

[ABOUT CSAIL](#)[RESEARCH](#)[NEWS + EVENTS](#)[RESOURCES](#)[PEOPLE](#)[ALUMNI & FRIENDS](#)

PEOPLE

[Principal Investigators](#)[All Members](#)[Student Spotlights](#)[Home](#) » [People](#) » [Manolis Kellis](#)

MANOLIS KELLIS



Position: Associate Professor

Office: [32-D524](#)

Phone: +1 (617) 253-2419

Email: manoli@mit.eduAreas of Study: Computational Biology:
Genomes, Networks, Evolution [Personal Website](#)

Last Update: January 16, 2014

[Download vCard](#)

PUBLICATIONS

[Evidence of Abundant Purifying Selection in Humans for Recently Acquired Regulatory Functions](#)

Ward, Kellis

[Science](#), doi:10.1126/science.1225057, Sep 5 2012.[An integrated Encyclopedia of DNA elements in the human genome](#)

ENCODE Project Consortium

[Nature](#) 489:57-74. Sep 6, 2012.[A high-resolution map of human evolutionary constraint using 29 mammals](#)

Lindblad-Toh, Garber, Zuk, Lin, Parker, Washietl, Kheradpour, Ernst, Jordan, Mauceli, Ward, Lowe, Holloway, Clamp, Gnerre, Alfoldi, Beal, Chang, Clawson, Palma, Fitzgerald, Flicek, Guttman, Hubisz, Jaffe, Jungreis, Kostka, Lara, Martins, Massingham, Moltke, Raney, Rasmussen, Stark, Vilella, Wen, Xie, Zody, Worley, Kovar, Muzny, Gibbs, Warren, Mardis, Weinstock, Wilson, Birney, Margulies, Herrero, Green, Haussler, Siepel, Goldman, Pollard, Pedersen, Lander, Kellis

[Nature](#), October 12, 2011.[Mapping and analysis of chromatin state dynamics in nine human cell types](#)Ernst, Kheradpour, Mikkelsen, Shores, Ward, Epstein, Zhang, Wang, Issner, Coyne, Ku, Durham, Kellis*, Bernstein*
[Nature](#), March 23, 2011.[A Cis-Regulatory Map of the Drosophila Genome](#)

Negre, Brown, Ma, Bristow, Miller, Kheradpour, Loriaux, Sealfon, Li, Ishii, Spokony, Chen, Hwang, Wagner, Auburn, Domanus, Shah, Morrison, Zieba, Suchy, Senderowicz, Victorsen, Bild, Grundstad, Hanley, Mannervik, Venken, Bellen, White, Russell, Grossman, Ren, Posakony, Kellis, White

[Nature](#), March 23, 2011.[Comprehensive analysis of the Drosophila melanogaster chromatin landscape differentiates among chromosomes, genes, and regulatory elements](#)

Kharchenko, Alekseyenko, Schwartz, Minoda, Riddle, Ernst, Sabo, Larschan, Gorchakov, Gu, Linder-Basso, Plachetka, Shanower, Tolstorukov, Bishop, Canfield, Sandstrom,

BIOGRAPHY

I am an associate professor of Computer Science at MIT in the area of Computational Biology. I am a member of the Computer Science and Artificial Intelligence Laboratory (CSAIL), and of the Broad Institute of MIT and Harvard.

My research interests are in the area of computational biology, genomics, epigenomics, gene regulation, and genome evolution. Specifically:

(1) in the area of genome interpretation, we seek to develop comparative genomics methods to identify genes and regulatory elements systematically in the human genome

(2) in the area of gene regulation, we seek to understand the regulatory motifs involved in cell type specification during development, understand their combinatorial relationships, and how these establish expression domains in the developing embryo.

(3) in the area of epigenomics, we seek to understand the chromatin signatures associated with distinct activity states, the changing chromatin states across different cell types and during differentiation, and the sequencing signals responsible for the establishment and maintenance of chromatin marks.

(4) in the area of evolutionary genomics, understanding the dynamics of gene phylogenies across complete genes, the emergence of new gene functions by duplication and mutation, and the algorithmic principles behind phylogenomics.

