Bridging Nordic Microscopy Infrastructure

BNMI

# BOOK OF ABSTRACTS

## BNMI 2026 Symposium

Hotel Levi Panorama, Levi, Finland

**November 23-27**



*Photo: Kassiopeia Hotels & Restaurants Image Bank*

# Contents

Welcome ..... 2
Program ..... 3
Pre-Symposium Workshops ..... 7
Abstracts ..... 12
Speaker abstracts ..... 12
Keynote EMBO speaker ..... 12
Invited speakers ..... 13
Contribution Talks ..... 20
Posters Abstracts ..... 36
Table of content ..... 36
Posters ..... 40
Social Program ..... 74
Organizing committee ..... 75
About BNMI ..... 76
Partners ..... 78
Sponsors ..... 79
Practical Information ..... 80

# Welcome

Welcome to the 5th meeting of the Bridging Nordic Microscopy Infrastructure (BNMI) network (https://bnmi.eu/). The goal of the BNMI2026 symposium is to bring the Nordic imaging infrastructures, leading imaging scientists, and industry representatives together for insightful discussions and collaboration to improve the quality and impact of microscopy in the Nordic countries. By bringing together experts from different imaging modalities and career stages, we aim to foster meaningful collaborations and offer a unique opportunity to stay updated on cutting-edge imaging technologies, learn new techniques, and build valuable connections within the imaging community.

The Finnish Advanced Microscopy Node of Euro-BioImaging hosts the symposium at the Levi Summit Event Centre & Hotel Levi Panorama.

# Program

| MONDAY, 23 NOVEMBER – PRE-SYMPOSIUM WORKSHOPS | | | |
|---|---|---|---|
| 13:00 | 17:00 | Arrival | |
| 12:00 | 15:00 | Lunch | |
| 15:00 | 19:00 | Registration | |
| 16:30 | 17:00 | Coffee | |
| **17:00** | **19:00** | **Pre-symposium Workshops** | |
| 19:00 | 21:00 | Dinner | |

| TUESDAY, 24 NOVEMBER – PRE-SYMPOSIUM WORKSHOPS & SYMPOSIUM INDUSTRY SESSION | | | |
|---|---|---|---|
| **09:00** | **11:00** | **Pre-symposium Workshops** | |
| 09:00 | 17:00 | Registration | |
| 11:30 | 13:00 | Lunch | |
| 13:00 | 13:30 | Welcome and Introduction | Irina Belaia, Oddmund Bakke |
| **13:30** | **14:25** | **Company talks** | Chair: Xian Hu |
| | | **CARL ZEISS** | Jesper Kielsgaard |
| | | **OY G. W. BERG & CO AB** | Mikko Nokkonen |
| | | **MILTENYI BIOTEC** | Christian Garm |
| | | **ABBELIGHT** | Sophie Ngo |
| | | **BRUKER LUXENDO** | Felix Weltzien |
| | | **FEMTONICS** | Péter Gál |
| 14:25 | 15:05 | Coffee and company exhibition | |
| **15:05** | **15:50** | **Company talks** | Chair: Dado Tokic |
| | | **BERGMAN LABORA AB** | Oliver Garner |
| | | **TRIOLAB OY** | Markku Saari |
| | | **THERMO FISHER SCIENTIFIC** | Harpreet Khinda |
| | | **HAMAMATSU PHOTONICS** | Ilya Stepanenko |
| | | **SARTORIUS** | Christopher Carroll |
| **15:50** | **16:50** | **Panel Discussion** | Moderator: Pasi Kankaanpää |
| | | **Who Builds the Future of Microscopy?** Shaping the Partnership Between Industry and Nordic Imaging Facilities | Panelists: Jesper Kielsgaard, Camilo Guzmán, Dennis Uhlenkamp, Clara Prats, Xian Hu |
| 16:50 | 19:00 | Free time | |
| 19:00 | 21:00 | Dinner | |

| WEDNESDAY, 25 NOVEMBER – SYMPOSIUM SESSIONS | | | |
|---|---|---|---|
| **09:00** | **10:30** | **SESSION 1 · Mesoscopy and 3D Imaging** | Chair: Veli-Pekka Ronkainen |
| 09:00 | | **Fibrillar collagen as an imaging biomarker for uterine health and pregnancy progression** | **Renata Prunskaite-Hyyryläinen** · University of Oulu, Finland |
| 09:35 | | **Automated atlas-based quantification of brain shuttles delivery using lightsheet microscopy** | **Judit Prat Duran** · Aarhus University, Denmark |
| 09:55 | | **Microscopy-driven characterization of rainbow trout hepatic 3D spheroids with multimodal analytical validation** | **Prem Chand** · University of Oslo, Norway |
| 10:00 | | **Whole-brain clearing and multi-channel light-sheet imaging for sex differences in mouse models of autism spectrum disorder** | **Moritz Negwer** · Radboud University, Netherlands |
| 10:30 | 11:15 | Coffee and company exhibition | |
| **11:15** | **12:45** | **SESSION 2 · Advances in Microscopy** | Chair: Hans Blom |
| 11:15 | | **Smart microscopy for adaptive imaging** | **Suliana Manley** · EPFL, Switzerland |
| 11:50 | | **Micro-stepping extended focus reduces photobleaching and preserves structured illumination super-resolution features** | **Xian Hu** · University of Oslo, Norway |
| 12:10 | | **Light as a probe for living systems** | **Antonio Fiore** · Turku Bioscience Centre, Åbo Akademi, Finland |
| 12:30 | | **Tracking sodium-potassium ATPases (NKA) using MINFLUX** | **Devinda Wijewardena** · KTH Royal Institute of Technology, Sweden |
| 12:45 | 14:00 | Lunch | |
| 14:00 | 16:00 | Free time | |
| **16:00** | **17:00** | **EMBO Keynote lecture** | Introduction: Oddmund Bakke |
| EMBO | | **Following lysosome dynamics and repair with light microscopy** | **Harald Stenmark,** Oslo University Hospital, Norway |
| 17:00 | 19:00 | Welcome Reception<br>Company exhibition & Poster session | |
| 19:00 | 21:00 | Dinner | |

| THURSDAY, 26 NOVEMBER - SYMPOSIUM SESSIONS | | | |
|---|---|---|---|
| **08:30** | **10:00** | **SESSION 3 · Imaging Applications** | Chair: Clara Prats |
| 08:30 | | **Pharmaceuticals under the nonlinear optical microscope** | **Clare Strachan** · University of Helsinki, Finland |
| 09:05 | | **Rapid ER remodeling by peptide-lipid complexes - peripheral ER collapse and vesiculation, nuclear ER expansion and nuclear shape change** | **Arunima Chaudhuri** · Lund University, Sweden |
| 09:25 | | **Cluster assembly dynamics drive fidelity of planar cell polarity polarization** | **Silas Boye Nissen** · Lund University, Sweden |
| 09:45 | | **Mitochondrial positioning by CDK1-MAP4 regulates focal adhesions, redox signaling and cell migration** | **Omkar Joshi** · University of Turku, Finland |
| 10:00 | 10:45 | Coffee, posters & company exhibition | |
| **10:45** | **12:00** | **SESSION 4 · Label-Free Imaging** | Chair: Jonathan Brewer |
| 10:45 | | **Structural diversity of amyloid aggregates across mouse models and human brain tissue revealed by vibrational imaging** | **Oxana Klementieva** · Lund University, Sweden |
| 11:20 | | **Digital holographic microscopy of biomolecular condensates in an electric field** | **Jennifer Tersteegen** · Aalto University, Finland |
| 11:40 | | **Coherent X-rays for imaging of wood — identifying challenges for hierarchical biological samples** | **Taissia Cheremnykh** · University of Jyväskylä, Finland |
| 12:00 | 13:30 | Lunch | |
| **13:30** | **15:00** | **SESSION 5 · High-Content Imaging and Image Analysis** | Chair: Antti Hassinen |
| 13:30 | | **Large-scale microscopy datasets for image-based profiling and model development** | **Lassi Paavolainen** · FIMM, University of Helsinki, Finland |
| 14:05 | | **Multiplexed high-content imaging for drug screening in rheumatoid arthritis synovial fibroblasts** | **Phatthamon Laphanuwat** · University of Zurich, Switzerland |
| 14:20 | | **Polar ordering during transition from dormant to migrating epithelia** | **Anna Lång** · Oslo University Hospital, Norway |
| 14:40 | | **Virtual multistaining of histological whole slide images based on generative AI and a panel of special stains** | **Sonja Koivukoski** · University of Eastern Finland, Finland |
| 15:00 | 15:30 | Coffee and company exhibition | |
| 16:00 | 19:30 | Social Program (Arctic Sauna World) | |
| 20:00 | 24:00 | Symposium dinner & party | |

| FRIDAY, 27 NOVEMBER - SYMPOSIUM SESSION | | | |
|---|---|---|---|
| **09:00** | **10:35** | **SESSION 6 · Electron Microscopy and Multimodal Imaging** | Chair: Sigurður Rúnar Guðmundsson |
| 09:00 | | **Cryo-Electron Tomography of the Baltic Sea microbiome** | **Linda Sandblad** · Umeå University, Sweden |
| 09:35 | | **From cells to molecules: multimodal bioimaging reveals the structural plasticity of the Staphylococcus aureus virulence peptide PSMα1** | **Sambhasan Banegjee** · Centre for Structural Biology, DESY, Germany |
| 09:55 | | **Membrane contacts between caveolae and the endoplasmic reticulum involved in fatty acid metabolism** | **Sebastian Rönfeldt**· Biochemical Imaging Centre Umeå, Sweden |
| 10:15 | | **Mechanosensitive membrane microdomains imaged through a lens of fluorescence and cryogenic electron microscopes** | **Markku Hakala** · University of Helsinki, Finland |
| 10:35 | 10:45 | Closing remarks | |
| 10:45 | 12:00 | Grab and go lunch and departure | |
| 11:30 | | Bus shuttle to Kittilä Airport | |

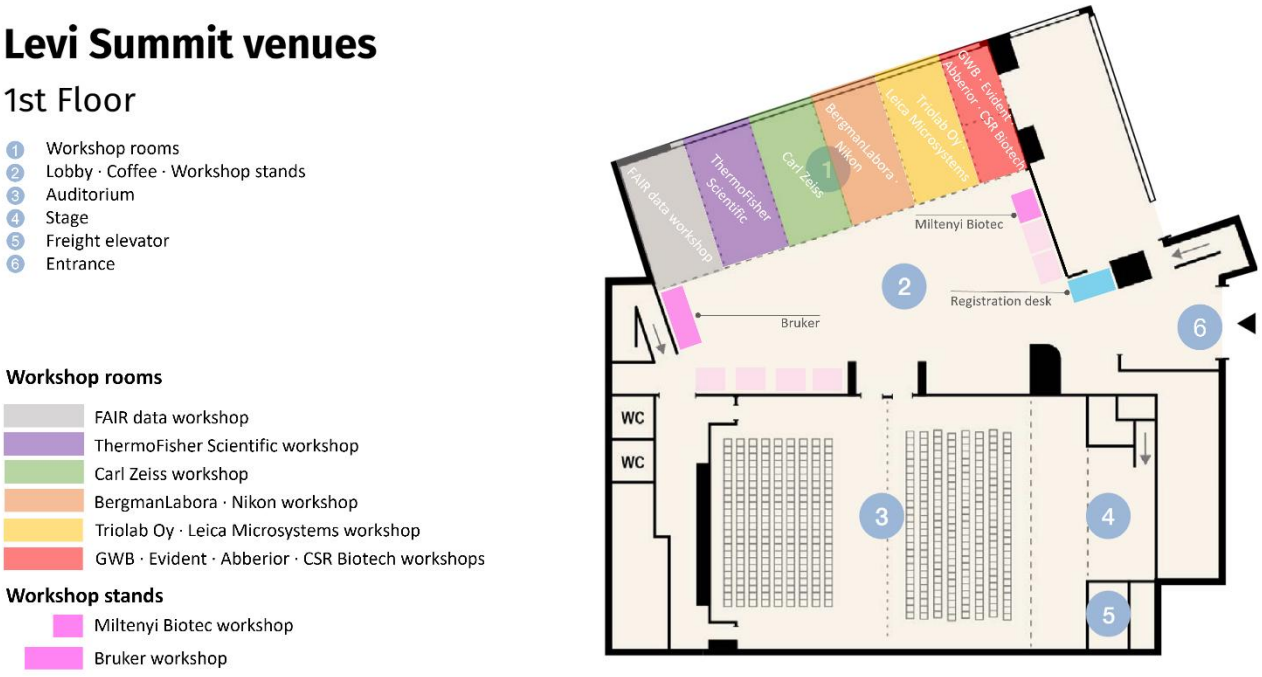
# Pre-Symposium Workshops

We are also organizing BNMI2026 pre-symposium technical workshops, which will be hosted by companies, Euro-BioImaging and Finnish Advanced Microscopy Node image analysts. Our workshops will run in parallel so that the symposium participants will have an opportunity to participate in several of them. Sessions on Monday and Tuesday will be identical.

*Time: Monday, 23 November (17:00–19:00) – Tuesday, 24 November (09:00–11:00)*

*Location: Levi Summit Event Center, Exhibition rooms, Tunturitie 205, 99130 Levi, Finland*

Venue setting for pre-symposium workshops:




Separate workshop registration is required. Workshop places are limited and allocated on a first-come, first-served basis.

## 1. ZEISS LATTICE LIGHTSHEET

***From 2D to 4D – seeing biology unfold in real time***

Join the pre-workshops on 23. or 24. November, including a remote live demonstration from the ZEISS demo lab in Germany. Discover how ZEISS Lattice Lightsheet 7 (LLS7) enables high-resolution, low-phototoxicity 4D imaging of living cells and how established 2D assays can be transformed into dynamic, quantitative 4D high-content experiments, including applications in 96-well plates and drug discovery.

Coming September 2026: Get a first look at the next-generation ZEISS Lattice Lightsheet 7 with SPIM-SMLM — bringing single-molecule localization microscopy to the Lattice Lightsheet platform with high SNR throughout the sample volume. One platform – from dynamic cell biology to single-molecule imaging.

## 2. SMART MICROSCOPY WORKSHOP – POWERED BY NIKON AX R NSPARC

Join us for demonstrations focused on Smart Microscopy pipeline development enabling high content imaging, automated analysis, and AI driven microscopy. You will have the opportunity to take a look at Nikons latest point scanning confocal – AX R with NSPARC super-resolution detector and learn more about how to leverage the NIS Elements software platform to maximise automation and data output. These demonstrations are ideal for researchers looking to increase throughput, improve reproducibility, and extract richer biological insight using advanced imaging and analysis tools.

## 3. OY G.W. BERG & CO WORKSHOPS

### Evident FV5000 New SILVIR detectors-See more with confocal

Our groundbreaking SilVIR™ detectors deliver photon-level quantitation, while redesigned scanner control enables 2K resonant and 8K galvo scanning to capture dynamic events with sharper precision. Smart automation streamlines workflows, and built-in stability ensures reproducible results. Built from legacy and driven by innovation, the FV5000 turns complex imaging into confident discovery.

### *CSR Biotech Cell Xtreme – Next generation live cell imaging platforms*

The Cell Xtreme is a state-of-the-art super-resolution platform combining MI–SIM with label-free Optical Diffraction Tomography (ODT) technology. This unique system combines spatial context with molecular specificity offering unparalleled insights into live-cell dynamics. Welcome to see first Super-resolution system combined with Label free ODT.

### *Abberior STEDYCON 2-confocal, STED, FLIM-uncompromised performance*

Transform any microscope into a powerful confocal, STED super-resolution, and fluorescence lifetime imaging system – within minutes. Compact, intuitive, and future-ready, STEDYCON delivers premium imaging performance in a remarkably small footprint. STEDYCON 2 is a next-generation, plug-and-play imaging solution designed to upgrade any existing microscope into a state-of-the-art confocal and superresolution platform. Welcome to see STEDYCON 2 together with Evident IX85 microscope.

## 4. LEICA MICROSYSTEMS and TRIOLAB OY WORKSHOP

### *Viventis SCAPE: New light sheet microscopy platform for high-speed 3D imaging using standard sample carriers*

Here we present the new Leica Viventis SCAPE, based on oblique plane microscopy (OPM) and swept confocally aligned planar excitation (SCAPE) technologies. This system is designed for high-speed, high-throughput volumetric light sheet imaging and is compatible with commonly used carriers, including glass slides, Petri dishes, and well plates. Viventis SCAPE enables fast 3D imaging without the need for specialized holders or deviations from common sample mounting protocols. Join this session to discover how Viventis SCAPE delivers fast, gentle, and accessible light sheet imaging – bringing high-speed 3D microscopy into standard laboratory workflows.

## 5. BRUKER WORKSHOP

***From Light-Sheet Imaging to Data Insight: An Integrated Workflow for 3D Microscopy***

Modern 3D microscopy workflows require not only rapid image acquisition, but also efficient solutions for handling, storing, and processing large imaging datasets. This workshop presents an integrated workflow combining imaging on the TruLive3D Light Sheet microscope with centralized data management and processing using Acquifer HIVE. The TruLive3D Imager enables multiplexed acquisition of large numbers of samples and experimental conditions within a single experiment, supporting scalable studies of organoids, spheroids, and other complex biological specimens. Expanded samples will be used to illustrate the workflow and demonstrate the generation of large-volume 3D datasets. Acquired data is seamlessly transferred to Acquifer HIVE, a multi-user high-performance platform for image data storage, management, visualization, and processing, providing a streamlined end-to-end workflow from image acquisition to data exploration and collaboration.

## 6. MILTENYI BIOTEC WORKSHOP

***Hands on light sheet imaging + A workflow combining 3D imaging with multiplex analysis***

Join us for a hands-on exploration of 3D light-sheet microscopy using the Ultramicrope Blaze. This workshop will cover the complete workflow, from sample preparation and labeling through 3D image acquisition, analysis, and data processing. We will demonstrate an integrated workflow combining high-throughput light-sheet microscopy with automated data processing, enabling scalable 3D imaging studies across a broad range of biological sample sizes – from organoids, whole organs or even whole specimens. The workshop will also provide a preview of upcoming R&D developments in multiplexing including 3D-2D multiplex imaging. Using interactive data visualization, we will showcase applications in both 2D and 3D multiplex imaging, including datasets reaching hundreds of molecular targets.

