Full Poster List (Alphabetical

Poster Session 1: Tuesday 9 Sept, 15:15–16:30

Poster Session 2 : Wednesday 10 Sept, 14:45 - 16:00

Last name	Frst name	N°	Poster session	abstract title
Abriata	Luciano Andres	J6	Poster session 2	moleculARweb tools for molecular graphics and modeling in web-based augmented and virtual reality -- as easy as browsing a webpage!
Agbo	Kenneth	V8	Poster session 2	Novel Protocols for Negative Peptide Generation and Feature Selection for Training Robust ML-based Peptide Classifiers
Ait Oumelloul	Mariam	B11	Poster session 1	Integrating genetics and metabolomics: A genome-wide association study of plasma metabolite profiles in people living with HIV
Angelino	Paolo	M5	Poster session 1	Toward Personalized Treatment: A Gene Signature to Predict nCRT Response in Rectal Cancer
Atanda	Halimat	L1	Poster session 1	Associating cancer-specific single nucleotide variants with methylation changes using models based on convolutional neural networks
Azbukina	Nadezhda	B4	Poster session 2	Perturbation screens reveal a spectrum of cell type-specific signal transduction response in human organoids
Babey	Arthur	F5	Poster session 1	HES-XPLAIN - An open platform for accelerating the development of eXplainable AI systems
Babey	Arthur	T10	Poster session 2	MOOSE-FS: Multiple-Objective Optimization for Ensemble Feature Selection
Bastian	Frederic	F2	Poster session 2	Comparative single-cell transcriptomics in dozens of species
Baumbach	Jan	L4	Poster session 2	Fake it till you make it - High-order epistasis detection with quantum computing
Benabbas	Anissa	K2	Poster session 2	Engineering brighter fluorescent proteins with DropSynth and machine learning methods
Bilous	Mariia	E8	Poster session 2	Enhancing Single-Cell Spatial Transcriptomics Analysis: Unraveling Bias, Variability and Correction Strategies Through Large-Scale Evaluation
Blume	Alexander	G1	Poster session 1	Cardiovascular disease biomarkers derived from circulating cell-free DNA methylation
Bojanić	Tamara	P4	Poster session 2	Evolution of the gene regulatory network within closely related bacterial strains
Bontempi	Dennis	F1	Poster session 1	Genetic and Prognostic Insights from Deep Learning Segmentation of Carotid Lumen Diameter
Bors	Sacha	U10	Poster session 2	Interpreting Visual Transformer RETFound in Retinal Phenotyping: Insights from Temporal Angle Predictions
Bosshard	Lars	B8	Poster session 2	Evaluating Network-Based Simulations of Single-Cell RNA-Seq Data for Robust Gene Co-Expression Analysis
Bost	Pierre	A8	Poster session 2	Next generation pipeline for next generation spatial transcriptomic data
Böttger	Leah	F3	Poster session 1	Sex-specific disease associations and genetic architecture of retinal phenotypes
Bouiller	Theophile	F12	Poster session 2	Benchmarking Foundation Models for in-silico Gene Perturbation Using scRNA-seq Data
Boulougouri	Maria	G9	Poster session 1	END-TO-END INTERPRETABLE GRAPH LEARNING FOR PATIENT CLASSIFICATION
Brandulas Camma	Alessandro	Q4	Poster session 2	Robust Data-driven gene expression inference for RNA-seq using intergenic regions as estimation of background noise
Breznikar	Rok	H12	Poster session 2	Accurate Small-Molecule Conformer Prediction and Its Transferability to Protein-Environment Conformations
Bugnon	Marine	G8	Poster session 2	Generating tailored high-quality datasets for evaluating structure-based computational drug design tools
Canal Pujol	Oriol	D3	Poster session 1	Targeted-CNV-Learner: A Machine Learning Framework for CNV Detection in Targeted Sequencing
CAPRON	Coralie	L5	Poster session 1	Integrated Multi-Omics Analysis Unveils a Functional Vulnerability Signature and New Therapeutic Targets to Eradicate Intestinal Cancer Stem Cells
Chammartin	Nylsa	B10	Poster session 2	Development of predictive models assessing the effects of SARS-CoV-2 drugs and their combinations on 3D tissue and mice research models, leveraging single-cell RNA sequencing
Coletti	Silvano	H1	Poster session 1	The Multiscale Phenotypic Interactome: An HPC-Accelerated ST-GNN Approach for Real-Time, Multimodal Health Monitoring
