



# Single Cell Omics

May 26–30, 2017 | Clarion Hotel Sign | Stockholm | Sweden

## Scientific Organizers:

**Sarah Teichmann**, Wellcome Trust Sanger Institute, UK

**Evan W. Newell**, Singapore Immunology Network, SigN, Singapore

**William J. Greenleaf**, Stanford University, USA

*Single cell omics is a new frontier in biology, where genome-wide data is captured at the resolution of individual cells. Single cell high-throughput technologies are being developed in the areas of imaging, mass spectrometry and DNA- and RNA-sequencing, and combinations thereof. The corresponding software and visualization tools are also a large active field of research. Single cell omics has important implications for all areas of development, differentiation and cellular decision-making, because these can now be studied at unprecedented resolution. Equally, single cell omics methods are shedding new light on immunity and cancer, due to the heterogeneous cell populations involved in both areas of biology. Therefore, these approaches are revolutionizing both basic biology as well as our understanding of disease, and technologies involved in translation to medicine. Since the field is in its infancy, and there are few meetings dedicated to this topic, there is a huge unmet need in the community to congregate and exchange ideas and information about new methods and the biological insights gained. A meeting such as this will be of continuing importance until single cell omics technologies become commonplace and established, and integrated into all areas of biology.*


## Session Topics:

- Single Cell DNA-Sequencing and Cancer
- Workshop 1: Making Sense of Single Cell Data (Visualization, Analysis)
- High-Throughput Imaging for Single Cell Analysis
- Single Cell Epigenomes
- Single Cell Transcriptomes
- Single Cell Nuclear Architecture
- Spatial Omics
- Single Cell Proteomics
- Workshop 2: Technology
- Single Cell Immunology

**Scholarship Application & Discounted Abstract Deadline: January 26, 2017**

**Abstract Deadline: February 28, 2017**

**Discounted Registration Deadline: March 28, 2017**



Note: Scholarships are available for graduate students and postdoctoral fellows and are awarded based on the abstract submitted.

Meeting Hashtag: #KSomics

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on Molecular and Cellular Biology

## Single Cell Omics (E3)

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Organized in collaboration with Knut and Alice Wallenberg Foundation and Science for Life Laboratory. Sponsored by Janssen R&D: Pharmaceutical Companies of Johnson & Johnson, Regeneron Pharmaceuticals, Inc. and Vertex Pharmaceuticals Incorporated.

Abstract & Scholarship Deadline: January 26, 2017 / Abstract Deadline: February 28, 2017 / Discounted Registration Deadline: March 28, 2017

### FRIDAY, MAY 26

#### Arrival and Registration

### SATURDAY, MAY 27

#### Welcome and Keynote Address

- \***Sarah Teichmann**, Wellcome Trust Sanger Institute, UK
- Alexander van Oudenaarden**, Hubrecht Institute, Netherlands  
*Revealing New Cell Types and Interactions Using Single Cell Omics*

#### Single Cell DNA Sequencing and Cancer

- \***Evan W. Newell**, Singapore Immunology Network, SigN, Singapore
- Anna Marciniak-Czochra**, University of Heidelberg, Germany  
*Mathematical Modeling of Heterogeneity, Clonal Selection and Emergence of Resistance in Acute Leukemias*
- Michael Stratton**, Wellcome Trust Sanger Institute, UK  
*Clonal Evolution of Cancers*
- Samuel Aparicio**, University of British Columbia, Canada  
*Clonal Dynamics in Cancer at Single Cell Resolution*
- Massimiliano Pagani**, Fondazione INGM, Italy  
*Short Talk: Single Cell Transcriptome Analysis of Human Tumor-Infiltrating T Regulatory Cells*
- Joanna Hård**, Karolinska Institutet, Sweden  
*Short Talk: Identification of Clonal Somatic Mutations in DNA Sequencing Data from Single Cells*