## 7. THERMO FISHER SCIENTIFIC HANDS-ON WORKSHOP

***Leveraging AI to accelerate image analysis***

Accurate alignment of serial sections and time-consuming manual segmentation remain major bottlenecks in microscopy image analysis, often limiting throughput, reproducibility, and quantitative consistency. This hands-on session focuses on building an efficient and scalable workflow in Amira Software, addressing these challenges through automated alignment, advanced pre-processing, AI-assisted segmentation, and robust 3D quantification. Participants will work directly within the software to streamline analysis, reduce manual intervention, and generate reliable quantitative insights from complex biological datasets.

NOTE: As this is a hands-on session, participants are required to bring their own laptop computer and mouse.

## 8. COMMUNITY-DRIVEN WORKSHOP

***FAIR data processes and tools***

Join this interactive workshop to explore practical approaches to making bioimaging data Findable, Accessible, Interoperable, and Reusable (FAIR). Through short lectures, community discussions, and live demonstrations, participants will learn about FAIR principles, metadata standards, data management strategies, and repositories for sharing imaging data. The workshop will introduce practical tools and workflows for converting and visualizing imaging datasets, managing structured metadata with OMERO, and preparing data for deposition in public repositories such as the BioImage Archive. Together, we will discuss common challenges in data management and explore solutions to support FAIR data practices in imaging facilities and research laboratories.

# Abstracts

## Speaker abstracts

### Keynote EMBO speaker



**Following lysosome dynamics and repair with light microscopy**

**Harald Stenmark**

Centre for Cancer Cell Reprogramming, Institute of Clinical Medicine, Faculty of Medicine, University of Oslo; Institute for Cancer Research, Oslo University Hospital, Montebello, Norway

Lysosomes are crucial for cell function and organ physiology. They play fundamental roles in the degradation of endogenous and exogenous macromolecules, pathogens and particles as well as damaged or superfluous organelles. In addition, the lysosome membrane is a docking and activation platform for protein complexes that orchestrate metabolic signalling in the cell. The integrity of their membrane is crucial for lysosomes to function as hubs for the regulation of cell metabolism. Various agents, including pathogens, nanoparticles and drugs, can compromise the integrity of the lysosome membrane, and lysosome membrane permeabilization causes leakage of proteases and cations into the cytosol, which can induce cell death pathways and innate immunity signalling. Multiple pathways have evolved to repair damaged lysosomes, and severely damaged lysosomes are degraded by an autophagic process, lysophagy. In this lecture I will discuss how we have been using various light microscopy methods to obtain insights into the mechanisms that ensure the maintenance of lysosomal membrane homeostasis.

## Invited speakers

### SESSION 1 · Mesoscopy and 3D Imaging



**Fibrillar Collagen as an imaging biomarker for uterine health and pregnancy progression**

**Renata Prunskaite-Hyyryläinen**

Faculty of Biochemistry and Molecular Medicine, University of Oulu, Finland

The uterine extracellular matrix (ECM), uterine glands, and implanted embryo are essential components of a functional uterus and fertility. However, they are rarely examined in relation to each other, and little is known about how the uterine endometrium and ECM change in 3D during the uterine life cycle, largely due to the lack of suitable study methods.

To address this, we applied second- and third-harmonic generation microscopy to develop and validate tools for assessing uterine fibrillar collagen. We established an original ex vivo method, **3DMOUSEneST** (PMID: 39868420), enabling label-free 3D visualization and quantification of uterine collagen deposition, early murine embryo growth, and prediction of pregnancy outcomes.

Using second-harmonic generation imaging, we quantified collagen dynamics in murine uteri across the estrous cycle in response to circulating sex hormones. Building on this, we developed a novel **SHG casting** (PMID: 41403834) method, which digitally fills glandular "hollows" defined by collagen scaffolds, allowing label-free 3D reconstruction and analysis of uterine gland morphology. This approach is supported by deep learning-based segmentation and is adaptable to a wide range of epithelial structures.

These methodological advances integrate reproductive biology and ECM research. We anticipate that **3DMOUSEneST** and **SHG casting** will have broad applications beyond uterine research, enabling analysis of diverse structures supported by fibrillar collagen-rich ECM.



## Whole-brain clearing and multi-channel light-sheet imaging for sex differences in mouse models of autism spectrum disorder

**Moritz Negwer**

Donders Institute for Brain, Cognition and Behaviour, Radboud University Medical Center, Nijmegen, Netherlands

Screening for cell-level differences on a whole-organ level is difficult to do with slice immunostainings - especially if done at scale, across hundreds of organs. This scale can be achieved with tissue clearing in combination with multi-channel staining.

Here, we investigate the cellular composition of mouse brains with a modified INSIHGT protocol [1] scaled to four channels. We use a combination of directly-tagged plant lectins (WFA) to label perineuronal nets, directly-tagged antibodies to visualize cell populations (TH for catecholaminergic neurons and Iba1 for microglia), and a near-infrared nuclear counterstain (NucSpot 750).

We then clear the brains and image them with a light-sheet microscope (Miltenyi Ultramicroscope II) at 4x, stitch and compress the images using the OME-Zarr format and detect the labelled cells in four channels using the DELiVR pipeline [2]. We custom-train the deep-learning segmenter with training data generated in virtual reality (VR).

As a result, we get the precise coordinates of every labelled cell, as well as the general cytoarchitecture via the nuclear counterstain. We use this approach to screen for sex-specific changes in the brains of model mice for Autism Spectrum Disorder (ASD). We are actively encouraging other groups with ASD mouse models to collaborate, so that we can get a broader view of 3D cytoarchitecture across as many mouse lines as possible.

References:
1. Yau et al., Nature Communications, 2024
2. Kaltenecker et al., Nature Methods, 2024

## SESSION 2 · Advances in Microscopy



### Smart microscopy for adaptive imaging

**Suliana Manley**

Laboratory of Experimental Biophysics, Institute of Physics, Interfaculty Institute of Bioengineering, EPFL SB-LEB, Lausanne, Switzerland

Fluorescence microscopy offers insights into subcellular dynamics, yet is often restricted by a limited photon budget. We developed “Event Driven Acquisitions,” a microscope feedback loop incorporating a neural network trained to recognize dynamic events and adapt the measurement in real-time. As a proof-of-concept, we detected mitochondrial dynamics, to prioritize capturing fission events. We then extended the EDA framework to include phase contrast microscopy and channel switching, allowing us to additionally capture mitochondrial pearling events, as well as organelle contacts. We use these methods to reveal new mechanisms for mitochondrial content management.

## SESSION 3 · Imaging Applications



### Pharmaceuticals under the nonlinear optical microscope

**Clare Strachan**

Division of Pharmaceutical Chemistry and Technology, Faculty of Pharmacy, University of Helsinki, Finland

Microscale chemical and physical behavior of drugs and dosage forms in different environments can profoundly affect pharmaceutical performance. Despite this, characterising such behavior can pose a real analytical challenge with established analytical methods. Non-linear optical microscopy, is a relatively new analytical technology that is, in many respects, ideally suited for such analyses. Collectively, it includes different non-linear optical phenomena, such as stimulated Raman scattering (SRS), sum frequency generation (SFG) and two-photon excited fluorescence (TPEF). Non-linear optical microscopy offers rapid, non-destructive, label-free, chemically and solid-state specific imaging with (sub)micron spatial resolution. It can reveal, for example, trace (changes in) solid-state forms, drug and excipient distributions in dosage forms, rapid phase changes during drug release (such as amorphous-amorphous phase separation), and nanoparticle localisation within in cells and tissues. The greatest analytical power is realised when different non-linear optical phenomena are correlatively combined based on their complementary sensitivities and specificities. This talk will put pharmaceuticals under the non-linear optical microscope, and, through the use of case studies, consider possibilities (and pitfalls) for revealing microscale secrets.

## SESSION 4 · Label-free Imaging



### Structural diversity of amyloid aggregates across mouse models and human brain tissue revealed by vibrational imaging

**Oxana Klementieva**

Laboratory of Medical Microspectroscopy, Department of Experimental Medicine, Lund University, Sweden

Amyloid accumulation in brain tissue is a key feature of neurodegenerative diseases, but these aggregates are not uniform – they vary in structure. It remains unclear how this structural variability relates to biological effects such as neurotoxicity and neuroinflammation.

Mouse models are widely used in research on memory research and specifically, in neurodegeneration. However, animal model relevance depends on how well they reflect the structural features observed in human Alzheimer's disease. We hypothesized that commonly used mouse models capture only part of the structural diversity found in humans. The key question was which models most closely resemble human amyloid structure.

To address this, we used high-resolution spectroscopic imaging to map amyloid structures directly in brain tissue. This novel label-free approach enables detection of specific aggregate structures at high spatial resolution without extraction or purification, allowing analysis of amyloid in its native tissue context and linking structure to local biological responses.

We compared several transgenic mouse models with human Alzheimer's disease brain tissue. The results show that amyloid structures differ between models and only partly match those observed in humans. Differences were detected both between plaques and within individual deposits.

We conclude, that even if each mouse model captures only a part of the structural diversity seen in human disease, understanding their limitations is therefore critical for selecting appropriate models and accurately interpreting disease mechanisms as mouse models remain an essential research tool that cannot be fully replaced by cultured cells or tissues.

## SESSION 5 · High-Content Imaging and Image Analysis



### Large-scale microscopy datasets for image-based profiling and model development

**Lassi Paavolainen**

Institute for Molecular Medicine Finland-FIMM, HiLIFE, University of Helsinki, Finland

I will present two large-scale microscopy datasets collected and prepared for data-driven discoveries and foundation model development. We have generated a Blood Cell Painting dataset including images from 50 million cells collected from 390 healthy donors for morphological profiling of immune cells. These images were profiled to extract donor-level features that we associate with donors' genetic background. Our study establishes Blood Cell Painting as a versatile method for immune cell profiling to uncover genetic, phenotypic and clinical determinants of immune cell morphology in health and disease. Further, we curated CHAMMI-75, an open access dataset of heterogeneous, multi-channel microscopy images from 75 diverse biological studies, for channel-adaptive microscopy model development. Our experiments show that training with CHAMMI-75 can improve performance in multi-channel bioimage profiling tasks through its high diversity in microscopy modalities. This work paves the way to cellular foundation model development for biological studies.

## SESSION 6 · Electron Microscopy and Multimodal Imaging



### Cryo-electron tomography of the Baltic Sea microbiome

**Linda Sandblad**

Umeå Centre for Electron Microscopy (UCEM), SciLifeLab Umeå, Sweden

Umeå Centre for Electron Microscopy (UCEM) is a Nordic hub for cryo-EM, electron tomography and volumeEM. The facility supports interdisciplinary research projects as a SciLifeLab platform, providing international open access to seven electron microscopes and sample preparation in dedicated cryo-EM facilities including plunge freezing, high pressure freezing, cryo-FIB lamella preparation and cryo-CLEM. In this presentation: Cryo-electron tomography enables a direct method to characterize cellular structures of marine microorganisms at nanometer resolution in their native state. We have developed a protocol for sampling of the microbial communities at the Umeå Marine Sciences Center. Compared with bacteria culture controls of sea water Cyanobacteria and soil Streptomyces. Collected cryo electron tomograms, using 300 kV cryo-TEM Titan Krios, of unique bacteria, reconstructed by SNARTomo, IMOD and visualized by Dragonfly. A research project with an aim to present a library of cryo-EM data of the microbiome. Direct visualization, containing structural information, cellular morphology and cryo-EM proteomics analysis will generate more reliable models of marine biomass and ecosystem predictions.

## Contribution Talks

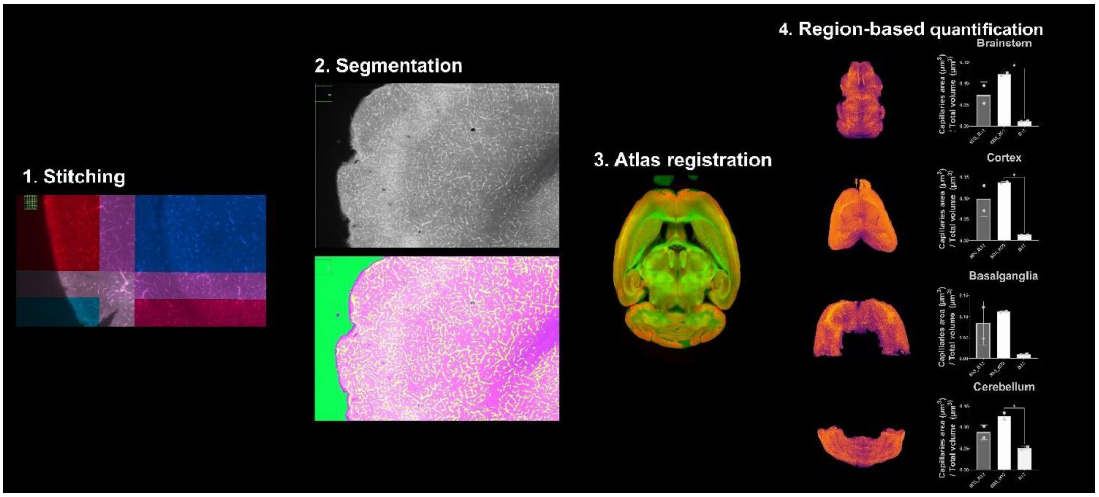
### SESSION 1 · Mesoscopy and 3D Imaging

**Automated atlas-based quantification of brain shuttles delivery using lightsheet microscopy**

**Judit Prat-Duran**[1]; Donato Sardella[1]; Kathrine Hyldig[1,2]; Rasmus Folmann Christiansen[1,2]; Morten S. Nielsen[1]

[1] Department of Biomedicine, Aarhus University, Denmark
[2] H. Lundbeck A/S, Valby, Denmark

The blood–brain barrier (BBB) is still the main challenge of brain drug delivery. Efforts have been placed on developing shuttles that cross the BBB, but current methods for studying brain penetration relay largely on brain homogenates, which cannot distinguish between capillary-bound signal and true parenchymal uptake, leading to an overestimation of BBB transport. We present an imaged-based re-producible pipeline for quantitative and spatially resolved assessment of brain shuttle distribution. First, shuttles are fluorescently labelled and administered via the desired route, followed by perfusion with 10% neutral formalin buffer. Brains are cleared using 20% N-Butyldiethanolamine and increasing tetrahydrofuran concentrations up to 100%, stored in ethyl cinnamate, and imaged on a Zeiss Light-Sheet7 microscope with a 5x objective, acquiring tiled z-stack datasets. Images are processed in Fiji (ImageJ 1.54p): tiles are stitched with BigStitcher, background corrected and segmented into capillary and parenchymal compartments using Labkit. Whole-brain datasets are registered to the Princeton Mouse Atlas using Elastix and BigWrap, enabling anatomical localization of the signal. Finally, capillary-bound and parenchymal signals are quantified across the brain regions of interest. This scalable pipe-line provides a standardized high-resolution framework for assessing BBB shuttle performance, and it is adaptable to different light-sheet microscopes, imaging objectives, and animal species.



**Microscopy-driven characterization of rainbow trout hepatic 3D spheroids with multimodal analytical validation**

**Prem Chand**[1, 2]; You Song[2]; Awadhesh Jha[3]; Tania Gomes[2]; Maria T. Hultman[2]

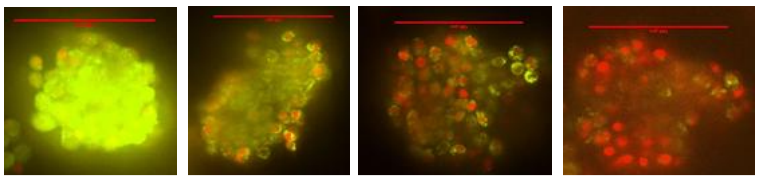
[1] University of Oslo, Norway
[2] Norwegian Institute for Water Research (NIVA), Norway
[3] University of Plymouth, United Kingdom

New Approach Methodologies (NAMs) are increasingly required to improve ecotoxicological risk assessment while reducing reliance on animal testing. This study proposes rainbow trout (Oncorhynchus mykiss) hepatic spheroids as a NAM for ecotoxicity testing, and being a relatively new model, they require further characterisation.

In this study, high-resolution confocal and two-photon microscopes were applied to examine spheroid architecture and functional integrity. Imaging endpoints included cytoskeletal organisation, nuclear structure, spatial viability, and hypoxia distribution, alongside subcellular responses such as reactive oxygen species (ROS) generation and mitochondrial membrane depolarisation. These approaches enabled spatially resolved assessment of spheroid health and stress responses.

Complementary multimodal detection platform-based assays (LDH, propidium iodide, WST-1, $H_2$DCFDA, and TMRM) supported and validated the microscopy data. Exposure (24–96 h) to chemicals with distinct modes of action, such as copper, 17α-ethinylestradiol, and carbonyl cyanide m-chlorophenyl hydrazone (CCCP), induced reproducible, mechanism-specific alterations detectable at both cellular and subcellular levels in spheroids.

Spheroids revealed consistent and reproducible stress responses, enabling sensitive detection of cytotoxicity, membrane depolarisation, and oxidative stress effects. These validation studies further strengthen this 3D cellular model as a potential tool for ecotoxicity



Contrl Low Medium High

**Qualitative assessment of cytotoxicity using confocal imaging.** Spheroids were exposed to different concentrations of copper (Cu) for 24 h and stained with H2DCFDA (green) propidium iodide (PI, red) to assess intracellular reactive oxygen species (ROS) and cell death. Scale bar = 100µm.

## SESSION 2 · Advances in Microscopy

### Micro-stepping extended focus reduces photobleaching and preserves structured illumination super-resolution features

**Xian Hu**[1]; Michael Sheetz[2]; Oddmund Bakke[3]; Felix Margadant[3]

[1] CanCell, Faculty of Medicine, University of Oslo, Norway
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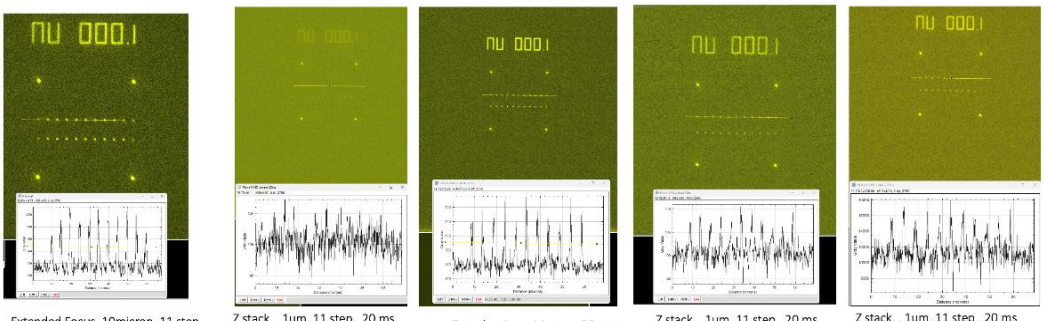
Despite the progress made in fast scan units, confocal systems still have insufficient temporal resolution for many volume imaging requirements, such as tracking movement of membrane vesicles in live cells. Researchers might sacrifice certain imaging modalities to achieve better performance in temporal resolution. This may result in imaging artifacts such as undersampling artifacts and limit the amount of analyzable data.

