

# POSTERS' LIST

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# Evolution & phylogeny

Poster session 1: Tuesday 25 June, 15:00 – 16:15

N°	Poster Title	Presenter's first name	Presenter's last name
A1	A comprehensive and accurate representation of human gene functions from large-scale evolutionary modeling and experimental Gene Ontology annotations	Marc	Feuermann
A3	Evolution of genome content and structure in bacteria: insights from E.coli ST131	Marco	Molari
A5	OMA	Adrian	Altenhoff
A7	Annotation matters: the effect of structural gene annotation on orthology	Silvia	Prieto
A9	The Least Diverged Orthologue Conjecture	Alex	Warwick Vesztry
A11	Orthology inference at scale with FastOMA	Stefano	Pascarelli
A13	Patchwork: Alignment-Based Retrieval and Concatenation of Phylogenetic Markers from Genomic Data	Felix	Thalen
A15	Exploring Indel Patterns in the HIV-1 Genome - A Comparative Analysis of Alignment and Ancestral Sequence Reconstruction Methods	Clara	Ighault
A17	Mutual Information-based feature selection of k-mers for phylogenetic placement	Nikolai	Romashchenko

# Genes and Genomes

Poster session 1: Tuesday 25 June, 15:00 – 16:15

N°	Poster Title	Presenter's first name	Presenter's last name
B1*	Variant effect predictors: a systematic review and practical guide	Cristian	Riccio
B3	Analysis of differential genomic interactions between experimental conditions in capture Hi-C data: Sharing data between neighbouring restriction fragments	Marco	Geigges
B5	Quality assessment of gene repertoire annotations with OMArk	Yannis	Nevers
B7	Comparative analysis of computational pipelines reveals robustness challenges in mouse prefrontal cortex single-nuclei data for autism spectrum disorder research	Peter	Degen
B9	Proteogenomics reveals new small proteins in Mycobacterium tuberculosis clinical reference strains	Benjamin	Heiniger
B11*	Scoary2: rapid association of phenotypic multi-omics data with microbial pan-genomes	Thomas	Roder
B13	Distinct 3' UTR Shortening Patterns associated with BRAF Inhibitor Resistance Types in Melanoma	Lisa	Fournier
B15	Subcellular compartmentalization of mRNA and their potential regulatory role during human motor neuron development	Zhi Ming	Xu
B17	Regulation of sperm mRNAs and long non-coding RNAs	Keigo	Shibata
B19	Copy number variation heterogeneity reveals biological inconsistency in hierarchical cancer classifications	Ziying	Yang
B21*	A Python Library for Enhancing Pathway Visualization in Genomics, Biochemistry, and Molecular Biology	Aparna	Pandey
B23	pgxRpi: Bridging Beacon v2 and R for Enhanced Genomics Data Discovery and Analysis	Hangjia	Zhao
B25	Quantitative genetics in the wild, the accuracy of low-coverage sequencing in a wild population	Alexandros	Topaloudis
B27	T2T haplotig phased genome assembly of the Argan tree ( <i>Argania spinosa</i> )	Laurent	Falquet
B29	Immunotherapy response biomarkers in colorectal cancer	Olesia	Kondrateva
B31	On the identification of differentially-active transcription factors from ATAC-seq data	Emanuel	Sonder

\*interactive screen

# Structural biology

Poster session 1: Tuesday 25 June, 15:00 – 16:15

N°	Poster Title	Presenter's first name	Presenter's last name
C1	TCRfp: a new fingerprint-based approach for TCR repertoire analysis	Francesca	Mayol Rullan
C3	Protein-Ligand Complex Prediction - Are we there yet?	Janani	Durairaj
C5	Open research data best practices for computational macromolecular models in ModelArchive	Gerardo	Tauriello
C7	The SWISS-MODEL server in the AlphaFold era	Gabriel	Studer
C9	Integration of DEER measurements allows structural modeling of the active Bax dimer	Anton	Hanke
C11	Improving affinity by capturing water	Roman	Aschwanden
C13	SwissDock 2024: major enhancements for small-molecule docking with Attracting Cavities and AutoDock Vina	Marine	Bugnon
C15	Computational antigen-targeted antiviral design	Océane	Follonier
C17*	SwissDrugDesign	Antoine	Daina

*\*interactive screen*

## Others

Poster session 1: Tuesday 25 June, 15:00 – 16:15

N°	Poster Title	Presenter's first name	Presenter's last name
D1	Using e-learning to complement synchronous bioinformatics training courses	Monique	Zahn
D3	SIB Software Stack: a collaborative effort between HPC centers in Switzerland to build and deploy a standardized software stack	Robin	Engler
D5	Exploring the Complex Etiology of Atopic Dermatitis Among African Children Through Systems Biology	Damir	Zhakparov

