



Translational Systems Immunology

January 28–February 1, 2018 | Cliff Lodge | Snowbird, Utah | USA

Scientific Organizers:

Sally John, Biogen, USA

Soumya Raychaudhuri, Brigham and Women's Hospital, Harvard Medical School, USA

Michael Vincent, Pfizer Inc., USA

Mark M. Davis, Stanford University, USA

Advances in large-scale data acquisition, immune phenotyping and computational biology are transforming immunology research and allowing unprecedented insights into the networks, pathways and systems that influence human health and disease. This conference will cover the exciting technology advances that are enhancing our ability to elucidate human immune function and networks as well as practical applications in drug and biomarker discovery and patient stratification. The meeting begins with a look at progress in human genetics and the use of sequencing to assign functional mutations to rare human immune phenotypes. The impact of common variants on immune function requires larger sample sizes, and speakers will cover how genome-wide high-throughput genomics in combination with detailed phenotyping and physiologically relevant perturbations are providing foundational data sets that allow an unbiased view of immune function in cells and tissues. Also discussed will be emerging computational and analytical methods that enable integration and interpretation of high-content molecular data. The meeting will then move on to look at the application of these technological advances, expanding investigation to study the immune response in tissues and organs to enable a deeper understanding of interaction between immune and non-immune cells and their respective roles in disease states. Critical to clinical progress is the translation of systems immunology research into novel therapies and diagnostic or prognostic tests. Sessions themed around infectious disease and vaccine development advances in immune-oncology and patient stratification in complex disease and treatment response aim to provide depth from foundational science to clinical translation. Finally, a key goal is fostering collaboration across disciplines and the development of novel ideas. The meeting will be relevant for immunologists, computational biologists and clinicians with an interest in molecular characterization of the immune system.

Session Topics:

- Human Phenotypic Validation via Rare Genetic Mutations
- Workshop 1: Friendly Debate
- Genetics and Epigenetics Variation in Human Immune Traits
- Advancing our Understanding of Immune Cell Repertoires
- Integrative Analysis, Dynamic Networks and Systems Immunology
- Systems Immunology at the Tissue Level
- Human Immune Response to Infectious Disease
- Immuno-Oncology from Basic Science to Clinical Practice
- Workshop 2: CyTOF
- Clinical Immunoprofiling and Patient Stratification

Scholarship Application & Discounted Abstract Deadline: October 2, 2017

Abstract Deadline: October 31, 2017

Discounted Registration Deadline: November 30, 2017



Note: Scholarships are available for graduate students and postdoctoral fellows and are awarded based on the abstract submitted. Submitting an abstract is an excellent opportunity to gain exposure for your work. Abstracts submitted by the abstract deadline will also be considered for short talks on the program.

Upper image of group A streptococcus bacteria on human neutrophil courtesy of the National Institute of Allergy and Infectious Diseases, NIH

Meeting Hashtag: #KSsysimm

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KEYSTONE SYMPOSIA

on Molecular and Cellular Biology

Translational Systems Immunology (A9)

January 28-February 1, 2018 • Snowbird Resort • Snowbird, Utah, USA

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Sponsored by AbbVie Inc., Biogen, Bioverativ Therapeutics, Merck & Co., Inc. and Theravance Biopharma

Abstract & Scholarship Deadline: October 2, 2017 / Abstract Deadline: October 31, 2017 / Discounted Registration Deadline: December 1, 2017

SUNDAY, JANUARY 28

Arrival and Registration

MONDAY, JANUARY 29

Welcome and Keynote Address

*Sally John, Biogen, USA

Sarah Teichmann, Wellcome Sanger Institute, UK
Immunogenomics One Cell at a Time

Human Phenotypic Validation via Rare Genetic Mutations

*Sally John, Biogen, USA

Danish Saleheen, University of Pennsylvania, USA
Human Knockout Program

Helen C. Su, NIAID, National Institutes of Health, USA
Elucidating Molecular Mechanisms of a Novel Inherited Immunodeficiency-Immudysregulation Disorder

Hakon Hakonarson, Children's Hospital of Philadelphia, USA
Exome Sequencing to Diagnosis and Treat Pediatric Immune Disease

Cecilia Dominguez Conde, CeMM/LBI-RUD, Austria
Short Talk: Insights into DOCK2 Deficiency through the Analysis of Protein Interactions

Michael P. O'Connell, NIAID, National Institutes of Health, USA
Short Talk: EXTL1- and NDST2-mediated Regulation of Allergic Disease