Collesano	Laura	M3	Poster session 1	Predicting the antigenic peptidome
Corà	Davide	N6	Poster session 2	A computational pipeline for the analysis of the role of proteins from unknown species in shotgun metagenomics data: application to the study of gut microbiota in a mouse model of Alzheimer's disease
Costa	Sara	O5	Poster session 1	Tumor mutational signature dynamics at single-cell resolution
Coudert	Elisabeth	T8	Poster session 2	Rhea, a FAIR resource of expert curated biochemical and transport reactions
Cuozzo Vilá	Alessandro	R1	Poster session 1	CytoxPred: efficient prediction of cancer cell lines targeted by cytotoxic small molecules
D'aes	Jolien	M2	Poster session 2	Genome database mining-derived unique genetic fingerprints allow genome-edited rice identification
Das	Asim Bikas	U1	Poster session 1	Artificial intelligence and network medicine-based framework to support subtype-specific precision therapy for gliomas
de Castro	Edouard	U2	Poster session 2	LitSABER: An Integrated System for Literature Curation
de Groot	Daan	B6	Poster session 2	Bonsai: How trees unlock the potential of single-cell omics data
Delgado Nungaray	Javier Alejandro	A7	Poster session 1	In silico analysis of the endogenous CRISPR-Cas system in Pseudomonas aeruginosa PAO1
Dennler	Olivier	I3	Poster session 1	Evaluating Sequence and Structural Similarity Metrics for Predicting Shared Paralog Functions
Dragan	Valeriia	F8	Poster session 2	Harmonizing immune receptor–epitope interactions into an extensible knowledge graph
Durairaj	Janani	H4	Poster session 2	Protein-Ligand Complex Prediction - Are we there yet?
Duvaud	Séverine	S12	Poster session 2	The semantic web community at SIB Swiss Institute of Bioinformatics
El Marrahi	Anissa	O3	Poster session 1	An Integrated Portrait of Prostate Cancer Progression
ElAbd	Hesham	A5	Poster session 1	Decoding immune repertoires by integrating immune sequencing techniques and large-scale functional antibody repertoire profiling methods
Ensmenger	Melissa	C10	Poster session 2	Application and Evaluation of Current Approaches for Spatially Resolved Omics Prediction from Histology Images
Esteban-Medina	Marina	D2	Poster session 2	Predicting cancer drug sensitivity across scales: From cell lines to single-cells with machinel learning and mechanistic models
Fadaei	Shakiba	T6	Poster session 2	Novel universal protein classification method
Feuermann	Marc	M6	Poster session 2	A compendium of human gene functions derived from evolutionary modelling
Follonier	Océane	G12	Poster session 2	From bytes to binders: design, score and optimize
Fournier	Lisa	C2	Poster session 2	Automated identification of molecularly defined breast cancer tumor domains from histopathology
Francisco	Serena	G4	Poster session 2	Structural consequences of a IAHSP-associated R-to-P substitution in an α-helix of Alsin

Gabriel	Aurélie	E6	Poster session 2	Annotating scATAC-Seq data using reliable chromatin accessibility signatures
Galal	Aya	E5	Poster session 1	Machine Learning-Based Identification of a Proteomic Panel for Parkinson's Disease Diagnosis
Galeota	Eugenia	C4	Poster session 2	CIA: A Clustering-Independent Annotation Tool for Accurate and Efficient Cell Type Identification in Single-Cell RNA Sequencing Data
Gandolfi	Giorgia	Q5	Poster session 1	nf-core/tumourevo: A Robust Bioinformatics and Machine Learning Pipeline for Analyzing Tumor Evolution from Whole-Genome Sequencing Data
Gankin	Dennis	G11	Poster session 1	Predicting Genetic Risk with Biologically Interpretable Neural Networks at the Scale of the UK Biobank
Garnica	Josep	E4	Poster session 2	When there is no ground truth: assessing consistency of transcriptomics-based cell type classifications using internal validation metrics
Gerber	Reto	A10	Poster session 2	Enhancing Imaging Mass Cytometry Analysis through Improved Marker Aggregation
Goldbach	Leander	N4	Poster session 2	Alternative RNA hydrogen-bonding schemes and their effect on the evolution of RNA structure.
