

Stanford University  
Palo Alto, California



June 8th-10th  
[encode2016.org](http://encode2016.org)

# ENCODE USERS MEETING 2016

Registration for the ENCODE 2016 Research Applications and Users Meeting is now open: [www.encode2016.org](http://www.encode2016.org)

This is a great opportunity for both novice and experienced users of genomic data to learn about ENCODE resources and how to leverage them for your own research. The meeting will take place **June 8th - June 10th, 2016**, at the Stanford Li Ka Shing Center, at 219 Campus Drive, Palo Alto CA, and will feature:

- Hands-on training workshops to learn to navigate, analyze, and integrate ENCODE and mouse ENCODE data into your research. No programming experience required.
- Leading-edge research applications from distinguished invited speakers.
- Tutorials on newly-available informatics pipelines that greatly facilitate working with ENCODE data.
- Short talks selected from abstracts.

***Registration is only \$100 for academic attendees and \$250 for non-academic attendees.  
This does not include transportation or lodging, but does cover meals.***

## KEYNOTE SPEAKER

Nancy Cox, Vanderbilt University

## CONFIRMED SPEAKERS

- Matthew Freedman, Dana Farber/Harvard Cancer Center
- Tom Gingeras, Cold Springs Harbor Laboratory
- Brenton Graveley, University of Connecticut Health Center
- Mathieu Lupien, Princess Margaret Cancer Centre
- Katherine Pollard, The Gladstone Institute at UCSF
- Tim Reddy, Duke University
- Bing Ren, University of California, San Diego
- Yijun Ruan, The Jackson Laboratory
- Michael Snyder, Stanford University
- Barbara Stranger, University of Chicago
- Zhiping Weng, University of Massachusetts Medical School
- Grace Xiao, University of California, Los Angeles

## WORKSHOP TOPICS

- Viewing, querying, and downloading ENCODE data
- Running ENCODE processing pipelines on your own data (including ChIP-seq, eCLIP-seq, RNA-seq, DNase-seq, DNA methylation)
- Integrating ENCODE data with those from your lab or other major projects
- Using ENCODE data to interpret human variation, personal genomes, and disease (including cancer) genomes
- Connecting regulatory elements to their target genes across the genome
- Integrative analysis
- See the website for more details about training workshops

The ENCODE Outreach Working Group  
[www.encode2016.org](http://www.encode2016.org)