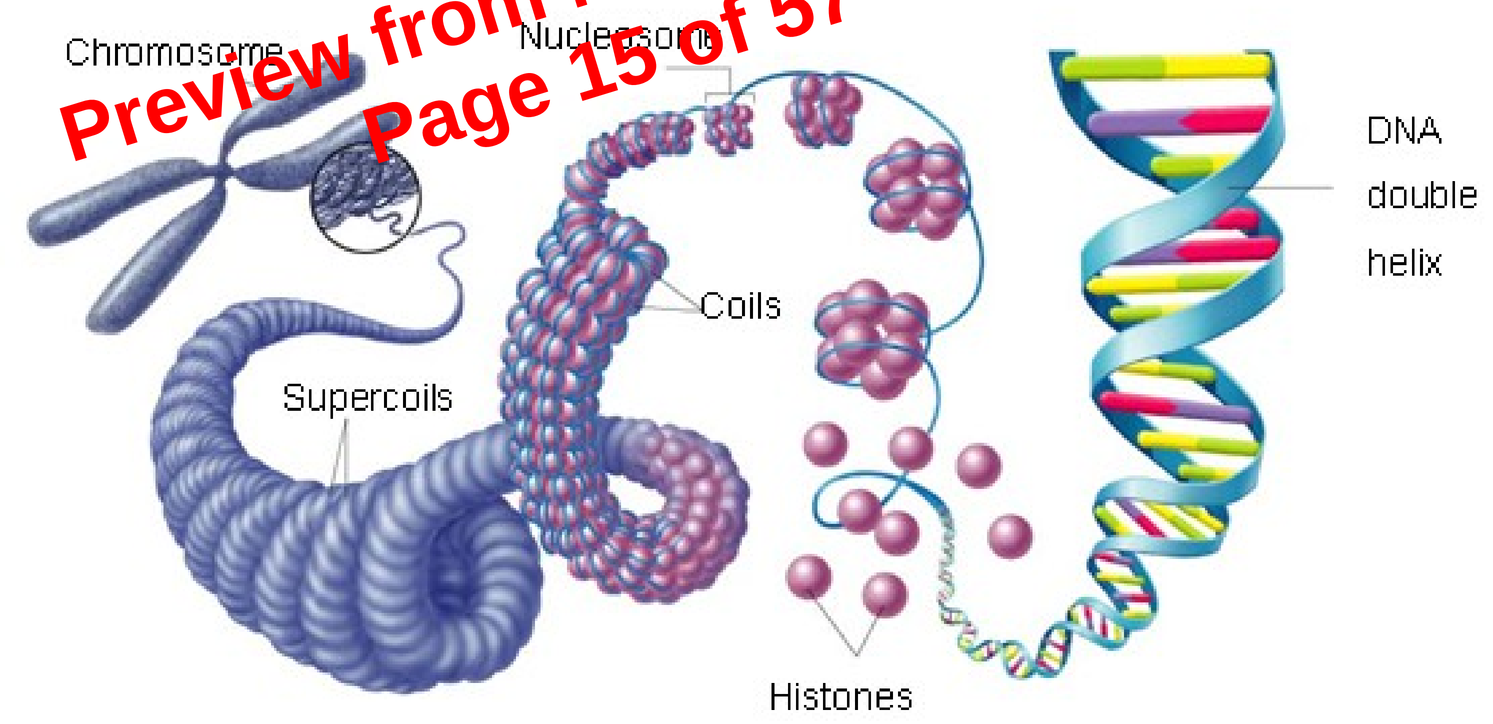
Regulation
of
Gene Expression

Overview of Gene Expression

- The control of gene expression is vital to the proper and efficient functioning of an organism.
- Cells control metabolism by either regulating enzyme activity –or- regulating the expression of genes coding for enzymes.

Chromosome Structure of Eukaryotes



Eukaryotic chromosomes contain DNA wrapped around proteins called *histones*. The strands of *nucleosomes* are tightly coiled and supercoiled to form chromosomes.

