

Distinguished Seminars on Epigenomics

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SEMINAR SERIES

Genomic mechanisms of gene regulation and chromatin organization

The large number of genes across eukaryotic genomes begs the question as to whether they are all fundamentally regulated in the same manner. Clearly, sequence-specific factors direct gene-specific regulation, but then do all downstream events proceed along a common path? To begin to address this question, we use ChIP-exo to map the precise contact points of proteins along genomic DNA. The near single-bp readout provides structural insights into how proteins are organized into complexes across genomes, and how they might position nucleosomes to regulate gene expression. Multiple classes of complexes occupy nucleosome-free promoter regions: an ensemble of sequence-specific factors and their coactivators, the core transcription machinery, chromatin remodelers and nucleosomes. This talk will focus on identifying common principles that determined how factors and chromatin organize themselves at promoters across co-regulated genes, and in genes in general.



ABOUT THE SPEAKER

B. Franklin Pugh, Ph.D.
Professor
Biochemistry and Molecular Biology
Pennsylvania State University, University Park

Frank Pugh is an academic scientist whose research interests lie in understanding the molecular mechanisms by which all genes within a eukaryotic genome are regulated. He received his PhD from the University of Wisconsin - Madison in 1987, and conducted postdoctoral research with Dr. Robert Tjian at the University of California Berkeley until 1991. Since then he has been on the faculty of the Pennsylvania State University - University Park in which he holds the rank of Professor of Molecular Biology (and holds the Willaman Chair, the Evan Pugh professorship, and is the director of the Center for Eukaryotic Gene Regulation).

Dr. Pugh's research highlights include the development of the first high resolution genome-wide ChIP-seq methods, that include MNase-based mapping of nucleosome positions and ChIP-exo to map protein-DNA interactions at near single bp resolution. Application of such maps in yeast and human model systems has produced a detailed understanding of how proteins work together to regulate gene transcription in response to environmental cues.

Thursday, December 10, 2015
3:00 pm, 310 Kelly Hall

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