#### Path to Publication

- \***Barbara Cheifet**, SpringerNature, USA

#### Workshop 1: Making Sense of Single Cell Data (Visualization, Analysis)

- \***Alexander van Oudenaarden**, Hubrecht Institute, Netherlands
- Joshua D. Campbell**, Boston University, USA  
*Don't Fear the Zeros: Identifying Transcriptional States and Cellular Populations in Sparse Single-Cell RNA-Seq Data with Bayesian Hierarchical Modeling*
- Dominic Grün**, Max Planck Institute for Immunobiology and Epigenetics, Germany  
*Single Cell RNA-Seq Reveals Cell Fate Bias of Multipotent Lymphoid Progenitors*
- Sue Hammoud**, University of Michigan, USA  
*Functional Heterogeneity of Spermatogenesis Revealed by >27,000 Single Cells of Mouse Testis*
- Martin Hemberg**, Wellcome Trust Sanger Institute, UK  
*VR Genome Browser - Using Virtual Reality to Visualize Complex Genomic Data*
- Bojan Losic**, Icahn School of Medicine at Sinai, USA  
*Predicting Peanut Allergic Reaction with Integrative Single Cell Models of T Cell Immuno-Synapse*
- Santiago J. Carmona**, University of Lausanne, Switzerland  
*Single-Cell Transcriptomics of Zebrafish Immune Cells Provides Insight into the Evolution of Vertebrate Immune Cell Types*

#### High-Throughput Imaging for Single Cell Analysis

- \***Ana Pombo**, Max-Delbrück-Centrum für Molekulare Medizin, Germany
- Rahul Satija**, New York Genome Center, USA  
*Learning the "Metadata" of a Cell with Single Cell Genomics*
- Long Cai**, California Institute of Technology, USA  
*Single Cell Expression Profiling and Lineage Dynamics by seqFISH and MEMOIR*
- Xiaowei Zhuang**, Harvard University, USA  
*In situ Transcriptome and Genome Imaging in Single Cells*
- Johan Elf**, Uppsala University, Sweden  
*Short Talk: Characterizing a library of cells at single molecule sensitivity*

#### Poster Session 1

### SUNDAY, MAY 28

#### Single Cell Epigenomes

- \***X. Sunney Xie**, Harvard University, USA
- Edith Heard**, Institut Curie, France  
*X Inactivation*
- William J. Greenleaf**, Stanford University, USA  
*Methods for Single Cell Epigenome Analysis*
- Arjun Raj**, University of Pennsylvania, USA  
*Single Cell Gene Expression*
- Oliver Stegle**, European Bioinformatics Institute, UK  
*Methods and Applications for Single Cell Epigenetics*
- Steffen Rulands**, Max Planck Institute for the Physics of Complex Systems, Germany  
*Short Talk: Genome Scale Oscillations of DNA Methylation during Exit from Pluripotency*
- Yasuyuki Ohkawa**, Kyushu University, Japan  
*Short Talk: ChILT - an Immunoprecipitation-Free Epigenome Profiling Technology*

#### Single Cell Transcriptomes

- \***Dana Pe'er**, Memorial Sloan Kettering Cancer Center, USA
- Sarah Teichmann**, Wellcome Trust Sanger Institute, UK  
*Understanding Cellular Heterogeneity*
- Alexandra-Chloé Villani**, Broad Institute of MIT and Harvard, USA  
*Discovery of Human Immune Cell Populations by Single Cell Profiling*
- Rickard Sandberg**, Karolinska Institutet, Sweden  
*Single Cell Gene Expression Analyses with Allelic Resolution*
- Sten Linnarsson**, Karolinska Institutet, Sweden  
*An Atlas of Mouse Brain Cell Types*

#### Poster Session 2

### MONDAY, MAY 29

#### Single Cell Nuclear Architecture

- \***William J. Greenleaf**, Stanford University, USA

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**Ana Pombo**, Max-Delbrück-Centrum für Molekulare Medizin, Germany  
*Genome Architecture Mapping, a New Single Cell Approach to Map Chromatin Contacts*

**X. Sunney Xie**, Harvard University, USA  
*Single Cell Genomics: When Stochasticity Meets Precision*

**Ulrike Litzenburger**, Stanford University, USA  
*Short Talk: Single-Cell Epigenomic Variability Reveals Functional Cancer Heterogeneity*

**Christoph Bock**, Austrian Academy of Sciences, Austria  
*Short Talk: CRISPR Screening with Single Cell Transcriptome Readout Establishes a High-Throughput Method for Dissecting Gene-Regulatory Mechanisms*