Graf	Alexandra	U4	Poster session 2	Stratification of Microbiome Metadata Using Machine Learning Techniques
Grob	Linda	D1	Poster session 1	KidsCan_01: In depth tumor profiling for children with high-risk, progressive & relapsed malignancies
Gueguen	Paul	Q1	Poster session 1	Single-cell and Spatial multi-omics identifies distinct central memory phenotypes in CTCL
Guerra	Concetta	C9	Poster session 1	AB-RELIEVE: an AI-designed next-generation antibody therapy resilient to SARS-CoV-2 variants
Guillen Ramirez	Hugo Armando	S4	Poster session 2	Advancing Multilingual Medical Terminology Analysis in Healthcare
Halter	Christian	T1	Poster session 1	Benchmarking tools for population-level exploratory single-cell data analysis
Hanimann	Jacob	S11	Poster session 1	The Spatially Resolved Transcriptional Landscape of Tumor Budding in Colorectal Cancer
Hariri	Ali	I4	Poster session 2	Graph rewiring for long range-aware protein learning
Hatos	András	H8	Poster session 2	OncoBoard: Aiding molecular tumor boards to improve variant interpretation
Haugland	Mathias Ramm	B2	Poster session 2	Learning a transparent representation of genes and their functions in single cells.
Heiniger	Benjamin	A11	Poster session 1	Proteogenomics identifies conserved and lineage-specific novel small proteins in clinical Mycobacterium tuberculosis reference strains
Hernández Velázqu	Rodrigo	O6	Poster session 2	ViromeXplore: integrative workflows for complete and reproducible viral characterization
Hoffmann	Anne	F9	Poster session 1	Exploring Obesity Variability through Machine Learning-Driven Patient Segmentation
Huang	Qingyao	V12	Poster session 2	Fostering Sustainability and Environmental Awareness at Work
Jambor	Helena	E1	Poster session 1	Enhancing Oncology Care with Visual Treatment Timelines
Kahraman	Abdullah	T11	Poster session 1	Heterogeneous and novel transcript expression in single cells of patient-derived ccRCC organoids
Kalhor	Mostafa	J4	Poster session 2	Prosit-XL: Accurate Fragment Intensity Prediction and Enhanced Cross-Linked Peptide Identification for Protein Structural and Interaction Studies
Kamal	Aryan	F6	Poster session 2	Transcriptional regulation of cell fate plasticity in hematopoiesis
Karabayev	Daniyar	R3	Poster session 1	Cell-free DNA methylation profiling for diffuse large B-cell lymphoma subtyping via whole-genome enzymatic methyl sequencing
Karmakar	Aparajita	J5	Poster session 1	Developing an Explainable AI Framework to Predict siRNA Gene Knockdown Efficacy
Kazan	Hilal	G2	Poster session 2	SCITUNA: Single-Cell data integration tool using network alignment
Kel	Alexander	L3	Poster session 1	Druggable master regulators of "orphan" death pathways
Kerschbamer	Emanuela	E12	Poster session 2	Spatial transcriptomics analysis of tuberculosis vaccination route in the mouse lung
Koenig	Natacha	T3	Poster session 1	Multiomics investigation of the action of CDK12/13 inhibitors in prostate cancer.
