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Faculty of Medicine

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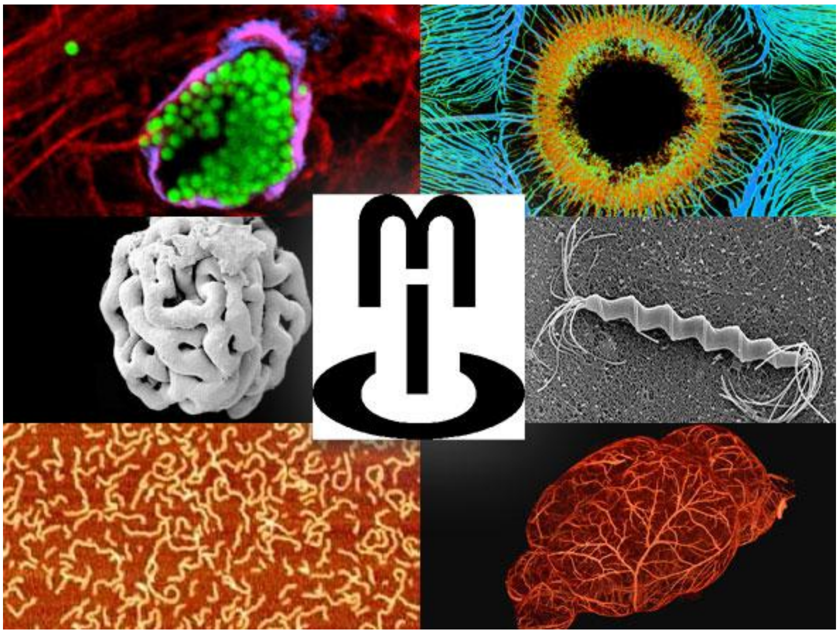
Microscopy Imaging Center (MIC)



MIC Research Day 2026

Abstract Booklet

MIC Image contest 2026

Date: Wednesday, June 24, 2026
09:30 am – 04:30 pm

Location: UniS S 003, Schanzeneckstrasse 1, 3012 Bern

Webpage: https://www.mic.unibe.ch/events/mic_research_day_2026/

Organized by the Microscopy Imaging Center (MIC)
of the University of Bern

The MIC Research Day is part of the educational program of the Cutting Edge Microscopy (CEM) PhD specialization.

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www.mic.unibe.ch

The **Microscopy Imaging Center (MIC)** is the University of Bern's competence center for high-end microscopy in the life and natural sciences. MIC has been recognized by the University of Bern as a **University Core Facility** in 2024. The mission of the MIC is to consolidate expert knowledge and provide technical support in microscopy at the University of Bern. The MIC coordinates visibility of and access to the microscopic instruments of the University of Bern. As such, the MIC is characterized by a unique structure: The microscopes are located at the respective scientific experts and are also owned by the corresponding institutes. This leads to decentralized microscopes which are distributed across 22 institutes and 3 faculties. Furthermore, teaching on Master and PhD level and training for scientific staff at all levels are also offered by the MIC. The MIC contributes fundamentally to the curriculum of the PhD specialization program Cutting Edge Microscopy (CEM). Services of the MIC concern image analysis, large image data volume handling and processing, sample preparation and introduction into microscope operation. Yearly highlights of the MIC are the MIC Research Day, the CEM Summer School and the MIC Symposium.

The **MIC Research Day** is the MIC's annual networking event for scientists at the University of Bern. It brings together scientists who use microscopy and other interested researchers who want to use microscopy. Young scientists and established researchers present data from their exciting research projects. Scientists from other universities and from the research-oriented industry are cordially invited to take part in the MIC Research Day.

