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. 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 University, 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”


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”


26. Silvia Angori (University Hospital Zurich, CH): “Molecular and functional characterization of papillary renal cell carcinoma”

27. 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”