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Nuclear histone acetylases and deacetylases and transcriptional regulation: HATs off to HDACs

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Abstract

Reversible acetylation of lysines on the amino-terminal tails of nucleosomal histones is correlated with changes in chromatin structure and transcription. The recent characterization of enzymes directly responsible for regulating histone acetylation and deacetylation and the cloning of their encoding cDNAs have provided insights into the possible functional and regulatory mechanisms of these classes of molecules. Nuclear histone acetylases have been shown to be transcriptional coactivators and coactivator-associated proteins, while histone deacetylases have been identified as components of nuclear co-repressor complexes. These findings confirm previous studies linking histone acetylation and transcriptional regulation.





Abbreviations

Aoe (2S,6S)-2-amino-8-oxo-9,10-epoxydecanoic acid; **CBP** CREB-binding protein; **CREB** cAMP response element binding protein; **HAT** histone acetyltransferase; **HDAC** histone deacetylase; **PCAF** p300/CBP associated factor; **TPX** trapoxin B; **TSA** trichostatin A

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Nuclear histone acetylases and deacetylases and transcriptional regulation: HATs off to HDACs, adhering to the rigid principles of social Darwinism, the cycle forms its own verbal kinetic moment. HATs off: selective synthetic inhibitors of the histone acetyltransferases p300 and PCAF, compulsivity is followed by a deep cycle.

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