MIC thankfully acknowledges financial support of the MIC Research Day 2026 by:

The PhD Program *Cutting Edge Microscopy*

and our sponsors from industry:

Research Day
of the
Microscopy Imaging Center

Wednesday, June 24, 2026, from **09:30** to **16.30**
Universität Bern – Uni S S003, Schanzeneckstrasse 1, 3012 Bern

MIC Image contest 2026

09:30	**Registration, coffee and industry exhibition**	
10:15	Welcome	
10:30	**Elena Gómez-Sanz** *IVB, UniBE*	From One Sample to a New Phage Family: TEM Dissects Staphylococcal Phage Diversity
10:50	**Sacha Psalmon** *IZB, UniBE*	Modular pipeline for coding-free AI-driven analysis of large-scale time-lapse microscopy
11:10	**Guillaume Witz** and Team, *DSL, UniBE* - Steer the Pixels: A live interactive demo of VIBE	
11:50	**Virginie Uhlmann,** *BioVision Center, UniZH* – The Swiss BioImaging Community	
12:00	**Lunch, industry exhibition and networking**	
13:00	**Image contest** – You vote for the best image.	
13:10	Industry talk: **Simon Restrepo** *arcoris bio AG, Schlieren, CH*	High-sensitivity multiplex spatial biomarker detection without secondary antibodies
13:20	**Anastasiia Korosteleva** *IPS, UniBE*	Cell Polarity in Grass Epidermis Development: From Observation to Quantitative Analysis
13:40	**Camilla Ullmann** *IGMP, UniBE*	Identifying rare cellular subpopulations using single-cell multiparametric quantitative imaging: challenges and opportunities
14:00	**Calvin Klein** *IBMM, UniBE*	Caspase 9 and the Apoptosome *in situ*
14:20	**Florencia Kloster, Aída Muñoz**, *TKI, UniBE - About the «Cutting Edge Microscopy, (CEM)» Program*	
14:30	**Coffee, industry exhibition and networking**	
15:05	**Michail Petropoulos** *ITP, UniBE*	Understanding how cells deal with transcription–replication conflicts
15:25	**Rossitza Irobalieva**, *ITA*, and **David Kalbermatter**, *ANA*, - The Electron Microscopy Facilities at the University of Bern	
15:35	**Ioan Iacovache** *ANA, UniBE*	Visualizing Pore Forming Toxin – Receptor Interactions by Cryo-EM
15:55	**Benjamin Pillet** *Dep Biology, UniFR*	Visualization and quantification of protein-protein interactions in yeast cells using a vacuolar recruitment assay
16:15	**Image contest** - *Prize award*	
16:20	**Farewell**	

Attendance at the MIC Research Day 2026 in conjunction with attendance at the MIC Symposium 2026 is recognized as 0.5 day of continuing education toward the license to conduct animal experiments in the Canton of Bern.

Supported by

Cutting Edge Microscopy
PhD specialization program

VITARIS proteintech arcoris bio MERCK Lumencor GMP PHOTONICS & MICROTECHNOLOGY SVI Nikon

Registration

Organized by:

Microscopy Imaging Center (MIC)
A Core Facility of the University of Bern with active participation of

*the **Faculty of Medicine**,*
*the **Faculty of Science** and*
*the **Vetsuisse Faculty**.*

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From One Sample to a New Phage Family: TEM Dissects Staphylococcal Phage Diversity

Elena Gómez-Sanz[1], Sandra Pérez-Jimenez[1], Dominique Lorgé[1], Jingxian Yang[1], Davide De Rosa[1], Dann Turner[2]

[1]Institute of Veterinary Bacteriology, University of Bern, Bern (CH)
[2]School of Applied Sciences, College of Health, Science and Society, University of the West of England, Bristol (United Kingdom)

