



## Program

### Sunday, May 5<sup>th</sup>

From 15:00	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 6th

### Session 1                      Molecular Engineering in Immunology

Chair: Bruno Correia

- 09:00–09:15                      FMV/CSF Welcome Address
- 9:15–09:50                      **William Schief**, The Scripps Research Institute, USA  
*Germline-targeting vaccine design for HIV*
- 09:50–10:10                      Fabian Sesterhenn, EPFL, CH  
*De novo designed epitope-focused immunogens elicit RSV neutralizing antibodies with finely controlled specificities*
- 10:10–10:30                      Aaron Sato, Twist Bioscience, USA  
*Synthetic DNA Technologies Enable Antibody Discovery and Optimization*
- 10:30–11:00                      *Refreshment break*
- 11:00–11:35                      **Melody Swartz**, The University of Chicago, USA  
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- 11:35–11:55                      Luca Piccoli, Institute for Research in Biomedicine, CH  
*Engineering the elbow: a novel approach to bispecific antibody design inspired by nature*
- 11:55–12:15                      Susan Thomas, Georgia Institute of Technology, USA  
*Overcoming transport barriers in the tumor immune microenvironment to enhance cancer immunotherapy*
- 12:15–12:35                      Daniel Adriano Silva Manzano, University of Washington, USA  
*De novo design of protein therapeutics*
- 12:35–14:00                      *Lunch*

Session 2                      Methods in Systems Immunology

Chair: Elisabetta Traggiai

- 14:00–14:35                      **Ning Jenny Jiang**, University of Texas at Austin, USA  
*Systems immunology enabled immune engineering*
- 14:35–14:55                      Simon Friedensohn, ETH Zurich, CH  
*Convergent selection of antibody specificity sequence patterns is revealed by deep learning*
- 14:55–15:15                      Gunilla Karlsson Hedestam, Karolinska Institute, SWE  
*Structural diversity in the human immunoglobulin heavy chain locus*
- 15:15–15:45                      *Refreshment Break*
- 15:45–16:20                      **Ron Germain**, National Institutes of Health, USA  
*From cell microstates to 3D tissue organization – factors controlling the operation of the immune “System”*
- 16:20–16:40                      Edward W. Green, German Cancer Research Center, GER  
*High-throughput, low-cost cloning of alpha/beta paired TCRs from 10x Genomics libraries into self-replicating, non-integrating S/MAR vectors as the basis for TCR validation and adoptive T cell therapies*
- 16:40–17:00                      Yannik Severin, ETH Zurich, CH  
*Donor identity and state revealed by deep immune phenotyping*
- 17:00–17:20                      David Gfeller, University of Lausanne, CH  
*Deep motif deconvolution across HLA peptidomes for robust epitope predictions*
- 17:20–17:40                      Kathrin Dienst, Bucher Biotec AG, CH  
*High-throughput workflows for isolation of antigen-specific B-cells and validation of drug candidates*
- 17:40-19:30                      **Poster session** (with free beers and soft drinks)
- 19:30                                      *Dinner*

## Tuesday, May 7<sup>th</sup>

### Session 3                      Programming and Reprogramming of Immune Cells

Chair: Sai Reddy

- 9:00–09:35                      **Johanna Olweus**, Oslo University Hospital, NOR  
*Expanding the repertoire of immunotherapy targets*
- 09:35–09:55                      Govinda Sharma, Michael Smith Genome Sciences Centre, CA  
*A novel high-throughput screening approach for the detection of cytotoxic T-cell receptor epitopes*
- 09:55–10:15                      Jurjen Tel, Eindhoven University of Technology, NL  
*Single cell analysis reveals functional heterogeneity within plasmacytoid dendritic cells and identifies environmental cues that drive type I IFN production*
- 10:15–10:45                      *Refreshment break*
- 10:45–11:20                      **Kathrin Schumann**, Technical University of Munich, GER  
*Functional dissection of gene networks that control human regulatory T cell identity*
- 11:20–11:40                      Lukas Jeker, University Hospital Basel, CH  
*Repairing Foxp3 mutations in T cells restores regulatory T cell function*
- 11:40–12:00                      Lena Gamboa, Georgia Institute of Technology & Emory University, USA  
*Heat-triggered CRISPR-dCas9 for the remote control of therapeutic T cells*
- 12:00–13:15                      *Lunch*
- 13:15–13:35                      Greta Giordano-Attianese, University of Lausanne, CH  
*STOP-CAR T Cells for Safety-Enhanced Cancer Immunotherapy*
- 13:35–13:55                      John Miles, James Cook University, AU  
*Using synthetic biology to generate hyper-stable vaccines*
- 13:55–14:15                      Justin Taylor, Fred Hutchinson Cancer Research Center, USA  
*B cells engineered to express pathogen-specific antibodies using CRISPR/Cas9 protect against infection*
- 14:30                                      *Excursion to Brissago Island*
- 19:00                                      *Conference Dinner at Brissago Island*



## Posters list

**Mariia Bilous**, *Department of Oncology, University of Lausanne, Switzerland*

Network approach for visualization and simplification of single-cell RNA sequencing data

**Felix Breden**, *Simon Fraser University, Canada*

iReceptor: a platform for querying and analyzing antibody/b-cell and t-cell receptor repertoire data across federated repositories

**Yiwei Chen**, *Institute for Research in Biomedicine, Switzerland*

The discovery of new insertions in antibodies against malaria

**Lucia Csepregi**, *ETH Zurich, Switzerland*

Uncovering the physiological network of B cell clonal lineages

**Simon Eggenschwiler**, *University of Lausanne, Switzerland*

Pan specific predictor for HLA-I ligands

**Roy E. Ehling**, *ETH Zurich, Switzerland*

Engineering an All-in-One Platform for the development and screening of bispecific antibodies in mammalian cells

**Lena Erlach**, *ETH Zurich, Switzerland*

Machine learning to design antibody variants with improved affinity

**Marianna Florova**, *University of Basel, Switzerland*

Crispr/Cas9-mediated B cell receptor engineering to control persistent viral infection

**Clemens Hermann**, *University of Cape Town, South Africa*

Using systems immunology to find correlates of protection in Tuberculosis in a controlled human lung-challenge model

**Sofya Kasatskaya**, *Skolkovo Institute of Science and Technology, Russia*

TCR repertoires clearly demonstrate thymic selection for human naïve Tregs but do not differentiate between RTE and mature naïve T cells

**Daehong Kim**, *University of Helsinki, Finland*

Proinflammatory cytokines, IL-15 and MCP-1, initiate genomic instability and hypermethylation through the activation of STAT3

**Sanjana Narang**, *Karolinska Institute, Stockholm, Sweden*

Allelic diversity of the human immunoglobulin heavy chain genes

**Daniel Neumeier**, *ETH Zurich, Switzerland*

Antibody discovery and engineering by enhanced CRISPR-Cas9 integration of variable antibody gene libraries

**Alessandro Pedrioli**, *ETH Zurich, Switzerland*

LCMV-specific antibody characterization upon chronic infection

**Duncan Ralph**, *Fred Hutchinson Cancer Research Center, United States*

Identifying high-affinity antibodies using tree shape metrics

**Marthe Solleder**, *University of Lausanne, Switzerland*

Deciphering the landscape of phosphorylated HLA-I ligands

**Nikita Subedi**, *Eindhoven University of Technology, Netherlands*

Decoding the effector function in natural killer cells using droplet based single cell analysis platform

**Tobias Wolf**, *ETH Zurich, Switzerland*

Quantitative analysis of protein synthesis in naïve T cells reveals posttranscriptional mechanisms for rapid activation