



PEMED 2018

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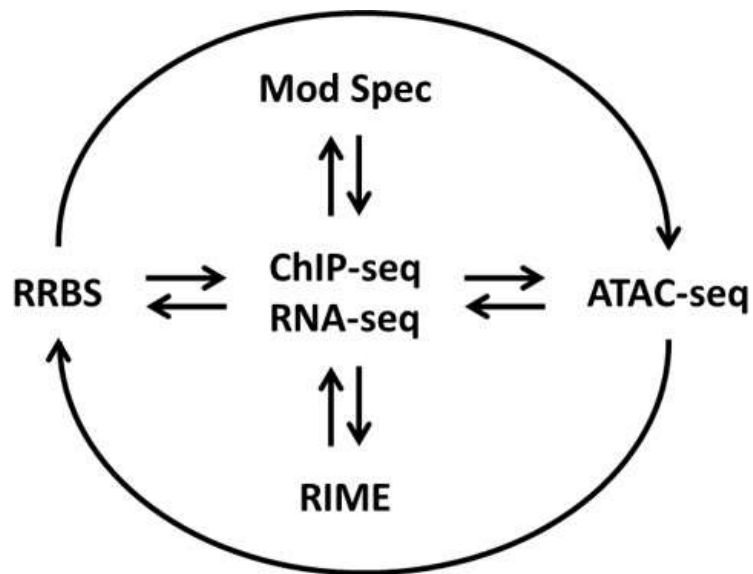
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A Multi-Omics approach to define the epigenetic profile of your model system

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Active Motif

Epigenetic profiling is critical for understanding the underlying mechanisms involved in cell fate decisions, cellular response to treatment and disease. Unfortunately, no single assay can provide a comprehensive view of the epigenetic state of your cells of interest. Here, we present different services offered by Active Motif that, when performed in union, can provide a comprehensive understanding of epigenetic determinants that are involved in your model system and be used for tumor profiling, biomarker and drug discovery research. Active Motif's comprehensive service offering includes: 1) **ATAC-seq** (Assay for Transposase-Accessible Chromatin using sequencing), which interrogates chromatin accessibility changes in your cells or tissues of interest; 2) **Mod Spec™**, which quantifies histone post-translational modifications by mass spectrometry, making it possible to measure global changes of greater than 80 different histone modification states in a single assay; 3) **ChIP-Seq** (Chromatin Immunoprecipitation Sequencing) experiment, an essential tool to study Chromatin and Transcription Biology using tumors cells or tissues as well as FFPE samples. Using specific antibodies, we can follow the binding pattern of chromatin proteins, elucidating their function and their correlation with different gene regulation pathways. 4) **RRBS** (Reduced Representation Bisulfite Sequencing) which provides single base-pair resolution methylation status at over 75% of CpG islands and over 50% of promoters; 5) **RIME** (Rapid Immunoprecipitation Mass Spectrometry of Endogenous Proteins) which can elucidate physically-interacting co-regulators that may be required in establishing the functional specificity of your target protein. Together, these assays will provide you with multi-dimensional mechanistic insight into the factors and pathways involved in the response of your model system.



Active Motif Assay Connectivity. Mod Spec and ATAC-seq are both great assays for researchers who know little about the role of epigenetics in their disease or model system. Mod Spec will identify differential histone modifications that can then be profiled on a genome-wide level using ChIP-seq. ATAC-seq differentials can point to important transcription factors or histone modifications that that should next be profiled with ChIP-seq. RRBS adds the DNA methylation component and RIME identifies additional protein co-regulators that influence differential gene expression