We propose an imaging modality producing fast projections from the field of depth which will shorten the imaging time by approximately an order of magnitude compared to volume imaging. The implementation requires merely a minimum two synchronized control signals that drive a piezo stage and trigger the camera exposure, a third, optional signal, blanks the laser output when the stage is in motion which mildly improves the stability and repeatability of the exposure. The device generating the signals has been tested on spinning disk confocal as well as on instant structured-illumination-microscopy (iSIM) microscopes. Our calibration images show that the approach provides highly repeatable and stable imaging conditions and does enable photometric measurements of the acquired data, in both the regular spinning disk setup as well as in the iSIM configuration. While light sheet microscopes can provide even faster projections of the same volume, the presented method provides more homogeneous optical sectioning and maintains the structured illumination characteristics.



Extended Focus, 10micron, 11 step , 202 ms exposure

Z stack, , 1um, 11 step , 20 ms exposure, Median intensity projection

Z stack, , 1um, 11 step , 20 ms exposure, Maximum intensity projection

Z stack, , 1um, 11 step , 20 ms exposure, Average intensity projection

Z stack, , 1um, 11 step , 20 ms exposure, SUM intensity projection



WF

Confocal

**Light as a probe for living systems**

**Antonio Fiore**[1]

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Light microscopy is a fundamental readout in all clinical and biomedical fields, supporting scientific discovery across research topics, spatial scales, and model organisms [1]. Modern microscopy leverages molecular tagging to visualize biomolecules with great sensitivity and resolution [2,3]; yet many foundational questions hinge on properties that cannot be easily quantified with traditional methods; for instance: the mechanical properties of cells and tissues [4], the architecture of extracellular matrix (ECM) [5], and the dynamics of ions in the brain [6]. This talk highlights technology developments to these readouts: i. Brillouin microscopy for biophysical characterization [7]; ii. Rhobo6, a dye for live ECM imaging [8]; iii. A new extracellular calcium sensor. Together, these methods extend microscopy capabilities to new mechanical, structural, and functional readouts, enabling researchers to access biological structure and function across scales.

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**Tracking Sodium-Potassium ATPases (NKA) using MINFLUX**

**Devinda Wijewardena**[1,2]; Hjalmar Brismar[1,2]

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Sodium-Potassium ATPase (NKA) pumps maintain intracellular ion balance and cell volume by extruding three Na+ ions and intruding two K+ ions, generating, a net outward current. NKA contributes to maintaining cell volume, and maintaining cellular signalling pathways. NKA function-irregularities are implicated in many diseases.

In this study, we are characterizing the dynamic behaviour of NKA pumps using MINFLUX nanoscopy. We use single-colour MINFLUX tracking to visualize the diffusion of NKA on the cell membrane surface under varied physiochemical conditions. The NKA was conjugated to Abberior-STAR-RED dyes. The NKA was expressed in human kidney HEK293A cells using Super-Ecliptic pHluorin (SEP), a Green Fluorescent Protein (GFP) variant. We vary buffer conditions to regulate the NKA diffusion rate, ATP concentrations, and pump activity. We quantify the diffusion of NKA, with the end objective of observing the localized rotations of individual NKA pumps, and their regulation mechanisms.

## SESSION 3 · Imaging Application

### Rapid ER remodeling by peptide-lipid complexes - peripheral ER collapse and vesiculation, nuclear ER expansion and nuclear shape change

Samudra Sabari[1]; Siddharth Chinchankar[1]; Ines Ambite[1]; Atefeh Nazari[1]; António Pedro N. B. M. Carneiro[1]; Axel Svenningsson[1]; Catharina Svanborg[1]; **Arunima Chaudhuri**[1]

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Conformationally fluid peptide-lipid complexes have been identified as potent tumoricidal agents in cellular models and clinical trials [1]. Here, we identify a novel ER response triggered by the tumoricidal complex alpha1-oleate, defined by a loss of peripheral ER structure, extensive ER vesiculation. Alpha1-oleate was present in the ER-derived vesicle (EDV) membranes, also decorated by ER-resident and interacting proteins, calnexin and ORP3, and in their lumen, also enriched for KDEL, confirming their ER origin distinct from lipid droplets. Rapid nuclear uptake of the complex constituents resulted in diffuse nuclear staining and the asymmetrical perinuclear enrichment of the collapsing ER with its content of alpha1-oleate created large invaginations lined by the ER, inner nuclear membrane markers and lamin nucleo-skeleton. In parallel a change in nuclear shape, resulted in a volcano-like structure. This newly discovered, potent ER response to alpha1-oleate may have evolved to package ER associated cellular contents in the nuclei of dying tumor cells thus sequestering toxic cell debris associated with apoptotic cell death [2].

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**Cluster Assembly Dynamics Drive Fidelity of Planar Cell Polarity Polarization**

**Silas Boye Nissen**[1,2,3]; Alexis T. Weiner[1]; Kaye Suyama[1]; Pablo Sanchez Bosch[1]; Maiya Yu[1,4,5]; Song Song[1]; Yuan Gu[6]; Alexander R. Dunn[3]; Jeffrey D. Axelrod[1]

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[2] The Novo Nordisk Foundation Center for Stem Cell Medicine (reNEW), University of Copenhagen, Copenhagen, Denmark
[3] Department of Chemical Engineering, Stanford University, Stanford, CA, USA
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In planar cell polarity (PCP) signaling, distinct molecular subcomplexes segregate to opposite sides of each cell, where they interact across intercellular junctions to form asymmetric clusters. Although proximal-distal asymmetry within PCP clusters is the defining feature of PCP signaling, the mechanism by which this asymmetry develops remains unclear. Here, we developed a method to count the number of monomers of core PCP proteins within individual clusters in live animals and used it to infer the underlying molecular dynamics of cluster assembly and polarization. Measurements over time and space in wild type and in strategically chosen mutants demonstrate that cluster assembly is required for polarization, and together with mathematical modeling provide evidence that clusters become increasingly asymmetric and correctly oriented as they increase in size. We propose that cluster assembly dynamics amplify weak and noisy inputs into a robust cellular output, in this case, cell and tissue-level polarization.

## Mitochondrial positioning by CDK1-MAP4 regulates focal adhesions, redox signaling and cell migration

**Omkar Joshi**[1]; Trinh Pham[1]; Monika Vaitkevičiūtė[1]; Michal Dibus[1]; James Conway[2]; Johanna Ivaska[1,3,4,5,6]

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Cell migration requires coordinated of focal adhesion (FA) dynamics, cytoskeletal remodeling and energy metabolism. Although mitochondria are proposed to support migration by supplying ATP at the cell periphery, it remains unclear whether functionally distinct mitochondrial subpopulations exist within migrating cells and how their spatial organization is regulated. Using live-cell imaging, dynamic micropatterning, and quantitative functional probes for mitochondrial membrane potential, ATP, calcium and ROS, we show that mitochondria move into protrusions during FA assembly, and retract from regions undergoing FA disassembly and membrane retraction. Contrary to the prevailing view, protrusion-localized FA-proximal mitochondria display lower membrane potential and ATP, but elevated ROS compared to their perinuclear counterparts, identifying them as a functionally distinct peripheral subpopulation. Phosphoproteomic profiling reveals that CDK1-mediated phosphorylation of the microtubule-associated protein MAP4 limits mitochondrial trafficking into protrusions, and that CDK1 inhibition or MAP4 depletion triggers mitochondrial streaming to the cell periphery and freezes FA turnover. Together, our data define a FA–CDK1–MAP4 regulatory axis that coordinates mitochondrial positioning with FA dynamics through spatially compartmentalized ROS signaling, and establish that mitochondrial mobility, rather than peripheral localization alone, is essential for efficient cell migration.

## SESSION 4 · Label-Free Imaging

### Digital holographic microscopy of biomolecular condensates in an electric field

**Jennifer Tersteegen**[1,2,5]; Adam L. Harmat[3,5]; Joshua T. Arrington[4]; Antti J. Mäkynen[1,3,5]; Pekka Peljo[3]; Mikko P. Haataja[4]; Maria Sammalkorpi[3,5]; Markus B. Linder[2,5]; Jaakko V. I. Timonen[1,5]

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[5] Centre of Excellence in Life-Inspired Hybrid Materials (LIBER), Aalto University, Espoo, Finland

Formation of biomolecular condensates via liquid-liquid phase separation has emerged as a crucial mechanism for biomaterials assembly and cellular processes. However, imaging of biomolecular condensates is challenging, as conventional techniques such as fluorescent labelling can alter condensate behavior or lead to misinterpretation of results. Label free techniques such as digital holographic microscopy (DHM) provide a promising alternative, allowing for clear identification of different phases based on refractive index changes correlating with a phase shift.

Here, we utilize DHM to image the electric field response of silk protein condensates. Condensates show diverse, voltage-dependent behavior, ranging from shape and interface changes at low voltages, to reversible disappearance at moderate voltages, and the emergence of electro convective patterns at high voltages. We connect our findings to electric field induced changes in wetting of condensates and to changes in the pH within the sample gap, leading to changes in the phase separation behavior of silk proteins. This highlights the use of electric fields to control and manipulate biomolecular condensates.

Our work shows the advantages of using DHM to capture the dynamic behavior of condensates but also points out limitations of this technique.

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**Coherent X-rays for imaging of wood — identifying challenges for hierarchical biological samples**

**Taisiia Cheremnykh**[1]; Maik Kahnt[2]; Paavo Penttilä[1]

[1] University of Jyväskylä, Finland
[2] MAX IV Laboratory, Sweden

Modern X-ray sources, such as the MAX IV synchrotron in Sweden, open up new avenues for Xray microscopy using coherent X-rays, and also provide the infrastructure necessary for the comprehensive characterisation of biological samples [1]. Forward X-ray ptychography requires and exploits the coherence of X-rays for phase retrieval [2]. This technique is available at the NanoMAX beamline [3] and enables label-free imaging of biological tissues based on phase contrast, with the phase being retrieved computationally. Depending on the properties of the sample, X-ray ptychography can provide nanoscale resolution of large specimens. Unlike other X-ray imaging techniques, the resolution in ptychography is not limited by the beam size, and scanning enables a large field of view. Scanning transmission X-ray microscopy (STXM) enables the rapid identification of regions of interest (ROIs) for ptychographic reconstruction. Tree is a great example of a biological sample with hierarchical structural organisation. Not only is it a source of advanced, sustainable wood-based materials that are highly relevant for Nordic countries [4], this hierarchical structure also serves as a stepping stone from plant to animal organisms in structural studies of biological samples. In our feasibility study, we used STXM to identify our ROIs. We confirmed the applicability of forward X-ray ptychography for imaging wood and identified challenges that are relevant to many other biological samples.

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## SESSION 5 · High-Content Imaging and Image Analysis

### Multiplexed High-Content Imaging for Drug Screening in Rheumatoid Arthritis Synovial Fibroblasts

**Phatthamon Laphanuwat**[1]; Christof Seiler[1]; Caroline Ospelt[1]

[1] Center for Experimental Rheumatology, Department of Rheumatology, University Hospital Zurich, University of Zurich, Zurich, Switzerland

Synovial fibroblasts (SFs) drive chronic inflammation and joint destruction in rheumatoid arthritis (RA), yet no standardized method exists to screen compounds modulating their pathogenicity. We present a multiplexed high-content imaging; HCI pipeline to address this gap. Building on prior observations of dysregulated autophagy, mitochondrial function, and lipid metabolism in activated SFs, we curated an FDA-approved library of 90 compounds targeting these vulnerabilities. Two fluorescence panels were deployed in 384-well format across six RA patient lines: Panel 1 (MitoSOX, LipidTOX, EdU) and Panel 2 (CYTO-ID, TMRM, SiR-Lysosome), with Cell Painting as a morphological readout. Screening of 30 compounds revealed distinct functional response profiles. Multidimensional imaging features were analyzed using a leave-one-out random forest classifier, with effect sizes displayed as volcano plots to identify significant shifts relative to control. Cell Painting flagged cytotoxic compounds, confirmed by an independent viability assay; only non-cytotoxic hits proceed further. Hits will be ranked by a composite feature score benchmarked against healthy SF profiles and validated by dose-response assays. Clinical relevance will be assessed retrospectively by examining disease activity in RA patients previously exposed to identified candidates. Future work will extend this pipeline to a 3D synovial microtissue model. This approach links preclinical HCI screening to clinical validation in RA.

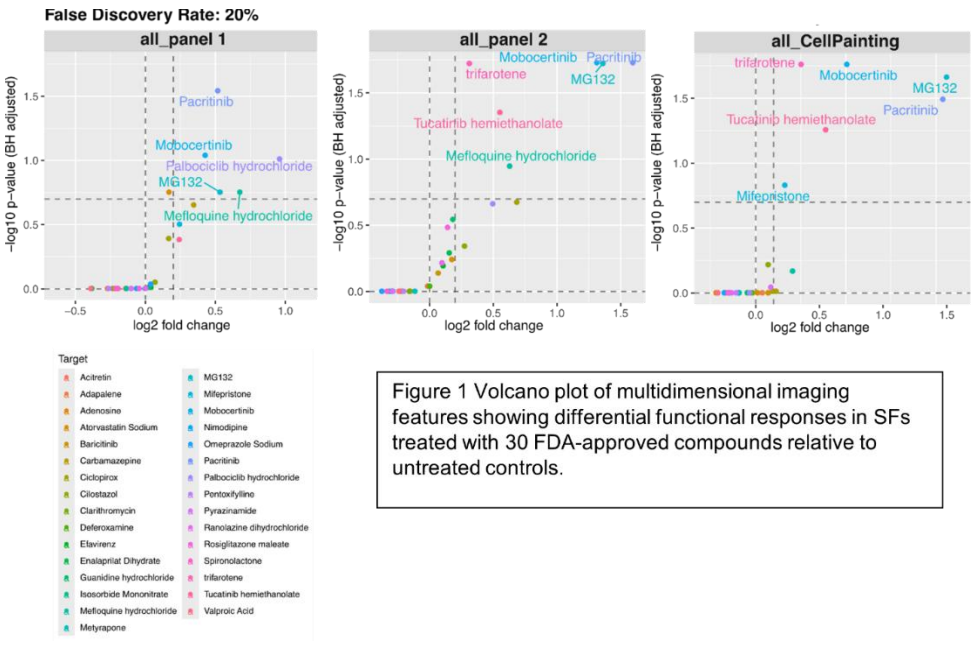


Figure 1 Volcano plot of multidimensional imaging features showing differential functional responses in SFs treated with 30 FDA-approved compounds relative to untreated controls.

**Polar ordering during transition from dormant to migrating epithelia**

**Anna Lång**[1]

[1] Oslo University Hospital, Oslo, Norway

The transition from dormancy to collective migration in epithelial tissues is crucial for wound healing, tissue patterning, and cancer invasion. We investigate this transition by tracking cell movements in keratinocyte monolayers after serum withdrawal and subsequent re-addition, an experimental approach that mimics static-to-dynamic state changes. High-content time-lapse imaging reveals that localized contractile sites nucleate +1 asters in epithelial monolayers after serum re-exposure, which in turn generate propagating polarity domain walls. Polar defects are created, transported, and annihilated along these walls, and the associated active flows drive defect coarsening at rates that exceed those expected from passive elastic relaxation. Numerical simulations using an active elastic model that couples actomyosin contractility to tissue deformation reproduce the experimental observations. Together, our results show that stress generated internally within the monolayer can drive topological reorganization in dormant epithelia. These findings provide a distinct route to polar ordering that is fundamentally different from classical flocking and unjamming transitions.

## Virtual multistaining of histological whole slide images based on generative AI and a panel of special stains

**Sonja Koivukoski**[1]; Hyder Abbas[2]; Siiri Sirviö[1]; Kirsikka Wirtanen[1]; Hesam Hakimnejad[2]; Pekka Ruusuvuori[2]; Leena Latonen[1]

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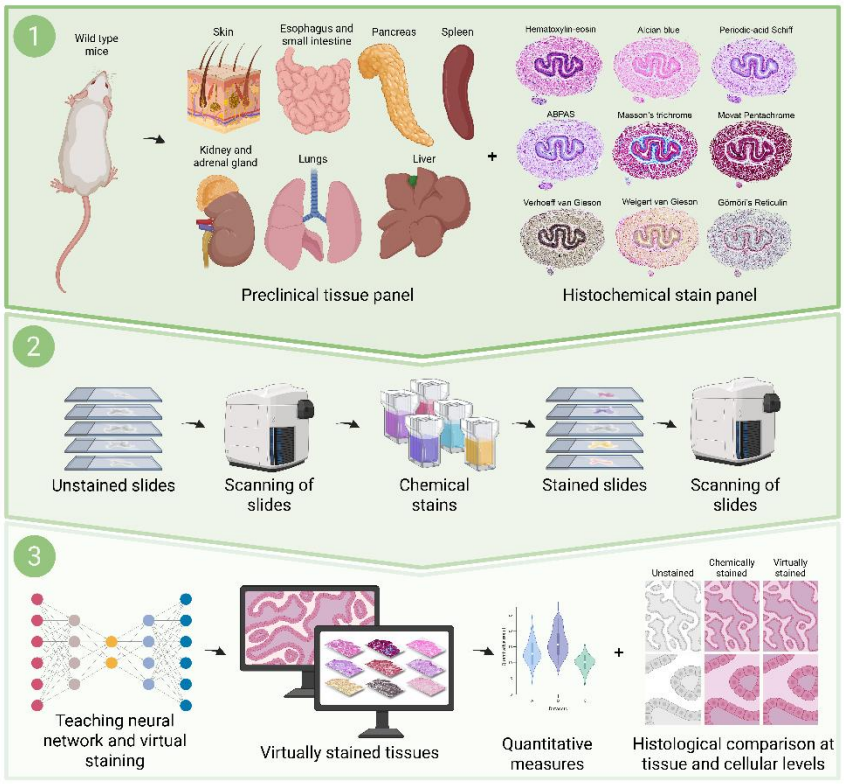


Histological tissue examination is based on the assessment of different morphological features in a variety of histological special stains. The purpose of the stains is to color the nearly invisible tissue specimens visible to the naked eye and highlight certain structures within the tissue. These methods, however, consume precious sample material, chemicals, and time. Our goal is to apply a previously established computational virtual staining method [1,2] to a tissue and staining panel (Figure), which includes the most common histological special stains and a large scale of different tissue structures. Our virtual staining algorithm utilizes machine learning and unstained tissue which enables faster tissue analysis and saves resources [1-3]. With this method, we could improve the currently very manual and laborious histological analysis methods in clinical laboratories and facilitate research by enabling more diverse single-cell–level analysis through multimodal approaches [3,4]. The results of this study show that the majority of the different stains and tissues perform well showing accurate histological details in the virtually stained images. These results could aid us in developing disease diagnostics for the future, which would allow patients to receive critical care faster.

