Poster Abstracts

1.
Beyond Dropout/Enrichment: Unlocking Advanced Phenotypic Profiling in Pooled CRISPR Screens
Awarded TDP

Hirofumi Noguchi, *hirofumi.noguchi@ki.se*

Traditional pooled CRISPR screens are based on guide dropout/guide enrichment in selected cell populations and are this limited to simple, sortable phenotypes. Single-Cell approaches such as Perturb-Seq and CROP-Seq link CRISPR perturbations to transcriptional profiling, capturing complex cellular states, but are expensive, poorly scalable and do not preserve spatial context. Optical Pooled Screening (OPS) and Spatial Omics Pooled Screening (SOPS) combine pooled CRISPR perturbations with high-content imaging, spatial transcriptomics, or spatial proteomics. These methods map genetic perturbations to complex morphological phenotypes, preserve spatial information, and enable functional studies. OPS and SOPS bridge the gap between genetic perturbation and rich, spatially resolved phenotypic readouts, to greatly expand the scope of functional genomic discovery.

2.
BRIDGE - Sweden
Awarded TDP

Niklas Berndt Thalén, *niklas.thalen@scilifelab.se*

Bridge Sweden is creating a platform to bridge the gap between expertise and research infrastructure in Sweden, supporting the development and commercialization of biological products and pharmaceuticals. Its goal is to strengthen Swedish Life Science and advance the next phase of biological product development.

3.
3D spatial profiling of transcripts and proteins in tissue
TDP 2026

Hans Blom, *hans.blom@scilifelab.se*

In this TDP we will develop 3D spatial transcriptome and proteome pipelines for thick tissue analysis, driving next-generation requests and services to deciphering life in true context.
Our TDP will provide a new level of understanding of tissue organization, cellular states, and molecular interaction, revealing spatial and biological information that cannot be captured by traditional 2D analysis, or with a single-omics modality. Characterizing and analyzing thick tissue biological complexity with multi-omics single-cell profiling will allow us to furthermore better understand healthy and diseased heterogeneities in 3D.

To drive this 3D development several SciLifeLab units with expertise in sample preparation, fluorescence imaging, spatial omics workflows, and bioimaging data analysis will join forces.
The end-goal being improved cross-platform services allowing linked characterization of gene expressions and protein levels in intact tissues (e.g., non-sliced biopsies, or spheroids/organoids).
Additionally, data analysis development will provide modular, scalable, and reusable software for in context insight of complex molecular organisation of transcripts and proteins in 3D.
Armed with improved diagnostics support we will moreover secure preparedness for future pandemics with 3D multi-omics tissue analysis (e.g., in retrospect better Covid-II multi-omics analysis of lung biopsies).

4.
AbPEA-NGS: Monitoring Antibody Reactivity Using High-Throughput Proximity Extension Assays
TDP 2026

HongXing Zhao, *hongxing.zhao@igp.uu.se*

Antibodies for specific infectious agents or self-targets represent important clinical biomarkers. Antibody reactivity in patient sera is also a frequent research topic, and it is routinely used to diagnose a broad range of diseases. Furthermore, mucosal antibody specificities represent a crucial first line of defense. However, despite its great importance, antibody reactivity remains relatively understudied for lack of suitable high-throughput analysis technologies.

Senior scientist Hongxing Zhao (SciLifeLab Affinity Proteomics) has developed a sensitive and efficient method for detecting many different antibody specificities by adapting the PEA (Proximity Extension Assay) for large-scale analyses of antibody reactivities - AbPEA. We have published two peer-reviewed studies where AbPEA was used to characterize antibody specificity against SARS-CoV-2. Ongoing work focuses on autoimmunity and increasing reactivity repertoires and sample throughput by introducing a sequencing readout.

The use cases proposed here are
1) to develop AbPEA panels to monitor urban wastewater for antibodies directed against infectious agents, and
2) to measure immune states against vaccines, infectious agents and autoantibodies in large sets of saliva, nasal swabs, plasma and serum.

For wastewater analyses, associate professor Anna Székely (SEEC-SLU) provides unique access to thousands of samples, and associate professor Nils Landegren contributes samples from healthy and autoimmune individuals.