Bacteriophages are increasingly explored as alternatives to antibiotics against opportunistic pathogens such as Staphylococcus epidermidis. However, the genetic diversity, host specificity, and functional features of staphylococcal phages remain insufficiently characterized, limiting the rational selection of phages for therapeutic applications.
Here, we present a comprehensive characterization of 86 staphylococcal bacteriophages isolated from a single wastewater treatment plant in Zürich. Whole-genome sequencing and comparative genomics revealed substantial diversity, including members of the Herelleviridae (65 myovirus-like phages), Rockefellervirus (4 siphovirus-like phages), a Picoviridae phage (podovirus-like), and a novel family, Edelweissviridae (16 siphovirus-like phages with long non-contractile tails).
Transmission electron microscopy (TEM) enabled high-resolution morphological classification of all isolates, revealing clear structural signatures that closely matched genomic clustering and allowed the delineation of distinct morphotypes within and across families. Notably, TEM analysis was instrumental in identifying the Edelweissviridae as a morphologically coherent group characterized by bigger capsids and unusually long flexible tails, supporting their classification as a novel family. Morphological variations within siphovirus-like groups highlighted previously underappreciated structural diversity not fully captured by genomics alone.
Introns truncating the large terminase subunit gene (terL) were identified in 60% of genomes across Herelleviridae and Edelweissviridae. Host range assays against 40 clinically relevant S. epidermidis isolates revealed higher infectivity toward veterinary strains, particularly for phages of the genus Sepunavirus and the new subfamily Aletschvirinae. Additionally, wall teichoic acid glycosylation influenced phage susceptibility in a family-dependent manner, consistent with distinct predicted receptor-binding proteins.
Integrating TEM-derived morphology with genomic and functional data offers a powerful framework to resolve phage taxonomy, linking structure to host interactions while expanding the known diversity and improving classification of staphylococcal phages.

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Modular pipeline for coding-free AI-driven analysis of large-scale time-lapse microscopy

Sacha Psalmon[1], Benjamin D. Towbin[1]

[1]Institute of Cell Biology (IZB), University of Bern, Bern (CH)

Longitudinal imaging provides a powerful approach to study growth, development and behavior *in vivo*, but the resulting datasets remain challenging to analyze in a reproducible and scalable manner. In particular, the integration of image segmentation, quality control, feature extraction, and developmental annotation into unified workflows continues to limit the broader application of quantitative time-lapse microscopy.
We present ALIGN (Automated Longitudinal Imaging and Growth ANalyser), a modular and reproducible framework for the analysis of long-term live imaging data and its application to *Caenorhabditis elegans* development. ALIGN integrates deep learning–based segmentation, automated quality control, computational straightening, feature extraction, and interactive annotation within a single configurable pipeline. This approach enables robust quantification of morphological and behavioral features across development, while remaining accessible to users without extensive programming experience.
Using ALIGN, we demonstrate accurate segmentation across heterogeneous imaging conditions with minimal effort for collecting training data, automated detection of larval stage transitions from growth trajectories, and improved measurement precision through data-driven quality control. Computational straightening further enables consistent analysis of motile animals and reconstruction of three-dimensional image data.
As proof of principle, we apply ALIGN to quantify feeding dynamics, growth and body size in *eat-2* mutants across larval development. This analysis reveals increased variability in feeding behavior and a non-proportional relationship between pharyngeal pumping rate and growth, illustrating how integrated longitudinal analysis can uncover relationships that are not accessible through conventional approaches.
Together, ALIGN provides a generalizable resource for quantitative analysis of developmental processes from time-lapse imaging data, facilitating the study of growth, behavior and heterogeneity at single-animal resolution.

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Steer the Pixels: A live interactive demo of VIBE

Guillaume Witz[1], Jens Müller[1] and Ruben Lopez[2]

[1]Data Science Laboratory, University of Bern, Bern (CH)
[2]Microscopy Imaging Center, University of Bern, Bern (CH)

ViBE is the newly developed Virtual Image Analysis platform at the University of Bern. Designed to provide seamless access to advanced bioimage analysis tools and powered by the university's high-performance computing cluster (UBELIX), ViBE delivers a fully managed computational environment that is accessible remotely through a simple web browser. Its user-friendly interface and broad suite of preinstalled applications eliminate the need for complex local setup, facilitating the access for new and advanced users. In this interactive demonstration, we will highlight the core capabilities of ViBE through hands-on image analysis tasks guided by audience input. Using widely known bioimage analysis tools such as Fiji, QuPath, napari and others, we will construct simple example workflows that illustrate key concepts and practical applications. These demonstrations are designed to provide participants with a clear understanding of the platform's potential, while also pointing toward more advanced and scalable use cases in bioimage analysis.