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## SESSION 6 · Electron Microscopy and Multimodal Imaging

### From cells to molecules: multimodal bioimaging reveals the structural plasticity of the *Staphylococcus aureus* virulence peptide PSMα1

**Sambhasan Banerjee**[1]; Valeriia Skoryk[2,3]; Bader Rayan[4]; Eilon Barnea[4]; Enrico Caragliano[1,5,6]; Alexander Golubev[1]; Nikolay Vinogradov[4]; David Flores[8]; Sindhuja Joel[1,2]; Mariana Pigozzi Cali[1,2]; Emil Gustavsson[1,2]; Jens Bosse[1,6,7]; Markus Zweckstetter[8, 9]; Thomas Gutsmann[1,10]; Oxana Klimentieva[3]; Meytal Landau[1,2,4,11]

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Phenol-soluble modulin α1 (PSMα1) is a virulence peptide secreted by Staphylococcus aureus that drives host-cell damage and biofilm formation, yet how its structural transitions govern function remains unknown. We combined confocal microscopy, cryo-electron microscopy, cryo-electron tomography, atomic force microscopy, X-ray fibre diffraction and optical photothermal infrared spectroscopy to visualise PSMα1 across cellular and molecular scales. Live-cell imaging shows that PSMα1 accumulates at the plasma membrane before membrane permeabilisation, identifying membrane association as the initiating event in cytotoxicity. This interaction is strongly inhibited by epigallocatechin gallate (EGCG). Cryo-EM resolves two polymorphic amyloid fibril architectures with a conserved hydrophobic core, while complementary structural imaging reveals that environmental pH redirects assembly into either canonical cross-β fibrils or thermally stable α-helical nanotubes that act as transient intermediates during fibril formation. Together, these findings reveal PSMα1 as an environment-responsive structural system in which assembly dictates membrane interactions and cytotoxic activity. More broadly, this work demonstrates how multimodal bioimaging can bridge molecular structure with cellular function, providing a powerful framework for understanding dynamic biomolecular assemblies in infection and beyond.

**Membrane contacts between caveolae and the endoplasmic reticulum involved in fatty acid metabolism**

**Sebastian Rönfeldt**[1,2,3]; Elin Larsson[2,3]; Björn Morén[2]; Alexander J Craig[4]; Lindon William Kirk Moodie[4]; Robert Glenn Parton[5,6]; Richard Lundmark[1,2,3]

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[4] Drug Design and Discovery, Department of Medicinal Chemistry, Uppsala University, Uppsala Biomedical Center, Uppsala, Sweden
[5] Institute for Molecular Bioscience, The University of Queensland, Brisbane, Queensland, Australia
[6] Centre for Microscopy and Microanalysis, The University of Queensland, Brisbane, Queensland, Australia

The vital process of cellular fatty acid metabolism involves uptake, metabolic trapping and storage of long-chain fatty acids (LCFAs) in different lipid species. Although several different enzymes like transporters and acyl-CoA synthetases are involved, the sequential mechanistic steps of the process are poorly understood. With different approaches we address the role of the caveola coat protein caveolin1 and the acyl-CoA synthetase FATP1 in this process as both have major impacts in the uptake and storage of fatty acids in vivo and in vitro. Using live cell microscopy and mass spectrometry-based quantification of LCFA metabolism, we take a look at uptake and metabolic processing. With correlative light and electron microscopy we tackle the question if membrane contact sites are formed between FATP1-enriched endoplasmic reticulum (ER) and caveolae. With particle tracking we analyse the temporal stability of such contacts differentiating between dynamic and persistent stages. While Structured Illumination Microscopy offers us the possibility to analyse the biological relevance of such contacts.

**Mechanosensitive membrane microdomains imaged through a lens of fluorescence and cryogenic electron microscopes**

Arda Kara[1]; Hanna Dahl[1]; Farha Mou[1]; **Markku Hakala**[1]

[1] Institute of Biotechnology, University of Helsinki, Finland

The plasma membrane (PM) serves as a critical barrier between the cell and its environment and plays a key role in mechanical sensing. It is highly complex in both lipid composition and associated proteins. PM lipids are distributed asymmetrically between the leaflets and are also laterally organized within the membrane. Membrane-interacting proteins are essential both in shaping cellular membranes and in organizing membrane lipids. Some proteins stabilize underlying lipids into distinct microdomains.

Here, we investigate how an N-BAR domain protein BIN1 remodels membranes and promotes lipid microdomain formation. The muscle-specific BIN1 isoform drives tubulation of the sarcolemma into T-tubules, which are connected to the sarcoplasmic reticulum through membrane contact sites. T-tubules are crucial for muscle's excitation-contraction coupling and must withstand mechanical stress to maintain normal muscle functions.

We use fluorescence correlation spectroscopy (FCS) and fluorescence recovery after photobleaching (FRAP) to measure diffusion of fluorescently labelled lipids in free membranes and under BIN1 protein coats. Using fluorescence lifetime imaging microscopy (FLIM) and the lipid-packing-sensitive probe Flipper-TR in reconstituted systems and living cells, we demonstrate how BIN1 alters membrane packing. Finally, cryogenic electron microscopy visualizes membrane microdomains and reveals structural details of how proteins organize lipids within membranes.

# Posters Abstracts

## Table of content


1. **LVB Imaging Centre – a core facility for advanced light microscopy at the Life Science Building (LVB) in Oslo**

**Anna Lång**, Oslo University Hospital, Oslo, Norway

2. **Aarhus University Health Bioimaging Core Facility**

**Anna Lorentzen**, Department of Biomedicine, Aarhus University, Denmark

3. **Advancing precision oncology through High-Content Imaging and Phenotypic Profiling**

**Antti Hassinen,** High Content Imaging and Analysis core unit, Institute for Molecular Medicine Finland (FIMM), Helsinki Institute of Life Science (HiLIFE), University of Helsinki, Helsinki, Finland

4. **Feedback microscopy for automated imaging of rare events in the Bioimaging Core Facility at the Danish Cancer Institute**

**Chris Dinant,** Bioimaging Core Facility, Danish Cancer Institute, Denmark

5. **Imaging and analysis of 3D patient-derived organoids using the Celigo Image Cytometer**

**Dean Shaw,** Revvity Cellular Technologies GmbH, Hamburg, Germany

6. **Live confocal imaging and image analysis of immune-cell chemotaxis in reconstructed skin**

**Dylan Salgues,** 1: Centre for Cellular Immunotherapy of Haematological Cancer Odense (CITCO), Department of Clinical Immunology, Odense University Hospital, University of Southern Denmark, Odense, Denmark; 2: Department of Biochemistry and Molecular Biology, University of Southern Denmark, Odense, Denmark

7. **Caveolin-1 loss drives morphological and drug sensitivity remodeling in high-grade serous ovarian cancer**

**Elina Multamäki**, Disease Networks Unit, Faculty of Biochemistry and Molecular Medicine, University of Oulu, Finland

8. **Stimulated Raman Scattering (SRS) and STED microscopy for chemical identification and super-resolution imaging of nanoplastics in cells**

**Gilia C. M. Ruiz,** Department of Biochemistry and Molecular Biology (BMB), Danish Molecular Biomedical Imaging Center (DaMBIC), University of Southern Denmark (SDU), Denmark

**9. ScopeOne: an adaptable, natively compiled platform for microscope control**

**Guillermo Moreno-Pescador,** 1: Department of Plant and Environmental Sciences, University of Copenhagen, Denmark; 2: Niels Bohr Institute, University of Copenhagen, Denmark

**10. Advanced light microscopy support across scales**

**Hans Blom,** Advanced Light Microscopy facility, Science for Life laboratory - Stockholm, Sweden

**11. A novel electrochemical biosensor for detection of plant extracellular vesicles (EVs)**

**Hassan Nasrollahpour,** Disease Networks Research Unit, Faculty of Biochemistry and Molecular Medicine, University of Oulu, Oulu, Finland

**12. STED/FLIM imaging of viral anchoring complexes: outcomes from a BNMI-supported visit to NorMIC**

**Hedvig Djupenström,** Faculty of Science and Engineering, Åbo Akademi University, Turku, Finland

**13. Tampere Imaging Facility – advanced light microscopy services for research and industry**

**Heidi Peussa,** Tampere University, Tampere, Finland

**14. Microscopy Image Browser 3: a scalable platform for segmentation and analysis of large vEM datasets**

**Ilya Belevich,** Electron Microscopy Unit, Institute of Biotechnology, HiLIFE, University of Helsinki, Helsinki, Finland

**15. Interdisciplinary software development for bioimage analysis in a core facility**

**Jesko Wagner,** Danish Bioimaging Infrastructure Image Analysis Core Facility, Denmark

**16. Enhancing brightfield high-content analysis: AI-driven segmentation and advanced organoid detection**

**Jonas Schwirz,** Revvity (Germany) GmbH, Hamburg, Germany

**17. Combining two-photon Laurdan generalized polarization and Stimulated Raman Scattering (SRS) microscopy to reveal lipid nanocarrier-skin interactions**

**Jonathan R Brewer,** Department of Biochemistry and Molecular Biology, Danish Molecular Biomedical Imaging Center (DaMBIC), University of Southern Denmark (SDU), Denmark

**18. Resolving Tau and α-Synuclein co-pathology dynamics in iPSC-derived cell systems**

**Kamelija Horvatović,** 1: Max Delbrück Center for Molecular Medicine, Berlin Institute for Medical Systems Biology, Berlin, Germany; 2: Charité Medical University, Berlin, Germany

**19. Reproducible microscopy image analysis in a shared facility environment**

**Ketan Gupta,** Centre for Cellular Imaging at the University of Gothenburg, Sweden

**20. Introducing SYLI, the Living Biobank - Cancer Laboratory**

**Kirsi Ketola,** Institute of Biomedicine, University of Eastern Finland, Kuopio, Finland

**21. Image Analysis at Turku BioImaging: services, tools, and cross-domain expertise**

**Linda Srbova,** Turku BioImaging, Åbo Akademi University and University of Turku, Turku, Finland

**22. CMIC – Cellular and Molecular Imaging Core – NTNU, Trondheim, Norway**

**Marianne Sandvold Beckwith,** Norwegian University of Science and Technology, Trondheim, Norway

**23. Fluorescence Lifetime Imaging for characterizing endosomal disruption and escape**

**Melissa Hendrén,** 1: Helsinki Institute of Life Sciences, University of Helsinki; 2: Faculty of Pharmacy, University of Helsinki, Finland

**24. A High-Throughput Image Analysis workflow for quantitative assessment of endosomal escape**

**Mengjie Wang,** 1: Helsinki Institute of Life Science HiLIFE, University of Helsinki, Finland; 2: Faculty of Pharmacy, University of Helsinki, Finland

**25. Ultrabright fluorescent nanoparticles for detection of rare RNAs and proteins**

**Niloufar Maghsoudnia,** Nano-Science Center & Department of Chemistry, University of Copenhagen, Copenhagen, Denmark

**26. Mechanism of effector-protein translocation via the type III secretion system**

**Nour Mustafa,** University of Turku, Turku, Finland

**27. Vimentin and PKM2: emerging partnership to regulate glucose metabolism and respiratory pathways in fibroblasts**

**Pallavi Devre,** Åbo Akademi University, Turku, Finland

**28. A Python-based image analysis pipeline for volume Electron Microscopy of *Plasmodium falciparum* ookinetes**

**Ramish Bibi,** Turku BioImaging, Åbo Akademi University and the University of Turku, Turku, Finland

**29. Viventis SCAPE: A single-objective, standard-carrier Light-Sheet microscope for high-speed, low-phototoxicity volumetric imaging**

**Rickard Linnskog,** Micromedic AB (authorized partners of Leica Microsystems in Sweden)

**30. Cyclic whole-brain imaging of RNA and protein in the intact mouse brain on standard light-sheet microscopy**

**Sara Sejer**, DANDRITE, Nordic-EMBL Partnership, and Department of Biomedicine, Aarhus University, Denmark

**31. A portable nanocomposite electrochemical platform for real-time monitoring of vitamin C as a therapeutic modulator in cancer**

**Sattar Akbari Nakhjavani**, Disease Networks Research Unit, Faculty of Biochemistry and Molecular Medicine, University of Oulu, Finland

**32. Analytical imaging at the Center for Advanced Bioimaging Denmark**

**Sebastian J Kjeldgaard-Nintemann**, Center for Advanced Bioimaging (CAB) Denmark, University of Copenhagen, Denmark

**33. The Core Facility for Integrated BioImaging, University of Copenhagen**

**Thomas Hartig Braunstein**, Center for Core Facilities, University of Copenhagen, Denmark

**34. Investigating tanycytes as a brain entry route for therapeutic cocaine- and amphetamine-regulated transcript Peptide (CARTp) analogs using advanced fluorescence imaging**

**Vilém Charvát**, Aarhus University, Department of Biomedicine, Aarhus, Denmark

## Posters

### 1. LVB Imaging Centre – a core facility for advanced light microscopy at the Life Science Building (LVB) in Oslo

**Anna Lång**[1]

[1] Oslo University Hospital, Oslo, Norway

The LVB Imaging Centre is a newly formed core facility for advanced light microscopy located in the Life Science Building (LVB) in Oslo. Bringing together microscopy expertise from the University of Oslo (UiO) and Oslo University Hospital (OUH), the centre provides an interdisciplinary environment that supports high-quality imaging across basic, translational, and applied life-science research.

The facility offers access to a broad range of imaging technologies, including confocal microscopy, super-resolution microscopy, high-content imaging, light-sheet microscopy, and multiplex imaging. These instruments enable studies ranging from subcellular structure and protein localization to dynamic processes in cells, tissues, organoids, and larger biological specimens. The centre will further invest in an upright two-photon confocal microscope, enabling deep-tissue imaging and live imaging in more complex samples.

The LVB Imaging Centre is open to all; students, researchers, and industry. We provide hands-on training, user support, image-acquisition assistance, and technical service when needed. By combining advanced instrumentation with dedicated microscopy specialists, the centre aims to make cutting-edge imaging accessible to a broad user community and to promote robust, reproducible, and innovative microscopy-based research in Oslo.

## 2. Aarhus University Health Bioimaging Core Facility

**Anna Lorentzen**[1]; Nina Burmeister[1]; Xiaoli Hu[1,2]; Morten Schallburg Nielsen[1]

[1] Department of Biomedicine, Aarhus University, Denmark
[2] Department of Clinical Medicine, Aarhus University, Denmark

Access to advanced imaging equipment and image analysis tools can be challenging. The Aarhus University Bioimaging Core Facility at the Department of Biomedicine provides access to a range of microscopes, software, expertise, and services supporting projects from whole-organ imaging to super-resolution microscopy.

The facility offers imaging platforms including SPIM, scanning and spinning-disc confocal microscopes, widefield systems, Airyscan, PALM/STORM on TIRF, multiphoton microscopy, high-content screening, and in vivo two-photon imaging. These technologies enable imaging across spatial scales, from intact organs and tissues to subcellular structures.

As multidimensional imaging technologies continue to evolve, image analysis and data management have become more complex. A key focus of the facility is therefore to support users with tailored image analysis solutions. Support includes freeware tools such as Fiji, Ilastik, and OMERO, as well as commercial software including Arivis, Imaris, ScanR, ZEN, and cellSens, helping researchers streamline image processing and quantitative analysis.

Facility staff provide comprehensive instrument training, assistance with developing customised imaging and analysis workflows, specialised courses and tutorials, and access to on-demand consultation and imaging services. The facility aims to enable high-quality, reproducible imaging research across diverse scientific disciplines.

## 3. Advancing precision oncology through High-Content Imaging and Phenotypic Profiling

Veikka Valtanen[1,2]; Lassi Paavolainen[2,3]; Isabel C Mogollon[1,2,3]; Vilja Pietiäinen[1,2,3]; **Antti Hassinen**[1,2]

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[2] FIMM, HiLIFE, University of Helsinki, Helsinki, Finland
[3] iCAN Digital Precision Cancer Medicine Flagship, University of Helsinki, Helsinki, Finland

Phenotypic imaging is a powerful approach for studying cancer biology, identifying therapeutic vulnerabilities, and advancing precision medicine. By capturing multidimensional cellular responses beyond conventional viability measurements, high-content imaging (HCI) enables characterization of disease phenotypes and treatment effects across diverse model systems. At FIMM High-Content Imaging and Analysis (FIMM-HCA; FIAM, Euro-Bioimaging), we provide automated high-content microscopy and advanced image analysis integrated with high-throughput drug screening. Our workflows support functional profiling of patient-derived and preclinical cancer models, including 2D cultures, 3D organoids, stroma–cancer co-cultures, and Cell Painting.

Collaborative projects demonstrate HCI's ability to resolve clinically relevant phenotypes and complex interactions. The co-developed Blood Cell Painting assay enables single-cell immunological profiling; analysis of >50 million cells from 390 healthy donors revealed immune-cell states associated with genetic and clinical variation (Högel-Starck et al., 2024). Deep learning-enabled analysis of 3D immune–cancer co-cultures has further revealed heterogeneous treatment responses in patient-derived renal cancer models that were not captured by conventional viability assays (Mogollon et al., 2024; Feodoroff et al., 2026).

Together, these studies highlight image-based phenotyping as a bridge between molecular characterization and functional precision oncology.