Kos	Pavel	D8	Poster session 2	Scalable and Reproducible Analysis of H&E-Stained Slides Using Machine Learning
Kraft	Agnieszka	T7	Poster session 1	Resolving malignant cell heterogeneity in tumor bulk RNA-seq data with CDState
Kuipers	Jack	C8	Poster session 2	Single-cell copy number calling and event history reconstruction
Kwee	Ivo	G3	Poster session 1	Combining multi-omics factorization methods for robust biomarker identification
Le Mercier	Philippe	A9	Poster session 1	Extending viral protein annotation with structural modeling: AlphaFold3 sheds light on reoviral capsid structures
Leary	Peter	P3	Poster session 1	MARMOT A Multifaceted R Pipeline for Analysing Spectral Flow Cytometry Data
Leone	Michele	O4	Poster session 2	Machine Learning integration of taxonomic sources to leverage genomic and biodiversity data
Lienhard	Matthias	D11	Poster session 1	Genetic Contributions to Non-Hereditary Acute Aortic Syndrome and Aneurysm: Towards Improved Risk Prediction
Litchfield	Cassandra	E3	Poster session 1	Integrating FFPE derived Whole Genome Sequencing into Routine Molecular Pathology: Validation and Establishment of a Bioinformatics Workflow
Litvinov	Daniil	K4	Poster session 2	Enhancing PPI prediction and interpretability with deep learning
Liu	Yan	I5	Poster session 1	Unraveling the molecular basis of cross-reactivity in TCR epitope recognition
Lu	Jing	F10	Poster session 2	Uncovering Cellular Senescence Through Machine Learning: Overcoming Marker Limitations with Integrated Transcriptomic and Interaction Analysis
Lukačišin	Martin	N3	Poster session 1	Prediction of drug interactions using isogrowth profiling
Luo	Siyuan	E10	Poster session 2	On metrics for subpopulation detection in single-cell and spatial omics data
Lütge	Mechthild	Q3	Poster session 1	Single-Sample Tumor Archetype Assignment for Clinical and Early-Phase Drug Development Applications
Maffei	Theo	S5	Poster session 1	Interpretable Graph Representation Learning on Spatial Omics
Malatesta	Marco	H2	Poster session 2	Integrating complementary functional association signals uncovers a novel partner in Coenzyme Q biosynthesis
Mallona	Izaskun	B12	Poster session 2	Omnibenchmark: well-defined, reproducible, extensible, and continuous benchmarking for computational biology
Marbach	Daniel	T5	Poster session 1	Generalizable AI predicts immunotherapy outcomes across cancers and treatments
Mariella	Elisa	J1	Poster session 1	Targeting oxidative metabolic vulnerabilities in sotorasib-tolerant lung cancer cells
Masson	Patrick	T4	Poster session 2	Modeling Human Functional Networks with Gene Ontology Causal Activity Models (GO-CAMs)
Maus	Irena	H5	Poster session 1	ELEAD: Increasing women's leadership, visibility, and impact in ELIXIR
Meijer	Eline	D9	Poster session 1	Batch effects and data representation in Matrix-Assisted Laser Desorption Ionization–Time of Flight Mass Spectrometry (MALDI-TOF MS) data for machine learning driven identification of microorganisms
Meylan	Marius	V10	Poster session 2	Genes, poop, and plaque and other stories in the Light of Evolution
Mikaeili	Arsham	C6	Poster session 2	Multimodal integration of gene expression and alternative splicing in single-cell and spatial transcriptomics
