The DNAProteome:
Recent Advances Towards Establishing the Protein-DNA Interaction Space
Herbert Auer – Erich Grotewold

Monday, April 20th 2009

9:00 - 9:15	Welcome remarks

Session I: The *cis*-regulatory element landscape of eukaryote genomes

9:15 – 9:55	**Gary Stromo**, Washington University, St. Louis, USA Prospects for a recognition code for DNA-protein interactions
9:55 - 10:35	**Greg Wray,** Duke University, Durham, USA Changes in transcriptional regulation across the genome during human origins
10:35 – 11:05	Coffee break
11:05 – 11:45	**Roderic Guigo** CRG, Barcelona, Spain The transcriptional complexity of the human genome: insights from next generation technologies
11:45 – 12:25	**Jan Karlseder**, Salk Institute, La Jolla, USA DNA binding proteins and control of telomere length in mammals and *C. elegans*
12:25 – 12:50	**Gerhard Mittler** MPI of Immunobiology, Freiburg, Germany The important contribution of quantitative proteomics for deciphering the gene-regulatory code of mammalian genomes
12:50 - 15:00	Lunch

Session II: Higher order structures in the protein-DNA space

15:00 - 15:40	**Tom Gingeras,** CSHL, Cold Spring Harbor, USA New classes of functional short RNAs and chromosome-wide transcriptional networks
15:40 – 16:20	**Rolf Ohlsson,** Uppsala Universitet, Uppsala, Sweden Novel techniques to analyse DNA and protein interaction in three dimensions
16:20 – 16:50	Coffee break
16:50 – 17:15	**Ola Söderberg,** Uppsala Universitet, Uppsala, Sweden Detection of individual endogenous protein interactions *in situ* using *in situ* PLA
17:15 – 17:55	**Vivian Cheung,** University of Pennsylvania, Philadelphia, USA Genetic mapping reveals regulatory landscape of human gene expression
17:55 – 20:00	Poster session and networking

Tue, April 21st 2009

Session III: Establishing gene regulatory networks

9:00 – 9:40	**Mike Snyder,** Yale University, New Haven, USA Analysis of transcription factor function and regulatory networks in eukaryotes
9:40 - 10:20	**Sarah Bray,** University of Cambridge, Cambridge, UK Decoding the Notch signal

10:20 – 10:45 **Albert Jordan**, CSIC, Barcelona, Spain
Depletion of human histone H1 variants uncovers specific roles in gene expression and cell growth
10:45 – 11:15 Coffee break
11:15 – 11:55 **Erich Grotewold,** Ohio State University, Columbus, USA
Systems approaches to unravel plant regulatory networks
11:55 – 12:35 **Duncan Odom,** Cambridge Research Institute, Cambridge, UK
The global control and evolution of transcription in mammalian tissues
12:35 – 13:00 **Leonid Mirny,** MIT, Cambridge, USA
Fundamentally different strategies of gene regulation revealed by analysis of binding motifs
13:00 - 15:00 Lunch

Session IV: Genome-wide transcription factor location analysis

15:00 - 15:40 **Joe Ecker,** Salk Institute, La Jolla, USA
Sequencing of Genomes, Epigenomes and Interactomes in Arabidopsis
15:40 – 16:20 **Bart Deplancke** EPFL, Lausanne, Switzerland
Novel genomic tools and resources for the systematic study of metazoan gene regulatory networks
16:20 – 16:50 Coffee break
16:50 – 17:30 **Thomas Graf,** CRG, Barcelona, Spain
17:30 – 18:10 **Eileen Furlong,** EMBL, Heidelberg, Germany
Transcription factor binding reveals spatial and temporal aspects of developmental networks
18:10 – 18:50 **Peggy Farnham,** UC Davis, Davis, USA
Genomic profiling reveals two classes of recruitment mechanisms for DNA binding factors
21:30 – open end: Speakers dinner

Wed, April 22nd 2009

Session V: Chromatin structure, histone and DNA modifications

9:00 – 9:40 **Dirk Schuebeler,** Friedrich Miescher Institut, Basel, Switzerland
Epigenetic determinants of genome function: insights from global analysis
9:40 – 10:20 **Robin Allshire,** University of Edinburgh, Edinburgh, UK
Synthetic heterochromatin, CENP-A chromatin and kinetochore assembly
10:20 – 10:45 **Federica Battistini**, University of Sheffield, Sheffield, UK
Sequence selectivity of DNA wrapping in the nucleosome
10:45 – 11:15 Coffee break
11:15 – 11:40 **Andrew Andrews,** Colorado State University, Fort Collins, USA
A coupled equilibrium approach to measuring nucleosome thermodynamics
11:40 – 12:20 **Saadi Khochbin,** Institut Albert Bonniot, Grenoble, France
Molecular basis of post-meiotic male genome reprogramming: essential role for histone hyperacetylation
12:20 – 13:00 **Manel Esteller,** IDIBELL-ICREA, Barcelona, Spain
Epigenomic and proteomic maps in health and disease

13:00 – 13:10 Closing remarks