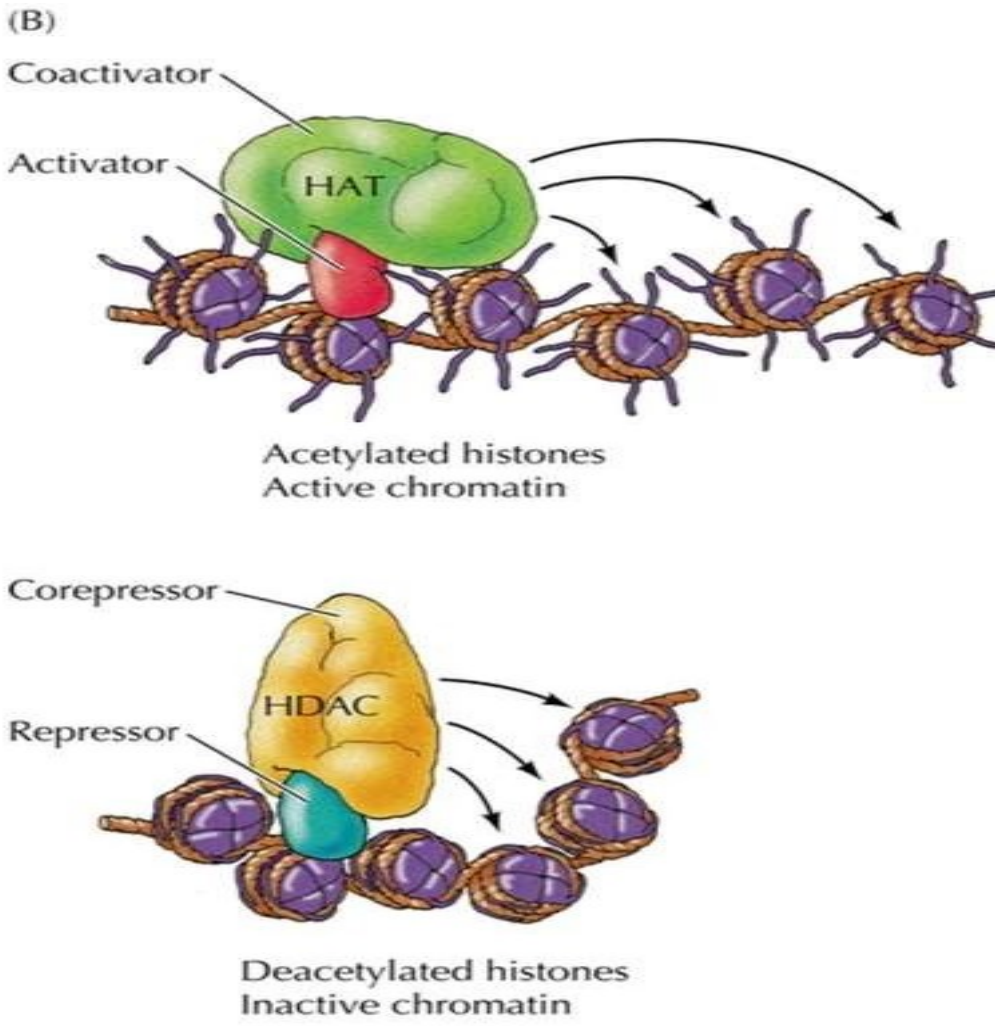


CETYLATION :

ATs and coactivators leads
euchromatin formation

IETHYLATION:

HDACs and corepressors leads
heterochromatin formation



ulation of Transcription:

ukaryotes – There are two types of promoters which are:

- **Basal promoters**
- **Upstream promoters**

Basal promoter or core promoter -These promoters reside within 40bp upstre
f the start site. These promoters are seen in all protein coding genes.