# Single cell

Poster session 1: Tuesday 25 June, 15:00 – 16:15

N°	Poster Title	Presenter's first name	Presenter's last name
E1	scFAIR: Enabling FAIR access to single-cell RNA-Seq data for reproducible analyses	Frederic	Bastian
E3	Coarse Graining Spatial Transcriptomics Data into Metaspots	Matei	Teleman
E5	Systematic capture of human receptor - ligand interactions as Gene Ontology Causal Activity Models	Patrick	Masson
E7	HiTME facilitates exploratory single-cell data analysis at the sample level, enabling unsupervised patient stratification	Christian	Halter
E9	Comparison of coronavirus infection in human and camelid primary airway epithelial cells with single-cell resolution	Vera	Flück
E11	Modeling chromatin accessibility in single cells in terms of transcription factor activities	Sarah	Morillo Leandro
E13	Characterizing the Tpex Phenotype in Tumor-Infiltrating Lymphocytes	Paul	Gueguen
E15	Evaluation of the single-cell transcriptome representations generated by short and long reads: A comparative assessment of the MAS-ISO-seq Approach	Hubert	Rehrauer
E17	Dissecting the impact of transcription factor dose on cell reprogramming heterogeneity using scTF-seq	Wangjie	Liu
E19	Multi-sample non-negative spatial factorization for spatial transcriptomics data	Yi	Wang
E21	Harmonizing cell type classification in the tumor microenvironment	Josep	Garnica Caparrós
E23*	Bonsai captures and visualizes the structure in single-cell transcriptomics	Daan	de Groot

\*interactive screen

## Medicine & Health

Poster session 2: Wednesday 26 June, 14:15 - 15:30

N°	Poster Title	Presenter's first name	Presenter's last name
A2	Linking genomic and genetic data to proteins in UniProtKB	Maria Livia	Famiglietti
A4	Leonhard Med - ETH's secure Trusted Research Environment for Personalized Health Research	Anna	Wiegand
A6	Enabling Secure Biomedical Research: The sciCORE+ Platform	Thierry	Sengstag
A8	BioMedIT: Switzerland's secure infrastructure for analysing biomedical data	Shubham	Kapoor
A10	MULTI-OMICS MODELS REVEAL CANDIDATE COMMON EFFECTORS OF NASH AND FIBROSIS IN MINIPIGS AND HUMANS	Josefina	Lascano Maillard
A12	dsMO: enabling non-disclosive federated multi-omics analysis on virtual cohorts	Thuong Van Du	Tran
A14	Interactive process mining of cancer treatment sequences with melanoma real-world data	Michel	Cuendet
A16	Characterisation of ultra-conserved "kill switch" exons in diffuse large B-cell lymphoma	Luciano	Cascione
A18	CytoxPred: efficient prediction of cancer cell lines targeted by cytotoxic small molecules	Alessandro	Cuozzo
A20	Unveiling Novel Adipose Populations Linked to Metabolic Health in Obesity	Adhideb	Ghosh

# New methods in Bioinformatics

Poster session 2: Wednesday 26 June, 14:15 - 15:30

N°	Poster Title	Presenter's first name	Presenter's last name
B2	Advancing FAIR meta-analyses of nucleotide sequence data with q2-fondue	Anja	Adamov
B4	BlgMAG: Board InteGrating Metagenome-Assembled Genomes quality metrics	Laurent	Falquet
B6	Predicting MHC-I ligands across alleles and species: How far can we go?	Daniel	Tadros
B8	Characterizing noncanonical binding modes of HLA molecules	Yan	Liu
B10	Towards Reproducible Biomedical Data Analysis: Balancing Standardization and Customization	Anne	Bertolini
B12*	CHIST-ERA Triple: improving data interoperability and federation across RDF knowledge graphs and Solid Pods	Ana-Claudia	Sima
B14	EnzChemRED, a rich enzyme reaction dataset for fine-tuning and benchmarking large language models to assist curation of the enzyme literature.	Elisabeth	Coudert
B16	Comprehensive analysis of the genetic variation in the LPA gene from short-read sequencing	Raphael	Betschart
B18	ISMARA: completely automated inference of gene regulatory networks from high-throughput data.	Mikhail	Pachkov
B20	Pseudotime estimation with deep learning for flow cytometry	Margarita	Liarou
B22*	Unlocking the potential of PMC supplementary data	Julien	Gobeill
B24	draugr: smart demultiplexing of short-read NGS data	Falko	Noé
B26	Bayesian Statistical Approach to Determine Immune Cell Responses from Gene Expression Data in the Tumor Microenvironment	Lukas Jonathan	Häuser
B28	CIAlign: A highly customisable command line tool to clean, interpret and visualise multiple sequence alignments	Charlotte	Tumescheit
B30	The impact of PCR duplication on bulk RNA-seq data generated using NovaSeq 6000, NovaSeq X, AVITI and G4 sequencers	Hubert	Rehrauer



