

## # POSTER

- 1 **Spatial Transcriptomic analyses in non-model organisms at the National Genomics Infrastructure**  
Xesus Abalo
- 2 **Nascent transcription uncovers functional genomic regions across the T2T-CHM13v2 reference genome**  
Serhat Aktay
- 3 **Highly multiplexed arrays with 1972 unique IDs of full length secretome proteins have been developed and can be used for antibody validation and autoantibody screening with a high multiplexing capacity and high sample throughput.**  
Eni Andersson
- 4 **Proteomic profiling of host proteins incorporated in SARS-CoV-2 viral particles**  
Sarah Andersson
- 5 **Cancer therapies based on nucleolar stress: Who should we treat?**  
Myriam Barz
- 6 **Advanced Light Microscopy**  
Hans Blom
- 7 **Towards a computational description of proton coupling in Xyle**  
Marta Bonaccorsi
- 8 **Metabolomics platform**  
**Bénilde Bonnefille**
- 9 **A generalized benchmark for all four categories of enrichment analysis methods based on a disease pathway network**  
Davide Buzzao
- 10 **Heterotypic tumor spheroid models for cellular immunotherapy**  
Valentina Carannante
- 11 **Mechanism of Ligand-dependent G-protein-coupled Receptor Activation Reveled by Free-energy Landscapes**  
Yue Chen
- 12 **Activity of projection-specific serotonergic neurons in anxiety and exploration-related behaviors.**  
Ana Costa
- 13 **Structure and dynamics of differential ligand binding in the human rho-type GABAA receptor**  
JOHN COWGILL
- 14 **Data-driven Exploration of the Inflammatory Proteome Associated with SARS-CoV-2 Infection and/or Vaccination from Home-sampled Blood Spots**  
Leo Dahl
- 15 **Strengthening population health surveillance and epidemics monitoring by microsampling**  
Matilda Dale
- 16 **Elucidating mechanisms to inactivate the chemoresistance factor SAMHD1 - targeting allosteric activation**  
Christopher Dirks
- 17 **The SciLifeLab Bioinformatics Platform NBIS**  
Pär Engström
- 18 **REFSTRA (REference-Free Single-cell Transcriptome Autotyping) for deconvolution of paired Spatial Transcriptomics data**  
Alper Eroglu

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| 19 | <b>Operations Office</b><br>Sandra Falck  |
| 20 | <b>Structural Insights into Opposing Actions of Neurosteroids on GABAA Receptor</b><br>Chen Fan   |
| 21 | <b>Large scale spatial UMI denosing</b><br>David Fernandez  |
| 22 | <b>fqseek: an integrated framework for reproducible and efficient processing of high-throughput sequencing data</b><br>Carlos Gallardo              |
| 23 | <b>Revealing the RBP regulome in hepatocellular carcinoma via consensus GRN inference</b><br>Mateusz Garbulowski                                    |
| 24 | <b>Hyperplexed immunofluorescence imaging analysis</b><br>Louise Gsell  |
| 25 | <b>Utilizing large-scale genomic data to explore variable disease penetrance</b><br>Sanna Gudmundsson   |
| 26 | <b>High-throughput biophysical mapping in health and diseases</b><br>Cenk Gurdap  |
| 27 | <b>The effect of SSRIs on the spatio-molecular organization of the serotonin system</b><br>Charlotta Henningson                                     |
| 28 | <b>MTHFD1/2 inhibitors for treatment of cancer</b><br>Martin Henriksson   |
| 29 | <b>Intestinal estrogen receptor beta modulates the inflammatory immune microenvironment during colitis and early carcinogenesis</b><br>Matilda Holm |
| 30 | <b>Deciphering the molecular mechanisms of purine analogue nelarabine in the treatment of childhood leukemia</b><br>Femke Hormann                   |
| 31 | <b>Cellular &amp; Molecular Imaging at SciLifeLab</b><br>Rebecca Howard   |
| 32 | <b>Identification of cancer-specific small RNAs in the TCGA cohort</b><br>Panagiotis Kalogeropoulos   |
| 33 | <b>The Coaching in Science Initiative</b><br>Linda Kvastad  |
| 34 | <b>Transcriptome-wide alterations in mRNA translation define breast cancer subtypes</b><br>Ola Larsson  |
| 35 | <b>Amino acid regulated gene expression and virulence</b><br>Per Ljungdahl  |
| 36 | <b>Single-cell genomics at NGI</b><br>Michelle Ljungmark  |