## 4. Feedback microscopy for automated imaging of rare events in the Bioimaging Core Facility at the Danish Cancer Institute

Tiina Naumanen Dietrich[1]; Victoria Bjerregaard[2]; **Chris Dinant**[1]

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[2] Cell Death and Metabolism Group, Danish Cancer Institute, Denmark

Feedback (or smart) microscopy combines real-time image analysis with automated microscope control. One example is targeted imaging, in which high-resolution, multi-channel images of rare objects are automatically acquired after detecting them in low-magnification scans via image analysis. We sought to set up targeted imaging in our Core Facility on two automated screening systems, the Zeiss Celldiscoverer 7, and the Molecular Devices ImageXpress Confocal HT.ai. Both systems provide tools for targeted imaging without the need for coding. Our use case was a 96-well study needing a uniform number of prometaphase nuclei per condition, with mitotic index spanning from scarce to abundant. The goal was to acquire a high-resolution, multi-channel z-stack of a defined number of prometaphase cells per treatment fully automatically. We were able to establish targeted imaging on both instruments. However, some system-specific limitations on the instruments prevented us from using these workflows on the specific use case. Therefore, we applied a simpler approach, called adaptive acquisition. This approach uses a simple image analysis for object detection during the high-resolution imaging and guides the system to move to next well upon reaching the desired number of objects.

## 5. Imaging and analysis of 3D patient-derived organoids using the Celigo Image Cytometer

Dmitry Kuksin[1]; William Rice[1]; Nathan Gödde[2]; Leo Chan[3]; **Dean Shaw**[4]; Olavi Ollikainen[4]; Kaupo Palo[4]; Hartwig Preckel[4]; Karin Boettcher[4]; Scott Cribbes[5]

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Imaging and analysis of primary organoids has traditionally been challenging due to the nature of organoid culturing as well as limited imaging and analysis platforms that are capable of performing such tasks. Traditionally, isolated progenitor cells, genetically engineered cells, or tissue fragments are grown in media supplemented with Matrigel®. These suspended cells eventually form organoids that can be used for downstream assays. Because the organoids are suspended in Matrigel, the imaging is typically performed by collecting a stack of images along the depth direction (Z-stack) using an epi-fluorescent microscope with a mounted camera. The acquired images are then manually processed using CellProfiler or ImageJ software. To help address these challenges, an assay has been developed for imaging and analysis of 3D organoids using Revvity's Celigo image cytometer, a plate-based multichannel brightfield and fluorescence imaging system. A "spin method" was created to facilitate the partial settling of the primary cells prior to Matrigel solidification, leading to the formation of organoids in a relatively flat focus field. This culturing method coupled with the Celigo image cytometer allowed for the capture and automatic analysis of an entire 96-well plate of formed organoids in less than 5 minutes. Because the Celigo image cytometer is capable of capturing brightfield and fluorescence images, it provides researchers with a tool for measuring the number of organoids per well, the sizes of each organoid as well as detection of fluorescent signals in a single assay. Here we successfully demonstrate how to perform culturing, imaging and analysis of patient derived organoids (PDOs) and murine derived organoids in 12, 24, 96, and 384-well formats using the Celigo image cytometer. The enhanced analysis capabilities that come with Revvity's Harmony high-content imaging and analysis software and Image Artist image analysis and management platform allows one to interrogate organoids in domes. Here we demonstrate that using multiple brightfield channels one can create Z-stacks of images of the Matrigel domes and analyse organoids in each of these stacks. These alternative methods in organoid imaging and data collection provide flexibility to the research community in their organoid research.

## 6. Live confocal imaging and image analysis of immune-cell chemotaxis in reconstructed skin

**Dylan Salgues**[1,2]; Mike Bogetofte Barnkob[1]; Jonathan Brewer[2]

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Cutaneous lupus erythematosus is a skin autoimmune disease causing malar rash, cutaneous lesions and photosensitivity. CLE is characterized by strong activation of the type I interferon pathway, leading to a recruitment of immune components [1]. There is a lack of models which come from the difficulty of integrating immune cells into reconstructed skin models, due to the limited compatibility of different cell types with a single culture medium, as well as the long reconstruction time required. Here, we establish a live-confocal-imaging workflow to monitor immune-cell migration and spatial integration in a reconstructed skin-compatible collagen matrix without disrupting the developing tissue. To achieve this, we have developed a custom-made support that spatially separates two collagen-matrix compartments: one containing a chemoattractant and the other containing lymphocytes. These two compartments are separated by a porous membrane allowing the passage of chemokines and cells. Fluorescent cell labeling enables live tracking of lymphocyte migration. Combined with image analysis, this approach can quantify cell position, motility, and migration direction within the collagen scaffold. Together, this approach provides a live-imaging framework for studying immune-cell migration during the development of reconstructed skin models.

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1. Wenzel, J. Cutaneous lupus erythematosus: new insights into pathogenesis and therapeutic strategies. Nat. Rev. Rheumatol. 15, 519–532 (2019).

## 7. Caveolin-1 loss drives morphological and drug sensitivity remodeling in high-grade serous ovarian cancer

**Elina Multamäki**[1]; Alice Dini[1]; Frida Rantanen[1]; Aino-Maija Kiiski[1]; Juuli Raivola[1,2]; Harlan Barker[1]; Emilia Piki[1]; Päivi Nummi[1]; Astrid Murumägi[3]; Daniela Ungureanu[1]

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[3] Institute for Molecular Medicine Finland (FIMM), Helsinki Institute of Life Science (HiLIFE), University of Helsinki

High-grade serous ovarian cancer (HGSOC) is the most lethal gynaecological cancer, with poor prognosis and limited treatment options. Caveolin-1 (CAV1), the core caveolae component, is frequently decreased in ovarian carcinomas and associated with poor prognosis (1), though its functional consequences remain unclear. CAV1 is directly involved in signaling through both caveolar and non-caveolar pathways, restraining multiple signaling proteins (2). We hypothesized that CAV1 loss releases this brake, activating downstream signaling and driving morphological and pharmacological changes in HGSOC cells.

To test this, we generated CAV1 knockout (KO) JHOS2 and OVCAR8 HGSOC cell lines. CAV1 loss depleted caveolar coat proteins and activated PI3K/AKT/mTOR and MAPK/ERK signaling. Cell Painting-based morphological profiling with machine learning-driven segmentation revealed a smoother, more circular cell shape, together with cell line-specific changes in actin organization. Drug sensitivity screening identified a shared NAMPT inhibitors resistance, alongside broader cell-specific shifts in drug response.

Together, these results show that CAV1 loss activates growth signaling in HGSOC, reshaping cell morphology and altering pharmacological response, and position CAV1 as a potential modulator of drug response.

References:
1. Zeng et al., 2020
2. Mani et al., 2026

## 8. Stimulated Raman Scattering (SRS) and STED microscopy for chemical identification and super-resolution imaging of nanoplastics in cells.

**Gilia C. M. Ruiz**[1]; Nicoline D. Daugaard[1]; and Jonathan R. Brewer[1]

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Nanoplastic pollution is an emerging environmental concern; however, elucidating its biological impacts remains challenging due to the difficulty of detecting and localizing these particles within complex biological systems. Addressing this challenge requires analytical approaches that combine high chemical specificity with nanoscale spatial resolution. Here, we integrate hyperspectral stimulated Raman scattering (SRS) and stimulated emission depletion (STED) microscopy to investigate nanoplastics in cellular environments. Fingerprint-region hyperspectral SRS enabled label-free discrimination of polystyrene (PS), polyethylene (PE), and polymethyl methacrylate (PMMA) based on their characteristic vibrational signatures. In differentiated Caco-2 monolayers exposed to 500 nm PS particles, SRS at the characteristic PS band (~1001 cm-1), combined with spectral analysis, identified particle-associated signals within the cellular background. Correlative fluorescence and depth-resolved SRS further supported their localization within the cell layer. STED microscopy complemented chemical imaging by providing super-resolved visualization of fluorescent 100 nm nanoplastics and their spatial relationship with cellular structures. SRS and STED provide complementary chemical and spatial information, establishing a correlative imaging strategy to identify and localize nanoplastics in complex biological environments.

## 9. ScopeOne: an adaptable, natively compiled platform for microscope control

Tianyi Zhao[1]; Staffan Persson[1]; **Guillermo Moreno-Pescador**[1,2]

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[2] Niels Bohr Institute, University of Copenhagen, Denmark

Control software for custom microscopes has converged on Python: µManager solved hardware abstraction, and Pycro-Manager and ImSwitch made it scriptable. That flexibility comes at a cost, because the Python layer sits in the path between camera and display.

We present ScopeOne, an adaptable, natively compiled (C++/Qt) control platform built on the µManager hardware abstraction layer, so existing device adapters work unmodified. Its modular design lets users add acquisition modes and processing steps, and the same functions are exposed through a local API with Python and MCP clients, making it scriptable for closed-loop and agent-mediated workflows.

Simultaneous control of heterogeneous cameras illustrates what the architecture allows. Micro-Manager has no native multi-camera mode; its Multi-Camera utility merges cameras into one logical device whose channels must share image dimensions and pixel type. In ScopeOne each camera runs in an isolated process with its own MMCore instance and transfers frames through shared memory, so detectors of different sensor size and pixel format acquire concurrently.

Median end-to-end display latency at 2048x2048 pixels was 99 ms, against 323 ms for Micro-Manager and 171 ms for napari-micromanager, and was unchanged under three-camera acquisition (two sCMOS at 100 fps plus an EMCCD), which the comparison platforms cannot run. The 99 ms floor is set by exposure and display refresh, not by software. ScopeOne is open source.

## 10. Advanced light microscopy support across scales

**Hans Blom**[1]

[1] Advanced Light Microscopy facility, Science for Life laboratory - Stockholm, Sweden

The mission of the facility is to give support with nanoscale biological visualisation by SIM, STED, SMLM, MINFLUX and ExM. In addition we support molecular analysis by fluorescence correlation spectroscopy methods and superresolution additions like STED-FCS and MINFLUX tracking for nanoscale dynamics. Moreover light-sheet fluorescence microscopy allow users to image live and/or optically cleared larger samples at unprecedented volumetric speed. Single cell ultra-fast volumetric imaging of biological processes at high-resolution is further provided by live lattice light-sheet microscopy.

## 11. A novel electrochemical biosensor for detection of plant extracellular vesicles (EVs)

**Hassan Nasrollahpour**[1]; Sattar Akbari Nakhjavani[1]; Marja Nissinen[2]; Niina Torniainen[2]; Ramila Mammadova[1]; Fabrizio Cillo[3]; Wilma Sabetta[4]; Susanna Kosamo[1]; and Seppo J. Vainio[1,5]

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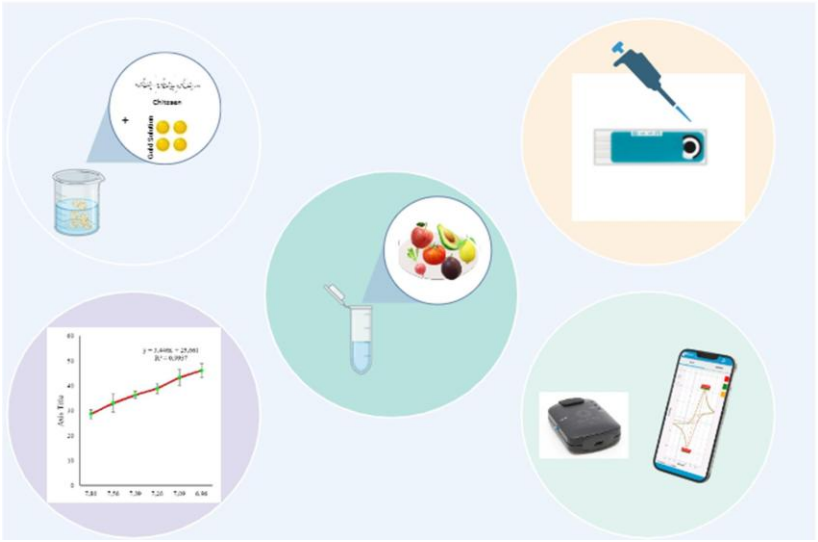
[5] Kvantum Institute, University of Oulu, Finland

INTRODUCTION

Extracellular vesicles (EVs) are membrane-enclosed particles secreted by almost all cell types both in human and plants. Due to their biomarker rich nature, they have been widely used for treatment, diagnostic and nutrition monitoring. The aim of this study is to detect specific plant EVs using an electrochemical assay.

METHODS



The sensing platform utilizes Screen-Printed Carbon Electrodes (SPCE) modified with chitosan/gold nanoparticles (AuNPs) to enhance both surface area and sensitivity. This modification provides a robust functional layer for the stable immobilization of an anti-EVs antibody (Ab), facilitating high-performance EV detection. In these experiments, a rabbit polyclonal Ab raised against the tomato (Solanum lycopersicum) Tetraspanin 8 (Solyc07g006280.3), a transmembrane protein considered a bona fide marker of EVs, was used as diagnostic reagent. Well-characterized EV isolates from tomato leaf tissues were used as testing material.

RESULTS

Preliminary results indicated that chitosan-AuNPs increased electrochemical signals. Subsequently, the antiEVs-Ab was immobilized onto the modified surface. This attachment decreased signal intensity due to increased steric hindrance determined by the Ab. After optimizing key performance parameters, the biosensor was applied to detect plant EVs. The sensing mechanism relied on the further increase in steric hindrance upon binding of plant EVs.

## 12. STED/FLIM imaging of viral anchoring complexes: outcomes from a BNMI-supported visit to NorMIC

**Hedvig Djupenström**[1]; Kaisa Rautaniemi[2]; Edna Xian Hu[3]

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[2] Advanced Imaging Core, Turku Bioscience Centre, University of Turku and Åbo Akademi University, Turku, Finland
[3] NorMIC Imaging Platform, Institute of Biosciences, University of Oslo, Norway

Kaposi's sarcoma herpesvirus (KSHV) establishes lifelong infections by maintaining viral episomes in the host cell nucleus. My PhD project investigates the multi-protein organization of this viral anchoring mechanism. STED microscopy is well suited for this question, but multi-protein imaging is limited by the number of simultaneous STED-compatible channels.

With support from a BNMI Short Term Scientific Mission, I visited the NorMIC Core Facility in Oslo together with Dr. Kaisa Rautaniemi from the Advanced Imaging Core in Turku. Hosted by Dr. Xian Hu (Edna), the visit focused on applying fluorescence lifetime imaging microscopy (FLIM) to expand the STED imaging beyond two-channels.

The main challenge was to separate two spectrally overlapping dyes, STAR RED and STAR 635. Although reference values suggested lifetimes of approximately 3.4 ns and 2.8 ns, both dyes initially appeared as one population around 2.4 ns in our biological samples. Using controls across various mounting media, together with expert troubleshooting of acquisition and fluorophore behaviour at NorMIC, we were able to shift the lifetimes to circa 1.2 ns and 1.9 ns and achieved separable phasor plots.

The STSM yielded useful data for my KSHV project and highlights the value of imaging core facilities: success was achievable by the combination of carefully prepared user controls and facility expertise willing to adapt advanced methods to non-ideal biological samples.

## 13. Tampere Imaging Facility – advanced light microscopy services for research and industry

Jenni Karttunen[1]; **Heidi Peussa**[1]; Outi Paloheimo[1]; Sanna Korpela[1]; Jani Mäkinen[1]; Teemu Ihalainen[1]

[1] Tampere University, Tampere, Finland

Tampere Imaging Facility – Light Microscopy Core unit of Tampere University (Tampere, Finland) provides state of the art light microscopy services for academic and industrial users. The facility hosts various high quality imaging systems and offers expert user training as well as contributions to teaching at Tampere University. Our instrumentation includes five confocal microscopes, six widefield systems, and several specialized modalities such as TIRF, FLIM, and SIM. Typical application areas span 2D and 3D imaging of (bio)materials, organoids, body on chip systems, tissue sections, and small model organisms (zebrafish and Drosophila melanogaster).

The facility currently supports more than 200 active users representing over 30 research groups. In 2024–2026, we have also contributed to the project “A collaborative platform for accelerating biomedical research and development through providing advanced microscopy services”, funded by the European Regional Development Fund. The project strengthens collaboration between companies in the region and Tampere University’s light microscopy services, expanding access to advanced imaging technologies and expertise. Tampere Imaging Facility is also part of a national roadmap infrastructure Euro Bioimaging Finland, uniting nine imaging organizations across seven universities and three university hospitals in Finland.

## 14. Microscopy Image Browser 3: a scalable platform for segmentation and analysis of large vEM datasets

**Ilya Belevich**[1]; Leena Leimio[1]; Eija Jokitalo[1]

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Volume electron microscopy routinely produces datasets that exceed computer memory, creating a bottleneck between acquisition and biological insight. Microscopy Image Browser (MIB) is a free, open-source application for processing, segmentation and visualization of multidimensional microscopy data. Here we present MIB3, a ground-up modernization designed for the scale and workflow demands of contemporary vEM.

MIB3 introduces a BigData engine that stores volumes as disk-backed, pyramidal OME-Zarr v3 files, enabling interactive browsing and segmentation of datasets larger than RAM. A level-map manager keeps edits consistent across resolutions, and export to OME-Zarr and standard formats ensures interoperability with other tools. BioFormats and OpenSlide integration extends BigData mode beyond vEM to whole-slide imaging.

Rebuilt on MATLAB's AppContainer framework, MIB3 provides a modern, dockable interface and an architecture that simplifies adding new formats, tools and plugins. Segmentation combines manual, semi-automatic and deep-learning tools, including DeepMIB and Segment-Anything-2 for interactive 2D and 3D workflows.

MIB3 runs as a MATLAB application or a standalone program compiled for academic research, remaining accessible to users without a MATLAB license.

## 15. Interdisciplinary software development for bioimage analysis in a core facility

Tricia Loo Yin Jun[1]; Julia Mertesdorf[1]; **Jesko Wagner**[1]

[1] Danish Bioimaging Infrastructure Image Analysis Core Facility, Denmark

Many bioimage analysts in core facilities create pipelines built for individual user projects, and publish them as reusable software, advancing FAIR principles and raising research quality. However, this model produces software only in response to biologist demand, potentially overlooking methodological advances from other disciplines. At the Danish Bioimaging Image Analysis Core Facility, we therefore also collaborate with computer scientists to translate new analysis methods into user-friendly software for biologists. We realise this approach by packaging solutions as napari plugins and standalone graphical tools. Pilot projects across our facility include the analysis of mitochondrial cristae, colocalisation of fluorescent markers, and knee-joint segmentation from MRI. These tools support accompanying publications and strengthen our services for future users. To improve user experience and code quality, we hold hackathons centred on testing and refining them. Such facility-led development frees analyst time while increasing the quality and transparency of analysis outcomes. By bridging scientific domains, it also speeds up adoption of emerging analysis methods. Looking ahead, we are exploring how these and future tools might support teaching, giving students experience with reproducible bioimage analysis. We welcome collaboration with other Nordic facilities in developing and sharing such tools.