5.
AICE – AI-guided Intracellular Cyclic-peptide Engine
TDP 2026

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Proximity-inducing agents (PIAs) are revolutionizing biomedical research by enabling precise control of protein interactions and cellular activities. Established modalities such as bispecific T-cell engagers (BiTEs), antibody-drug conjugates (ADCs), and small-molecule molecular glues have demonstrated the power of event-driven pharmacology. Newer classes including PROTACs, RIPTACS, LYTACs, and AbTACs are extending this strategy to proteins once considered “undruggable.”

In parallel, peptide-based therapeutics are experiencing renewed success, exemplified by GLP-1 receptor agonists and other incretin peptides. Peptides offer exceptional specificity, favorable safety profiles, and compatibility with modern delivery technologies such as mRNA-based systems.

This TDP proposal integrates two SciLifeLab PULSE entrepreneurial postdoctoral projects into a unified platform for AI-guided design and intracellular production of cyclic peptide tools. Artificial intelligence will drive the optimization of peptide sequences, structural stability, and target-binding efficiency. The platform will not only generate lead cyclic peptides for proximity-induced pharmacology but will also explore mRNA delivery systems that enable target cells to self-produce circular peptides intracellularly.

Impact: This project will establish a next-generation, AI-enabled discovery engine that merges computational design, synthetic biology, and mRNA therapeutics - unlocking new opportunities to target challenging intracellular proteins and advancing Sweden’s position in innovative drug discovery.

6.
BioVAT - Biodiversity Variant Analysis Toolkit
TDP 2026

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Genetic variation is the basis for evolution and enables species to adapt to changing environments. Despite its relevance for many fundamental questions, variant analysis for non-model organisms is not a solved issue. Existing pipelines are often optimized for human data, or do not give the necessary output for downstream analyses. We here suggest a modular population genomics pipeline called BioVAT (BIOdiversity Variant Analysis Toolkit), fully adaptable to any organism. It will be available as a service through NBIS support, and be used by NBIS experts in projects on population genomics, conservation genomics, etc. Key features include ability to deal with different data types, choice of variant caller, functionality to deal with reference-bias, a full range of filters adaptable to the specific study, control over output including the possibility to report non-variant sites, and a range of population genomics downstream analyses. The pipeline facilitates reproducibility and supports full reports for use in publications, and will be available open source following FAIR standards. It will be able to interface with data producing facilities such as the National Genomics Infrastructure, and the output is standardized to facilitate easy upload to the European Variant Archive and the DDLS-developed DivBase service.

7.
Capture-based long-read metagenomics for detection of pathogens and antimicrobial resistance
TDP 2026

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Accurate pathogen detection in low-bacterial-load samples is challenging, culture often fails and current molecular methods lack sensitivity and provide limited information. Shotgun metagenomics can detect species and antimicrobial resistance (AMR) genes but requires deep, costly sequencing. Recent advances in targeted metagenomics and long-read sequencing now enable simultaneous identification of pathogens, AMR markers, and virulence factors even from minimal input. Hybridization-based capture enriches bacterial DNA, allowing culture-independent, high-resolution genomics for fastidious or unculturable pathogens. Long-read-adapted capture further improves genome recovery, reduces sequencing depth requirements, and enables detection of novel pathogens due to probe mismatch tolerance and recovery of large DNA fragments.
The project aims to develop and validate a capture-based long-read metagenomics workflow, providing species-level resolution of priority pathogens, detection of AMR and virulence determinants, and flexible probe-panel design. Work packages include probe design, optimization of long-read library preparation, development of automated bioinformatic pipelines, validation in clinically relevant matrices, and benchmarking of Twist vs. Agilent panels. The workflow will be implemented as a modular service within Clinical Genomics, with automated library preparation ensuring scalability. This will enhance Sweden's capacity for infectious disease genomics, AMR surveillance, and pandemic preparedness by providing a sensitive, standardized, and flexible sequencing approach for low-bacterial-load samples.

