



WISCONSIN INSTITUTES FOR  
**DISCOVERY**

MORGRIDGE INSTITUTE FOR RESEARCH  
WISCONSIN INSTITUTE FOR DISCOVERY



## **EPIGENETICS SEMINAR SERIES**

**Dr. Benjamin A. Garcia**

**Princeton University**

# **Quantitative Proteomics for Interrogating the Histone Code**

**Thursday, August 18<sup>th</sup>, 2011, 10:00 A.M.**

**H.F. DeLuca Forum, WI Institutes for Discovery**

Co-Sponsored by

**Wisconsin Institute for Discovery**

**Department of Chemistry**

**Department of Biomolecular Chemistry**

**ABSTRACT:** Histones are small post-translationally modified proteins that package DNA into chromosomes and regulate gene expression. Nevertheless, what type of effect single or multiple distinct combinations of simultaneously occurring histone modifications (Histone Codes or patterns) have upon cellular events is not yet fully understood. One reason for this is that there is a lack of robust high-throughput methods available for quantitative characterization of Histone Codes by any standard biological, immunological or physical technique. We plan to specifically address this deficiency by developing novel mass spectrometry based proteomic methods and accompanying bioinformatics to quantitatively characterize molecular level descriptions of combinatorial Histone Codes, and apply these methods to study how these dynamic Histone Codes influence gene expression under different biological conditions. Here we present proteomics data that describes: (i) high-throughput comparison of histone modifications from multiple cellular states (ii) developing mass spectrometry methods for quantitative tracking of combinatorial Histone Codes (iii) monitoring in vivo Histone Code dynamics, and (iv) investigating the role of Histone Code interpreting proteins in recognizing distinct Histone Codes. Ultimately, we will work towards the goal of taking any defined part of the genome and accurately quantifying the Histone Codes, detecting all the non-histone proteins that reside on these distinct pieces of chromatin, and then mapping this proteomic data back to specific genomic locations, therefore taking a proteomic snapshot of what that chromosome landscape looks like during any nuclear event. These studies in combination with biological experiments will help provide a systems biology outlook on gene expression that will lay down the basic scientific foundation to advance several applications, such as cancer progression.