## 16. Enhancing brightfield high-content analysis: AI-driven segmentation and advanced organoid detection

**Jonas Schwirz**[1]; James Hutt[2]; Astrid Canivet[3]; David Sagnat[3]; Kaupo Palo[4]; Olavi Ollikainen[4]; Sten-Oliver Salumaa[4]; Hartwig Preckel[5]; Karin Boettcher[5]; Angelika Foitzik[5]; Alexander Schreiner[5]

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[4] Revvity Tallinn, Estonia
[5] Revvity Cellular Technologies Hamburg, Germany

Brightfield microscopy provides rich morphological data without fluorescent labeling, yet its low contrast poses significant challenges for robust automated segmentation. We introduce two innovative approaches that address these challenges and enable reliable, scalable analyses

Advanced 3D organoid detection in brightfield - Find Organoids building block in Harmony high-content imaging and analysis software delivers up to 2-fold increase in detection via '2.5D' segmentation, robustly handling overlapping objects, variable morphologies, and complex ECM optical properties.

AI-powered brightfield analysis - Phenologic.AI achieves >95% detection accuracy for label-free nuclear and cytoplasm segmentation, and artifact- reduced digital phase contrast reconstruction for reduced phototoxicity in extended time-lapse studies.

## 17. Combining two-photon Laurdan generalized polarization and Stimulated Raman Scattering (SRS) microscopy to reveal lipid nanocarrier-skin interactions

Gilia CM Ruiz[1]; Morten F Ebbesen[1]; **Jonathan R Brewer**[1]

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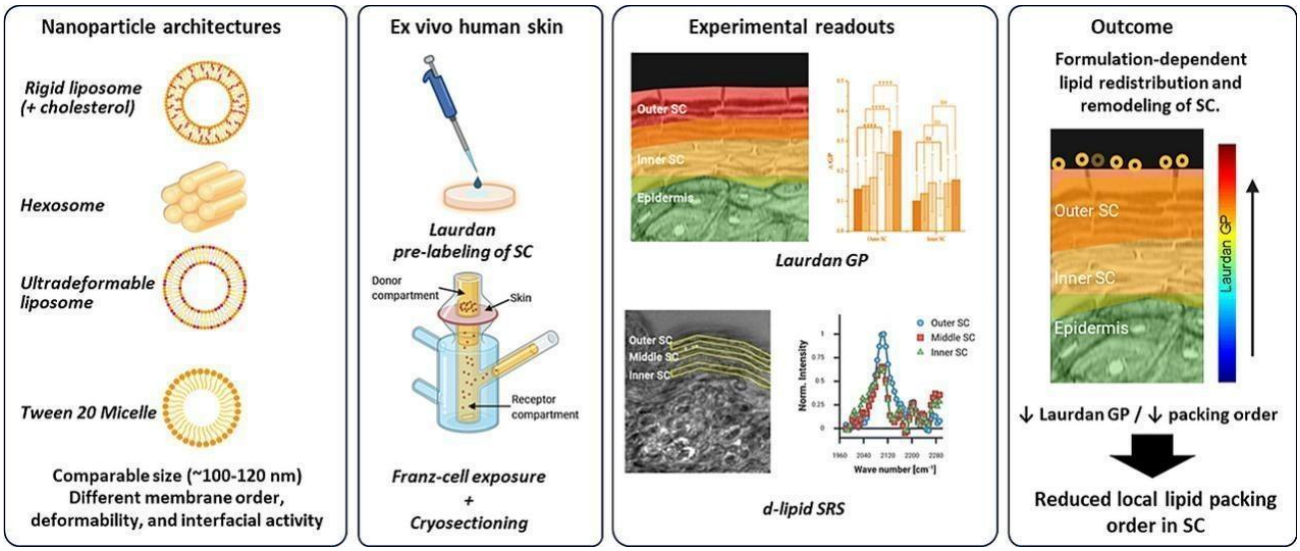
Lipid nanocarriers can enhance skin drug delivery, but how their supramolecular properties modulate the stratum corneum (SC) lipid barrier remains understood. We combined depth-resolved two-photon Laurdan generalized polarization (GP) imaging, DiD fluorescence, and hyperspectral stimulated Raman scattering (SRS) microscopy to map lipid remodeling and formulation-derived material in ex vivo human skin after 4 h exposure to conventional liposomes, hexosomes, ultradeformable liposomes, and Tween 20 micelles. Laurdan GP revealed formulation- and depth-dependent reductions in SC lipid packing, strongest in the outer SC. Hexosomes induced larger outer-SC GP reductions than conventional liposomes (ΔGP ~0.25-0.33 vs ~0.14-0.18), while ultradeformable liposomes produced stronger remodeling than rigid liposomes or surfactant alone. DiD fluorescence localized formulation-associated material predominantly within the SC, while SRS imaging of deuterated phospholipids provided a fluorophore-independent chemical readout of lipid distribution. SRS revealed distinct depth-dependent distributions, with rigid liposomes predominantly localized to the outer SC, whereas ultradeformable vesicles showed lipid signals extending into the middle and inner SC. By integrating biophysical and chemical imaging, our results reveal formulation-dependent lipid redistribution and remodeling within the skin barrier and demonstrate the value of multimodal microscopy for resolving nanocarrier–tissue interactions.



## 18. Resolving Tau and α-Synuclein co-Pathology dynamics in iPSC-derived cell systems

**Kamelija Horvatović**[1,2]; Paula Santos[1,3]; Anna Oliveras-Martinez[1]; Malcolm Hain[1,4]; Melissa Birol[1,3]

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Alzheimer's disease and Lewy body dementia share overlapping tau and alpha-synuclein pathology, yet despite the high prevalence of co-pathology reported post-mortem, their mechanistic interaction remains insufficiently explored. It is unclear whether one protein seeds or precedes the other, and whether their interaction reflects direct molecular co-assembly or convergence in shared compartments. Both proteins are independently implicated in lipid perturbations, suggesting a possible metabolic link, yet post-mortem tissue and conventional 2D culture systems cannot capture these early, dynamic interactions. We use two complementary human iPSC-derived neuronal lines to dissect tau-alpha-synuclein interactions at endogenous and exogenous levels: EDi, endogenously SNAP-tagged for alpha-synuclein, and BiH009, doxycycline-inducibly SNAP-tagged for tau, with an untagged control. Cultures are exposed to recombinant fluorescent alpha-synuclein-647 or tau-647, allowing endogenous and exogenous protein pools to be compared. Confocal imaging of tagged and recombinant proteins alongside BODIPY-labeled lipid droplets reveals where the two proteins colocalize and which compartments they occupy, while calcium imaging captures whether network activity shifts alongside this convergence. Together, this system initially maps where and how tau and alpha-synuclein interact in living neurons, and whether convergence coincides with early shifts in lipid handling and network function.

## 19. Reproducible microscopy image analysis in a shared facility environment

**Ketan Gupta**[1]

[1] Centre for Cellular Imaging at the University of Gothenburg, Sweden

Microscopy core facilities increasingly support users who generate complex light and electron microscopy data, but who lack the programming experience needed to quantitatively analyse images. This contribution discusses image analysis as a service and making pipelines which are transparent, adaptable and reusable across projects. We focus on ways to distribute and reproduce pipelines, drawing on experience teaching Python-based image analysis and on facility projects using YOLO for object detection [1], image denoising, flat-field correction, thresholding, watershed segmentation [2], and feature extraction. As an example, we describe an OMERO-connected YOLO workflow to train object-detection models on user-annotated data, run inference, and return reviewable results to non-programming users. Key elements include Python-backed visual interfaces such as napari plugins [3], documented processing parameters and model versions, quality-control metrics, modular workflows, and support for repository-ready data in line with FAIR principles and data-driven life sciences. By embedding analysis in documented, interactive workflows, microscopy facilities can help users validate outputs and convert diverse imaging datasets into quantitative, reusable evidence.

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## 20. Introducing SYLI, the Living Biobank - Cancer Laboratory

Aleksanteri Seppälä[1]; Mikko Karjalainen[1]; **Kirsi Ketola**[1]

[1] Institute of Biomedicine, University of Eastern Finland, Kuopio, Finland

Translating discoveries made in cancer research into clinical and societal impact requires a coordinated effort between basic science, technology development, and medical innovations. SYLI, the Living Biobank-Cancer Laboratory, has been established to accelerate this process by integrating multidisciplinary expertise and advanced technologies into a unified framework. The aim of the project is to combine existing equipment and the related special expertise, and key investments to form a new RDI infrastructure, the Cancer Laboratory. This will create an operating concept and a comprehensive service model for close cooperation between the University of Eastern Finland (UEF) and regional businesses. The long-term goal of the development and investment project is to create a comprehensive service package for translational cancer research in North-Savo for both academia and industry. The impact of the new RDI services will strengthen the infrastructure at UEF, will create opportunities for new business-oriented innovations and potentially benefit the healthcare provided to the general population.

## 21. Image Analysis at Turku BioImaging: services, tools, and cross-domain expertise

**Linda Srbova**[1]; Junel Solis[1]; Ramish Bibi[1]; Chris Bühling[1]; Dado Tokic[1]; Irina Belaia[1]; Pasi Kankaanpää[1]

[1] Turku BioImaging, Åbo Akademi University and University of Turku, Turku, Finland

In Turku BioImaging, image analysis services (www.bioimaging.fi/image-data-team/) are provided by a team bringing together diverse expertise, with members specializing in different methodological and domain areas. The team's work is primarily centered on the development of analysis tools for biological and biomedical image data. While the user base has traditionally consisted of academic researchers, rapidly growing interest has been observed from regional development projects, industry customers, and adjacent fields such as digital agriculture, water ecosystem monitoring, geospatial engineering, and signal processing. These services are available on an open-access basis to academic, public-sector, and private-sector users alike, both nationally and internationally, through the Finnish Advanced Microscopy Node of Euro-BioImaging (https://eurobioimaging.fi/FiAM/), with funded access available for image analysis support.

Turku BioImaging services range from consultation to the development of custom-made automated analysis pipelines, in which both conventional and deep learning methods can be employed. Consultation includes guidance on good practices in the imaging workflow and on publishing data in line with FAIR principles. Additionally, support in data collection is also available.

An important focus is placed on the creation of scalable and reproducible image processing and analysis workflows, combined with the resources supported by the IT Center for Science (CSC), the Finnish state-funded provider of high-performance computing and data storage infrastructure. Given the complex and iterative nature of image analysis outputs, each project is provided with a standardized, sample-level PDF report, enabling an intuitive and efficient overview of the results. In addition, cloud-ready image and data visualization formats are used to provide interactive, cross-referenced results, giving users the ability to directly see connections between raw data and image analysis results.

## 22. CMIC – Cellular and Molecular Imaging Core – NTNU, Trondheim, Norway

**Marianne Sandvold Beckwith**[1]; Bjørnar Sporsheim[1]; Alberto Diez Sanchez[1],

[1] Norwegian University of Science and Technology (NTNU), Trondheim, Norway

Here we present the Cellular and Molecular Imaging Core facility (CMIC) at NTNU in Trondheim (Norway). At CMIC we offer instruments, services and expertise within advanced light microscopy and histology. Some of our applications include siRNA screens with high-content imaging (spinning disk), screening of large sets of patient samples (slide scanner), precise molecular localization studies (DNA paint, STED and single molecule-FISH), and cyclic imaging with automated fluid exchanges. We also develop and provide support for automated image analysis, facilitating FAIR and efficient data processing.

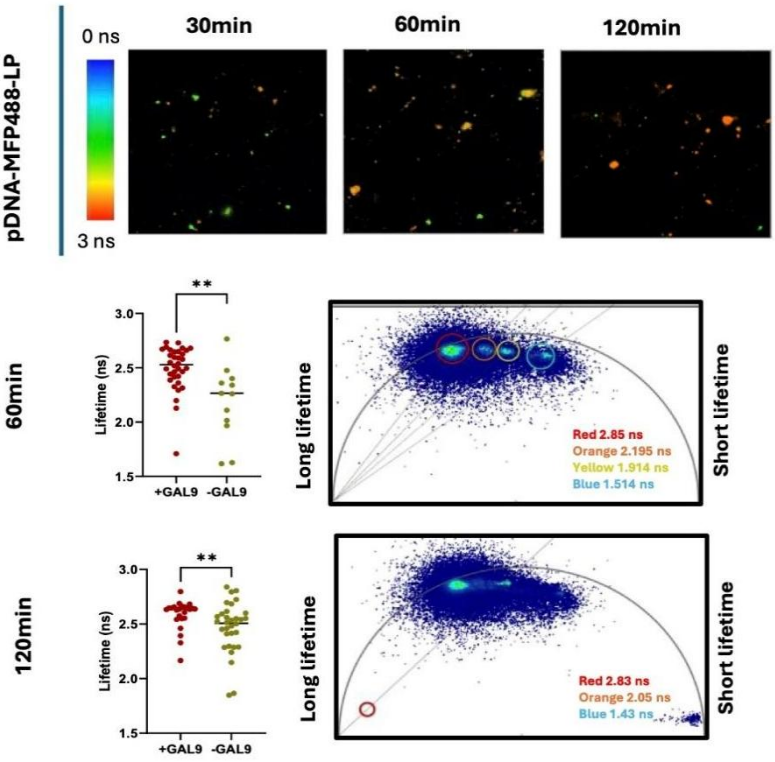
Situated within the university hospital campus, we foster close collaboration with the clinical environment and medical research groups. We have approximately 100 unique users annually, predominantly from the medical faculty, the faculty of natural sciences, and the hospital. Through our users we encounter a diversity of samples and model systems, ranging from cell lines and primary cells to organoids, plants, marine animals and diverse human and animal tissue (e.g., brain, intestine, placenta and tumors). In the coming year we aim to explore expansion microscopy as a (for us) new method, and are happy to connect with any fellow expansion microscopists at BNMI!

## 23. Fluorescence Lifetime Imaging for characterizing endosomal disruption and escape

**Melissa Hendrén**[1,2]; Elina Vuorimaa-Laukkanen[3]; Jonas Burmester[1,2]; Nova Räsänen[1,2]; Ali Karimi[1,2]; Vuokko Toivanen[1,2]; Shiqi Wang[1,2]

[1] Helsinki Institute of Life Sciences, University of Helsinki, Helsinki, Finland
[2] Faculty of Pharmacy, University of Helsinki, Helsinki, Finland
[3] Faculty of Engineering and Natural Sciences, Tampere University, Tampere, Finland

Currently, less than 2% of administered oligonucleotide-based drugs encapsulated in lipid nanoparticles reach the cytoplasm [1]. This makes the delivery of the oligonucleotides for translation and transcription highly inefficient. Main bottleneck contributing to the inefficient delivery is endosomal escape. By utilizing fluorescent lifetime imaging together with traditional endosomal rupture markers (Galectin-9). By labeling the payload, we can combine lifetime imaging and protein markers to obtain a better understanding of how and when the payload escapes the endosome.




Plasmid DNA was used as model payload and labeled with MFP488 via covalent binding to the oligonucleotides encapsulated in lipoplexes (LPs) and transfected into the cells. HEK293 cell line was used, which had been modified to continuously express mCherry–Galectin9 fusion protein [2]. Imaging of modified HEK293 cells after LP transfection, shows an increase of high intensity spots of mCherry-GAL9, indicating endosomal rupture. FLIM data of labelled particles delivered to cells, shows a clear shift in lifetime over two hours, indicating a significant change in the particle microenvironment. Particles co-localized with GAL9 have consistently a longer lifetime than particles non-colocalized (Figure). By utilizing FLIM imaging method to track lipoplexes, we were able to distinguish lipoplexes outside, internalized and ruptured endosomes.

References:

1. Gilleron et al., Nat. Biotechnol. 2013
2. Munson et al., Commun. Biol. 2021

## 24. A High-Throughput Image Analysis Workflow for quantitative assessment of endosomal escape

**Mengjie Wang**[1,2]; Melissa Hendrén[1,2]; Zhuoyuan Lin[3]; Shiqi Wang[1,2]

[1] Helsinki Institute of Life Science HiLIFE, University of Helsinki, Helsinki, Finland
[2] Faculty of Pharmacy, University of Helsinki, Helsinki, Finland
[3] Department of Chemistry, Tsinghua University, Beijing, China

Endosomal escape is a critical factor of mRNA delivery by lipid nanoparticles (LNPs) (1). However, how the apparent pKa of LNP regulates the endosome escape compartment remains unclear. Fluorescence microscopy has become a powerful tool for studying endosome escape by following single escape events, but quantitative mapping of escape events remains challenging due to their small size and the lack of robust high-throughput image analysis workflows.

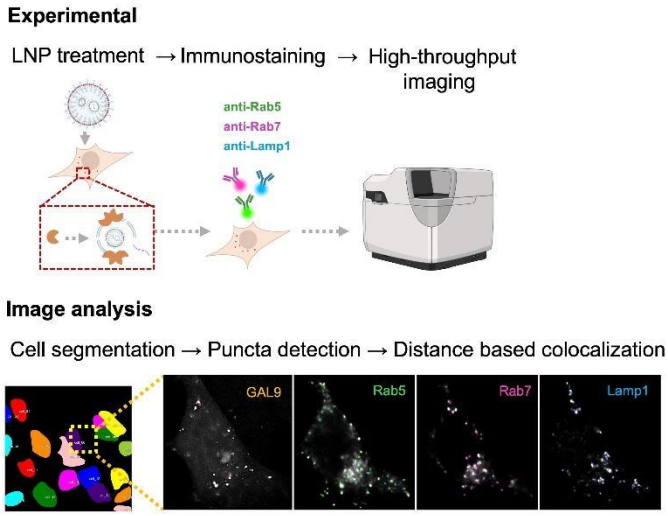



Fig 1. High-throughput imaging workflow for quantitative assessment of endosome escape

Here, we developed a high-throughput image analysis workflow for quantifying endosomal escape using multichannel fluorescence microscopy (Fig 1). The workflow integrates automated cell segmentation (Cellpose) (2), puncta detection (StarDist) (3), distance-based colocalization, and batch image analysis to generate endosomal compartments profiles. We formulated a library of LNPs with apparent pKa values from 5.5 to 7.0 and quantified endosomal escape in mCherry-GAL9 HEK293 cell line (4). Immunostaining of endosomal compartments enabled spatial localization of escape throughout endosome maturation.