8.
Cell-specific Proteome 3D Structural Atlas by Structural Elucidation of Proteins in Cellular Environment (SEPCE)
TDP 2026

Massimiliano Gaetani, *massimiliano.gaetani@ki.se*

This project will establish a fundamentally new way to study protein structure and function directly in the cellular environment. The proposed method, Structural Elucidation of Proteins in Cellular Environment (SEPCE), integrates two recent proteomics innovations with the addition of with AI-based structural prediction: HOLSER, which measures local proteolytic accessibility of thousands of proteins; and PISA, which quantifies their solubility states. Together, HOLSER and PISA will generate

proteome-wide experimental constraints for refining OpenFold models, enabling the reconstruction of a complete three-dimensional protein structural landscape of a given cell.

SEPCE will be applied to reveal how protein structures remodel in response to drugs, stress, and viral infection, and to identify molecular interfaces that govern protein-protein and protein-ligand interactions. By producing hundreds of thousands of experimental structural parameters at once, SEPCE will transform structural biology from a single-molecule discipline into a quantitative systems-level science. This low-risk, high-gain project will create the first cell-specific Proteome Structural Atlas, opening unprecedented opportunities for mechanistic biology, drug discovery, and precision medicine. With single-cell proteomics techniques rapidly advancing, the Proteome Structural Atlas will be possible to construct for a single cell.

9.
Development of a High-Accuracy, High-Throughput Droplet-PTA Platform for scWGS
TDP 2026

Julia Bräunig, *julia.braunig@med.lu.se*

This project will deliver Sweden's first high-throughput droplet-based single-cell whole-genome sequencing (scWGS) service, combining precision, scale, and versatility to transform microbial and human genomics. Using Primary Template-directed Amplification (PTA) in semi-permeable capsules (SPCs), the platform captures individual cells—including hard-to-lyse microbes—while enabling near-complete genome recovery with accurate SNV/CNV detection. Clinical Genomics Lund (CGL), with extensive expertise in translational single-cell applications, will lead wet-lab development, optimizing droplet workflows and benchmarking performance. Pilot studies, conducted together with Clinical Genomics Uppsala (CGU), will interrogate antimicrobial resistance and microbiome diversity, as well as tumor clonal evolution and somatic mosaicism.
Laura Carroll (DDLS fellow, UmU) and Johan Henriksson (SciLifeLab Group Leader, UmU) will develop two software tools, Bascet and Biscvi, in collaboration with NBIS, ensuring FAIR-compliant pipelines and standardized analysis. Integration with the SciLifeLab Data Centre (Liane Hughes, UU) and Swedish Pathogens Portal (SPP) provides nationwide, load-balanced access to interactive datasets. By combining cutting-edge technology with a coordinated national network, this project establishes a modular, scalable method for single-cell genomics in Sweden—enabling translational research, pathogen surveillance, antimicrobial resistance monitoring, and interactive visualization.

10.
Enabling the next big transformation in Genomics: Combining Pangenomes and the Ancestral Recombination Graph
TDP 2026

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Genomics is currently undergoing two major revolutions. First, pangenomes are transforming comparative genomics by enabling the distinction between core (regions shared across all samples) and variable genomic regions (regions shared by a subset of species, populations or individuals). Second, ancestral recombination graphs (ARGs) are reshaping population genomics by providing a substantially more detailed representation of genealogical relationships across the genome.

Each approach has independently yielded striking insights. For example, ARG-based analyses have uncovered the deep coalescence (6 million-year-old) of ABO blood group alleles in humans, a signal that traditional population genomic methods failed to detect. Similarly, pangenome studies often recover >50% more sequence length and thousands of additional genes compared to single-reference genomes, revealing extensive hidden variation or "dark genetic matter".

Here, we propose to unify these two advances through the development of a novel and containerised software pipeline, PanARG, and to offer this as a service through NBIS support. The pipeline will enable researchers to test new hypotheses about genomic variation, adaptation, and evolutionary history at unprecedented resolution.

Importantly, this proposal represents a collaboration between two infrastructures (the Bioinformatics and Genomics platforms at SciLifeLab), a DDLS fellow and the international network of both.

