

Abdelaal, Tamim		
Enhancing spatial transcriptomics using scRNA-seq		38
Ágg, Bence		
Searching for cardioprotective microRNA families by bioinformatics analysis of cross-species transcriptomic datasets		39
Alcala, Nicolas		
Exploring spatial and temporal tumor evolution in thoracic cancers using integrative multi-omic analyses		40
Alishayeva, Saudat		
The role of age-associated chromatin changes in Hematopoietic Stem Cells in Acute Myeloid Leukemia		41
Aranciaga, Nicolas		
Multi-omics approach to understanding dairy cow subfertility		42
Behrens, Drew		
Impact of tRNA abundance and codon demand on mRNA translation dynamics		43
Behruznia, Mahboobeh		
Genome wide sequencing analysis of E. coli isolated from septic tank systems in Canberra, Australia		44
Benfatto, Salvatore		
Pan Cancer Inferred Synthetic lethalties (PARIS) to exploit genetic dependencies in cancer cells		45
Berest, Ivan	Presenters: Berest, Ivan; Arnold, Christian	
Quantification of differential transcription factor activity and multiomics-based classification into activators and repressors: diffTF		46
Björklund, Stefan	Presenters: Rentoft, Matilda; Jonsson, Viktor	
Decoding the role of the Arabidopsis Mediator complex in abiotic stress		47

Blätke, Mary-Ann	
Integrated Multi-Omic Analysis Reveals the Post-Transcriptional Component of Tomato Fruit Ripening Regulation	48
Boos, Felix	
In the wrong place at the wrong time - When mitochondrial proteins launch an attack on the cytosol	49
Bouhaddou, Mehdi	
Integrating Multiple Unbiased Proteomics Datasets using Network Propagation to Reveal Mechanisms of Cancer Drug Resistance	50
Brochet, Pauline	
Multi omic analyses to decipher the pathogenic process associated to chagas disease	51
Browne, Christopher	
Incorporating Chemoproteomics into a Broader Multiomics Strategy to Facilitate Drug Discovery	52
Bunina, Daria	
Pathological mutations in LSD1 interfere with ZEB1 transcription factor and alter developmental gene expression	53
Burge, Chris	
Understanding RNA binding protein function through integrative analysis of in vitro and in vivo data	54
Cabbia, Andrea	
Distance metrics for genome-scale metabolic models	55
Cantini, Laura	
Benchmarking of multi-omics joint Dimensionality Reduction approaches for cancer studies	56
Canzler, Sebastian	
Prospects and Challenges of Multi-Omics Data Integration in Toxicology	57

Cao, Wei	
Global analysis of epigenetic heterogeneity identifies divergent drivers of esophageal squamous cell carcinoma	58
Cherkaoui, Sarah	
Characterization of cancer cell lines metabolic heterogeneity	59
Cheyne, Ashleigh	
Applying multi-omics technologies to better understand host-pathogen interactions during Mycobacterium tuberculosis infection	60
Ciuffa, Rodolfo	
Time- and space-resolved absolute composition of the Tumor necrosis Factor receptor signaling complex	61
Coltell, Oscar	
Crosstalk between smoking and the genome in older subjects with metabolic syndrome through genomics, epigenomics and transcriptomics	62
Cominetti, Ornella	
Obesity shows preserved plasma proteome in large independent clinical cohorts	63
Conesa, Ana	
Tools for transforming multiomics data into disease models	64
Cordoba, Javier	
Integrative analysis of transcriptomic and proteomic data of Euglena gracilis in mixotrophic conditions	65
Corella, Dolores	
Genome-wide association analyses of weight loss in a randomized controlled trial of lifestyle intervention, and combined transcriptome-wide associations in a Mediterranean population	66
Crook, Oliver	
Uncertainty Quantification for Dynamic Spatial Proteomics Experiments	67

Daga, Neha	
Understanding genetic and epigenetic T-cell regulatory mechanisms in autoimmune diseases	68
Dasgupta, Abhijit	Presenter: De, Rajat
An in silico model integrating biochemical pathways and metabolomics data	69
Dasgupta, Abhijit	
Uncovering Altered Cell Cycle Dynamics in Human Cancer Cells by Integrating Biochemical Pathways and Genomics Data	70
Diels, Sara	
Targeted multi-omics approach indicates regulatory effect of PON1 on metabolic relevant pathways	71
Dobrinic, Paula	
A time-resolved study of PRC1-mediated gene repression	72
Dugourd, Aurelien	
Linking signalling and metabolomic footprints with causal networks	73
Edgar, Rachel	
Functional Interpretation of Genetic Variants in Inflammatory Bowel Disease	74
Faeth Savitski, Maria	
Multiplexed proteome dynamics profiling reveals impact of NEDD8 inhibition on protein degradation	75
Faqui, Tariq	
Handling Missing Values in Untargeted Metabolomics Data	76
François, Liesbeth	
Insights into biological mechanisms of an in vitro epilepsy model by leveraging gene coexpression modules	77

