

*The Bioinformatics Colloquium Series presents*

# Laura Elnitski

*Head, Genomic Functional Analysis Section,  
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## **“Regulatory and Epigenetic Landscapes of Mammalian Genomes”**

**Fri., Oct. 24 @ 11:10 a.m.—12 p.m.  
Stocker Center 103**

Knowledge of the human genome will greatly affect our understanding of basic human health and provide new therapies for many diseases. Although the genome has been fully sequenced, many mysteries still hide in its code. The well-known gene accounts for less than 2 percent of the sequence, while other functional elements, which provide important regulatory instructions, create up to 50 percent of the genome. Recent evidence suggests that these regulatory elements play a larger role in human disease than previously thought. Understanding non-coding functional elements is crucial to our understanding of how a cell functions properly. Elnitski's tutorial will discuss conventional and cutting edge ways to address the genome's functional regions through computational and experimental approaches.

**– Refreshments will be provided –**

### ***Career Experience & Awards:***

- Ph.D, biochemistry and molecular biology, Penn State University
- NIH Research Scholar Award for postdoctoral research in computational biology
- Outstanding Research Achievement Award, International Symposium on Bioinformatics Research and Applications, 2007
- Associate editor, *Genome Research* journal
- Ad hoc reviewer, NIH scientific grant review panel study section

*Sponsored by the Russ College of Engineering and Technology's School of Electrical Engineering and Computer Science; Biomedical Engineering program; Center for Intelligent, Distributed and Dependable Systems; and Bioinformatics Laboratory; the College of Arts and Sciences' Molecular and Cellular Biology program; the Ohio University Genomics Facility; and The Edison Biotechnical Institute*