When a transcription process wants to start, the histones need to be modification then DNA can be exposed to reaction. During transcription, Histone H3 will be methylated at lys^4 by a specific methylase. This methylation facilitated the binding of histone acetyltransferase(HATs), an enzyme that acetylates particular Lys residues. Where chromatin is being activated for transcription, the nucleosomal histones are further acetylated by nuclear (type A) HATs. HATs contain three famlies which are MYST, GNAT, and p300. Acetylation of particular Lys residues is critical for the interaction of nucleosomes with other proteins. When transcription of a gene is no longer required, the extent of acetylation of nucleosomes in that vicinity is reduced by the activity of histone deacetylases (HDACs), as part of a general gene-silencing process that restores the chromatin to a transcriptionally inactive state. Acetylation histones can be read by regulatory proteins which will bind to bromodomains. Bromodomains recognise only a short sequence of four amino acids, (including the acetylated lysine) so target specificity must depend on interactions with other regions.

There is an example of histone acetylation that controls the life of plants. The flowering in Arabidopsis is controlled by histone deacetylase. There is a gene called FLC in arabidopsis which is expressed to prevent the flowering of itself. After the plants experience a period of low temperature, the plants consider that spring is coming. So there is another gene called FLD that will express an enzyme which can deacetylate the FLC which can turn off the FLC gene. Then there is no enzyme to prevent flowering. Then the Arabidopsis is able to initiate flower only in spring by the corporation of FLC and FLD gene.

Histone methylation also plays an important role. The addition of methyl groups to histone tails is specifically located on Lysine and Arginine and commonly modified on H3 and H4. Methyl groups can active or inactive chromatin and can be attached to more than one group at one time. The histone methyltransferase HMT and histone lysine methyl transferase HKMTs catalyst methylation with the SET domain. The effector protein can recognise the methylation domain and bind to methylated lysines via chromodomains which are the readers of histone methylation. These effector proteins have enzymatic activities and can lead to chromatin remodelling which could activate or repress the effect on transcription without changing the overall charge of histones.