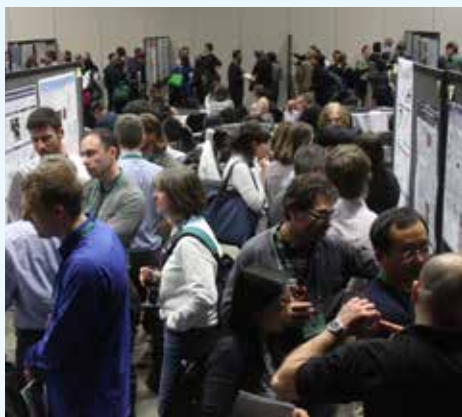




Join Keystone Symposia
for the 2016 conference on:

Systems Immunology: From Molecular Networks to Human Biology

January 10–14, 2016

Big Sky Resort | Big Sky, Montana | USA

Scientific Organizers:

Ronald N. Germain, Aviv Regev, Nir Hacohen and Dana Pe'er

This meeting will place emphasis on understanding how biological function emerges from the interaction of multiple components in networks and pathways, on the construction of quantitative models that permit predictions about systems behavior that can be tested experimentally, and on identification of reliable biomarkers and insight into disease pathogenesis that can be acquired from deep analysis of large-scale, multi-parameter data collection in humans.

Session Topics:

- Immunoreceptor Signaling I: Receptors and Pathways
- Immunoreceptor Signaling II: New Methods for Probing Cell Signaling
- Modeling Signaling Pathways and Transcriptional Networks
- Cellular Communication, Migration and Dynamics I & II
- Systems Analysis of Cancer and Model Organisms
- Human Systems Immunology I: Data Collection Methods and Analytical Technology
- Human Systems Immunology II: Biomarkers, Models and the Microbiome



Submitting an abstract is a great way of participating in the conference through poster presentation and possible selection for a short talk.

Scholarship & Discounted Abstract Deadline: Sep 21, 2015

Abstract Deadline: Oct 20, 2015

Discounted Registration Deadline: Nov 10, 2015

For additional details, visit www.keystonesymposia.org/16A1.

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KEYSTONE SYMPOSIA

on Molecular and Cellular Biology

Systems Immunology: From Molecular Networks to Human Biology (A1)

January 10-14, 2016 • Big Sky Resort • Big Sky, Montana, USA

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Sponsored by Cell Signaling Technology, Inc. and Takeda Pharmaceutical Company Limited

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SUNDAY, JANUARY 10

Arrival and Registration

MONDAY, JANUARY 11

Welcome and Keynote Address

Uri Alon, Weizmann Institute of Science, Israel
Evolutionary Tradeoffs and the Geometry of Biological Shape Space

Immunoreceptor Signaling I: Receptors and Pathways

Nir Hacohen, Massachusetts General Hospital, USA
Network and Pathway Analysis in TLR Activated Dendritic Cells

Facundo D. Batista, Cancer Research UK, London Research Institute, UK
B Cell Signaling

Suzanne Gaudet, Dana-Farber Cancer Institute/Harvard Medical School, USA
NF-kappaB Signaling Dynamics and the Control of Transcription and Cell Fate

Short Talk(s) Chosen from Abstracts

Workshop 1

Short Talks Chosen from Abstracts

Immunoreceptor Signaling II: New Methods for Probing Cell Signaling

Veit Hornung, Ludwig-Maximilians-University Munich, Germany
CRISPR/Cas Approaches to Analysis of Immune Cell Signaling

Bernard Malissen, Centre d'Immunologie de Marseille-Luminy, France
Engineered Systems for Analysis of Signaling Pathways in Primary Lymphocytes Using Quantitative Proteomics

Iain D.C. Fraser, NIAID, National Institutes of Health, USA
Interrogating Immune Signaling Systems with High-Throughput/High Content Screening

Short Talk Chosen from Abstracts

Poster Session 1

TUESDAY, JANUARY 12

Modeling Signaling Pathways and Transcriptional Networks

Alan Aderem, Center for Infectious Disease Research, USA
Dissecting the Innate Immune System Using Tools of Systems Biology

Aviv Regev, Massachusetts Institute of Technology/Broad Institute, USA
Signaling Networks in Th17 CD4 T Cells

Harinder Singh, Cincinnati Children's Hospital Medical Center, USA
Gene Regulatory Networks Orchestrating Cell Fate Dynamics of Activated B Cells

Ellen V. Rothenberg, California Institute of Technology, USA
Transcriptional Networks in Developing Lymphocytes

Short Talk(s) Chosen from Abstracts

Workshop 2

Short Talks Chosen from Abstracts

Single Cell Analysis Modeling I

Ronald N. Germain, NIAID, National Institutes of Health, USA
Imaging Immunity: Creating a Quantitative Spatiotemporal Understanding of Host Defense

Catherine A. Blish, Stanford University School of Medicine, USA
Defining Protective Immunologic Signatures

Michael Meyer-Hermann, Helmholtz Centre for Infection Research, Germany
Germinal Centres in vivo and in silico

Short Talk Chosen from Abstracts

Poster Session 2

WEDNESDAY, JANUARY 13

Single Cell Analysis Modeling II

Dana Pe'er, Columbia University, USA
Modeling Cellular Responses

Sarah Teichmann, EMBL European Bioinformatics Institute, UK
Understanding Cellular Heterogeneity

Grégoire Altan-Bonnet, Memorial Sloan Kettering Cancer Center, USA

Modeling the Spatio-Temporal Heterogeneity of Cell-to-Cell Communications

Martin Meier-Schellersheim, NIAID, National Institutes of Health, USA

Computational Modeling Elucidates how MAPK Crosstalk Regulates Sensitivity of Macrophages Toward TLR4 Stimulation

Short Talk(s) Chosen from Abstracts

Systems Analysis of Cancer and Model Organisms

Andrea Califano, Columbia University, USA
Systematic Elucidation of Druggable Dependencies in Human Malignancies: A New Take on Precision Medicine

Kathryn Miller-Jensen, Yale University, USA
Discovering Macrophage Paracrine Signaling Networks from Single-Cell Data

Catherine A.A. Beauchemin, Ryerson University, Canada
Modelling Viral Infection in Vivo and in Vitro

Short Talk Chosen from Abstracts

Poster Session 3

THURSDAY, JANUARY 14

Human Systems Immunology: Methods

Damien Chaussabel, Sidra Medical and Research Center, Qatar
Bioinformatics Approaches to Understanding Human Immunology

Harlan Robins, Fred Hutchinson Cancer Research Center, USA
Repertoire Analysis

Garry P. Nolan, Stanford University, USA
Mass Spectrometry Methods for Analysis of Cell Phenotype and State

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John Tsang, NIAID, National Institutes of Health, USA

Meta-Analysis of Human Immunity

Short Talk(s) Chosen from Abstracts

Workshop 3

Short Talks Chosen from Abstracts

Human Systems Immunology: Biomedical Applications

Yasmine Belkaid, NIAID, National Institutes of Health, USA

Long-term Consequences of Infection for Tissue Immunity and Metabolism

Anne O'Garra, Francis Crick Institute, UK

Systems Studies of Human Immune Responses to Infection

Arup K. Chakraborty, Massachusetts Institute of Technology, USA

How to Hit HIV Where it Hurts by Integrating Sequencing, Statistical Inference, Mechanistic Models and Human Data

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

FRIDAY, JANUARY 15

Departure