11.
From Correlation to Causation: Linking CRISPR Perturbation with Cell- and Tissue Profiling at Scale
TDP 2026

Bernhard Schmierer, *bernhard.schmierer@ki.se*

Pooled CRISPR screens are a cornerstone of functional genomics and enable large-scale identification of gene function. Classical pooled screens rely on physical separation of phenotypes, which restricts readouts to cell fitness or other sortable traits. However, many biological questions require richer phenotyping to capture morphological, molecular, and spatial features of cell state after perturbation.
High-content imaging, spatial omics and other cell- and tissue profiling methods now provide unprecedented insights into cellular organization and tissue architecture. However, in the absence of genetic perturbation, these methods remain largely descriptive and fail to assign causal relationships between genes and phenotypes.
Here, we will integrate massively parallel, CRISPR-based genetic perturbation with morphological and spatial omics profiling. Building on seminal papers in 2019/2022 and a surge of method papers in 2025, we will establish scalable methods to functionally interrogate complex phenotypes in cells, organoids and tissues. We will implement cost-efficient, cross-platform service pipelines that are anticipated to eventually also involve the Genomics platform and NBIS.
In summary, we will shift high-content profiling platforms from passive observation to uncovering causal relationships between genes and phenotypes. These methods will equip SciLifeLab users with powerful new tools to understand cellular mechanisms, tissue organization, and disease-relevant pathways. Causal, multimodal, and context-rich datasets will help move from descriptive cell mapping to predictive, mechanistic modeling - a critical step toward building a virtual cell.

12.
High-Resolution Multiomics: Advanced integrated Spatial Multiomics for next-generation diagnostics
TDP 2026

Carolina Oses Sepulveda, *carolina.oses@scilifelab.se*

*Advanced spatial instruments such as Xenium (targeted spatial transcriptomics up to 5000 genes) and PhenoCycler and COMET (for high-plex protein detection up to ≈ 60 protein markers), allow researchers to interrogate tissue biology at single-cell resolution. Today, these two technologies are offered independently at the ISS (In Situ Sequencing) and SP (Spatial Proteomics) units. Over the last year, we have received several user requests for integrating these two modalities. This has a high scientific impact, as this would allow for mapping transcripts and proteins onto the same cells within the intact tissue. This combination of Xenium and PhenoCycler/COMET takes advantage of the high multiplexing transcript detection from Xenium, with the high image resolution of proteins on the PhenoCycler/COMET platform. Specifically, this combination allows users to move from discovery with Xenium to more hypothesis-driven questions and validation of interesting signatures with PhenoCycler/COMET.
*
We have tested this combination on two user projects, yielding promising preliminary data that demonstrate the feasibility of this integrated workflow. However, optimizations and testing across sample types are needed before it can be offered as a service. While having the resources to do this work, dedicated funding is critical to afford the reagents needed for these optimizations. <p>

13.
HOT-Lab: Anticipatory and Reactive Structural Biology Technologies for Pandemic Preparedness
TDP 2026

Cecilia Persson, *cecilia.persson@nmr.gu.se*

Protein structure prediction has transformed viral research and pandemic preparedness by enabling the identification of conserved folds, host–virus interfaces, and potential therapeutic or vaccine targets. Yet, the absence of integrated, scalable technologies linking predictive modelling with experimental validation limits our ability to act rapidly when new or re-emerging viral threats arise.
This Technology Development Project HOT-Lab (High Outbreak Threat Preparedness Laboratory) will establish anticipatory and reactive structural biology technologies for pandemic preparedness, driven by the Integrated Structural Biology (ISB) platform in close collaboration with NBIS/LU-Fold and the Atkinson lab at Lund University. The project will combine large-scale AI-based structure prediction pipelines with experimental structural validation to create a responsive infrastructure capable of producing, refining, and delivering viral protein structures on demand whilst also having direct opportunities for small molecule fragment library screening and hit validation.
By integrating computational and experimental workflows into a unified, deployable technology, HOT-Lab will enable both anticipatory coverage of high-risk viral families and reactive model validation during emerging outbreaks. The resulting infrastructure will strengthen SciLifeLab's capacity to provide rapid, high-confidence structural insights to the Swedish research and public-health communities, enhancing national preparedness for future viral threats.

