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SnapShot: Histone Readers

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Posttranslational modifications (PTMs) of histone proteins and methylation of DNA are major components of the epigenetic machinery that regulates the structure and dynamics of chromatin, gene transcription, DNA replication, DNA recombination, and DNA repair. The PTMs alter direct interactions between histones and DNA and serve as docking sites for epigenetic effectors. A number of PTMs have been identified in the flexible histone tails that protrude from the nucleosomal core and are readily accessible to histone acetyltransferases (HATs), histone deacetylases (HDACs), histone lysine methyltransferases (HKMTs), kinases, phosphatases, and other enzymes capable of depositing or removing PTMs. The list of PTMs is rapidly growing and includes acetylation, methylation, ubiquitination, and SUMOylation of lysine residues, methylation and citrullination of arginine residues, phosphorylation of serine and threonine residues, and ADP-ribosylation of glutamate and arginine residues.

The histone PTMs are recognized by protein modules, referred to as epigenetic effectors, histone-binding domains, or simply "readers" of PTMs. Binding of the effectors recruits or stabilizes various transcription factors, chromatin remodeling complexes, and other components of the transcriptional network at chromatin. Many chromatin-associating proteins contain multiple copies of an effector or several different effectors, often specific for distinct PTMs. This provides a multivalent mechanism for targeting to a particular genomic site and ensures the proper biological outcome. Furthermore, the effectors are commonly found in macromolecules that either possess catalytic activities or act as scaffolding proteins that tether multisubunit enzymatic complexes to chromatin. These, in turn, further modify the epigenetic landscape by "erasing" PTMs, "writing" new epigenetic marks, or cleaving off the entire tail. This SnapShot shows the histone-binding effectors, their atomic-resolution structures, and the reported specificities for PTMs.

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