ENCODE Phase 3: Participants and Projects

ENCODE Production Centers

Research Group	Institution	Major Research Goals
Bradley Bernstein	Broad Institute of MIT and Harvard	Map histone modifications using chromatin immunoprecipitation followed by high-throughput sequencing.
Thomas Gingeras	Cold Spring Harbor Laboratory	Identify protein-coding and non-protein coding RNA transcripts using high-throughput sequencing, and identify transcription start sites using cap analysis.
Brenton Graveley	University of Connecticut Health Center	Identify human RNA sequence elements bound by proteins, and investigate their function.
Richard Myers	HudsonAlpha Institute for Biotechnology	Identify transcription factor binding sites in the human genome, identify RNA transcripts in mouse and human cells, and identify DNA methylation sites in human cells.
Bing Ren	LICR/University of California, San Diego	Catalog chromatin structure in mouse cells by mapping histone modifications and identifying sites of DNA methylation. Functionally characterize regulatory elements using transgenic mice.
Michael Snyder	Stanford University	Identify transcription factor binding sites in the human genome, and functionally characterize regulatory elements.
John Stamatoyannopoulos	University of Washington, Seattle	Map chromatin structure and transcription factor binding sites in human and mouse cells using DNaseI.

ENCODE Data Coordination Center

Research Group	Institution	Goals
Michael Cherry	Stanford University	Collect, organize, store, manage, and provide access to data from ENCODE and related projects.

ENCODE Data Analysis Center

Research Group	Institution	Research Goals
Zhiping Weng	University of Massachusetts Medical School, Worcester	Coordinate and assist in the integrative analysis of data produced by the ENCODE Consortium.

ENCODE Computational Analysis Awards

Research Group	Institution	Research Goals
Peter Bickel	University of California	Develop statistical methods to enable integration of high dimensional ENCODE data.
David Gifford	Massachusetts Institute of Technology	Improve resolution for experimental identification of functional elements, and learn enhancer grammar to predict enhancers.
Sunduz Keles	University of Wisconsin, Madison	Develop computational methods to annotate repetitive regions, and integrate datasets in repetitive regions.
Robert Klein	Sloan-Kettering Institute for Cancer Research	Develop computational methods to integrate ENCODE data with GWAS data, to find functional variants and critical cell types.
Jonathan Pritchard	Stanford University	Develop statistical and computational methods for interpreting ENCODE data with respect to gene expression.
Xinshu Xiao	University of California, Los Angeles	Provide in-depth analysis of ENCODE data to identity functional variants regulating mRNA metabolism.

ENCODE Technology Development Effort

Research Group	Institution	Research Goals
Christopher Burge	Massachusetts Institute of Technology	Develop technology for genome-wide identification of RNA branch points.
Barak Cohen	Washington University in St. Louis	Functionally characterize regulatory elements using high-throughput assays in cell lines and primary cells.
Peggy Farnham	University of Southern California	Functionally characterize transcription factor hotspots in situ using site-specific nuclease technology.

Raymond Hawkins	University of Washington	Improve the sensitivity of ChIP-seq assays, to increase power to identify functional elements.
Christina Leslie	Memorial Sloan-Kettering Cancer Center	Develop computational predictions of transcription factor binding sites and predict cell-specific gene expression.
Jason Lieb	University of North Carolina, Chapel Hill	Highly parallel functional characterization of enhancers, promoters, insulators, and silencers.
Mats Ljungman	University of Michigan	Develop new assays (BruChase-seq and BrUV-seq) to identify promoters and enhancers, and to measure RNA metabolism.
Tarjei Mikkelsen	Broad Institute of MIT and Harvard	Functionally characterize enhancers, silencers, insulators, splicing regulators, and RNA stability/translation, using high-throughput assays with integrated reporters.
Jay Shendure	University of Washington	Functionally characterize regulatory elements using massively parallel assays in cell lines and mice.
Alexey Wolfson	Advanced RNA Technologies, LLC	Develop improved RNAi method using self-deliverable RNAs.
Guo-Cheng Yuan	Harvard School of Public Health	Develop novel computational methods to characterize chromatin states and predict chromosomal interactions.

Additional ENCODE Participants

Research Group	**Institution**	**Research Goals**
Michael Beer	Johns Hopkins University	Develop sequence-based models to predict regulatory elements and determine their function.
Jennifer Harrow	Wellcome Trust Sanger Institute	GENCODE Project: Annotate gene features using computational methods, manual annotation, and targeted experiments.
David Gilbert	Florida State University	Investigate the relationship of replication timing to other chromatin properties and developmental gene expression patterns.
Anton Valouev	University of Southern California, Keck School of Medicine	Generate and analyze nucleosome-binding and gene regulatory data, and develop novel computational methods for such analyses.

Last Updated: September 17, 2018