The workflow revealed that apparent pKa is strongly associated with whether and where escape happens, although it does not simply match the pH of the compartment from which escape occurs. Early endosome escape is the strongest indicator of mRNA-LNP transfection efficiency.

References:
1. Patel et al., Trends in Pharmacological Sciences, 2021
2. Stringer C, et al. Nature Methods, 2021.
3. Schmidt U, et al. MICCAI, 2018
4. Munson et al., Communications Biology, 2021

## 25. Ultrabright fluorescent nanoparticles for detection of rare RNAs and proteins

**Niloufar Maghsoudnia**[1]; Junsheng Chen[1]

[1] Nano-Science Center & Department of Chemistry, University of Copenhagen, Copenhagen, Denmark

Fluorescence imaging of low-abundance biomolecules remains challenging due to the limited brightness and photostability of conventional fluorescent probes. Ultrabright organic fluorescent nanoparticles (NPs) based on molecular self-assembly, known as SMILES (Small-Molecule Ionic Isolation Lattices), exhibit exceptionally high fluorescence brightness (1). However, their broader application in biological environments is restricted by insufficient stability under physiological conditions. In this work, we develop a silica-coating strategy for SMILES nanoparticles that significantly improves their stability while preserving and enhancing their fluorescence properties. The silica shell further provides a versatile platform for surface functionalization with targeting ligands such as nanobodies and single-stranded DNA probes.

The ultimate objective of this project is to develop targeted fluorescent probes for the visualization of rare RNAs and proteins involved in cellular stress-response pathways. The resulting silica-coated SMILES nanoparticles are intended for use in advanced fluorescence microscopy applications, including fluorescence lifetime imaging microscopy (FLIM), where their high brightness and improved stability may enable sensitive detection of low-abundance biomolecular targets.

References:
1. Chen et al. Ultrabright Fluorescent Organic Nanoparticles Based on Small-Molecule Ionic Isolation Lattices. Angew Chem Int Ed. 2021; 60:9450–8.

## 26. Mechanism of effector-protein translocation via the Type III Secretion System

**Nour Mustafa**[1]; Henri Malmi[1]; Anton Zavialov[1]

[1] University of Turku, Turku, Finland

The Non-Flagellar Type III Secretion System (T3SS) is a virulence factor in gram-negative bacteria. Through this secretion system, called the injectisome, bacteria can directly translocate effector proteins into host cells and induce various reactions, which allows for hijacking host cells and disrupting their functionality (Hauser, 2009). When T3SS is disturbed, bacteria expressing it can be rendered non-pathogenic (Duncan et al., 2012). The functionality of the T3SS depends on the precise and timely coordination between its different components during assembly, where each protein can perform its part only when needed (Deng et al., 2017). Plaguing this system with nonfunctional mutants/deletions of certain subunits can mean the dysfunctionality of the whole system.

In our model of the Yersinia injectisome, substrates to be secreted are delivered by dedicated chaperone proteins to a nanomeric gate protein, YscV (Jensen et al., 2020; Xu et al., 2021). It has been shown that an early substrate-chaperone complex YscXY acts as a gatekeeper to the initiation of effector protein translocation. However, the binding mechanism of YscXY to YscV and subsequent secretion steps remain poorly understood. It has been shown, however, that without the presence of functional YscXY complexes in bacteria, the secretion of effector proteins, is completely halted (Bröms et al., 2005; Iriarte & Cornelis, 1999).

We are exploring the assembly of the T3SS using Cryo-EM and structural biology techniques.

## 27. Vimentin and PKM2: emerging partnership to regulate glucose metabolism and respiratory pathways in fibroblast

**Pallavi Devre**[1,2]; Ponnuswamy Mohanasundaram[1,2]; Giulia Sultana[1,2]; John Eriksson[1,2]

[1] Åbo Akademi University, Turku, Finland
[2] University of Turku, Turku, Finland

Vimentin is a cytoskeletal intermediate filament protein that plays a crucial role in various cellular functions, including cell proliferation, migration, and oxidative stress protection. We observed that the absence of vimentin reduces cell proliferation in mouse embryonic fibroblasts (MEFs), thereby contributing to delayed wound healing in vimentin knockout mice. The primary objective of my research is to comprehend the molecular mechanisms underlying vimentin's role in cell proliferation and growth. In cancer and highly proliferating cells, most glucose molecules switch to the pentose phosphate pathway instead of oxidative phosphorylation. This shift supports macromolecule synthesis and generates NADPH, crucial for maintaining the cell's redox status. Our findings indicate that vimentin knockout results in a reduced GSH/GSSG ratio and glucose-dependent cell proliferation. Additionally, we discovered that vimentin interacts with pyruvate kinase M2, acting as a gatekeeper for the pentose phosphate pathway. Based on our observations, we hypothesize that vimentin may regulate glucose metabolism by modulating PKM2 activity, which is essential for maintaining growth signals and redox levels in highly proliferative cells. Our research aims to explore the role of vimentin in glucose metabolism and cell growth.

## 28. A Python-based image analysis pipeline for volume Electron Microscopy of *Plasmodium falciparum* ookinetes

**Ramish Bibi**[1]; Junel Solis[1]; Irina Belaia[1]; Pasi Kankaanpää[1]; Pablo Suárez-Cortés[2]; Týč Jiří[3]

[1] Turku BioImaging, Åbo Akademi University and the University of Turku, Turku, Finland
[2] Max Planck Institute for Infection Biology, Berlin, Germany
[3] Institute of Parasitology, Biology Centre of the Czech Academy of Sciences, České Budějovice, Czechia

Malaria remains a global health challenge, with *Plasmodium falciparum* causing the most severe infections. A critical stage in its transmission cycle occurs in the mosquito midgut, where ookinetes initiate infection. Understanding the ookinete stage requires high-resolution, three-dimensional imaging, yet the data volumes generated by volume electron microscopy (vEM) are massive, often exceeding terabytes. Traditional image analysis tools struggle with the scale and complexity of such data. To meet this challenge, we developed an end-to-end image-analysis pipeline that blends classical computational workflows with advance image analysis methods to extract meaningful insights.

Raw vEM data – composed of tens of thousands of 2D tiles – are first stitched into contiguous slices. These slices are converted to the OME-Zarr format to enable memory-efficient parallel access. Where needed, AI-based denoising models are applied to enhance contrast, followed by automated cropping to focus on regions containing the parasite. A semi-automated Z-registration workflow aligns the slices into coherent 3-D volumes. The reconstructed volumes are segmented using a combination of manual annotations and an AI-powered segmentation network, which accelerates the delineation of parasite membranes and sub-cellular structures by learning from sparse labels. Quantitative features such as sizes, volumes, surface areas and organelle spatial distributions are computed directly from the segmentation masks.

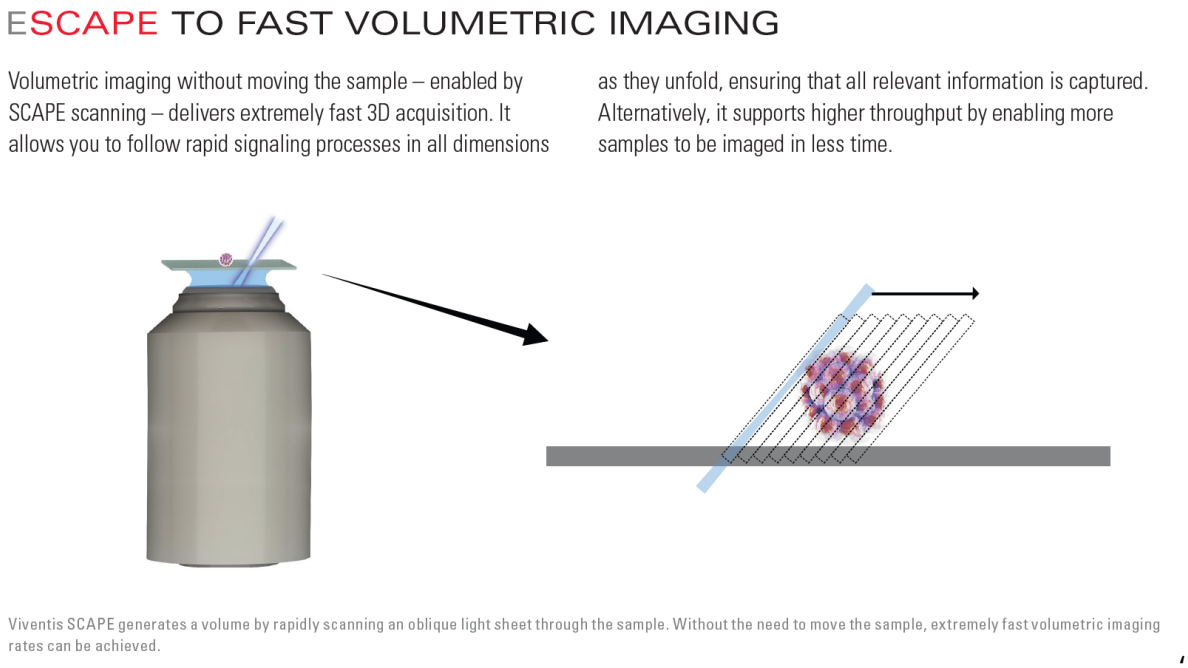
## 29. Viventis SCAPE: a single-objective, standard-carrier Light-Sheet Microscope for high-speed, low-phototoxicity volumetric imaging

**Rickard Linnskog**[1]

[1] Micromedic AB (authorized partners of Leica Microsystems in Sweden)

Light-sheet fluorescence microscopy (LSFM) offers optical sectioning, high speed and reduced photodamage relative to confocal and widefield imaging, since only the imaged plane is illuminated. Conventional LSFM geometries use two or more objectives arranged orthogonally around the sample, typically requiring dedicated holders, embedding media or open-top adaptations, and limiting parallel sample numbers. This has restricted routine light-sheet use for standard multi-well plates, dishes or slides, or for studies needing large sample numbers for statistically robust comparisons.

Leica Viventis SCAPE is a single-objective, inverted light-sheet microscope built on swept confocally-aligned planar excitation (SCAPE) and oblique-plane microscopy (OPM) principles, first described by Huisken et al. (2004, Science) and developed for high-speed volumetric acquisition by Hillman and colleagues. By combining illumination and detection through one objective, it is designed to make light-sheet imaging compatible with unmodified, flat-bottom sample carriers, allowing researchers to work with 3D cell culture models, organoids and complex in vitro models, and small model organisms — applications in which throughput, temporal resolution and specimen viability have historically been in tension with one another in light-sheet microscopy.



## 30. Cyclic whole-brain imaging of RNA and protein in the intact mouse brain on standard light-sheet microscopy

**Sara Sejer**[1]; Noor De Jong[1]; Dong Won Thomas Kim[1]

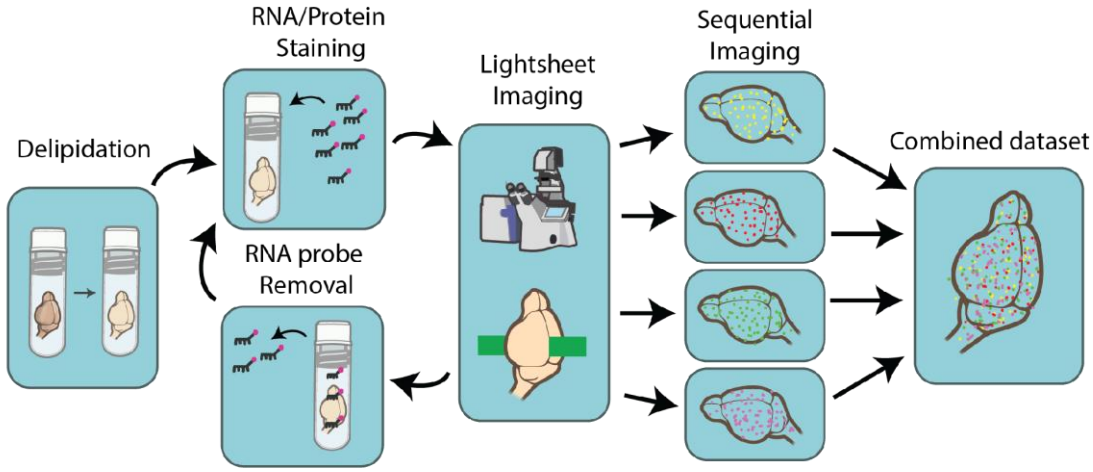
[1] DANDRITE, Nordic-EMBL Partnership, and Department of Biomedicine, Aarhus University, Denmark

Tissue sectioning is the standard approach for spatial analysis of the brain, but it can lose rare or spatially distributed signals. Whole-brain clearing now enables RNA imaging or multiplexed protein imaging in intact tissue. However, cyclic detection of RNA and protein in the same sample has so far been limited to thick sections. Many multiplex approaches also require custom barcoded reagents, limiting cost-effectiveness and accessibility.

We present IRIS, a pipeline for cyclic imaging of RNA and protein in the same intact adult mouse brain. IRIS uses iterative stripping and re-staining with conventional antibodies and mRNA probes, commercially available reagents, and a standard light-sheet microscope. We currently demonstrate up to four imaging cycles, with sample preparation completed within 10 days from brain harvest to imaging.

To manage datasets exceeding 150 GB per brain, we built a semi-automated data-handling pipeline that isolates individual brain regions and reduces data size. This pipeline combines open-source tools with Python-based processing.

IRIS enables direct, region-level comparison of RNA and protein expression across the whole brain within a single sample. We are extending it toward integration with single-cell reference atlases and applying it to neuronal vulnerability in Alzheimer's disease models. By using standard equipment and off-the-shelf reagents, IRIS aims to make whole-brain spatial multi-omics accessible beyond specialized laboratories.



## 31. A portable nanocomposite electrochemical platform for real-time monitoring of vitamin C as a therapeutic modulator in cancer

**Sattar Akbari Nakhjavani**[1]; Hassan Nasrollahpour[1]; Susanna Kosamo[1]; Seppo Vainio[1]

[1] Disease Networks Research Unit, Faculty of Biochemistry and Molecular Medicine, University of Oulu, 90014 Oulu, Finland

Introduction

Vitamin C (ascorbic acid, AA) is a promising nutrient which presents a dual functionality as an antioxidant and a prooxidant. Here, a portable nanocomposite-based electrochemical (EC) sensing platform was designed for sensitive and selective detection of AA in biofluids.

Methods

Screen-printed carbon electrodes (SPCEs) were modified with a conductive polymer/gold nanoparticle (cPol/AuNP) nanocomposite using controlled cyclic voltammetry (CV). Experimental parameters, including electrolyte pH and deposition cycles, were optimized.

Results and discussion

EC characterization confirmed successful modification and enhanced electron transfer properties. The sensor exhibited a robust response toward AA, indicating high sensitivity and rapid signal transduction. The fabricated sensor displayed a limit of detection of 15 µM within a linear detection range of 0-2 mM and an LOD of 63 µM for linear detection range of 2-50 mM. As proof of its application, the engineered sensor demonstrated excellent performance in detecting Vitamin C in biological fluids, including serum, tears, and sweat.

Conclusion

By enabling real-time, point-of-care quantification of AA, the developed sensor holds strong potential in paving the way toward its integration into next-generation personalized healthcare system.

Acknowledgement

The authors would like to acknowledge MSCA COFUND Data4Healthcare Program and University of Oulu for financial support.

## 32. Analytical imaging at the Center for Advanced Bioimaging Denmark

**Sebastian J Kjeldgaard-Nintemann**[1]; Nynne M Christensen[1]

[1] Center for Advanced Bioimaging (CAB) Denmark, University of Copenhagen, Denmark

The Center for Advanced Bioimaging (CAB) Denmark at the University of Copenhagen offers expert training and access to a comprehensive bioimaging instrument park to users from a broad spectrum of research areas. Available modalities range from routine widefield microscopy to electron microscopy and high-end confocal and multiphoton microscopy for imaging label-free and in-depth. CAB is specialized in live imaging and has vast experience in imaging of plants as well as mammalian cells/organs under physiological conditions. A recent focus of CAB is the exciting field of label-free, analytical imaging with new microscopes that allow for fluorescence lifetime imaging (FLIM), coherent Raman scattering (CRS) and EDS-transmission electron microscopy.

## 33. The Core Facility for Integrated BioImaging, University of Copenhagen

**Thomas Hartig Braunstein**[1]

[1] Center for Core Facilities, University of Copenhagen, Denmark

The Core Facility for Integrated BioImaging (CFIB) was officially inaugurated in September 2010. It is located at the Faculty of Health and Medical Sciences, University of Copenhagen.

CFIB offers a broad selection of advanced light and electron microscopes and a 9.4T NMR scanner. Researchers and students gain access not only to cutting-edge instruments and preparation equipment but also to essential technical guidance and support. We had around 550 unique users using the facility throughout the last year. Traditionally, light, electron microscopy and preclinical equipment have been separated entities with limited interaction. As our name suggests, our mission is to integrate diverse bioimaging techniques and strengthen interdisciplinary approaches to scientific imaging and make advanced multimodal workflows possible.

## 34. Investigating tanycytes as a brain entry route for therapeutic cocaine- and amphetamine-regulated transcript Peptide (CARTp) analogs using advanced fluorescence imaging

**Vilém Charvát**[1]; Andrea Pačesová[2]; Lenka Maletínská[2]; Morten Schallburg Nielsen[1]

[1] Aarhus University, Department of Biomedicine, Aarhus, Denmark
[2] Institute of Organic Chemistry and Biochemistry of the Czech Academy of Sciences – IOCB Prague, Prague, Czech Republic

CARTp is a neuropeptide involved in energy homeostasis and neuronal survival. Novel CARTp analogs from the IOCB Prague exhibit anorexigenic and neuroprotective effects following peripheral administration. However, despite decades of research, the CARTp receptor remains unknown, and the mechanism by which these peptides access central nervous system targets has not been elucidated.

Recent evidence suggests that hypothalamic tanycytes (Fig.1A) transport circulating metabolic peptides into the brain. We hypothesize that tanycytes similarly mediate the uptake and trafficking of CARTp analogs.

To address this question, primary rat tanycytes were exposed to FITC-labeled CARTp analogs and analyzed by immunofluorescence and Airyscan confocal microscopy. Preliminary results demonstrate time-dependent peptide internalization and localization within intracellular vesicular compartments (Fig.1B). Colocalization studies with endosomal markers indicate active intracellular trafficking through the endosomal system. Ongoing studies aim to characterize the peptide trafficking, identify candidate receptors involved in cellular uptake, and define the intracellular route followed by CARTp analogs.