Thurman, Stamatoyannopoulos, Kellis, Elgin, Kuroda, Pirotta, Karpen
[Nature](#), March 23, 2011.

[Identification of functional elements and regulatory circuits in Drosophila by large-scale data integration](#)

The modENCODE Consortium, Roy, Ernst, Kharchenko, Kheradpour, Negre, Eaton, Landolin, Bristow, Ma, Lin, Washietl, Arshinoff, Ay, Meyer, Robine, Washington, Di Stefano, et al, Cherbas, Graveley, Lewis, Micklem, Oliver, Park, Celniker, Henikoff, Karpen, Lai, MacAlpine, Stein, White, Kellis
[Science](#), Dec 24, 2010.

[Discovery and characterization of chromatin states for systematic annotation of the human genome](#)

Ernst, Kellis.
[Nature Biotechnology](#). doi:10.1038/nbt.1662, July 25, 2010

[A Bayesian approach for fast and accurate gene tree reconstruction](#)

Rasmussen, Kellis.
[Molecular Biology and Evolution](#). Advance Access, July 25, 2010, DOI 10.1093/molbev/msq189.

[The modENCODE Project: Unlocking the secrets of the genome](#)

Celniker, Dillon, Gerstein, Gunsalus, Henikoff, Karpen, Kellis, Lai, Lieb, MacAlpine, Micklem, Piano, Snyder, Stein, White, Waterston; modENCODE Consortium.
[Nature](#). 2009 Jun 18;459(7249):927-30.

[Evolution of pathogenicity and sexual reproduction in eight Candida genomes](#)

Butler*, Rasmussen, Lin, Santos, et al, Birren, Kellis*, Cuomo*.
[Nature](#). 2009 Jun 4;459(7247):657-62.

[Histone modifications at human enhancers reflect global cell-type-specific gene expression](#)

Heintzman, Hon, Hawkins, Kheradpour, Stark, et al, Crawford, Kellis, Ren.
[Nature](#). 2009 May 7;459(7243):108-12. Epub 2009 Mar 18.

[Chromatin signature reveals over a thousand highly conserved large non-coding RNAs in mammal](#)

Guttman, Amit, Garber, French, Lin, et al, Bernstein, Kellis, Regev, Rinn, Lander
[Nature](#), Feb 1, 2009

[Discovery of functional elements in 12 Drosophila genomes using evolutionary signature](#)

Stark, Lin, Kheradpour, Pedersen, Parts, Carlson, Crosby, Rasmussen, Roy, Deoras, Ruby, Brennecke, FlyBase curators, Berkeley Drosophila Genome Project, Hodges, et al, Pachter, Kent, Haussler, Lai, Bartel, Hannon, Kaufman, Eisen, Clark, Smith, Celniker, Gelbart, Kellis
[Nature](#), 2007 Nov 8; 450:203-218, 14 pages

[Systematic discovery of regulatory motifs in human promoters and 3' UTRs by comparison of several mammal](#)

Xie, Lu, Kulbokas, Golub, Mootha, Lindblad-Toh, Lander, Kellis
[Nature](#) 2005 Feb 27,
doi: 10.1038/nature03441

[Proof and evolutionary analysis of ancient genome duplication in the yeast Saccharomyces cerevisia](#)

Kellis, Birren, Lander
[Nature](#) 2004 Apr 8; 428 pp. 617-24

[Sequencing and comparison of yeast species to identify genes and regulatory motifs](#)
Kellis, Patterson, Endrizzi, Birren, Lander
[Nature](#) 2003 May 15; 423 pp. 241-254

AWARDS

Athens Technology Center for Research and Education (AIT): Niki Award (2011)

National Science Foundation: United States Presidential Early Career Award for Scientists and Engineers (PECASE) (2010)

MIT: Karl Van Tassel Career Development Professorship (2007)

National Science Foundation: CAREER award (2007)

Technology Review: TR35 - Top 35 Innovator Under the Age of 35 (2006)

Genome Technology: Top Young PIs (2006)

MIT: Distinguished Alumnus (1964) Career Development Chair (2005)

MIT EECS: Sprowls Doctoral Dissertation Award (2003)

[submit new awards here](#)

(CSAIL members only)