Asmat, Mohd Shamoon
Elucidating the anti-aggregatory potential of anti-tuberculosis drugs D-cycloserine and pyrazinamide against neurodegenerative diseases: A comparative biophysical insight

Beuke, Katharina
Computation of changes in the immune response to infectious diseases during immunosuppressant treatment

Boileau, Etienne
A landscape of RNA splicing and translation in the mammalian heart

Bonafonte Pardàs, Irene
Transcriptomic analysis reveals immunological processes associated with the response to abatacept in rheumatoid arthritis

Chianale, Federica
Precision medicine in practice: Preclinical evaluation of a novel tumor-targeting fluorescent probe for image-guided surgery

Corleone, Giacomo
Understanding genetic and epigenetic hierarchies in cancer for precision medicine

Erdos, Balazs
A computational modelling approach to characterizing postprandial glucose responses in individuals

Fitriani, Annisa
Genome-wide association study (GWAS) of biomarker linking maternal depression and hypertensive disease of pregnancy (HDP)

Garcia, Sara
Predict nephrotoxicity associated with cisplatin-based chemotherapy in testicular cancer patients

Gruber, Andreas
The whole-genome landscape of endometrial cancer
Ho Xuan, Hung
Noncoding RNA-encoded microproteins regulated under metronomic chemotherapy

Jakob, Petra
Loss of N-glycanase 1 alters transcriptional and translational regulation

James, Tojo
Integration of deep multi-omics and digital monitoring in 96 people during a data-driven lifestyle intervention

Kayvanpour, Elham
Precision medicine: Combining myocardial fibrosis burden and genotype to predict outcome in non-ischemic dilated cardiomyopathy (DCM)

Keömley-Horváth, Bence
Protein-wide simulations to drive the design of new therapies from multi-omics data

Kieron, Marcelina
Identification of regulatory non-coding variants associated with early-onset Alzheimer's disease based on targeted sequencing of open chromatin regions

Kriegova, Eva
A risk evaluation tool utilizing the multiple gene polymorphisms for identification of patients with genetic susceptibility to total joint arthroplasty failure

Kudelka, Milos
Patient similarity network (PSN) analysis for identification of risk patient groups: The first step for precision medicine

Kurilov, Roman
Drug response prediction in primary blood tumor cells using models trained on cell line data

Lai, Mang Ching
Multiomic landscape of human bone marrow mesenchymal stromal cells in ageing
Langova, Ralitsa
Analysis of DNA methylation patterns and epigenetic drug response of acute myeloid leukemia

Lee, Seoeun
Genome-wide RNA sequencing analysis reveals CG11671 gene by hyperbaric normoxia treatment which alleviates tauopathy of Drosophila model

Li, Chen
PCprophet: A machine-learning tool for accurately prediction of protein complexes and their functions from proteomic data

Linnemann Nielsen, Rikke
Data integration for prediction of weight loss in clinically controlled dietary trials

Lysenkov, Vladislav
Predicting risk of neuropsychiatric disorders using genotypes and neural networks

Moon, Yesol
Genome-wide RNA sequencing analysis reveals senescence marker protein 30 gene by hyperbaric normoxia treatment which alleviates tauopathy of Drosophila model

Mossotto, Enrico
Sequencing data modelling identifies mutations in monogenic inflammatory bowel disease genes that translate to distinct clinical phenotypes

O'Callaghan, Nathan
Salivary a-amylase copy number is not associated with weight trajectories and glycemic improvements following clinical weight loss: results from a 2-phase dietary intervention study

Okoniewski, Michal
Secure research platforms for biomedical big data analysis and management
Peixoto, Carolina
Sparse models and network-based regularizers for the analysis of RNA-seq data from colorectal cancer

Pobiruchin, Monika  
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Generative modelling: Using real world clinical data for deriving Markov models

Popova, Anna
Enabling precision oncology: Highly miniaturized chip-technology for testing live patient-derived cancer cells with anti-cancer compounds to reveal individual drug sensitivity and resistance

Rams, Mona
Module detection from RNA-seq data via dictionary learning

Richter-Pechanski, Phillip
Deep learning approaches outperform conventional strategies in de-identification of German medical reports

Schraivogel, Daniel
Targeted transcriptome analysis of perturbations enables genome-scale genetic screens in single cells

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Network-based bioinformatics approaches towards precision medicine

Story, Ben
Investigating leukemia using targeted single-cell multi-omics

Ustyantseva, Elizaveta
Development of the stem cell-based platform for studying the neurodegeneration mechanisms using genetically-encoded biosensors

Vus, Kateryna
High-throughput screening of potential inhibitors of amyloid fibril formation
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Blood RNA splicing analysis reveals unprecedented impact of rare genetic diseases variants on splicing

Yaung, Stephanie
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Assessment of a highly-curated somatic oncology mutation database to aid in the interpretation of clinically important variants in NGS results