14.
Multiplex Spatial Interactomics Integrating in-situ Proximity Ligation Assay and Cell Painting for AI-Powered Drug Discovery and Precision Medicine
TDP 2026

Malin Jarvius, *malin.jarvius@uu.se*

Understanding how proteins interact and undergo modifications within their native spatial context is fundamental to decoding biological signaling, disease mechanisms and drug responses. Protein–protein interactions and posttranslational modifications (PPIs and PTMs) form the basis of signaling cascades, and their spatial organization, and their temporal dynamics determine the outcomes of pharmacological interventions. Yet, current interactomic and imaging approaches fail to capture this complexity at sufficient resolution or throughput.

We have recently pioneered a multiplex in-situ proximity ligation assays (misPLA) capable of visualizing multiple PPIs and PTMs within cells. There is high potential to combine the technology with cell painting, to link molecular interaction patterns to cellular phenotypes in a spatially indexed manner. This proposal aims to develop and establish a new technology—Spatial Interactomics with Cell Painting (SIXP)—that reveals high-throughput molecular activity with morphology mapping and AI-supported image analysis. As a proof-of-concept, we will apply SIXP to dissect the biased activation of GLP-1 receptor (GLP-1R) signaling, a key pathway in diabetes therapy. Once implemented, the developed technology can be implemented within the CBGE platform broadly applied across basic biology including for the Alpha Cell project and a wide range of precision medicine and therapeutic areas.

15.
Next-Generation Spatial Omics: Enabling Host–Microbe–Immune Insights via SmT and Spatial VDJ
TDP 2026

Remi-André Olsen , *remi-andre.olsen@scilifelab.se*

Our proposal aims to further develop and implement two cutting-edge spatial omics technologies, Spatial metaTranscriptomics (SmT) and Spatial VDJ, into NGI and offer both as a novel nation-wide service. These methods, which are not yet commercially available, enable simultaneous spatial profiling of host transcriptomes, microbial communities, and immune clonotypes from the same tissue

section, offering transformative insights into host–microbe–immune interactions. Developed locally by Stefania Giacomello, Camilla Engblom, and Kim Thrane, the technologies will be adapted for compatibility with commercial platforms (i.e., 10x Genomics Visium HD) and supported by user-friendly computational pipelines. Funding will support technology development, method transfer, optimization, and consumables, ensuring rapid deployment and accessibility. Deliverables include standardized workflows, long-read sequencing capabilities, and scalable infrastructure services. This initiative will position NGI as the first facility globally to offer integrated spatial microbial and immune profiling, reinforcing Sweden's leadership in spatial biology innovation and providing the national research community with ground-breaking tools for infection biology, immunology, and data-driven discovery.

16.
Reshaping Bio NMR by AI: Fully automated assignment and structure in hours
TDP 2026

Ulrika Brath, *ulrika.brath@gu.se*

NMR spectroscopy provides uniquely detailed, atomistic insight into molecular systems under near physiological conditions. Despite the advantages, NMR experiments are lengthy and analysis by experienced personal requires significant time. This often becomes a major time and cost bottleneck in integrative structural biology.

In this project, we will streamline and integrate multiple Deep Learning driven methods into the NUSTA-DL platform, which will be offered to users of the Swedish NMR Centre hosted by the Gothenburg and Umeå Universities. The NUSTA-DL workflow will combine technologies for NMR data acquisition, peak picking, assignment and structure determination. We will:

- *Implement the latest state-of-the-art methods for automated NMR spectra collection and analysis, with a 10-fold decrease in experiment and analysis time relative to the existing setup.*
- *Build a fully automated workflow for protein assignment, structure characterization and data deposition. This ensures autonomous access for Swedish PIs to the most advanced DL-based NMR assignment and protein structure elucidation protocols.*
- *Implement a user-friendly interface, enabling the user to go directly from sample to structure.*
- *Validate the NUSTA-DL performance for users with protein samples from the ISB platform.*

Our goal is to achieve an over 10-fold faster timeline from experiment to structural insight.