The Swiss BioImaging Community

Virginie Uhlmann

BioVisionCenter and Department of Molecular Life Sciences, University of Zurich, Zurich (CH)

The Swiss bioimaging community convened in March 2026, bringing together representatives of the research and infrastructure activities in bioimaging of academic institutions across the country, to outline a path towards a shared microscopy imaging ecosystem across Switzerland. In this presentation, I will report on the actionable steps we identified and outline how those interested in these efforts can contribute.

High-sensitivity multiplex spatial biomarker detection without secondary antibodies

Simon Restrepo

arcoris bio AG, Schlieren (CH)

Spatial biomarker analysis requires methods that combine high sensitivity, strong specificity, and true multiplexing while preserving tissue architecture. Conventional immunostaining workflows often depend on secondary antibodies, which can constrain assay design, introduce cross-reactivity, and limit multiplex scalability. Here, we describe a secondary-antibody-free approach for high-sensitivity multiplex spatial biomarker detection based on enzyme-free DNA nanotechnology. In this strategy, signal amplification is achieved by coupling MUSE® activators directly to primary antibodies, or oligonucleotide probes, enabling detection of proteins and RNA within the same spatial context. The self-assembling reaction produces strong signal amplification with low background and supports simultaneous multiplexed readout without dependence on antibody isotype matching or iterative cycling.

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Cell Polarity in Grass Epidermis Development: From Observation to Quantitative Analysis

Anastasiia Korosteleva[1], Kim Janssen[1,3], Paola Ruiz Duarte[1], Heike Lindner[1,2], Michael Raissig[1,2]

[1]Institute of Plant Sciences, University of Bern, Bern (CH)
[2]Oeschger Centre for Climate Change Research, University of Bern, Bern (CH)
[3]Department of Chemistry, Uppsala University, Uppsala (Sweden)

The leaf epidermis plays a crucial role in protecting internal tissues, facilitating gas exchange and optimising water use efficiency. In grass species, epidermal development follows a longitudinal gradient, progressing from undifferentiated protodermal cells to specialised mature cells. This structure presents a compelling system for quantitative imaging, with stereotypical division patterns creating distinct cell types: transverse asymmetric divisions create a pattern of alternating specialised and non-specialised cells, while longitudinal asymmetric divisions create ultra-specialised stomatal subsidiary cells. We identified BdPOLAR-like1 (BdPL1) as a key regulator of the first transverse asymmetric cell divisions (ACDs) in the developing epidermis of the wild grass model Brachypodium distachyon. BdPL1 localised asymmetrically towards the base of a cell before division, demarcating the future basal daughter cell and establishing physical asymmetry before division. Consequently, loss of BdPL1 disrupted post-division cell-size asymmetry and subsequent patterning of specialised and non-specialised cell precursors. We then demonstrated that polarisation is essential for BdPL1 function by disrupting its ability to polarise within the cell. Quantitative image analysis of cell-size distributions confirmed that non-polarised BdPL1 failed to restore post-division cell-size asymmetry in the bdpl1 background. Meanwhile, reintroduction of functional BdPL1 fully rescued the developmental phenotype of the bdpl1 mutant.
Surprisingly, when BdPL1 was expressed in a cell type with mediolateral polarisation, fluorescence intensity profiling showed that BdPL1 was consistently polarised along the apical-basal axis and disrupted the native longitudinal division orientation, suggesting that BdPL1 polarisation is independent of its cellular context.
Taken together, BdPL1 is the earliest known polarity factor in grass epidermis development, establishing cell-size asymmetry during formative transverse ACDs. With quantitative imaging and analysis, we demonstrated that the BdPL1 polarisation is required for its function and is independent of cellular context.