Minotto	Thomas	H10	Poster session 2	Exploring homology detection via k-means clustering of proteins embedded with a large language model
Mirzaie	Mehdi	K6	Poster session 2	Unrevealing Protein Evolution Through Energy Landscapes: A computational Approach
Mock	Andrea	S1	Poster session 1	Predicting therapy response in breast cancer patients using spatial proteomics of metastatic lymph nodes
Molari	Marco	L2	Poster session 2	Quantifying the Evolutionary Dynamics of Structure and Content in Closely Related E. coli Genomes
Moreno	Dana Lea	P1	Poster session 1	MixTCRclean: a tool to improve TCR data quality by detecting and correcting errors in TCR sequences
Morillo Leonardo	Sarah	D10	Poster session 2	Modeling chromatin accessibility in single cells in terms of tran- scription factor activities
Moustafa	Ahmed	V6	Poster session 2	Comparing CNN and BERT Models for 16S rRNA Taxonomic Classification

Msomi	Nosihle	B1	Poster session 1	Deciphering Seasonal Human Coronaviruses: Linking Viral Evolution, Immune Exposure, and Global Surveillance
Neuner-Jehle	Nadia	L6	Poster session 2	Phylogenetic Analysis of Non-Polio Enteroviruses to Develop a Scalable Nomenclature System
Noé	Falko	G7	Poster session 1	Multiomics Integration for Exercise Personalisation: Insights from the ACTIBATE Trial on Brown Adipose Tissue Activation
Nyamari	Marion	V4	Poster session 2	Comparison of genome alignment and transcriptome mapping for non-model species
Okawa	Marchi	D7	Poster session 1	Identification of genes associated with X chromosome inactivation using tensor decomposition.
Pagani	Lisa	A3	Poster session 1	Cross-scale effect of microbiome dynamics on resistance
Pandey	Aparna	H9	Poster session 1	KeggMapWizard: interactive and versatile biochemical pathway maps
PASCHOAL	ALEXANDRE	U12	Poster session 2	Generative AI improves the mirtrons classification
Pasqualini	Jacopo	P6	Poster session 2	Genome context interpretation of dark protein functions in the human gut microbiome
Peralta Viteri	Christian	K5	Poster session 1	Revisiting the Reverse Paradigm: A Deep Learning Approach for Targeted Cancer Therapy Efficacy Prediction
Perez Gomes	Marta	R5	Poster session 1	TCRpcDist: In Silico Tool for Advancing Cancer Immunotherapies
Pourcel	Lucille	V2	Poster session 2	Enzyme and transporter annotation in UniProtKB using Rhea and ChEBI
Presby	David	R6	Poster session 2	Supporting Shaky Foundations: Manually Derived Image Features Complement Foundation Models for Genetic Associations and Disease Predictions
Prieto	Silvia	R2	Poster session 2	Harnessing ancestral gene order reconstruction to refine gene loss inference in a domesticated crop
Purushothaman	Srinithi	B9	Poster session 1	Screening for rectal colonization with multidrug-resistant pathogens: usage of rapid metagenomic long-read technology
Qoku	Arber	A4	Poster session 2	Prismo: A Unifying Factor Model Framework for Domain-informed Multi-omics Data Integration
Rabuzin	Lovro	D12	Poster session 2	GRASS-MIL: Graph-based Representation and Analysis of Spatial Structures with Multiple Instance Learning
Ramirez Alvarez	Carlos	B5	Poster session 1	Defining an interferon-clock: a precise description of the interferon response kinetic