17.
Spatial miRNomics
TDP 2026

Rapolas Spalinskas, *rapolas.spalinskas@scilifelab.se*

Spatial miRNomics aims to implement a novel, high-plex spatial method for mapping microRNAs (miRNAs) in tissues, fully integrated with the 10x Genomics Xenium platform and compatible with existing in situ sequencing (ISS) transcriptomic workflows. miRNAs are essential regulators of gene expression, and their dysregulation is implicated in the development of diverse pathologies. Despite an extensive body of research, their spatial distribution in tissues remains largely unexplored due to technical limitations, and no existing national or international platforms currently provide this service. Spatial miRNomics will, for the first time, offer researchers a dedicated infrastructure service for spatial miRNA profiling. Recently, Mats Nilsson's group developed a highly efficient method for tissue miRNA mapping based on inhouse ISS-chemistry. The TDP will adapt and implement this approach on the 10X
Genomics Xenium platform, establishing robust protocols, validated probe panels, and operational know-how to advise users effectively. It will be applicable across diverse tissues, with optional multimodal spatial setups for joint miRNA-mRNA and protein profiling.
In the long term, Spatial miRNomics will be established as a routine service within the SciLifeLab ISS facility, the first of its kind internationally, integrating spatial miRNA profiling with transcriptomic analysis, strengthening SciLifeLab's international leadership in spatial omics and enabling new biological and translational discoveries.

18.
Spatial Multi-Omics on a Single Tissue Section
TDP 2026

Katarina Tiklova, *katarina.tiklova@scilifelab.se*

This project aims to develop a novel workflow for analyzing multiple modalities on the same tissue section by combining imaging-based spatial transcriptomics using In Situ Sequencing (ISS) with Mass Spectrometry Imaging (MSI)—a combination not currently available. ISS maps thousands of RNA transcripts at high spatial resolution, while MSI detects peptides, lipids, glycans, and metabolites. Integrating these modalities on a single section will enable direct correlation of transcriptomic and molecular profiles within a shared cellular and microenvironmental context.
The project will focus on optimizing sample preparation, preserving signals for all modalities, and achieving accurate spatial registration between datasets. The ultimate goal is to establish this workflow as a new integrated service between the ISS and MSI units, providing a multi-omic spatial mapping platform that supports the creation of comprehensive molecular atlases, drives novel biological insights, and facilitates advanced spatial data integration.

19.
Spatial multiomics integration
TDP 2026

Åsa Björklund, *asa.bjorklund@scilifelab.se*

Spatial Biology has become a prominent area of development at Scilifelab and the natural next step is the combination of multiple spatial omics from the same samples. The Spatial Omics Platform is currently working on several projects that combine multiple modalities on the same section.

However, methods for aligning spatial data from different omics and subsequent multimodal analysis of the data require further development. This application suggests a collaboration with the Joakim Lundeberg laboratory which has access to unique samples from human development and insight into the biological system. We suggest running all the different technologies offered at the Spatial Biology Platform on the same set of samples.

The main deliverables for this project will be: i) streamlined pipelines and methods for image registration across modalities, ii) a framework for multimodal integration and iii) a graphical interface for data visualization for all the modalities.

20.
Case studies using Integrated Structural Biology
Other Platform Posters

Cecilia Persson, *cecilia.persson@nmr.gu.se*

Three recent user cases are presented.

21.
Cellular & Molecular Imaging (CMI) Platform
Other Platform Posters

Reba Howard, *rebecca.howard@scilifelab.se*

Cellular and molecular imaging enables the visualization of biological systems from atomistic to tissue levels. Typical methods involve the transmission, absorption, reflection, or refraction of a focused beam of visible light or electrons by a microscopic sample of interest. In the life sciences, such samples may be biological macromolecules, cells, small organs or organisms of interest to biomedical or planetary biology research. At SciLifeLab, imaging staff assist users from academic, industry, and clinical settings to identify and implement relevant techniques for sample preparation and for the collection, processing, analysis, and sharing of imaging data, with a focus on methods and instruments not generally accessible to individual research groups or local facilities. Key SciLifeLab imaging

services include cryogenic electronic microscopy (cryo-EM) and tomography (cryo-ET), super-resolution and other advanced methods in fluorescence microscopy, focused ion-beam milling scanning electron microscopy (FIB-SEM), correlative array tomography (CAT) and nanoscale secondary ion mass spectrometry (nanoSIMS), along with a range of imaging modalities in support of structural biology and spatial omics.