Gaidar, Daria		
Workflow for TF knockout simulations on transcriptome primed whole genome metabolic model reconstructions for 10 antibiotic resistant E. coli strains		78
Garcia-Albornoz, Manuel		
Integrated OMICs data of the bone marrow microenvironment in homeostasis and human leukaemia		79
Haghverdi, Laleh		
A Soft Alignment of Multiple t-SNEs		80
Hailemariam, Dagnachew		
Comparative multi-omics approach to understand the physiological underpinnings of feed efficiency in dairy cows		81
Harwood, Janet		
Transcriptome-wide association studies (TWAS) in Alzheimer's disease		82
Heyer, Christian		
Cancer subtyping and treatment prediction through longitudinal multi-omics analysis		83
Holinski, Alexandra	Presenters: Holinski, Alexandra; Burke, Melissa	
Multiomics Training at EMBL-EBI		84
Huang, Zhiqin		
Neoantigen prediction for cancer vaccine across entities		85
Huth, Frauke		
The Role of DNA Methylation in Chromatin Structure and Transcription Factor Binding		86
Ibarra, Ignacio		
Mechanistic insights into transcription factor cooperativity and its impact on protein-phenotype interactions		87
Iliou, Aikaterini		
A Metabolome-wide association study for colorectal cancer genetic variants in humans		88

Imrie, Lisa	
A Multi-omics approach to eye tissue biomarker identification in Keratoconus & Fuch's Dystrophy patients	89
Jackson, Heather	
Integrating multiple levels of 'omics datasets to better diagnose febrile children	90
Jeffery, Heather	
Single molecule nanopore sequencing for chromatin accessibility	91
Jyoti, Poonam	
Integrating multiomics approaches to decode the systems features of <i>Ralstonia solanacearum</i>	92
Kalxdorf, Mathias	
Integrated multi-omics analysis of clinical brain tumor samples	93
Kawata, Kentaro	
Development of simultaneous measurement system for transcription and RNA degradation rates using modified nucleic acid	94
Kiniry, Stephen J.	
Trips-Viz: A transcriptome browser for multi-omics data	95
Kokki, Krista	
Transcription factor CWO is putative sugar-responsive regulators of amino acid balance in <i>Drosophila</i>	96
Kokova, Daria	
A metabolic map of opisthorchiasis at the chronic stage of infection	97
Konki, Mikko	
Peripheral blood DNA methylation differences in twin pairs discordant for Alzheimer's disease	98

Kracher, Barbara	
Multiomics analysis of neutrophin signaling activation by a TrkB agonistic antibody	99
Krapp, Anne	
Early nitrate signaling in plants	100
Kraus, Milena	
Unsupervised disease subtype detection on multiple omics and clinical data in the complex disease of aortic stenosis	101
Lai, Mang Ching	
The Accessible Chromatin Landscape of Human Mesenchymal Stromal Cells in Ageing	102
Ledezma-Tejeida, Daniela E.	
Identification of transcription factor signalling molecules by coupling gene expression and metabolomics	103
Leutert, Mario	
Uncovering signaling network dynamics by rapid-robotic-phosphoproteomics (R2-P2)	104
Levin, Michal	
Genome-free proteotranscriptomics: gene annotation and spatial proteomics in non-model organisms	105
Li, Nan	
Landscape of X chromosome inactivation in female human pluripotent stem cells	106
Licholaj, Sabina	
CircularRNA as microRNA trap in pathogenesis of abdominal aortic aneurysm	107
Lin, Yi-Ting	
Targeted Metabolomics to identify potential biomarkers of blood pressure progression	108