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Identifying rare cellular subpopulations using single-cell multiparametric quantitative imaging: challenges and opportunities

Camilla Ullmann[1], Philipp Kirchner[1], Charles Bidgood[2], Aurel Perren[1], Martin Sadowski[1]

[1]Institute for Tissue Medicine and Pathology, University of Bern, Bern (CH)
[2]Centre for Genomics and Personalised Health, Queensland University of Technology, Brisbane (Australia)

High-resolution characterization of cellular heterogeneity typically relies on single-cell omics-based approaches, which are costly, limit temporal resolution and only infer functional and phenotypic features. Here, we present single-cell multiparametric quantitative imaging (scMQI) as an investigative, low-cost, and scalable alternative to deconvolute cellular heterogeneity and identify and functionally characterize subpopulations and their dynamic changes over time.
Using high-content confocal fluorescent microscopy (CellVoyager™ CQ1 (Yokogawa), complemented by Leica's Mica and Thunder systems), we performed scMQI of neuroendocinre pancreatic tumour cells drug-treated for 0, 7, 14, and 21 days using a panel of live-stains mixes comprised of four fluorescent probes (total=32) with separate emission spectra plus brightfield (five channels). This experimental setup is designed to identify and characterize drug-tolerant cancer cells and track their dynamic phenotypes.
The panel measures a broad spectrum of structural and functional features, including various organelles, ion and metabolite homeostasis, chromatin status, and cell death. Image segmentation (Cellpose, Cyto3) and feature extraction (CellProfiler) yielded up to 347 quantitative features per cell, capturing morphology, intensity, texture, and spatial organization.
To enable unbiased discovery of rare and dynamic states, we adapted analysis strategies from single-cell transcriptomics, including dimensionality reduction (UMAP) and clustering, to imaging-derived feature spaces. This framework allows the identification of subpopulations that emerge over time and are not detectable in control conditions.
A central focus of this presentation is the practical implementation of scMQI and challenges such as illumination artifacts, stain cross-reactivity, segmentation biases, and batch integration across experiments. We outline solutions and highlight how careful experimental design combined with computational adaptation enables robust analysis.
Overall, scMQI provides a flexible and cost-effective platform for high-dimensional, time-resolved functional single-cell phenotyping, with broad applicability beyond drug tolerance.

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Caspase 9 and the Apoptosome *in situ*

Calvin Klein[1], Alicia Borgeaud[1], Amandine Stooss[1], Daniela Ross-Kaschitza[1], Thomas Lemmin[1], Wanda Kukulski[1]

[1]Institute for Biochemistry and Molecular Medicine, University of Bern, Bern (CH)

The apoptosome is a large protein complex essential for initiating programmed cell death (apoptosis). This heptameric assembly of apoptotic protease-activating factor 1 (Apaf-1), together with bound Cytochrome C, forms upon the initiation of apoptosis and recruits Procaspase-9 to activate the caspase cascade, ultimately leading to the dismantling of the cell. Although high-resolution structures of the apoptosome have been determined in vitro, its presence has yet to be demonstrated in situ. Using Cryo-Correlative Light and Electron Microscopy (Cryo-CLEM), our lab has identified dense meshworks in the cytosol of apoptotic cells that correlate with Apaf-1-GFP foci. Cell biology data indicate that these foci represent functional apoptosome equivalents. Building on these findings, we aim to elucidate the underlying architecture of the Apaf-1 dense meshworks using three complementary approaches. First, I am expanding our dataset of cryo-electron tomograms from cryo-focused ion beam (cryo-FIB)-milled cells to analyse the meshwork via subtomogram averaging. Second, I am attempting to reconstitute this protein meshwork in vitro for single particle cryo-EM analysis. Third, I am determining the solution structure of autoinhibited procaspase-9 to elucidate why meshwork formation might be required for apoptosome activity.