**Suman Bose**, Massachusetts Institute of Technology, USA  
*Short Talk: A Microfluidic Platform for High-Throughput Micro-RNA Profiling of Single Cells*

**Anita Göndör**, Karolinska Institute, Sweden  
*Short Talk: Novel Feedback Loops between 3D Genome Organizers and the Circadian Clock Regulate Rhythmic Chromatin Transitions in the Nuclear Architecture*

**Thomas Norman**, University of California, San Francisco, USA  
*Short Talk: Interpreting Genetic Screens using Perturb-seq*

**Jeanette Baran-Gale**, University of Edinburgh, UK  
*Short Talk: The Complexity of Promiscuous Gene Expression in Medullary Thymic Epithelial Cells*

### Spatial Omics

**Mark D. Lynch**, Fluidigm Corporation, USA  
*Single Cell Omics and Functional Analysis*

\***John Marioni**, European Bioinformatics Institute, EMBL-EBI, UK  
*Modeling Cell Fate Decisions during Early Development*

**Je H. Lee**, Cold Spring Harbor Laboratory, USA  
*In situ Sequencing Platforms for Investigating Cellular Variations and Lineage*

**Mats Nilsson**, Science for Life Laboratory, Sweden  
*Short Talk: Spatial Neuron Cell-Type Mapping in Mouse Brain by in situ Sequencing*

### Poster Session 3

#### TUESDAY, MAY 30

##### Single Cell Proteomics

\***Shalin H. Naik**, Walter & Eliza Hall Institute, Australia

**Evan W. Newell**, Singapore Immunology Network, SigN, Singapore  
*High-Dimensional Cellular Immune Profiling in Health and Disease*

**Garry P. Nolan**, Stanford University, USA  
*System-Wide Order, from Disorder, at the Cancer-Immune Interface*

**Dana Pe'er**, Memorial Sloan Kettering Cancer Center, USA  
*Machine Learning for Data Analysis and Visualization*

**J. Christopher Love**, Massachusetts Institute of Technology, USA  
*Integrated Single Cell Analysis for Discovery and Development*

**Bogdan Budnik**, Harvard University, USA  
*Short Talk: Single Cell Proteomics by Mass Spectrometry (SCoPE-MS) New Technique for Quantification of Proteomes of Single Mammalian Cells*

**Emma K. Lundberg**, SciLifeLab Stockholm and School of Biotechnology, KTH, Sweden  
*Short Talk: The Cell Atlas of the Human Protein Atlas*

### Poster Session 4

#### Workshop 2: Technology

\***Emma K. Lundberg**, SciLifeLab Stockholm and School of Biotechnology, KTH, Sweden

**Kylie R. James**, Wellcome Trust Sanger Institute, UK  
*Resolving CD4+ T Helper Fate Bifurcation during Malaria*

**Nemanja Despot Marjanovic**, Massachusetts Institute of Technology, USA

*Longitudinal Profiling of Tumor Evolution in Autochthonous Mouse Models of Kras-Driven Human Lung Adenocarcinoma*

**Wissam H. Hamou**, Icahn School of Medicine at Mount Sinai, USA  
*Flexible Single Cell Isolation Technologies Combined with High-Throughput Targeted Sequencing Enable the Characterization of Intratumor Heterogeneity*

**Linda Kvastad**, Royal Institute of Technology, Sweden  
*In Situ Quality Control Assay Generates a Spatial Heat Map of RNA Integrity with Single Cell Resolution*

**Leeat Keren**, Stanford University, USA  
*Characterization of Tumor Immune Microenvironment in Breast Cancer using Multiplexed Imaging*

**Amina Ann Qutub**, Rice University, USA  
*Communication between Developing Neural Cells*

### Single Cell Immunology

\***Garry P. Nolan**, Stanford University, USA

**Richard Conroy**, NIH Common Fund, USA  
*HuBMap*

**Nir Friedman**, Weizmann Institute of Science, Israel  
*Clonal Expansion under the Microscope: Imaging Collective T Cell Responses with Single Cell Resolution*

**Shalin H. Naik**, Walter & Eliza Hall Institute, Australia  
*Clonal Multi-Omics*

### Meeting Wrap-Up: Outcomes and Future Directions (Organizers)

#### WEDNESDAY, MAY 31

##### Departure