

# Systems Biology of Adaptive Immunity



14–17<sup>th</sup> May 2017

Congressi Stefano Franscini, Monte Verità, Ascona, Switzerland

Main organizer: Sai T. Reddy (ETHZ, CH)  
Co-organizers: Annette Oxenius (ETHZ, CH)  
Fabio Luciani (UNSW, AU)  
Elisabetta Traggiai (Novartis, CH)  
Victor Greiff, Ulrike Menzel, Enkelejda Miho (ETHZ, CH)

## Sunday, May 14<sup>th</sup>

From 16:00	Registration
17:15–18:00	<b>Sai T. Reddy</b> , ETH Zurich, Switzerland Welcome lecture
18:00 – 19:00	<i>Welcome drink</i>
19:00	<i>Dinner</i>

# Monday, May 15<sup>th</sup>

## Session 1                    Adaptive immune repertoires and recognition

Morning session - Chair: Fabio Luciani, Co-Chair: Victor Greiff

9:00–09:15                    FMV/CSF Welcome Address: Lorenzo Sonognini, Chiara Cometta

9:15–10:15                    **Keynote Lecture: Ido Amit**, Weizmann Institute, Israel  
The power of ONE: Immunology in the age of single cell genomics

10:15–10:45                    **Ramit Mehr**, Bar-Ilan University, Israel  
Immune repertoire analysis in health and disease

10:45–11:00                    **Enkelejda Miho**, ETH Zurich, Switzerland  
Large-scale network analysis reveals that antibody repertoires are reproducible, redundant and robust

11:00–11:30                    *Refreshment break*

11:30–12:00                    **Andrew Sewell**, Cardiff University, UK  
Challenging the immunology textbook: A systems view of T-cell immunity

12:00–12:15                    **Nike Kräutler**, ETH Zurich, Switzerland  
Antibody evolution in acute and chronic viral infections

12:15–14.00                    *Lunch*

Afternoon session - Chair: Annette Oxenius, Co-Chair: Enkelejda Miho

- 14:00–14:15 **Samuele Notarbartolo**, Inst. for Research in Biomedicine, CH  
Transcriptional control of immuno-regulatory human TH17
- 14:15–14:30 **David Gfeller**, University of Lausanne, Switzerland  
Deciphering HLA specificities across large HLA peptidomics datasets accurately predicts neo-antigens
- 14:30–14:45 **Martin Corcoran**, Karolinska Institutet, Sweden  
Individualized germline databases produced with IgDiscover demonstrate the extent of allelic variation in human populations
- 14:45–15:00 **Mikhail Shugay**, Institute of Bioorganic Chemistry RAS, Russia  
Decoding the antigen specificity of T-cell receptor repertoires
- 15:00–15:30 *Refreshment Break*
- 15:30–15:45 **Katja Fink**, Singapore Immunology Network, Singapore  
Human anti-viral B cells responses on a single cell level
- 15:45–16:00 **Johannes Trück**, University of Zurich, Switzerland  
B cell receptor repertoire sequencing in patients with primary immunodeficiency
- 16:00–16:15 **Hans-Jörg Warnatz**, MPI for Molecular Genetics, Germany  
Easy and efficient generation of high-affinity monoclonal antibodies using a novel method for paired immunoglobulin chain sequencing from large B cell populations
- 16:15–16:45 **Lélia Delamarre**, Genentech, USA  
**Neoantigens in cancer immunotherapy**
- 16:45–17:00 **Simone Rizzetto**, UNSW, Australia  
Linking phenotype with transcriptomic and clonotype of human B and T cells using VDJPuzzle
- 17:00–19:00 Poster session (with free beers and soft drinks)
- 19:00 *Dinner*

## Tuesday, May 16<sup>th</sup>

### Session 2                    Cellular and molecular dynamics and regulation of the adaptive immune response

Chair: Elisabetta Traggiai, Co-Chair: Ulrike Menzel

- 9:00–10:00                    **Keynote Lecture: Antonio Lanzavecchia, ETH Zurich, CH**  
Dissecting human antibody responses: useful, basic and surprising findings
- 10:00–10:30                    **Philippe Bousso, Institute Pasteur, France**  
Decoding immune responses to cancer or infection using intravital imaging
- 10:30–10:45                    **Victor Greiff, ETH Zurich, Switzerland**  
Quantifying the balance of predetermination and stochasticity in the diversity of immune repertoires
- 10:45–11:15                    *Refreshment Break*
- 11:15–11:30                    **Mario Novkovic, Kantonsspital St. Gallen, Switzerland**  
Topological small-world organization of the fibroblastic reticular cell network determines lymph node functionality
- 11:30–11:45                    **Stefan Ewert, Novartis Pharma AG, Switzerland**  
The good, the bad and the ugly antigen: Deep sequencing analysis of selection outputs is revealing antigen-specific enrichment patterns
- 11:45–12:00                    **Santiago Carmona, University of Lausanne, Switzerland**  
Single-cell transcriptome analysis of fish immune cells provides insight into the evolution of vertebrate immune cell types
- 12:00–12:15                    **Rajagopal Murugan, DKFZ, Germany**  
Clonal evolution of human memory B cell responses
- 12:30–15:00                    *Lunch and free time*
- 15:15                            Excursion to Brissago Island
- 19:00                            Conference Dinner at Brissago Island

## Wednesday, May 17<sup>th</sup>

Session 3                      Recent advances in high-throughput technologies and translational systems medicine

Chair: Sai T. Reddy

8:30–9:30                      **Keynote Lecture: George Georgiou, University of Texas, USA**  
TBA

9:30–9:45                      **Scott Brown**, University of British Columbia, Canada  
Exploring the clinical relevance of the personalized self-immunopeptidome

9:45–10:00                      **Klaus Eyer**, ESPCI, France  
High-throughput single-cell deep phenotyping of immunoglobulin G secreting cells for high-resolution immune monitoring

10:00–10:15                      **Chaim A Schramm**, NIH, USA  
Gene-specific mutability and substitution bias play dominant roles in modulating antibody somatic hypermutation

10:15–10:30                      **Raissa Fonseca**, University of São Paulo, Brazil  
Ontogeny and developmental plasticity of the resident memory CD8+ T cell subset

10:30–11:00                      *Refreshment Break*

11:00–11:30                      **Ziv Shulman**, Weizmann Institute, Israel  
B cell-ICAMs are gatekeepers for GC entry

11:30–11:45                      **John M. Lindner**, Novartis, Switzerland  
High-throughput functional BCR screening: A method and its applications in human health and disease

11:45–12:15                      **Dmitriy Chudakov**, Inst. of Bioorganic Chemistry RAS, Russia  
Extraction and comparative post-analysis of immune repertoires

12:15–12:30                      **Ganesh Phad**, Karolinska Institutet, Sweden  
Production of individualized V gene databases reveals high levels of immunoglobulin genetic diversity

12:30–12:45                      CSF and Systlms Awards

12:45                              *Lunch and departure*