

$$\sum_n V_n [BID]_n \left( \frac{s_{CB}[p18]_n}{s_{CB}[p18]_n} \right) \left( \frac{s_{F1}[Pr_{ER} F_1]_n}{s_{F1}[Pr_{ER} F_1]_n} \right)$$

# Poster Abstracts

## POSTERSESSION 1 Monday, 19 June, 17:00–19:00

ID 01

Inference of the gut microbiota interaction mechanisms on the mucus composition through mathematical modeling  
**Isaac Elías Vázquez Rivera**

ID 02

Outlier Detection in Steatosis Data using Bayesian Uncertainty Quantification via FAIR Modelling Tools  
**Sebastian Höpfl**

ID 03

Spatio-temporal modeling of immune cell interaction  
**Patrick Brunner**

ID 04

Progression-dependent altered metabolism in osteosarcoma resulting in different nutrient source dependencies  
**Raphaëla Fritsche**

ID 05

A detailed Molecular Network Map and Model of the NLRP3 Inflammasome  
**Marcus Krantz**

ID 06

To be AI, or not to be AI: A checklist to prove a product contains AI  
**Schöttler Jonas**

ID 07

NeDRex – an integrative and interactive network medicine platform for drug repurposing  
**Sepideh Sadegh**

ID 08

Both clinically informed and brain region agnostic approaches identify neuroimaging-derived phenotypes associated with genetically regulated gene expression of late-onset Alzheimer's disease genes  
**Ting-Chen Wang**

ID 09

Deterministic and Stochastic Modelling of Interferon-driven Immune Cell Priming in Viral Infections  
**Rosa Luna Kreider**

ID 10

Liebig's law of the minimum in the TGF- $\beta$  pathway  
**Zhike Zi**

ID 11

Multi-omics analysis of endothelial cells reveals cell type-specific metabolic patterns governing cellular phenotypes  
**Stephan Durot**

ID 12

The CytoScanner platform for model-based optimization of drug concentration trajectories  
**Stefan Kallenberger**

ID 13

Neighbor-based normalization in CITE-seq  
**Javier Marchena Hurtado**

ID 14

Mathematical modelling of the dynamics of renal function and immunosuppression in kidney transplant recipients  
**Nelida Elizabeth López-Palau**

ID 15

Rate of change of insulin resistance in prediabetes and a carrying capacity for beta cell function  
**Aurore Woller**

ID 16

Identification of Alterations in HGF-induced Signal Transduction as a Hallmark of Hepatocyte Dysregulation in Liver Disease  
**Svenja Kemmer**

ID 17

Integrated circulating metabolites and clinical parameters for multi-cancer screening and accurate diagnosis  
**Yan Li**

ID 18

Drugst.One – Closing the gap from protein analysis to disease module identification and drug prioritization on your website  
**Michael Hartung**

$$\sum_n V_n [BID]_n \left( \frac{s_{CR}[p18]_n}{s_{F1}[Pr_{ER}F_1]_n} \right)$$

ID 19

Single-cell transcriptomics deciphers molecular effects of Elexacaftor/Tezacaftor/Ivacaftor in upper airway cells of children with cystic fibrosis

**Jennifer Loske**

ID 20

Cord blood DNA methylation pattern predicts food allergy development later in children`s life

**Laura Matzner**

ID 21

Deficient viral recognition and IFN response may explain the severe disease courses in RSV compared to SARS-CoV-2 infections in young children

**Ismail El-Shimy Hassanin**

ID 22

Unanticipated heterogeneity in poorly differentiated large-cell neuroendocrine neoplasia pinpoints cell type-specific treatment targets

**Olivia Debnath**

ID 23

DNA methylome and scRNA sequencing of nasal cells from COVID-19 patients reveal altered cilia function and chemokine receptor expression

**Marey Messingschlager**

ID 24

Pooled multiomic single-cell CRISPRi screen of schizophrenia risk genes pinpoints disturbed neuronal differentiation as a potential disease mechanism

**Anniqve Claringbould**

ID 25

Single-cell-resolved interspecies comparison identifies a shared inflammatory axis and a dominant neutrophil-endothelial program in severe COVID-19

**Stefan Peidli**

## **POSTERSESSION 2 Tuesday, 20 June, 13:20–15:20**

ID 26

A novel framework for cross-platform DNA methylation-based pan-cancer classification

**Dongsheng Yuan**

ID 27

Multiscale mathematical modelling of JAK/STAT cell signaling pathways for prediction of inflammatory markers in IBD

**Gemma Douilhet**

ID 28

2-D or not 2-D? Ovrl.py as a Quality Control Tool for Spatially Resolved Transcriptomics Analysis

**Sebastian Tiesmeyer**

ID 29

Data-driven construction of tissue-aware gene- to organism-level knowledge graphs

**Khue Nguyen**

ID 30

Inference of Human Genotype-to-Phenotype Relationships via differentiable Transcriptome Imputation

**Leonhard Kohleick**

ID 31

Systematic Analysis of Data Quantity for Deep Learning Models in Survival Analysis using Metabolomic Markers

**Tillmann Rheude**

ID 32

Identifying therapeutic treatment options for muscle invasive bladder cancer

**Alexander Malt**

ID 33

Unlocking performance improvements in machine learning on human genetic data through transfer learning and improved feature selection

**Leonard Eckhoff**

ID 34

Harmonisation of electronic health records across populations cohorts for applications in machine learning and statistical analyses

**Leylanur Bodur**

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ID 35

T1 weighted brain MRI predicts phenome-wide disease onset

**Minh Duc Do**

ID 36

Computational modeling of the Hes1 oscillator for the self-renewal of muscle stem cells

**Zsófia Bujtár**

ID 37

A mathematical model reveals the regulatory logic of interferon- $\beta$  expression

**Allison Schiffman**

ID 38

Computational identification of transcriptional regulators affecting lipid droplet morphology in adipocytes

**Danaí Stella Zareífi**

ID 39

A Concept to visualize genome-scale metabolic Networks of Microbiomes and Multi-Tissue Systems

**Emanuel Lange**

ID 40

Combining mechanistic and inferred network construction approaches to investigate lymphatic endothelial cell behavior in pathological conditions

**Sophie Bekisz**

ID 41

Towards a mechanical model of vascular endothelial cell morphology in the context of the interaction of blood flow and vascular geometry

**David Outland**

ID 42

Evolutionary Dynamics of Oligodendrogliomas

**Sarah Benedetto**

ID 43

From Nephron Physiological Map to Kidney Disease Ontologies: a Systems Biology Approach for in Silico Toxicology

**Alessio Gamba**

ID 44

Cell Decision Making in Lymphoid Organs

**Lisa Li**

ID 45

Oxygen-dependent systematic control of protein-RNA interactions by JMJD6

**Maike Gräff**

ID 46

Dynamics of the circadian clock in triple negative breast cancer

**Carolin Ector**

ID 47

A computational model of the DNA damage-induced IKK/NF- $\kappa$ B pathway reveals a critical dependence on irradiation dose and PARP-1

**Fabian Konrath**

ID 48

Analysis of the robustness of oscillations in a mixed mechanism double phosphorylation system with respect to total kinase concentrations

**Kim-Joao Grasse**

ID 49

Neuroendocrine tumors of the small intestine are not driven by genomic mutations

**Niklas Müller-Böttcher**

ID 50

Genomic Landscape of relapsing Multiple Myeloma

**Shashwat Sahay**