

ENCODE Phase 4: Participants and Projects

Grantees	Institution	Title	Grant Number
Mapping Awards			
Bradley Bernstein, Chad Nusbaum	Broad Institute of Harvard and MIT	A Catalog of Cell Types and Genomic Elements in Tissues, Organoids and Disease	UM1 HG009390
Erez Lieberman Aiden	Baylor College of Medicine	Genome-Wide Mapping of Loops Using In Situ Hi-C	UM1 HG009375
Mats Ljungman	University of Michigan	Mapping of Novel Candidate Functional Elements with Bru-Seq Technology	UM1 HG009382
Richard Myers, Eric Mendenhall	HudsonAlpha Institute for Biotechnology; University of Alabama in Huntsville	An ENCODE ChIP-seq pipeline using endogenously tagged human DNA-associated proteins	UM1 HG009411
Yijun Ruan	The Jackson Laboratory	Comprehensive Mapping of Long-Range Chromatin Interactions in Human and Mouse Genomes	UM1 HG009409
Michael Snyder	Stanford University	Production Center for Mapping Regulatory Regions of the Human Genome	UM1 HG009442
John Stamatoyannopoulos	Altius Institute for Biomedical Sciences	ENCODE Mapping Center - A Comprehensive Catalog of Dnase I Hypersensitive Sites	UM1 HG009444
Barbara Wold, Ali Mortazavi	California Institute of Technology; University of California, Irvine	High Precision Human and Mouse Transcriptomes	UM1 HG009443
Functional Characterization Awards			
Nadav Ahituv, Jay Shendure	University of California, San Francisco; University of Washington	Massively parallel reporter assays and genome editing of ENCODE predicted regulatory elements	UM1 HG009408
William Greenleaf, Michael Bassik	Stanford University	High-throughput systematic characterization of regulatory element function	UM1 HG009436
John Lis, Haiyuan Yu	Cornell University	High-throughput functional characterization of human enhancers	UM1 HG009393
Len Pennacchio, Axel Visel	Lawrence Berkeley National Laboratory	In Vivo Characterization of Major ENCODE-Predicted Classes of Noncoding Variants	UM1 HG009421
Tim Reddy, Maria Ciofani, Gregory Crawford, Charles Gersbach	Duke University	Regulatory Mechanisms Of CD4+ T Cell Differentiation	UM1 HG009428
Pardis Sabeti	Broad Institute	Comprehensive Functional Characterisation And Dissection of Noncoding Regulatory Elements And Human Genetic Variation	UM1 HG009435
Yin Shen, Bing Ren	University of California, San Francisco; University of California, San Diego; Ludwig Institute for Cancer Research	High-throughput CRISPR-mediated functional validation of regulatory elements	UM1 HG009402
Kevin White	University of Chicago	Center For Functional Validation and Evaluation Of ENCODE Enhancer Regions	UM1 HG009426
Computational Analysis Awards			
Michael Beer	Johns Hopkins University	Systematic Identification of Core Regulatory Circuitry from ENCODE Data	U01 HG009380
Christina Leslie	Memorial Sloan Kettering Cancer Center	Encoding genomic architecture in the encyclopedia: linking DNA elements, chromatin state, and gene expression in 3D	U01 HG009395
Alkes Price, Soumya Raychaudhuri	Harvard University; Brigham and Women's Hospital	Functionally specialized components of disease heritability in ENCODE data	U01 HG009379
Jonathan Pritchard	Stanford University	Decoding the regulatory architecture of the human genome across	U01 HG009431

		cell types, individuals and disease	
Ting Wang, Barak Cohen, Cedric Feschotte	Washington University; University of Utah	Connecting transposable elements and regulatory innovation using ENCODE data	U01 HG009391
Xinshu Grace Xiao	University of California, Los Angeles	Analysis of functional genetic variants in RNA processing and expression	U01 HG009417
Data Coordination Center			
J. Michael Cherry	Stanford University	A Data Coordinating Center for ENCODE	U24 HG009397
Data Analysis Center			
Zhiping Weng, Mark Gerstein	University of Massachusetts Medical School; Yale University	EDAC: ENCODE Data Analysis Center	U24 HG009446

Affiliate Members

Name	Institution
Brenton Graveley, Gene Yeo	University of Connecticut Health Center
Guo-Cheng Yuan	Dana-Farber Cancer Institute
Alexander Dobin	Cold Spring Harbor Laboratory

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