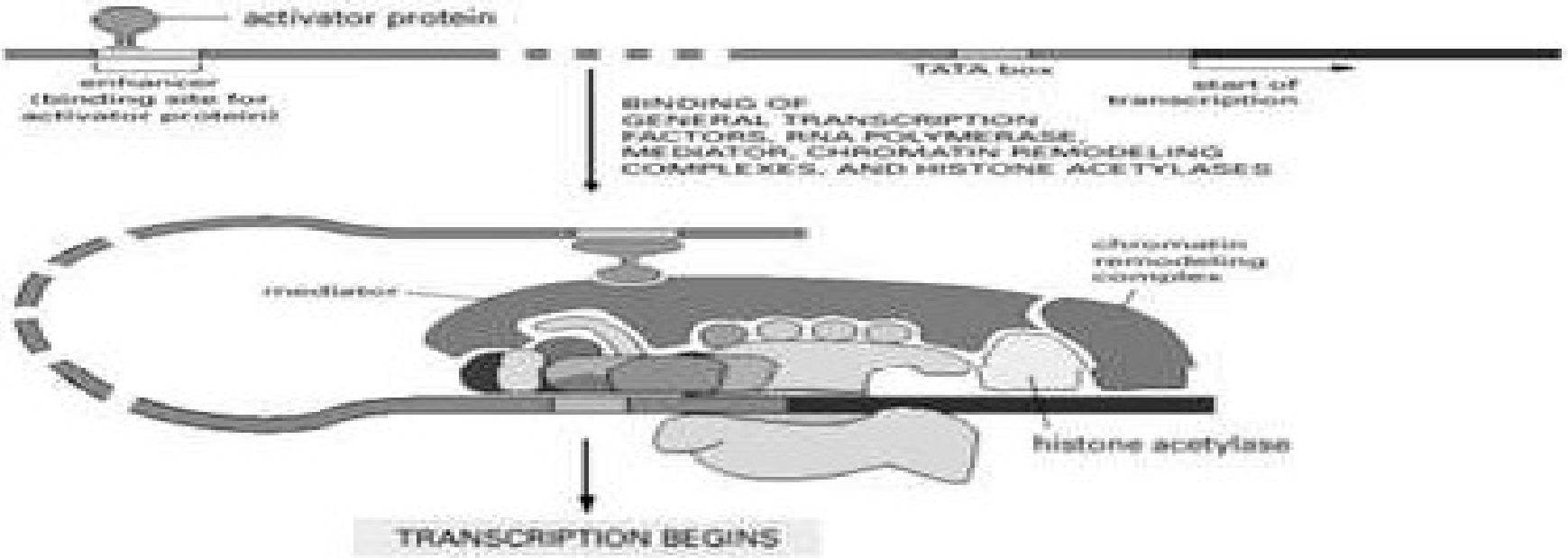
Upstream promoters - These promoters may lie up to 200bp upstream of the anscriptional initiation site. The structure of this promoter and the associated binding facto eeps varying from gene to gene.

anscriptional control:

controlling when and how often a given gene is
anscribed

gure 6. Genes can be expressed with different efficiencies.
ene A is transcribed and
nslated much more efficiently than gene B. This allows the amount of
otein A in the cell to bemuch greater than that of protein B.

Transcriptional control – regulation by RNA polymerase:



hancers

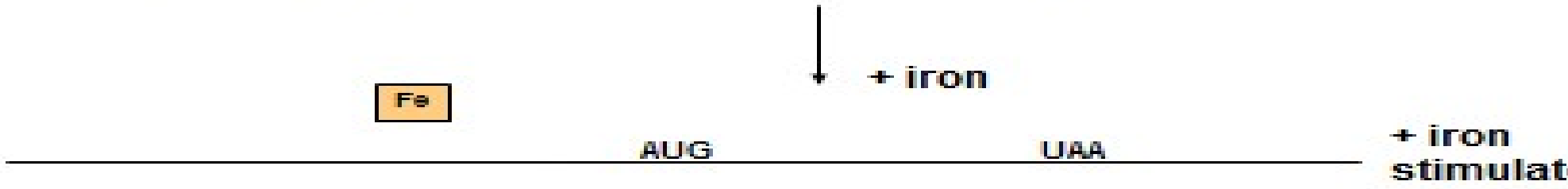
- Enhancers can be located upstream, downstream or within the gene that is transcribed
- The binding of these enhancers with enhancer binding proteins (transcription factors) increases the rate of transcription of that gene to a greater extent.
- Promoters are capable of initiating lower levels of transcription.
- Enhancers are responsible for the cell or tissue specific transcription.
- Each enhancer has its own transcription factor that it binds to.

Control at mRNA stability

A stem loop is stabilised by the 90 kDa protein in the absence of iron

This time, the stem loop is at the 5' end of the mRNA.

The presence of the stem loop prevents translation of this mRNA by blocking the progress of the ribosomes along the mRNA.



In the presence of iron, the hairpin is lost, the ribosomes can transla the mRNA and ferritin protein synthesis is increased.