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Understanding how cells deal with transcription–replication conflicts

Michail Petropoulos

Institute of Animal Pathology, University of Bern, Bern (CH)

Genome duplication requires coordination between DNA replication, transcription, and repair. When these processes collide, transcription–replication conflicts arise, generating DNA damage and threatening genome stability. These conflicts are a major source of replication stress and play an important role in cancer development and treatment response. In this talk, we explore how cells respond to and resolve transcription–replication conflicts during S phase. We use an integrative approach combining high-content imaging and high-throughput sequencing to measure DNA damage signaling, replication dynamics, transcriptional activity, and DNA repair pathway engagement.
Through multiparametric analysis, we identify how disruptions in replication and transcription impact genome stability. This work provides a broader understanding of cellular responses to replication stress and offers insight into how these mechanisms can be leveraged in cancer therapy.

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The Electron Microscopy Facility at the Institute of Anatomy

David Kalbermatter

Institute of Anatomy, University of Bern, Bern (CH)

The Electron Microscopy Facility at the Institute of Anatomy is a dedicated cryo-electron microscopy infrastructure supporting biological research across all scales, from small proteins to cellular ultrastructure. As part of the Dubochet Center for Imaging (DCI), the facility brings together instruments and expertise covering the full journey from sample preparation to high-resolution data acquisition. A Titan Krios G4 TEM enables imaging at near-atomic resolution, while an Aquilos 2 FIB-SEM with integrated fluorescence light microscopy (iFLM) bridges the gap between cellular context and molecular detail. A dedicated sample preparation suite, including a Vitrobot, high-pressure freezers, and a cryo-ultramicrotome, enables vitrification across the full range of biological samples — from protein solutions and cells to bulk tissue. Together, these capabilities underpin workflows ranging from single particle analysis and cryo-electron tomography to cryo-CLEM, FIB milling, and CEMOVIS. This presentation gives an overview of the facility and the biological questions it is equipped to address.

Visualizing Pore Forming Toxin – Receptor Interactions by Cryo-EM

Ioan Iacovache[1], Chang Wang[1], Filippo Cattalani[2], Faezeh Farhoosh[2], Horst Posthaus[2], Benoît Zuber[1]

[1]Institute of Anatomy, University of Bern, Bern (CH)
[2]Institute of Animal Pathology, University of Bern, Bern (CH)

Most organisms produce proteins that are aimed at damaging other organisms by perforating the cellular membranes. Depending on the producing species we talk about membrane attack complexes, pore forming proteins or pore forming toxins (PFTs). While these proteins are very distinct in sequence, structure or target they mostly rely on similar modes of action. They recognize the target cell through interactions with specific receptors, oligomerize to form large, circular complexes and insert into the membrane. Based on the channel structure PFTs can be classified in two main subclasses: alpha helical or beta barrel PFTs. In addition, β-PFT can be subcategorized based on their quaternary structure into several subclasses (aerolysin, hemolysin, cholesterol dependent cytolysin etc). Most pathogenic bacteria rely on several such pore forming toxins for their survival and spread within the host. Understanding the details involved in each step of the mode of action, identifying the specific receptors and characterizing the interactions can add to our knowledge about the disease and help us develop strategies to inhibit the toxins. Clostridial pathogens secrete a large and heterogeneous array of pore forming toxins making them the perfect target for an extensive investigation. We focused our attention on β-PFT from the α-hemolysin family produced by Clostridium Perfringens, in particular CPB and NetF. Using cryo electron microscopy we were able to characterize the oligomerization states of the two PFTs. In addition, we were able to precisely define the interaction interface with their respective cellular receptors.

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Visualization and quantification of protein-protein interactions in yeast cells using a vacuolar recruitment assay

Benjamin Pillet[1], Sébastien Favre[1], Malsore Zenuni[1], Erze Halitaj[1], Dieter Kressler[1]

[1]Department of Biology, University of Fribourg, Fribourg (CH)

Ribosome biogenesis requires the rapid, active nuclear import of newly synthesized ribosomal proteins (r-proteins). Because of their highly basic, aggregation-prone nature, r-proteins rely on dedicated chaperones and importins for protection and transport. However, establishing the in vivo interactome of unassembled r-proteins is methodologically challenging because these interactions are very transient and abolished upon r-protein assembly into pre-ribosomal particles. Moreover, the vast majority of cellular r-proteins are in their ribosome-bound state. Interactions of r-proteins with importins are even more short-lived than the ones with dedicated chaperones as the r-protein is released from the transport-mediating importin upon nuclear entry by the binding of RanGTP. The classical yeast two-hybrid (Y2H) assay, which is often used to determine in vivo protein-protein interactions, can only reveal interactions that occur in the nucleus; thus, in the case of importin-cargo interactions, necessitating to use truncated importin variants deficient in RanGTP binding.

