Decoding the epigenomic landscape by histone reader ZMYND8

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Chromatin is the physiological template for all genomic processes in eukaryotic cells. The core histones in chromatin get extensively posttranslationally modified and “reader/effector” proteins get recruited onto local chromatin which then dictate the “on” or “off” state of the underlying genes. The readers may interpret a histone posttranslational modification (PTM) via monovalent or multivalent recognition. In multivalent recognition readers recognize one histone modification intra/inter nucleosomally. An accessible surface is provided by these readers (such as a cavity or surface groove) which accommodates the modified histone residues and determines the modification (e.g. acetylation vs. methylation of lysine) or state specificity (e.g. mono vs. tri methylation of lysine). So far a huge family of proteins have been identified harbouring chromatin binding modules having a distinct preference for their binding signatures (i.e. modified histones). The readers can be chromatin architectural proteins, chromatin remodellers or chromatin modifiers. They may harbour catalytic functions or act as scaffolding proteins that are responsible to tether the multi-subunit enzyme complexes to chromatin. This recruitment further modify the epigenetic landscape by erasing old PTMs and writing new ones.

Human transcription factor Zinc finger MYND-type containing 8 (ZMYND8) is an important intermediate of the transcription regulatory network and can promote chromatin silencing. A modest chromatin binding affinity and interaction with core histones H3 and H4 is accomplished through its putative chromatin binding reader/effector modules: a PHD finger, a bromodomain and a Pro-Trp-Trp-Pro (PWWP) motif (PBP module in combination). The preferential interaction of this transcription factor with the epigenetic signatures could explain its distinct role in controlling gene expression in chromatin context.