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| 37 | <b>Biochemical and Cellular Assay Unit</b><br>Bo Lundgren  |
| 38 | <b>Variational Autoencoder for Imaging Mass Spectrometry</b><br>Fei Luo  |
| 39 | <b>Molecular profiling of the indoor and outdoor airborne exposome by passive sampling on silicone foam</b><br>Jonathan Martin             |
| 40 | <b>Specifying cellular context of regulons for exploring transcriptome-derived gene regulatory networks</b><br>Mariia Minaeva              |
| 41 | <b>Deciphering riboregulation in healthy and diseased cells</b><br>Riccardo Mosca  |
| 42 | <b>Machine Learning for Predicting Protein-Protein Interactions</b><br>Sarah Narrowe Danielsson  |
| 43 | <b>Autoantibody profiling and serology testing of human body fluids using high density protein arrays</b><br>Jennie Olofsson               |
| 44 | <b>AlphaFold2-driven molecular dynamics simulations of the mitochondrial carriers transport mechanism</b><br>Andrea Pasquadibisceglie      |
| 45 | <b>Identifying genetic vulnerabilities of senescence</b><br>Oneka Perea Ariznabarreta  |
| 46 | <b>FunCoup 5: Functional Association Networks in All Domains of Life, Supporting Directed Links and Tissue-Specificity</b><br>Emma Persson |
| 47 | <b>The discovery of a novel inhibitor of macropinocytosis with antiviral activity</b><br>Bartłomiej Porebski                               |
| 48 | <b>Gene Length Times the Production of Heat Shock Proteins</b><br>Adelina Rabenius   |
| 49 | <b>A guideline for quantitative characterization and application of environment-sensitive probes</b><br>Franziska Ragaller                 |
| 50 | <b>Dual laser strategy allows the profiling of virus host surface protein on SARS-CoV-2 viral particles</b><br>Maryam Sahi                 |
| 51 | <b>agoTRIBE detects microRNA-target interactions transcriptome-wide in single cells</b><br>Vaishnovi Sekar                                 |
| 52 | <b>Converting Cold into Hot Tumors by Mitotic MTH1 Inhibitor TH1579 Treatment</b><br>Jianyu Shen   |
| 53 | <b>Accurate protein fitting into cryo-EM maps using multiple conformers generated by AlphaFold2</b><br>Tatiana Shugaeva                    |
| 54 | <b>Development of a highly specific and sensitive multiplex serological COVID-19 assay</b><br>Lovisa Skoglund                              |

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| 55 | <b>Hepatoprotective effects of estrogen receptor agonists uncover novel biomarkers and targets for NAFLD</b><br>Christian Sommerauer |
| 56 | <b>High-dimensional screening of serological responses to all routine immunizations</b><br>William Stauch                            |
| 57 | <b>Cancer Immunotherapy</b><br>Renhua Sun  |
| 58 | <b>Plastic recycling by designer enzymes</b><br>Per-Olof Syrén   |
| 59 | <b>Barcode-free prediction of cell lineages from scRNA-seq datasets</b><br>Marcel Tarbier  |
| 60 | <b>SpLitter: Diploid genome assembly using TELL-Seq reads and assembly graphs</b><br>Ivan Tolstoganov                                |
| 61 | <b>Quantification of DNA replication at the nanoscale</b><br>Bruno Urién González  |
| 62 | <b>Direct observation of Na-K-ATPase oligomers in the plasma membrane of living cells by FRET-FCS</b><br>Stefan Wennmalm             |
| 63 | <b>Chemical Exposomomics in Human Plasma</b><br>Hongyu Xie   |
| 64 | <b>Exploiting nucleotide metabolism to potentiate nucleoside analogue-based cancer therapies</b><br>Miriam Yagüe Capilla             |
| 65 | <b>Searching Deep Proteomics Data for Specific Proteoforms Using Long-read mRNA-seq Data</b><br>Yuqi Zheng                           |