## Bioinformatics Day February 20, 2024: Participant Poster Presenters

|                       | February 20, 2024 9:30-17:00 Small Letter Hill of the Blumedical Center (BMC).  |
|-----------------------|---|
| Egert, Luisa          | All roads lead to astrocyte identity  |
| Ehm Tamara            | . Decoding the COVID-19 Molecular Mosaic: Integrated Analysis of Protein Expression Dynamics and Histone Post-Translational Modifications in Circulating Immune Cells   |
| Fallon, Conrad        | . The quantitative effect of transcription factor binding site affinity and sequence on enhancer activity.  Wencke Walter w. Maria Solovey was Dex Gabriele Lubatti sawa Markus Schmidt was Schmidt was Tobias Straub was Anna Danese was Wasim |
| Gill, Jaskaran Singh  | . Applications of Deep Learning in Population history inference   |
| Janßen, Philipp       | . Gene expression evolution in early primate development  |
| Kliesmete Zane        | . Regulatory and coding sequences of TRNP1 co-evolve with brain size and cortical folding in mammals  |
| Kowalewski, Rafal     | . Pinpointing positions of single proteins in cells   |
| Latzko, Lisa          | . Evaluating Whole Genome Sequencing as Comprehensive Approach for Cancer Diagnostics   |
| Lin, Luming           | . Genome-wide association analysis identifies three loci associated with post-TB lung function in African adults  |
| Merchant, Kevin       | . Comprehensive structure activity relationship analysis for optimization of N23P-based IPF therapeutics using metaSAR model  |
| Mourra Diaz, Carlos I | <b>Michel</b> Unraveling the evolutionary dynamics of transcription factor binding site acquisition within retrotransposon regulatory elements  |
| Pamar, Daksh Pratap   | Singh Generalizing gRNA-design for CRISPRi from humans to other primates  |
| Pförtner, Felix       | . Improving bulk RNA-seq protocols  |
| Prexler, Carolin      | . Germline Variation in Pediatric Cancer Patients to Analyze Genetic<br>Predisposition - a Trio WES Study   |
| Puzek, Barbara        | . Genetics influence COVID-19 vaccine response  |
| Rabuffo, Claudia      | . Comprehensive analysis of the 3D organization of unconventional genomes   |
| Richter, Maria        | . Improving library size normalization in scATAC-seq data   |
| Rong, Yuying          | . New laboratory and computational workflow to reveal the recombination landscapes in Brassica species through single-nucleus pollen sequencing   |
| Rosales-Becerra, Par  | <b>Ilina</b> Comprehensive nascent RNA analysis based on metabolic labeling and nucleotide conversions  |
| Samoju, Rushmitha.    | . Pyocyanin: A boon indeed  |
| Schmid, Katharina     | . Benchmarking single cell copy number variant callers  |
| Térmeg, Anita         | . Cross-species comparison of gene regulatory networks  |
| Tüysüz, Irem          | . Identify patterns in mRNA to predict transcript half-lives in Trypanosoma using Saluki  |
| Vieth, Beate          | . powsimR2: Using simulations for power analysis of cell type identification from single cell and single nuclei RNA-sequencing data   |
| Zhdanovich, Yauheni   | ya Single nucleus RNA profiling reveals potential therapeutic vulnerabilities in  |

sinonasal carcinomas