Lisitsyna, Anna	Presenters: Forcisi, Sara; Lisitsyna, Anna	
Pattern recognition methods for mass spectrometry based untargeted metabolomics		109
Liu, Po-Yu		
Functional Characteristics of the Flying Squirrel's Cecal Microbiota under a Leaf-Based Diet, Based on Multiple Meta-Omic Profiling		110
Luschnikova, Anna	Presenter: Onyan, Anastasia	
Cationic peptides induce selective tumor cell apoptosis through interaction with nucleolin and nucleophosmin as overexpressed target proteins		111
Madgwick, Matthew		
Identification of prognostic indicators with a machine learning based systems biology approach using gut microbiome data		112
Maehara, Kazumitsu		
Modeling latent flows in single cell data		113
Maji, Pradipta		
Scalable Regularized Canonical Correlation Analysis for Multimodal Omics Data		114
Mantini, Giulia		
Co-expression analysis of proteomics data to reveal biology and prognostic biomarkers in pancreatic ductal adenocarcinoma		115
Mari, Tommaso		
Multi-omics characterization of neuroblastoma cell lines		116
Masood, Fareha		
GenPro: An android application for the analysis of genomic and proteomic data		117
Mastela, Anna		
Combined 'omics and synthetic biology approaches to characterize cellular bottlenecks in the production of 'difficult-to-express' proteins in CHO cells		118

Mathew, Mano Joseph		
Knowledge-based diagnosis and prediction using omics and artificial intelligence		119
Mathioudaki, Anna		
Investigating the interplay between mesenchymal stem cells and leukemic cells in ageing combining single-cell multiomics and imaging		120
Meier, Karin		
Metabolic landscape of the mammalian digestive tract		121
Merilahti, Johannes		
A three-omics approach to identify cleavage-dependent TYRO3, AXL and MER receptor tyrosine kinase signaling pathways in melanoma		122
Michel, Audrey		
Characterizing the nature of ribosomal footprints in the 3' trailers of annotated transcripts		123
Mwai, Kennedy		
protGear: A tool for protein micro-array data pre-processing		124
Nalpas, Nicolas		
Integration of Individualised Proteogenomics Datasets to Analyse Single Amino Acid Variants in Cancer		125
Nicolet, Benoit P.		
Circular RNA in erythropoiesis and megakaryopoiesis are abundant but not efficiently translated		126
Nielsen, Sofie V.		
Structural destabilization and chaperone-assisted proteasomal degradation of MLH1 as a mechanism for Lynch syndrome		127
Nöh, Katharina	Presenters: Nöh, Katharina; Theorell, Axel	
Metabolic Network Inference with Bayesian Model Averaging: Benefits and Challenges		128

Ohkawa, Yasuyuki Chromatin integration labelling Technology for expanding multi-omics	129
Okendo, Javan Integration of clinical, immunological and Omic datasets from Tuberculosis patients to provide new insight into the drivers of TB disease and correlates of protection	130
Oki, Shinya High resolution spatial transcriptomics method by photo-isolation chemistry	131
Ortmayr, Karin Metabolic adaptation to cellular quiescence in cancer cells	132
Otte, Kathrin Evolution of the <i>Drosophila simulans</i> molecular phenotypes in response to adaptation to a novel temperature environment	133
Otto, Georg W Towards a multi-omics approach for identifying biomarkers of anti-drug antibody development in interferon-β treatment	134
Paludo, Gabriela Prado Cestode strobilation: Identification of developmental genes and pathways	135
Parvizi, Poorya Network-based embedding methods for multi-omics data analysis	136
Patel, Mohana Kumara Spatial and temporal distribution of rohitukine and its analogues, an anticancer compounds in <i>Dysoxylum binectariferum</i> (Meliaceae)	137
Peterson, Tim Cell fitness is an omniphenotype	138

Porcelli, Carlotta	
Data analysis and integration of different methods to study the mechanisms and functions of m6A-YTH modules in Arabidopsis thaliana	139
Pstrag, Natalia	
Multi-level approach to deciphering the function and deregulation of TMEM72 and TMEM116 in clear cell renal cell carcinoma	140
Puchala, Weronika	
HaDeX: Analysis of data from hydrogen-deuterium exchange mass spectrometry experiments	141
Quintero, Andres	
Single-cell transcriptome and chromatin accessibility data integration reveals cell specific signatures	142
Rang, Franka	
Mapping histone post-translational modifications in single cells	143
Raposo de Magalhaes, Claudia	
Using an integrated multi-omics approach to validate more robust welfare biomarkers in gilthead seabream	144
Renard, Claire	
Multi-omics determinants of carcinogen-mediated cell transformation following carcinogen exposure	145
Reyes, Jaime	
DNMT3A mediates epigenetic and transcriptional inflammatory-signaling response in hematopoietic stem cells throughout aging	146
Romanov, Natalie	
Disentangling Genetic and Environmental Effects on the Proteotypes of Individuals	147
Ryback, Brendan	
Systematic identification of flux regulation through enzyme phosphorylation	148