Ranzani	Valeria	D4	Poster session 2	IRescue: uncertainty-aware quantification of transposable elements expression at single cell level
Rehrauer	Hubert	U8	Poster session 2	GEO Uploader: Simplifying the data deposition in the GEO repository
Reznik	Lidia	H3	Poster session 1	Multimodal generative AI assistant for all cancer modalities
Righetti	Camilla	S8	Poster session 2	Single-Cell RNA and TCR sequencing suggests a key role for tissue-infiltrating EOMES+Tr1-like cells and their circulating precursors in autoimmune diseases
Riina	Jacob	P2	Poster session 2	Lightning-Fast Simulations on Large Fitness Landscapes
Roder	Thomas	C11	Poster session 1	Assembly Curator: rapid and interactive consensus assembly generation for bacterial genomes
Rodrigues de Goes	Fabiana	J3	Poster session 1	From Data to Discovery: Exploring Microprotein for Cancer AI-Driven Analysis
Roehrig	Ute	H6	Poster session 2	Attracting Cavities 2.1: Accelerating High-Confidence Docking with the SwissDock Webserver
Romanovsky	Eva	K1	Poster session 1	CG>TG mutation frequency as negative predictor of homologous recombination deficiency in ovarian and breast cancer
Romashchenko	Nikolai	Q6	Poster session 2	OMAmer 2: Improved protein (sub-)family classification with sequence and structural data
Rooney	Ashley	C5	Poster session 1	Swab comparison for ease-of-use assessment and oral microbiota characterization
Rossier	Victor	S2	Poster session 2	Improving Varroa resistance in Apis mellifera using short- and long-read metagenomics
Roux	Julien	F11	Poster session 1	Rapid and long-lasting remodelling of the blood transcriptome following bariatric surgery
Ruiz Rodríguez	José Luis	C3	Poster session 1	Microbiota and mosquito-borne diseases: A meta-transcriptomics workflow for the taxonomic and functional profiling of these unexpected guests
Runge	Jan-Niklas	E7	Poster session 1	Real-world performance of AI-based tumor cell content quantification
Saadat Varnosfade	Ali	N1	Poster session 1	From Mutation to Degradation: Predicting Nonsense-Mediated Decay with NMDEP
Schieler	Carlotta	S7	Poster session 1	Integrative Multi-Omics Profiling Unveils Enhanced Antibody Responses in Cancer Patients Post-Influenza Vaccination
Sesta	Luca	C1	Poster session 1	Detecting epistasis from SARS-CoV-2 genomic data
Shah	Ekta	E2	Poster session 2	BaM-SVA improves batch correction for better scRNA transcriptomics data integration
Shichkova	Polina	N5	Poster session 1	Identification of predictive and monitoring biomarkers with plasma proteomics in NSCLC patients
Singh	Aakanksha	S9	Poster session 1	Evaluating the impact of experimental factors on deconvolution accuracy in multimodal transcriptional data: A benchmarking study
SMITH	Alex	T12	Poster session 2	Developmentally-corrected Omics Time Course Analysis in C. elegans
Sonder	Emanuel	D6	Poster session 2	A platform for obtaining cell type-specific TF binding predictions
Stambolliu	Alen	S3	Poster session 1	Deciphering Retrotransposable Elements dynamics in tumor-infiltrating lymphocytes through combination of short- and long-read single-cell RNA sequencing
Stefaniak	Filip	H7	Poster session 1	Machine Learning and Explainable Artificial Intelligence for prediction and understanding of RNA-small molecule interactions.