1. Chromatin Modifications

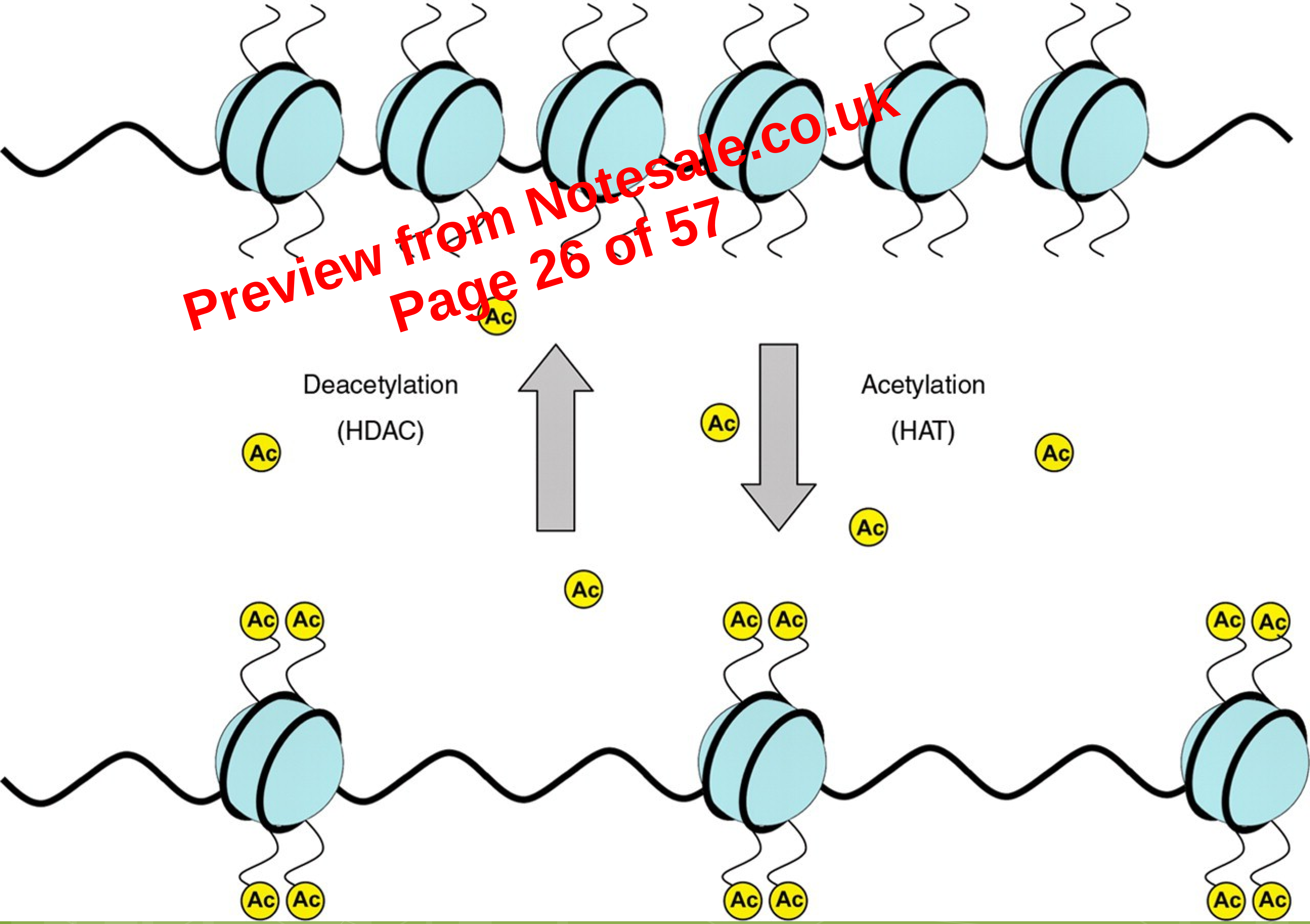
- Chromatin modifications affect the availability of genes for transcription:
  - The physical state of DNA in or near a gene is important in helping control whether the gene is available for transcription.
  - Genes of heterochromatin (highly condensed) are usually not expressed because transcription proteins cannot reach the DNA.
- **DNA methylation** seems to diminish transcription of that DNA.
- **Histone acetylation** seems to loosen nucleosome structure and thereby enhance transcription.