22.
COMPIS: Computational Chemistry & Cheminformatics at SciLifelab
Other Platform Posters

Evert Homan, *evert.homan@scilifelab.se*

Computational chemistry and cheminformatics are indispensable tools in modern early drug discovery, with a demonstrated track record of reducing both lead times and costs in drug development. With the recent advent of AI, computational chemistry has the potential to revolutionize the field further by accelerating hit identification, optimizing lead compounds, and enabling more accurate predictions of relevant properties.
At SciLifeLab, computational chemistry and cheminformatics are applied across multiple platforms and nodes, including CBGE and DDDP, with active groups in Stockholm, Uppsala, and Umeå. Computational chemists from these sites have now joined forces in COMPIS — COMPutational chemistry and chemInformatics at SciLifeLab — to exchange expertise on software, tools, and workflows, and to collaborate on joint technology development projects.
For scientists at SciLifeLab and beyond, COMPIS will serve as a central resource for computational chemistry expertise and support, lowering the barrier to adopting state-of-the-art methods and strengthening cross-disciplinary collaboration across the Swedish life science community.

23.
Exposomics: high-resolution mapping of environmental chemical exposures in human and ecosystem health
Other Platform Posters

Stefano Papazian, *stefano.papazian@aces.su.se*

The exposome encompasses the full spectrum of environmental exposures encountered throughout life and is increasingly recognized as a key determinant of health and disease. These exposures include pharmaceuticals, consumer-product chemicals, industrial contaminants, dietary compounds, and biologically derived molecules originating from the microbiome and environment.

The Exposomics Unit at the SciLifeLab Metabolomics and Exposomics Platform, hosted at Stockholm University, provides state-of-the-art infrastructure and expertise for comprehensive chemical exposome characterization using high-resolution mass spectrometry (GC- and LC-HRMS). The unit supports researchers across academia, healthcare, and government through end-to-end services spanning study design, sample preparation, targeted analysis, suspect screening, and large-scale nontargeted chemical profiling.

The unit is able to generate and support interpretation of exposome-scale datasets from both human and environmental samples, enabling discovery of known and previously unrecognized chemical exposures, implementing advanced computational workflows for chemical annotation, data integration, and exposome-wide analyses. By combining cutting-edge analytical technologies with scalable data-processing capabilities, the Exposomics Unit provides a national resource for investigating the environmental determinants of health and supporting next-generation exposome research.

24.
From Discovery to Quantification: Mass Spectrometry-Based Metabolomics at SMC and CMSI
Other Platform Posters

Annika Johansson, *annika.johansson01@umu.se*

The Chalmers Mass Spectrometry Infrastructure (CMSI) and the Swedish Metabolomics Centre (SMC) provide complementary mass spectrometry-based metabolomics capabilities that support a broad

range of life science research. This poster presents two representative user projects that highlight the strengths of untargeted and targeted metabolomics approaches and their application to diverse scientific questions.
The first case study, conducted at CMSI, demonstrates the use of untargeted metabolomics for comprehensive metabolic profiling and discovery-driven research. By capturing a wide range of metabolites without prior assumptions, the approach enables the identification of metabolic patterns and biomarkers associated with complex biological systems, generating new insights and hypotheses for further investigation.
The second case study, performed at SMC, showcases a targeted metabolomics application supported by recent method development. The project highlights how optimized analytical workflows can improve sensitivity, selectivity, and quantitative performance, enabling robust measurement of biologically relevant metabolites and supporting hypothesis-driven research.
Together, these examples illustrate the complementary nature of untargeted and targeted metabolomics, from broad metabolic exploration to precise quantitative analysis. The showcased projects demonstrate the expertise, analytical platforms, and collaborative opportunities available through CMSI and SMC, highlighting the value of advanced mass spectrometry methodologies in addressing contemporary research challenges across multiple scientific disciplines.

