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Genomics and chromatin analysis methods for profiling protein, RNA and DNA interactions in chromatin

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Chromatin immune-precipitation provides an in vivo picture of protein association within the dynamic cellular chromatin environment. Over the past decade, additional resolution on chromatin structure has been elucidated using other techniques that capture proteins or nucleic acids to uncover the composition of the components of chromatin, including regulatory proteins, modified histones, modified genomic DNA and the new putative chromatin regulatory molecule, non-coding RNAs. These precipitation techniques, both immune based as well as nucleic acid capture based, allow dissection of the role of these molecules in establishing and characterizing chromatin state. The methods can be easily combined with current library construction techniques to provide genome wide views of these interactions under experimental treatments & genetic backgrounds. The information provided by ChIP (Chromatin Immuno-Precipitation), Nuclear RIP (RNA Binding Protein Immuno-Precipitation of chromatin) and ChIRP (Chromatin Isolation by RNA) will be discussed.

Biography

John M Rosenfeld received his BS from Georgetown University, and received his PhD in molecular biology & biochemistry from the University of California, Irvine. He performed his Post-Doctoral training in the laboratory of Dr Ronald Evans at the Salk Institute on the topic of profiling transcriptional targets of orphan nuclear receptors. He joined Merck-Millipore in 2003, and has been developing research tools to explore gene regulation for the past 11 years. In addition to developing research tools and assays for epigenetic analysis, he is now responsible for managing platform technology development and external innovation for EMD Millipore and is part of the bioscience scientific networking group in this company.

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