B32	The ELIXIR Cloud - Federated and secure analysis of genome-scale data	Alexander	Kanitz
B34	Exploring the footprints of T-cell receptor generation rules in single-cell TCR repertoire data	Dana	Moreno
B36	Coding a pipeline to extract cryptic pockets from all structures in Protein Data Bank	Pedro	Febrer Martinez
B38	BiotXplorer: navigating biotic interaction the literature	Emilie	Pasche
B40	Synthetic gene circuit design: exploiting cell-to-cell variability	Baptiste	Turpin
B42	PocketNet: Ligand-guided Pocket Prediction for Blind Docking and Target Identification	Matthew	Masters
B44	The LEM Framework for Continuous Benchmarking in Bioinformatics: Use Cases in Taxonomic Profiling and BUSCO	Mosé	Manni
B46	Enhancing Ligand-Based Virtual Screening with 3D Shape Similarity via a Distance-Aware Transformer Model	Manuel	Sellner
B48	Antigen specificity of human regulatory CD4+ T cells revealed by integrating bulk TCR sequencing and single-cell analysis	Alessio	Murgia

*\*interactive screen*

# Ecology

Poster session 2: Wednesday 26 June, 14:15 - 15:30

N°	Poster Title	Presenter's first name	Presenter's last name
C2	The Microbe Atlas database: Global trends and insights into Earth's Microbial Ecosystems	Janko	Tackmann
C4	Towards Comparative QTLomics	Irene Consuelo	Julca Chavez

# Proteins and proteomes

Poster session 2: Wednesday 26 June, 14:15 - 15:30

N°	Poster Title	Presenter's first name	Presenter's last name
D2*	Recon4IMD: Leveraging UniProt, Rhea, and SwissLipids to develop improved human metabolic models for inherited metabolic diseases	Anastasia	Sveshnikova
D4	Network-Oriented multi-Omics Data Analysis and Integration (NOODAI)	Tiberiu	Totu
D6	Rhea, a FAIR resource of expert curated biochemical and transport reactions	Parit	Bansal
D8	Annotation of transport reactions in UniProtKB using Rhea and ChEBI	Lucille	Pourcel
D10	CHIST-ERA TRIPLE: VOID and what it enables	Jerven Tjalling	Bolleman
D12	Enhancing Mass Spectrometry Imaging Accuracy via Spatially Informed Mass Recalibration	Leonardo	Schwarz
D14	Glycosaminoglycan-binding profiles as potential probes for the virulence of human pathogens	Frédérique	Lisacek
D16	UniLectin: the second pillar of Glyco@Expasy	Boris	Schnider
D18	High-Throughput Proteomics in Lymphoma for Mechanistic Insights and Clinical Applications	Lopamudra	Chatterjee
D20	Advancing Precision Dermatology: Tape Strip Proteomics	Philipp	Gessner
D22	A novel framework for deep glycoproteome characterisation with data-independent acquisition (DIA) mass spectrometry (MS)	Xindong	Sun
D24	Challenging the current view on protein prenylation in T helper cells using experimental data and information on protein 3D structures	Jana	Koch
D26*	A workflow to analyze and integrate a phospho-enriched dataset and the respective total proteome dataset using prophosqua	Jonas	Grossmann
D28	ViralZone enzymes: improved overview of the viral reaction landscape	Philippe	Le Mercier
D30	A map of predicted mechanistic impacts of human protein missense variants	Jürgen	Jänes

\*interactive screen

## Remarkable outputs

Poster session 2: Wednesday 26 June, 14:15 - 15:30

N°	Poster Title	Presenter's first name	Presenter's last name
E2	The Protein Universe Atlas - a guide into the unknowns of natural protein space	Janani	Durairaj
E4	Glittr.org encourages re-use and co-development of FAIR training materials	Geert	van Geest
F6	Attracting Cavities 2.0: Precise Docking of Noncovalent and Covalent Small Molecules	Ute	Roehrig