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”


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”


10. Tanieyman Yildirim (Istanbul Medipol University / International School of Medicine, TR): “Gut microbiota, neurocytometry, amyotrophic lateral sclerosis and Huntington’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. Ahashil 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”


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”


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”