

[BC]2 and EMBO Flash Talks

* Flash talks take place in room San Francisco (3rd floor, same as poster exhibition area). Presentations are mixed from abstracts submitted to the [BC]2 and EMBO pillar and are presented in the order mentioned below. Each flash talk takes 2 minutes.

- 1. Lekshmi Dharmarajan** (ETH Zurich, CH): *“A simple and flexible computational framework for inferring sources of heterogeneity from single-cell dynamics”*
- 2. Agathe Morand** (University of Basel, CH): *“Deciphering the role of Nrf2-related glutathione pathways in malignant cancer cells”*
- 3. Jeremie Breda** (University of Basel, CH): *“Realizing Waddington's metaphor: Inferring regulatory landscapes from single-cell gene expression data”*
- 4. Serej Ley** (Swiss Tropical and Public Health Institute, CH): *“MDR to preXDR to XDR tuberculosis: whole genome sequencing reveals several different evolutionary strategies”*
- 5. Nicolas Ochsner** (ETH Zurich & Institute of Molecular Systems Biology, CH): *“Representation learning of disease associated cell subsets from single-cell RNA sequencing data”*
- 6. Talita Diniz Melo Hanchuk** (Unicamp, BR): *“HABP4 is required for colon tumorigenesis in the murine colitis-associated carcinoma model”*
- 7. Sara Fonseca Costa** (University of Lausanne, CH): *“The challenges of annotation and integration of scRNA-Seq into Bgee”*
- 8. Madhwi Ojha** (Banasthali Vidyapith, IN): *“Discovery of potent anthranilic acid derivatives for the treatment of chronic inflammation”*
- 9. Maido Remm** (University of Tartu, EE): *“An alignment-free method for predicting phenotypes of sequenced bacterial isolates”*
- 10. Suleyman Yildirim** (Istanbul Medipol University / International School of Medicine, TR): *“Gut microbiota, neuropsychometric test scores and neuroimaging differentiate cognitive impairment in Parkinson's disease”*
- 11. Ninon Mounier** (University Center for Primary Care and Public Health, CH): *“Leveraging correlated risks to increase power in Genome-Wide Association Studies”*
- 12. Ville Laitinen** (Turku Universit, FI): *“Non-parametric modeling of state shifts in microbial communities”*
- 13. Monica R. Ticlla** (Swiss Tropical and Public Health Institute, CH): *“Insights into lung microbiome dysbiosis in patients with active pulmonary tuberculosis: a nested case-control study”*
- 14. Anneke Brümmer** (University of Lausanne, CH): *“Codon bias in lincRNAs: a mechanism to prevent translation?”*
- 15. Nicholas Noll** (University of Basel Basel, CH): *“Tracking bacterial pathogens in the regime of fast horizontal gene transfer”*
- 16. Julien Racle** (University of Lausanne, CH): *“Deep motif deconvolution of HLA-II peptidomes for robust class II epitope predictions”*
- 17. Van Du T. Tran** (SIB Swiss Institute of Bioinformatics, CH): *“Condition-specific series of metabolic sub-networks and its application for gene set enrichment analysis”*
- 18. Aashil A. Batavia** (University Hospital Zurich, CH): *“Characterisation of wild-type Von Hippel-Lindau ccRCC with the application of both a bottom-up and a top-down multi-omic integrative approach”*
- 19. Qaaifah Gillani** (University of Kashmir, IN): *“PCTAIRE1 kinase overcomes PolST induced mitotic arrest and cell death”*
- 20. Eva Dazert** (Biozentrum / University of Basel, CH): *“Cracking the HCC code - a multi-OMICS study of liver cancer to understand its development and therapy response”*
- 21. Deepak K. Tanwar** (Swiss Institute of Bioinformatics, CH): *“shortRNA: a flexible framework for the analysis of short RNA sequencing data”*
- 22. Shuguang Yuan** (Shenzhen Institutes of Advanced Technology, Chinese Academy of Sciences, CN): *“Explore a new ligand binding site of G protein-coupled receptors”*
- 23. Martin Fox** (SIB Swiss Institute of Bioinformatics, CH): *“A national infrastructure network to enable secure biomedical data processing: the BioMedIT project”*
- 24. Tsering Wüthrich** (University of Bern, CH): *“A bioinformatic workflow to enable species assignment directly from metagenetic sequencing”*
- 25. Antoine Daina** (SIB Swiss Institute of Bioinformatics, CH): *“SwissTargetPrediction: web tool update and large-scale evaluation of protein target prediction for bioactive small molecules”*
- 26. Mathieu Seppey** (University of Geneva, CH): *“LEMMI: a live evaluation of computational methods for metagenome investigation”*
- 27. Athos Fiori** (University of Basel, CH): *“Microbial population in fluctuating environments, how the size influences the strategy”*
- 28. Silvia Angori** (University Hospital Zurich, CH): *“Molecular and functional characterization of papillary renal cell carcinoma”*
- 29. Mahmoud Hallal** (University of Bern, CH): *“Characterization of kinase activities inferred by phosphoproteomics in myeloid cell lines treated with targeting compounds for the identification of driving and bypassing oncogenic signaling pathways”*
- 30. Mitsugu Shimobayashi** (University of Basel, CH): *“Loss of hexokinase 2 causes insulin resistance”*