DNA Methylation

- **DNA methylation** is the attachment of methyl groups (-CH_3) to DNA bases after DNA is synthesized.
  - Methylation renders DNA inactive.
  - Inactive DNA, such as that of inactivated mammalian X chromosomes (Barr bodies), is generally highly methylated compared to DNA that is actively transcribed.
  - Comparison of the same genes in different types of tissues shows that the genes are usually more heavily methylated in cells where they are not expressed.
  - In addition, de-methylating certain inactive genes (removing their extra methyl groups) turns them on.
- At least in some species, DNA methylation seems to be essential for the long-term inactivation of genes that occurs during cellular differentiation in the embryo.

Histone Acetylation

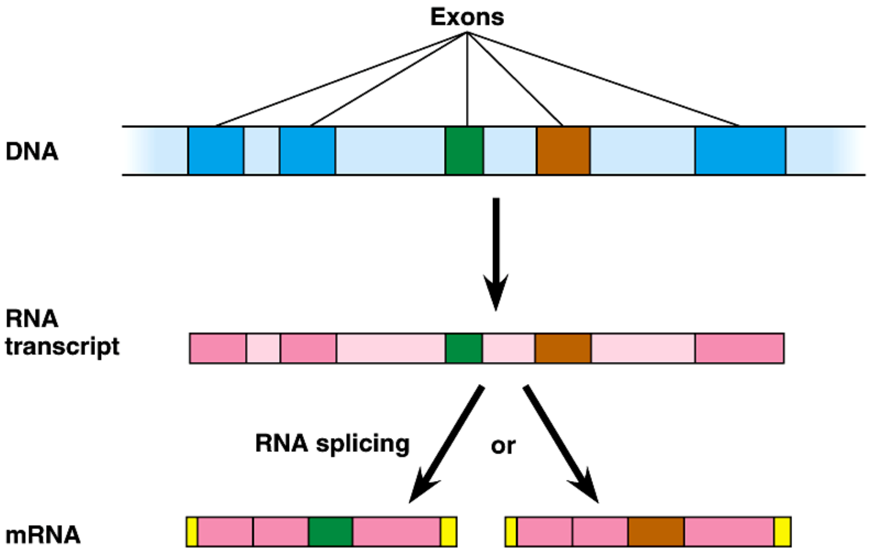
- **Histone acetylation** is the attachment of acetyl groups (-$COOH_3$) to certain amino acids of histone proteins; de-acetylation is the removal of acetyl groups.
  - When the histones of nucleosome are acetylated, they change shape so that they grip the DNA less tightly.
  - As a result, transcription proteins have easier access to genes in the acetylated region.


Ac
Deacetylation
(HDAC)
Acetylation
(HAT)
Ac
Ac
Ac
Ac
Ac
Ac Ac
Ac Ac
Ac Ac
Ac Ac
Ac Ac
Ac Ac

- It appears that TEs travel at will, showing up whenever and wherever they please.

- How they pull off this trick isn’t completely clear because TEs have several options when it comes to travel.
- They take advantage of breaks in DNA, but not just any break will do — the break must include little overhanging bits of single-stranded DNA .

Alternative Splicing Offers New Combinations of Exons = New Proteins



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The RNA transcripts of some genes can be spliced in more than one way, generating different mRNA molecules.

With alternative splicing, an organism can get more than one type of polypeptide from a single gene.