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Proteomic approaches for epiproteome analysis

A particular chromosome activity, such as gene transcription, can be defined by the specific epiproteome at the chromosomal location. The epiproteome includes the particular proteins involved in the activity as well as the histone posttranslational modifications at the specific region of the chromosome. Defining different epiproteomes has been limited by the lack of technologies that can comprehensively identify the proteins and histone posttranslational modifications in high resolution at specific genomic sites. Recent advances in targeted chromatin enrichment and proteomics have provided evidence that epiproteomes can be measured with near nucleosomal resolution. In this talk, I will present three technological platforms we have developed for the analysis of site specific epiproteomes.

Biography

Alan J Tackett has obtained his PhD from University of Arkansas for Medical Sciences in 2002. Currently, he is working as Associate Professor in University of Arkansas. He is serving as an editorial member of several reputed journals like Conference Papers in Biology. He has authored 41 research articles/books. In 2011 he received UAMS Founders Society Research Award.

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