Workshop 1: Translation from Mice to Man: Friendly Debate

*Michael Vincent, Pfizer Inc., USA

*Mark M. Davis, Stanford University School of Medicine, USA

Jeffrey Barrett, Genomics plc, UK
Using Human Genetics for Target Discovery in Inflammatory Bowel Disease

Richard M. Siegel, NIAMS, National Institutes of Health, USA
A Systems Approach to Defining Contributions of TNF-Family Cytokines to Autoimmune Disease Susceptibility Reveals a Protective Role for TL1A/TNFSF15 in IBD

Adam Laing, King's College London, UK
Immune Parameters Are Constrained within a Multidimensional Shape that Describes Immune Competence

Genetics and Epigenetics Variation in Human Immune Traits

*Sally John, Biogen, USA

Julian C. Knight, University of Oxford, UK
Genetic and Epigenetic Modulators of Monocyte Activation in Health and Disease

Anjana Rao, La Jolla Institute for Allergy and Immunology, USA
Transcriptional and Epigenetic Regulation in Cancer and Cancer Immunotherapy

Nicole Soranzo, Wellcome Trust Sanger Institute, UK
Human Genetic Variation of Hematological Parameters

Dafni Glinos, Wellcome Trust Sanger Institute, UK

Short Talk: Genetic Effects on Transcriptional Variation of Human T Regulatory Cells

Poster Session 1

TUESDAY, JANUARY 30

Advancing our Understanding of Immune Cell Repertoires

*Michael Vincent, Pfizer Inc., USA

Aleksandra Walczak, École Normale Supérieure, France
Diversity of Immune Receptor Repertoires

Mark M. Davis, Stanford University School of Medicine, USA
T-Cell Repertoires and How to Read Them

Harlan Robins, Fred Hutchinson Cancer Research Center, USA
Reading the Cellular Adaptive Immune System to Diagnose Disease

George Georgiou, University of Texas at Austin, USA
The Human Serological and BCR Antibody Repertoires in Cancer, Autoimmunity or following Vaccination

Nathaniel D. Chu, Massachusetts Institute of Technology, USA
Short Talk: Longitudinal Immunosequencing in Healthy Individuals Reveals Persistent T Cell Receptors Rich in Public Receptors

Scott Nicholas Furlan, Seattle Children's Research Institute, USA
Short Talk: Dissecting the Mechanics of T Cell Alloproliferation

Integrative Analysis, Dynamic Networks and Systems Immunology

*Soumya Raychaudhuri, Brigham and Women's Hospital, Harvard Medical School, USA

Kasper Lage, Massachusetts General Hospital, USA
Human Gene and Protein Networks Perturbed by Genetics to Identify Therapeutics

Manolis Kellis, Massachusetts Institute of Technology, Broad Institute, USA
Talk Title to be Announced

Shai S. Shen-Orr, Technion, Israel
Connect the Dots – An Integrative Cell-Centered View of Immunity

Jiyang Yu, St. Jude Children's Research Hospital, USA
Short Talk: NetBID, a Novel Systems Biology Approach, Identifies Hippo Signaling as a "Hidden" Driver Selectively Programming CD8 α + Dendritic Cell Activity

Poster Session 2

WEDNESDAY, JANUARY 31

Systems Immunology at the Tissue Level

*Nicole Soranzo, Wellcome Trust Sanger Institute, UK

Betty Diamond, Feinstein Institute for Medical Research, USA
Deconstructing Lupus Nephritis through a Single Analysis of Immune Cells in the Kidney

Soumya Raychaudhuri, Brigham and Women's Hospital, Harvard Medical School, USA
Single Cell Sequencing in Rheumatoid Synovial Tissue

Carolyn B. Coyne, University of Pittsburgh, USA
Immunology of the Human Placenta

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Elham Azizi, Memorial Sloan Kettering Cancer Center, USA
Computational Approaches to Understanding Cellular Heterogeneity in the Tumor-Immune Microenvironment

Zoltan Maliga, Harvard Medical School, USA
Short Talk: Deep Immunophenotyping of Idiopathic and ICI-Induced Skin Disease with Cyclic Immunofluorescence Microscopy

Michelle Miron, Columbia University, USA
Short Talk: Human Lymph Nodes Maintain Resident Memory T Cells with High Proliferative Capacity and Clonal Diversity