25.
Multimodal Mechanism-of-Action Elucidation at the CBGE platform
Other Platform Posters

Bernhard Schmierer, *bernhard.schmierer@ki.se*

The SciLifeLab platform Chemical Biology and Genome Engineering (CBGE) combines chemical biology, chemical proteomics, cell painting, and CRISPR-based functional genomics to study the biological effects of small molecules. We integrate phenotypic profiling, genome-wide perturbations, and proteome-wide target engagement to identify molecular targets, pathways and networks that govern the activity of a small molecule or other agent. We aim at the integration of multimodal datasets to generate testable hypotheses from high-throughput data. By providing access to advanced technologies and expert guidance, we enable researchers to translate phenotypic observation into mechanistic insight.

26.
NanoSIMS Imaging– A New Tool to Unveil Nanostructures in Life Science
Other Platform Posters

Yanan Yang & Nhu Phan, *yanan.yang@gu.se*

27.
Pharmacometabolomics - ADME of Therapeutics (ADMEoT/UDOPP) Unit
Other Platform Posters

Valentina Ramundi, Ioanna Tsiara, *pawel.baranczewski@uu.se*

A dedicated Metabolomics Capability for Drug Discovery (Pharmacometabolomics) was established at Uppsala University in January 2026. The capability is integrated within the ADME of Therapeutics (ADMEoT) unit at SciLifeLab Drug Discovery and Development (DDD) and operates in close collaboration with the Globisch Laboratory, Department of Chemistry for Life Sciences, Uppsala University, led by Professor Daniel Globisch.
The primary objective of Pharmacometabolomics is to investigate prototype drug-induced alterations in the metabolome. By integrating metabolomics into the drug discovery process, this approach helps bridge the gap between genetic variation and phenotypic outcomes, providing a more comprehensive understanding of target engagement and mechanism of action. Metabolomic profiling generates biochemical fingerprints of drug responses, enabling the characterization of pharmacological effects, the assessment of safety liabilities, and the identification of candidate biomarkers for efficacy and toxicity.

In our poster, we present the Metabolomics capability, including its available resources, analytical platforms, workflow, and highlight how metabolomics can support decision-making throughout the drug discovery and development pipeline.

28.
Rapid nanopore sequencing for detection of actionable mutations in acute myeloid leukemia
Other Platform Posters

Panagiotis Baliakas, *marcela.davila@gu.se*

Background: Genetic characterization of acute myeloid leukemia (AML) is crucial for risk-stratification and treatment decision making. The mutational status of several actionable genes requires short turn-around-time (TAT), which in the clinical setting leads to multiple parallel testing.
Materials and methods: We have designed an amplicon-based panel [15 amplicons, 2161-3495bp] using a multiplex PCR approach, covering regions of interest in TP53, FLT3, IDH1, IDH2, and NPM1. Libraries were generated for Oxford Nanopore (ONT) sequencing on the Flongle and the MinION platforms. Variant calling was performed using ClairS-TO, Vardict, and Deepsomatic.
Results: Forty AML patient samples with 68 mutations previously characterized by a short-read sequencing somatic panel have been analyzed. Variant allele frequencies (VAFs) ranged between 1-83% (TP53: n=48, VAF 2-83%; NMP1: n=3, VAF 39-48%; IDH1: n=4, VAF 4-35%; IDH2: n=2, VAF 9-49%; FLT3 TKD: n=3, VAF 7-40%; FLT3 internal tandem duplications: n=8, 10-177 bp, VAF 1-31%). Limit of detection was defined to 3%. All variants were detected with both Flongle and MinION platforms (Flongle R2 = 0.97, MinION R2 = 0.98).
Conclusion: ONT amplicon sequencing in AML can serve as a single test that provides clinically relevant results with a short TAT, allowing early personalized treatment options. This is to our knowledge the first application of long read sequencing for rapid diagnostic in AML to this scale.

29.
SciLifeLab Genomics platform
Other Platform Posters
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Information about the SciLifeLab Genomics platform

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