This study provides new insights into the cellular mechanisms that may enable peripherally administered CARTp analogs to reach hypothalamic targets and highlight advanced fluorescence imaging approaches for investigating neuropeptide transport at the brain–circulation interface.

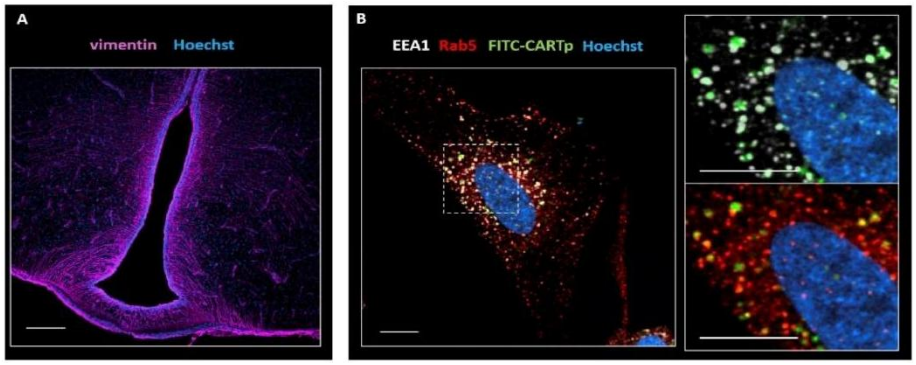



Fig.1: A – Hypothalamic tanycytes stained for cytoskeletal protein vimentin (magenta). Rat brain slice imaged at ZEISS LSM confocal microscope equipped with Airyscan detector. Scale bar is 100 µm. B - Representative image of primary rat tanycytes treated with 2 µM FITC-CARTp for 30 min. Intracellular colocalization of FITC-CARTp (green) with markers of early endosomes – EEA1 (white) and Rab5 (red). Fixed and stained cells were imaged at ZEISS LSM confocal microscope equipped with Airyscan detector. Scale bar is 10 µm.

# Social Program

**Thursday, November 26, 2026**

**Arctic Sauna World**




As part of the symposium social program, you will have the opportunity to enjoy a two-hour sauna experience at Arctic Sauna World, located by the beautiful Lake Jerisjärvi in Finnish Lapland. Arctic Sauna World offers several traditional Finnish saunas, each with its own atmosphere and style of heat, combined with the possibility of refreshing in an ice-swimming hole. You can also relax in the lounge while enjoying views of the lake and surrounding fells.

In case you are not a sauna-goer, you can spend time at the beach restaurant Jierra, where the bar will be open. Refreshments and snacks will be provided. In addition, the surrounding area offers a nice setting for hikes if someone wants to go for a brisk walk.

Time
Transportation is included
16:00 Hotel Levi Panorama (departure) – 16:40 Arctic Sauna World (arrival)
16:40 – 18:40 Sauna time
18:50 Arctic Sauna World (departure) – 19:30 Hotel Levi Panorama (arrival)

Place:
Arctic Sauna World, Jerisjärventie 91, 99300 Muonio
Webpage: https://harriniva.fi/en/arctic-sauna-world/

Note: Swimwear is required, and separate changing rooms are available for men and women. Towels will be provided.

**Symposium dinner & party**



The symposium dinner and party will be held at the Hotel Levi Panorama. Dress code is casual & smart casual.

Time:
20:00 – 00:00

Place:
Restaurant Panorama, 2nd floor,
Hotel Levi Panorama, Tunturitie 205, 99130 Levi

# Organizing committee

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- Pasi Kankaanpää (Åbo Akademi University, University of Turku),
- Junel Solis (Åbo Akademi University),
- Camilo Guzmán (Euro-BioImaging ERIC),
- Veli-Pekka Ronkainen (University of Oulu),
- Antti Hassinen (University of Helsinki),
- Hanna Grobe (University of Eastern Finland)

### Contact information

Email bnmi-2026@ibv.uio.no if you have any questions.

# About BNMI

The **Bridging Nordic Microscopy Infrastructure** (**BNMI**, https://bnmi.eu/) initiative was launched in 2021, creating a functional and dynamic network to strengthen Nordic collaboration. Through workshops, symposia, staff exchanges, and research mobility grants, BNMI has supported the use of advanced microscopy, driven innovation, and strengthened expertise, ensuring that the Nordic region remains at the forefront of scientific discovery. This collaborative effort has empowered researchers to utilize state-of-the-art microscopy technologies regardless of their location, enabling transformative discoveries in biology, medicine, and beyond.

In 2025, NordForsk has granted funding for five more years to **BNMI-II**, which was built on this successful foundation, to deepen Nordic collaboration and ensure long-term sustainability. It aims to strengthen Nordic collaboration through researcher and staff mobility, joint training and knowledge exchange, technological and methodological innovation, improved data management and FAIR practices, and the promotion of early-career development.

All participating countries in this infrastructure; Norway, Denmark, Iceland, Sweden and Finland have already established infrastructures and network organizations at the national level that provide a full spectrum of biological imaging tools that are easily accessible to both academic and industry users. BNMI-II aims to facilitate more efficient Nordic collaboration and a long-term partnership between these countries. All these bioimaging infrastructures are united under the Euro-Bioimaging ERIC (www.eurobioimaging.eu/), leading the whole Europe working toward a better research, diagnostics and patient care.

In **Norway**, the **Norwegian Advanced Light Microscopy Imaging Infrastructure Network** (**NALMIN**, http://nalmin.no) was established in 2014. NALMIN has until now secured two major infrastructure grants from the Norwegian Research Council, in addition to major support from its host institutions. Today, NALMIN is a well-established network of imaging platforms with facilities located in all major life science research organizations in Norway.

In **Denmark**, the **Danish BioImaging Infrastructure** (**DBI-INFRA**, www.danishbioimaging.dk) was launched in April 2022 as a national distributed bioimaging infrastructure that brings together open-access bioimaging platforms supporting imaging technologies across scales. The DBI-INFRA consortium comprises seven partner institutions - Aalborg University, Aarhus University, the University of Southern Denmark, Roskilde University, the Danish Cancer Institute, the Technical University of Denmark, and the University of Copenhagen - hosting ten open-access imaging core facilities.

In **Iceland**, the **Biomedical Center, University of Iceland** (**BMC-UI**, http://lifvisindi.hi.is/) is an official collaboration between research groups working in biomedical molecular life sciences in Iceland across institutions. The primary goal of BMC-UI is to establish core facilities that bring together researchers in Iceland under a unified framework, maximizing the use of available infrastructures and fostering cross-disciplinary collaborations.

In **Sweden**, the **Swedish National Microscopy Infrastructure** (**NMI**, http://nmisweden.se/). Since 2016, the National Microscopy Infrastructure has operated as a distributed research platform with specialized nodes at Stockholm University, University of Gothenburg, Umeå University, and the Royal Institute of Technology (KTH), which serves as the host institution. Additionally, since 2024, Karolinska Institute and Lund University have joined as associate partners. NMI's mission is to provide researchers in academia and industry open access to cutting-edge microscopy technologies and expertise.

In **Finland**, the **Finnish Advanced Microscopy Node** (**FiAM**, https://eurobioimaging.fi/FiAM/) is a national roadmap infrastructure offering open access to state-of-the-art biological imaging technologies, training, and image data analysis services. FiAM comprises eight imaging facilities hosted by the University of Helsinki, the University of Turku, Åbo Akademi University, and the University of Oulu, with the University of Eastern Finland and Tampere University as associate partners. It operates in close collaboration with the Finnish Biomedical Imaging Node; together, they form Euro-BioImaging Finland, a national roadmap infrastructure and lighthouse supported by the Research Council of Finland.

## SAVE THE DATE

**6th BNMI Symposium**

When: August 30 – September 3, 2027

Where: Hótel Örk, Hveragerði, Iceland

Host: Biomedical Center Imaging Core Facility School of Health Sciences, University of Iceland



About Hveragerði:

Nestled in a highly active geothermal area, Hveragerði is often called the "hot spring capital" of the world. The town is defined by pillars of steam rising from the ground year-round, creating a spectacular backdrop for scientific exchange.

More information: https://www.visithveragerdi.is/en

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On behalf of the organizers, special thanks for supporting the 5th BNMI symposium!





















## Sponsors

We would like to extend our warm thanks to all our sponsors for their generous support and valuable contribution to this symposium. Your partnership plays an important role in bringing together researchers, imaging specialists, and industry representatives to exchange knowledge, share expertise, and foster new collaborations. By supporting the BNMI2026 symposium, you help create an environment where scientific discovery meets technological innovation. Your participation also provides our attendees with valuable opportunities to explore emerging imaging technologies, learn about the latest developments, and connect with industry experts.

We greatly appreciate your commitment to the microscopy and imaging community and thank you for helping make the BNMI symposium possible!



# Practical Information

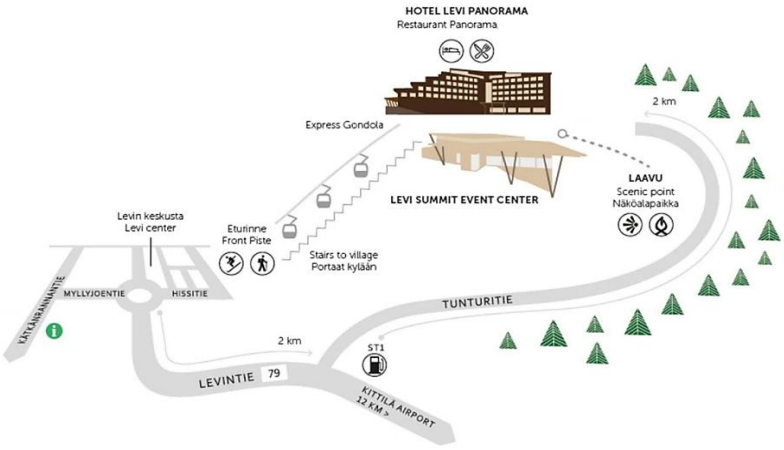
**Symposium webpage:** https://eurobioimaging.fi/FiAM/bnmi2026/

**Symposium venue**

Levi Summit Event Center,
Tunturitie 205, 99130 Levi, Finland

Webpage:
https://www.kassiopeia.fi/levi-summit/en/

Opening hours: 8:00 – 19:00




**Accommodation**

Hotel Levi Panorama, Tunturitie 205, 99130 Levi, Finland (connected to Levi Summit Event Center)

Webpage: https://www.kassiopeia.fi/hotel-levi-panorama/en/

Check-in from 15:00, Check-out by 11:00

Contact: panorama@kassiopeia.fi



**Registration desk**

Opening hours:

- Monday, 23 November: 15:00-19:00
- Tuesday, 24 November: 08:00-17:00

Participants should wear their name badges throughout the symposium. Name badges are required for access to symposium activities, meals, and company exhibitions.

**Meals and catering**

Breakfasts, lunches and dinners (except on Thursday, November 26) will be served at Restaurant Panorama, 1st floor, Hotel Levi Panorama. Coffee breaks and welcome reception will be served in the lobby of the Levi Summit Event Center.

For exact times, check the program (pages 3-6).

**WiFi**

- Summit business network
- Password: LeviSummit

**Exhibition**

Opening hours:

- Sunday, November 22: 9:00-17:00 – Monday, November 23: 9:00-16:30 (installation)
- Tuesday, November 24: 14:25-15:05
- Wednesday, November 25: 10:30-11:45, 17:00-19:00
- Thursday, November 26: 10:00-10:45, 15:00-15:30
- Friday, November 27: 9:00-17:00 (disassembling)

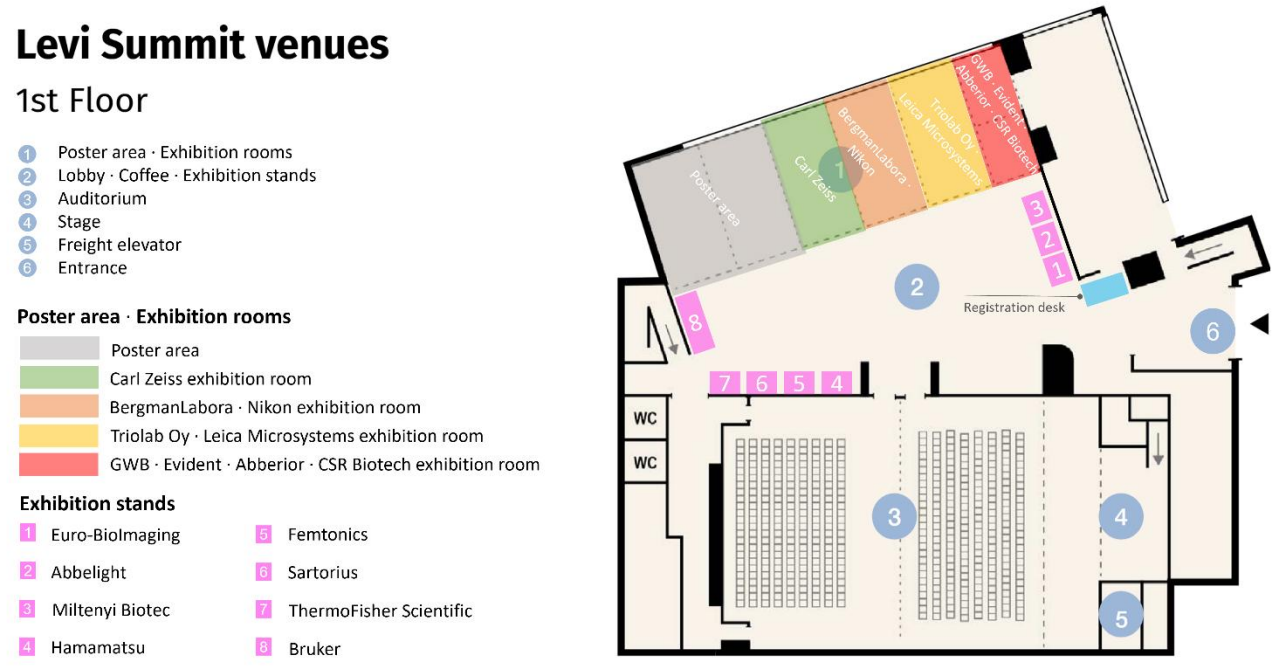
**Posters**

- Tuesday, November 24: 13:00-19:00 – Wednesday, November 25:9:00-13:00 (poster setup)
- Wednesday, November 25, 17.00–19.00 (poster session)
- Thursday, November 26, 10.00–10.45 (poster session)
- Friday, November 27, 9:00-11:00 (disassembly)

Poster size (maximum dimensions): 80 cm (width) x 165 cm (height).
Poster numbers will be given to poster presenters at the registration desk.

**Venue setting for symposium**

Tuesday, November 24, 13:00 onwards



## Getting to Levi

### By plane – Kittilä

Kittilä Airport is an international airport located in the heart of Lapland, about 14 kilometers from the Hotel Levi Panorama. The airport has scheduled flights from major European cities and multiple daily connections from Helsinki. Check flights to Levi from Europe: https://www.levi.fi/en/info/general/arrival-at-levi/

Kittilä Airport transfer

Tunturilinjat Oy operates a shuttle service from Kittilä Airport to Levi, with a stop at Hotel Levi Panorama upon request (approximately 14 km). For schedules, prices, and more details, visit: https://tunturilinjat.fi/en/schedules/

Important information about return transfers

The return trip to Kittilä Airport must be booked at the hotel reception at least 24 hours in advance. The bus does not stop at the hotel automatically; reception will inform the driver about passengers to be picked up from the hotel.

On Friday, November 27, the shuttle bus will be organized for the symposium participants:

11:30 -11:50 - bus transfer Levi Hotel Panorama - Kittila Airport

### By plane – Rovaniemi

Rovaniemi Airport is international airport located about 170 kilometers from the BNMI2026 symposium venue. The airport is serviced by flights from most major European cities and daily connections from Helsinki.

### By train – Rovaniemi

You can reach Rovaniemi by train from several Finnish cities, with direct daily connections operated by VR, https://www.vr.fi/en. Cities with train connections to Rovaniemi: Helsinki, Tampere, Oulu, Turku. Some trains are car-carrier trains, so you can reach Rovaniemi by train and drive the rest of the trip to Levi in your car.

### Transportation from Rovaniemi to Levi

The distance from Rovaniemi to Levi is approximately 170 km, with a driving time of around 2-2.5 hours. Take the E75 north from Rovaniemi, then turn onto road 79 towards Levi. Several daily bus connections operate between Rovaniemi and Levi, especially during the winter season. For schedules, prices, and ticket bookings, visit: https://www.matkahuolto.fi/

**Levi ski resort**

Levi Ski Resort is Finland's leading ski resort and a year-round activity park, growing and evolving amidst Lapland's Arctic nature. Levi's downhill and cross-country skiing season typically opens in the first week of October. Along with its unique location on the slopes, Hotel Levi Panorama is the only ski-in ski-out hotel in Levi. Levi Village is easily accessible from the hotel via the Levi Express gondola (scenic cabin lift), or participants can take Panorama Stairs, which also bring you to Levi Village.

Opportunities available around the hotel:

- Levi Express Gondola: connects Hotel Levi Panorama with Levi Village
- Panorama Stairs: An alternative walking route to Levi Village (weather and conditions permitting)
- Skiing: Hotel Levi Panorama offers ski-in/ski-out access and a ski equipment storage & maintenance room for participants
- Ski passes: available at the hotel reception
- Equipment rental: available through Zero Point Rental: https://www.levi.fi/en/services/zero-point-rental/
- Levi Ski Resort webpage: https://www.levi.fi/en/info/levi-ski-resort/
- Slopes: https://www.levi.fi/en/ski/slopes-and-lifts/front-slopes/
- Samiland Exhibition: https://samiland.fi/en/
- Santa's Cabin: https://www.levi.fi/en/activities/places-to-visit/santas-cabin/
- More Levi's travel tips: https://www.kassiopeia.fi/en/travel-levi/

Late November in Levi is typically cold, with winter conditions and possible snowfall. Outdoor temperatures can fall well below freezing. We recommend bringing:

- Warm winter clothes
- Winter boots with good grip
- Skiing equipment if you plan to ski
- Swimwear for the sauna activities

**Contact information**

- Emergency services 112
- Kittilä and Levi Taxi +358 200 99800
- Rovaniemi Taxi +358 200 88000
- Hotel Reception +358 16 336 3000, panorama@kassiopeia.fi
- Symposium Chair, Irina Belaia +358 50 569 8336, irina.belaia@abo.fi
- Symposium Organizers bnmi-2026@ibv.uio.no