

Expanding the Toolbox for Characterizing Epigenetic Protein-Protein Interactions Mediated by Post-translational Modifications

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Post-translational modification of histone proteins, including lysine methylation and acylation, regulates gene expression through recruitment of reader proteins to the nucleosome. Dysregulation of these events is prevalent in a wide range of diseases, such that there is much interest in characterizing these modifications and their binding partners as well as developing inhibitors for these protein-protein interactions. I will discuss using both traditional structure-activity relationships and Genetic Code Expansion to study the protein-protein interactions that are mediated by these post-translational modifications and to develop new tools to sense them.