Salokas, Kari	
Supplementing proteomics approaches with public transcriptomics data to understand GTF2IRD1-ALK oncofusions	149
Saw, Nay Min Min Thaw	Presenters: Saw, Nay Min Min Thaw; Williams, Rohan
Metabolome-guided multi-omics reveal the metabolic function of member taxa in complex microbial communities	150
Sawikowska, Aneta	
Networks in research on omic changes in barley under drought	151
Schastnaya, Evgeniya	
Phosphoregulation of E. coli central metabolism	152
Schulte-Schrepping, Jonas	
Utilizing single cell -omics of peripheral blood to develop novel biomarkers for patients with inflammatory bowel disease	153
Scott-Boyer, Marie Pier	
A framework to integrate multi-omics longitudinal dataset	154
Seiple, Colin	
Breaking point: Computational interrogation of structural variation in cancer	155
Sigalova, Olga	
Identifying mechanisms regulating gene expression variation during embryonic development	156
Singh, Pranika	
Elucidating risk assessment mechanisms in toxicology through bioinformatics	157
Sussulini, Alessandra	
Multi-omics data integration for IN VITRO studies aiming at the identification of depression and ayahuasca treatment molecular signatures	158

Swirski, Michal		
Combining promoteromics, transcriptomics, translaticomics and molecular phylogenetics to define transcript-level translational landscape		159
Szydlowska, Kinga		
Searching for epileptogenesis/epilepsy biomarkers - circulating microRNA levels changes in the rat model of temporal lobe epilepsy		160
Temba, Godfrey	Presenter: Pecht, Tal	
Multi-omics interrogation of urbanization in a healthy Tanzanian cohort		161
Teppo, Jaakko		
Molecular characterization of the brain peri-infarct region after post-stroke MANF administration		162
Thomas, Cecilia Engel		
Multimomics signatures predictive of early diabetes remission following bariatric surgery: An IMI-DIRECT study		163
Timasheva, Yanina		
Dissecting shared pathophysiological mechanisms of cardiovascular disease and type 2 diabetes		164
Timmermans, Steven		
Multimomics and data integration for studying sepsis		165
Tinti, Michele		
Data analysis of non-model species		166
Tiwari, Vijay		
Local DNA biophysical features encode the regulatory potential of genomic loci		167
Treveil, Agatha		
Studying the role of Bifidobacteria on Paneth cells using multi-omics approaches		168

Ulas, Thomas	
A favorable clinical outcome to influenza infection in neonates is linked to reprogramming of monocytes towards a less inflammatory phenotype with metabolic shift	169
Valgepea, Kaspar	
Unraveling regulatory features in the ancient metabolism of acetogens	170
Vališ, Karel	
Computational technique for prediction of individual transcriptional programs	171
van de Haar, Lieke	
Single-cell RNAseq analysis identifies cellular subset-specific gene expression in the developing mouse habenula	172
Vaparanta, Katri	
A novel algorithm for steady-state signaling cascade inference from multiomics data	173
Vashisht, Shikha	
Integrative multi-omics data analysis approach to identify key gene-regulatory mechanisms responsible for congenital heart disease	174
Verhey, Theodore B.	
Identifying oncogenic co-mutation patterns using networks of expressed clonal mutations	175
Vermeirssen, Vanessa	
Integrating copy number alterations and RNA-seq in regulatory networks of neuroblastoma	176
Vierlinger, Klemens	
Bioinformatic method for the identification of patient-specific antibodies from longitudinal immunomics data and integration with genetic data	177

Walch, Philipp	
Global mapping of host-pathogen interactions in the context of Salmonella infection	178
Wang, Yun-Lin	
Systematic Analysis of the Effect of UTR Variants on RNA Stability	179
Weinberger, Michael	
Heterogeneity in the developing zebrafish epicardium	180
Wörheide, Maria Anna	
A network-based approach for the identification of multi-omics modules associated with complex human diseases	181
Yanovich-Arad, Gali	
Proteogenomics of Glioblastoma Associates Molecular Patterns with Survival	182
Zachariou, Margarita	
Network-based multi-source integration as a backbone for network rewiring	183
Ziebell, Frederik	
Multi-omic data integration methods to align chemical and genetic perturbations in HAP1 cells	184