Steuer	Jakob	I6	Poster session 2	Understanding Molecular Switches in Bacterial Gene Regulation
Stickley	Luca	G5	Poster session 1	Microbiome as a predictor of long-term pulmonary outcomes in severe SARS-CoV-2 survivors
Sturm	Gregor	D5	Poster session 1	Data Science Operations (DSO) - A command line helper bringing DevOps principles to data analysis projects
Sundar	Sneha	Q2	Poster session 2	Diversity of F-like plasmid transfer genes in livestock-associated E.coli
Sur	Saubashya	G6	Poster session 2	ADMET profiling, molecular docking, and simulation analysis help identify appropriate natural products as inhibitors of isocitrate lyase in Mycobacterium abscessus
Taguchi	Y-h.	E9	Poster session 1	Tensor Decomposition based unsupervised feature extraction applied to Bioinformatics
Tang	Simon	A1	Poster session 1	Bulk and single-cell transcriptomic insights into treatment-induced changes in tuberculosis patients from Tanzania
Tauriello	Gerardo	G10	Poster session 2	Working with Computational Models in the AlphaFold Era using SWISS-MODEL and ModelArchive
Teleman	Matei	A2	Poster session 2	SuperSpot: coarse graining spatial transcriptomics data into metaspots
Timonen	Veera	A12	Poster session 2	Blood Cell Painting enables large-scale genotype-phenotype discovery in immune cells
Timonina	Valeriia	B3	Poster session 1	Clonal Hematopoiesis in People Living With HIV: Association With Aging and Inflammation
Tostes	Katiane	M1	Poster session 1	Metabolic Gene Signatures as Predictive Biomarkers of Response to Immune Checkpoint Inhibitors in NSCLC
Trickovic	Matija	C7	Poster session 1	Human gut microbiota subspecies carry implicit information for in-depth microbiome research
Trofimova	Olga	E11	Poster session 1	Deep learning aging marker from retinal images unveils sex-specific genetic and clinical signatures
Trottet	Cécile	F7	Poster session 1	Deep Hierarchical Subtyping of Multi-Organ Systemic Sclerosis Trajectories
van Geest	Geert	U6	Poster session 2	SIB promotes open and FAIR educational materials in bioinformatics
van Gerwen	Julian	S6	Poster session 2	Predicting cellular functions of human phosphosites
van Rijen	Paul	S10	Poster session 2	Cell-Triage: Using Domain-Specific Language Models for Full-Text Triage in Cell Line Biocuration

Vazquez Mendoza	Luis Heriberto	K3	Poster session 1	Multicomplex-based Pharmacophore Modeling Targeting the Estrogen Receptor β. Towards the search for breast cancer drugs
Vazquez Montes de	Sergio	I1	Poster session 1	Predicting Immunotherapy Response in Advanced Bladder Cancer: A Meta-Analysis of Six Independent Poster √
Vlachou	Evi	T9	Poster session 1	Human Bone Marrow Niche Remodelling After Allogeneic Hematopoietic Cell Transplantation
Voitl	Laura	N2	Poster session 2	Identifying Genetic Variants for a Mendelian Trait using Long Read Sequencing in Three Domestic Animal Species
Wandinger	Caroline Sophie	P5	Poster session 1	Sparse Canonical Correlation Analysis as an Unbiased Approach to Explore Gene Expression Co-Regulation Across Cell Types
Wang	Jiayi	A6	Poster session 2	Expression biomarkers for aldosterone-producing adenomas: genotyping individual cells using long-read single-cell transcriptomic data
Waterhouse	Robert	R4	Poster session 2	From literature to biodiversity data: mining arthropod organismal and ecological traits with machine learning
Wei	Wei	J2	Poster session 2	Astromime: Graph-Based Learning for the Detection of Protein Local Surface Mimicry
Yadav	Deepak	I2	Poster session 2	Training graph neural network to classify SNARE proteins structures
Yepes García	Jeferyd	O2	Poster session 2	Fine-tuning Large Language Models for lignocellulose-related sequence annotation in a metagenomics context and comparison against specialized classical tools
Zahn	Monique	T2	Poster session 2	How does SIB support open software and databases?
Zielinska	Karolina	C12	Poster session 2	Single-cell transcriptomic analysis of the bone marrow stromal networks during chemotherapy
Zielinska	Karolina	O1	Poster session 1	Genomic and Transcriptomic Insights into the Pathogenesis of Therapy-related Acute Myeloid Leukemia from TP53-mutant Clonal Hematopoiesis
Zurich	ETH	M4	Poster session 2	A Multi-Omics Framework for Decoding Disease Mechanisms: Insights from Methylmalonic Aciduria
Zwaans	Antoine	F4	Poster session 2	Modelling incomplete sequencing of lineage tracing barcodes for robust single-cell phylogenetic inference
		B7	Poster session 1	