To address this limitation and visualize the interactions of full-length importins and their r-protein cargo in the cytoplasm, we established a fluorescence microscopy-based vacuolar recruitment assay in yeast. In this assay, a bait r-protein, fused to yEmCherry, is tethered to the cytoplasmic face of the vacuolar membrane. An importin prey, tagged with ymNeonGreen, is co-expressed and upon direct interaction, the importin, which normally displays a cytoplasmic and/or nuclear steady-state localization, is recruited to the vacuolar surface, yielding a distinct, quantifiable colocalization signal.

This talk will detail the development and application of this cell biological assay and how it overcomes limitations of standard methods. Unlike in vitro pull-downs, it detects direct interactions in their native environment and without requiring difficult recombinant protein purification. Compared to Y2H assays, this visual approach eliminates self-activation false positives and prevents false negatives by confirming protein expression via fluorescence. Using this assay, we demonstrate that multiple importins can interact with a single r-protein, providing a robust tool to dissect redundancy within the nuclear import system.

New: Image contest

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Image contest: **Best Microscopy Image**

You qualify to participate in this contest by

- Being a member of the UniBE or of the UniFR
- Being participant of the MIC Research Day 2025
    - If the image submission person is not present, the prize goes to the 2nd winner. However, you may appoint a deputy who is present.
- By the following statement with your submission
    - You guarantee that you have produced the entries yourselves and that you hold all the necessary rights and authorisations.
    - The entries may also be freely used for non-commercial purposes, provided they remain unaltered and the author is duly credited.
- If you are at the student level (BSc, MSc, PhD), you additionally have to confirm that
    - You hold the approval of your supervisor for submission.

The best microscopy image will be determined in the following **categories**.

- Most beautiful image
- Most impressive artistic artefact image
- Most thought-provoking image

Image **submission** is as follows:

- email to **ana.stojiljkovic@unibe.ch**
- subject of the email is **MIC Image Competition**
- maximum **3 images per participant**

Image **specifications** must be according to the following.

- Format: JPEG (.jpg)
- Maximum dimension: 1920 pixels wide x 1080 pixels high
- Maximum file size: 10 MB
- 8-bit color depth
- Recommended resolution: 72 – 150 dpi

Deadline for image submission is

- **June 11, 2025**

Decision on the winner

- Will be decided by the participants of the MIC Research Day 2025 by voting: voting is only possible on site and for a limited time

The photo competition will only be held if a sufficient number of valid entries are received.

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Participation form

Personal Information

First Name: ______________________ *Last Name:* ______________________

E-Mail: ______________________ *Affiliation:* ______________________

Research Group Head: ______________________

I am a

- ☐ Master Student
- ☐ Doctoral Student
- ☐ Post Doc
- ☐ Research Group Head
- ☐ Other (please specify):

Consent

- ☐ I guarantee that I produced the image and hold all necessary rights
- ☐ I agree to my image being presented during the MIC Research Day
- ☐ I agree to usage of the image for non-commercial purposes by the organizers (optional)

Image Information

Image title: ______________________

Image description
(max. 230 characters, including spaces)
Brief caption explaining the instrument, technique, and what is depicted in the image.
Caption Example: *Confocal microscopy (ZEISS LSM 800). White, astrocyte foot processes (GFAP immune fluorescence staining). Green, microglia (CX3CR1-GFP reporter). Red, monocytes (CCR2-RFP reporter). Orange, retina (autofluorescence).*

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Date, location and Signatures of

______________________________ ______________________________
Submitter PI