Human Immune Response to Infectious Disease

***Mark M. Davis**, Stanford University School of Medicine, USA

Bali Pulendran, Stanford University School of Medicine, USA
Microbiome and B Cell Responses

Purvesh Khatri, Stanford University, USA
Adventures of a "Data Parasite": Translational Medicine using Heterogeneous Public Data

Máté Manczinger, MTA Szegedi Biológiai Kutatóközpont, Hungary
Short Talk: Pathogen Diversity Drives the Evolution of Promiscuous Peptide Binding of Human MHC-II Alleles

Susanna S. Ng, QIMR Berghofer Medical Research Institute, Australia
Short Talk: Identifying Novel Immune Checkpoint Molecules that can be Targeted to Improve CD4+ T Helper Cell Function during Chronic Infection

Poster Session 3

THURSDAY, FEBRUARY 1

Immuno-Oncology from Basic Science to Clinical Practice

***Kasper Lage**, Massachusetts General Hospital, USA

Shannon J. Turley, Genentech, Inc., USA
Leukocyte Function and Positioning in Diverse Stromal Niches

Alexandra Snyder, Adaptive Biotechnologies, USA
T Cell Receptor Sequencing (TCR) in Immuno-Oncology: Systemic, Intratumoral and Antigen-Specific Immunity

Cassian Yee, University of Texas MD Anderson Cancer Center, USA
Terminators: No Fate but What You Make

Wendy Broom, Genocea Biosciences, USA
Neoantigen Identification using ATLAS Across Multiple Tumor Types Highlights Limitations of Prediction Algorithms

Pauline L. Gonnord, INSERM UMR1043, France
Short Talk: High-Dimensional Immunophenotyping of Chronic Lymphocytic Leukemia (CLL) Patients Reveals Remodeling of the CD8+ T Cell Compartment by Tumor Progression and Predicts Need for Therapy

Daniel Wells, Parker Institute for Cancer Immunotherapy, USA
Short Talk: Genetic Mechanisms of Immune Evasion in Colorectal Cancer

Mazlina Ismail, University College London, UK
Short Talk: Characterising the T Cell Receptor Repertoire of Patients with Non-small-cell Lung Cancer (NSCLC) within the Lung TRACERx Study

Workshop 2: CyTOF Change to Human Immunoprofiling

***Soumya Raychaudhuri**, Brigham and Women's Hospital, Harvard Medical School, USA

Petter Brodin, Karolinska Institutet, Sweden
Convergence of Immune Systems in Diverse Newborn Children during the First Months of Life

Jean-Louis Palgen, CEA, France
Prime and Boost Vaccination Elicit a Distinct Innate Myeloid Cell Immune Response

Luis Miguel Franco, National Institutes of Health, USA
Immune Regulation by Glucocorticoids Can Be Linked to Cell-Lineage-Specific Transcriptional Responses

Oisin Huhn, University of Cambridge, UK
Characterizing the Architecture of the Decidual Natural Killer Cell Niche using Time of Flight Mass Cytometry

Ainhoa Perez-Diez, NIAID, National Institutes of Health, USA
Antibody Profiling Identifies a Strong and Widespread Auto-Immune Response in Idiopathic CD4 Lymphopenic Patients

Arnon Arazi, Broad Institute, USA
Beyond Clustering: Using scRNA-seq Data to Generate Quantitative, Testable Models of Human Disease

Ning Jenny Jiang, University of Texas at Austin, USA
High-Throughput Detection of T Cell Antigen Reactivity at Single T Cell Level using de novo Generated DNA-Linked MHC Tetramers

Clinical Immunoprofiling and Patient Stratification

***David M. Sansom**, University College London Medical School, UK

Holden T. Maecker, Stanford School of Medicine, USA
Comprehensive Immune Profiling and Functional Analysis of Human Aging / Response to Therapy

Sally John, Biogen, USA
A Network Approach to Understanding the Role of the Immune System in Neurodegenerative Disease

Sathya Baarathi Shanthi Ravichandran, Indian Institute of Science, India
Short Talk: Identification of a Robust Blood-Based Biomarker Signature for Chronic Systemic Inflammation through a Meta-Analysis of Disease Networks

Maria Gutierrez-Arcelus, Harvard Medical School, USA
Short Talk: Cis Regulatory Variation Determines Time Dependent Allelic Expression of HLA-DQB1 during T Cell Activation

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

FRIDAY, FEBRUARY 2

Departure