



“RESOLVING SINGLE CELL HETEROGENEITY

SYSTEMS MICROSCOPY MEETS SINGLE CELL OMICS”

SEPTEMBER 25TH, 2015, AT NOBEL FORUM,
KAROLINSKA INSTITUTET, STOCKHOLM, SWEDEN

09:00-18:00

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Program

Time	Title
	SESSION 1: RESOLVING PHENOTYPIC HETEROGENEITY IN CELL POPULATIONS CHAIR: SABRINA SPENCER
09:00-09:05	Welcome , Staffan Strömblad
09:05-09:35	Chris Bakal , ICR, London, UK “How the behavior of dynamical systems leads to the emergence of phenotypic heterogeneity in cancer”
09:40-09:55	Staffan Strömblad , Karolinska Institutet, Huddinge, Sweden “Heterogeneity in mesenchymal motility reflects adaptive switching between two distinct migration modes”
10:00-10:30	Coffee
10:30-11:00	Daniel Gerlich , IMBA, Vienna, Austria “Cellular phenotype discovery by outlier detection in high-content screening”
11:05-11:20	Yael Korem , Weizmann Institute, Rehovot, Israel “Understanding single-cell gene expression data using Pareto optimality theory”
11:25-13:00	Lunch
	SESSION 2: MOLECULAR HETEROGENEITY OF SINGLE CELLS CHAIR: STEN LINNARSSON
13:00-13:30	Sabrina Spencer , University of Colorado, Boulder, Colorado, USA “Single-cell dynamics of the proliferation-quiescence decision”
13:35-14:05	Savas Tay , ETH Zurich, Switzerland “Microfluidic single cell analysis”
14:10-14:40	Jan Ellenberg , EMBL, Heidelberg, Germany “Systems biology of the human cell using light microscopy”

14:45-15:00	Peter Horvath , Hungarian Academia of Sciences, BRC, Szeged, Hungary "CL2M: Correlative light-light microscopy, a novel tool for single cell isolation"
15:05-15:35	Coffee
	SESSION 3: GENOMIC HETEROGENEITY OF SINGLE CELLS CHAIR: DANIEL GERLICH
15:35-15:50	Ulf Landegren , Uppsala University, Uppsala, Sweden "Analyzing the phenotype of single cells, expressed at the level of transcripts and proteins"
15:55-16:10	Petter Brodin , Science for Life Laboratories, Stockholm, Sweden "The systems biology of a million single cells using Mass cytometry"
16:15-16:45	Sten Linnarsson , Karolinska Institutet, Solna, Sweden "Molecular anatomy of the mouse nervous system by high throughput single-cell RNA-seq"
16:50-17:20	Rickard Sandberg , Karolinska Institutet, Solna, Sweden "Single-cell gene expression analyses reveal principles of allelic transcription in mammalian cells"
17:25-17:40	Mats Nilsson , Stockholm University, Stockholm, Sweden "Resolving mutation and gene expression heterogeneity in tissue sections by in situ sequencing"
17:45-17:50	Round – up Staffan Strömblad

Organizers:

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