

SYMPOSIUM

THE ENCODE PROJECT Ten years after the human genome sequence

10

July 20, 2010 · PRBB Auditorium

INVITED SPEAKERS

Ewan BIRNEY, European Bioinformatics Institute
Laura ELNITSKI, National Human Genome Research Institute
Elise FEINGOLD, National Human Genome Research Institute
Morgan GIDDINGS, The University of North Carolina at Chapel Hill
Tom GINGERAS, Cold Spring Harbor Laboratory
Peter GOOD, National Human Genome Research Institute
Ross HARDISSON, Penn State University
Tim HUBBARD, Wellcome Trust Sanger Institute
Jim KENT, University California Santa Cruz
Elliott H. MARGULIES, National Human Genome Research Institute
Richard M. MYERS, Hudson Alpha Institute for Biotechnology
Kate ROSENBLUM, University of California Santa Cruz
Mike SNYDER, Stanford University
John STAMATOYANNOPOULOS, University of Washington
Scott A. TENENBAUM, State University of New York
Zhiping WENG, University of Massachusetts Medical School
Barbara WOLD, California Institute of Technology

SCIENTIFIC COMMITTEE

Roderic GUIGÓ, Centre for Genomic Regulation
Ian DUNHAM, The Wellcome Trust Sanger Institute

www.crg.cat/encode_symposium

Centre for Genomic Regulation (CRG)
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CO-ORGANIZERS



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SUPPORTED BY:

THE ENCODE PROJECT

Ten years after the human genome sequence



08:45 - 09:20 Registration

09:25 - 09:30 Welcome

Session 1

Chair: Luis Serrano, Coordinator of the Systems Biology Programme, CRG

09:30 - 09:50 Ewan Birney, European Bioinformatics Institute
"Heritable chromatin differences in humans"

09:50 - 10:10 Tim Hubbard, The Wellcome Trust Sanger Institute
"Large scale computational motif finding"

10:10 - 10:30 Richard M. Myers, HudsonAlpha Institute for Biotechnology
"Whole genome analysis of transcription factor binding, methylation and transcription"

10:30 - 10:50 Zhiping Weng, University of Massachusetts Medical School
"Identification of transcriptional factor binding sites in the human genome"

10:50 - 11:10 John Stamatoyannopoulos, University of Washington
"Mapping and footprinting the human regulatory genome"

11:10 - 11:30 Laura Elnitski, National Human Genome Research Institute
"Cis-acting transcriptional elements with negative regulatory function"



11:30 - 11:50 COFFEE BREAK

Session 2

Chair: Xavier Estivill, Coordinator of the Genes & Disease Programme, CRG

11:50 - 12:10 Scott A. Tenenbaum, State University of New York
"RIP-Chip: Using RNA-Binding Proteins and microRNA Targeting to Study the Human Regulatory Code"

12:10 - 12:30 Tom Gingeras, Cold Spring Harbor Laboratory
"Eukaryotic Transcriptomes: compartmentalized and elegant"

12:30 - 12:50 Ross Hardisson, Penn State University
"Epigenetic Landscape of Erythroid Gene Regulation"

12:50 - 13:10 Elliott H. Margulies, National Human Genome Research Institute
"Using evolution to characterize non-coding somatic variants in tumor genomes"

13:10 - 13:30 Morgan Giddings, The University of North Carolina at Chapel Hill
"Mining the Genome using the Proteome - from mass spectrometry to informatics"

13:30 - 13:50 Jim Kent, University of California Santa Cruz
"Who's in charge here? Finding and characterizing regulatory regions in the human genome"

14:00 - 15:30 LUNCH

Special Session

Presentation: Montserrat Vendrell, CEO, Biocat

Chair: Roderic Guigó, Coordinator of the Bioinformatics & Genomics Programme, CRG

15:30 - 16:30 Elise Feingold / Peter Good, National Human Genome Research Institute
"The Future of Genomics"