KBC DAYS 2026

Dynamic Worlds

Responses and Transformations from Molecules to Landscapes



10–11 NOVEMBER 2026 • UMEÅ, SWEDEN

Conference Programme - Research Infrastructures - Abstracts - Participants

KBC CHEMICAL BIOLOGICAL CENTRE

A collaboration between

UMEÅ UNIVERSITY

SLU

DAY 1, Tuesday 10 November

SESSION 1: OPENING and KEYNOTE LECTURE I

Chair: Nicolò Maccaferri

9.00 **Welcome and Opening of the KBC DAYS 2026**
Stefan Björklund
Scientific Coordinator of KBC

9.10 **Umeå Doctoral Student Society (UDSS)**
Emma Dehan
President, Umeå Doctoral Student Society

9.15 **RECEM - Research School for Excellence in Cementitious Materials Science**
Nils Skoglund
Department of Applied Physics and Electronics, UMU

9.25 **KEYNOTE LECTURE I: Electron waves and light: Exploring matter in motion**
Prof. Claus Ropers
Director, Department of Ultrafast Dynamics, Max Planck Institute for Multidisciplinary Sciences, Göttingen, Germany

10.10 *Smile & Recharge*

10.15 *Coffee break*

SESSION 2: NEW FACULTY MEMBERS, AWARDS and GRANT RECIPIENTS from KBC

Chair: Stefan Björklund

10.40 **Harnessing Bacterial Proteins and Membrane Vesicles for Cancer Therapy: Mechanisms and Therapeutic Opportunities**
Sun Nyunt Wai
Department of Molecular Biology, UMU, Recipient of the Bo and Barbro Hammarström Prize at Umeå University for 2026

10.55 **Wood in trees – from evolutionary footprints to protein interactomics**
Leonard Blaschek
Department of Forest Genetics and Plant Physiology, Umeå Plant Science Centre, SLU

11.10 **Data-driven biology or biology-driven data? A *PhysiOmics* approach to neurobiology**
José Davila Velderrain
Department of Molecular Biology, UMU

11.25 **Genomics of forest trees in a changing world**
Susan McEvoy
Department of Forest Genetics and Plant Physiology, Umeå Plant Science Centre, SLU

DAY 1, Tuesday 10 November

11.40 **One laser, many worlds: ultrafast light for electronics, biology, and chemistry**
Markus Ludwig
Department of Physics, UMU

12.00 *Lunch*

SESSION 3: KEYNOTE LECTURE II and ELEVATED TALKS PRESENTATIONS by PhD and FORSKARASPIRANT PROGRAMME STUDENTS

Chair: Andreas Kohler

13.00 **Elevator talks presentations** *(2 min each)*

1. From Mine Waste to Functional Clays: Redox-Driven Mineral Transformation for Sustainable Environmental Barriers (Poster#1)
Trung Nguyen, *Department of Chemistry, UMU*

2. The ageing paradox: increasing heat resistance despite decline in protein quality control (Poster#2)
Sofia Morney, *Department of Molecular Biology, UMU*

3. From Air to Minerals: The Interplay of Chemistry and Material Properties in CO_2 Capture (Poster#3)
Romana Viktoria Szakal, *Department of Chemistry, UMU*

4. Human *in vivo* genetic screening for novel CAR T cell design (Poster#4)
Florian Albrecht, *Department of Molecular Biology, UMU*

5. From serum to structure: sequencing antibodies by mass spectrometry
Léa Maheux, *Department of Physics, UMU*

6. Neutrophils, NETs and IL-18 in the world of COVID-19 (Poster#6)
Emelie Backman, *Department of Clinical Microbiology, UMU*

13.15 **KEYNOTE LECTURE II: "Molecular Mechanisms Underlying the Energy Currents of Life"**
Prof. Ville R. I. Kaila
Department of Biochemistry and Biophysics, Arrhenius Laboratories for Natural Sciences, Stockholm University, Stockholm, Sweden

INTERACTION / POSTER SESSION

14.00 **Poster presentations by PhD and Forskaraspirant Programme students and research infrastructures**
and *Coffee*

DAY 1, Tuesday 10 November

SESSION 4: NEW FACULTY MEMBERS, AWARD and GRANT RECIPIENTS from KBC

Chair: Anna Arnqvist Björklund

15.00 **Shaped by water: hydraulic control of plant growth**
Juan Alonso-Serra
Department of Forest Genetics and Plant Physiology, Umeå Plant Science Centre, SLU

15.15 **Application of human organoid models for the study of emerging pandemic respiratory viruses**
Meaghan Flagg
Department of Clinical Microbiology, The Laboratory for Molecular Infection Medicine Sweden (MIMS), UMU

15.30 **Complex Trait Genetics and Plasticity for Resilient Plants**
Yanjun Zan
Department of Plant Physiology, Umeå Plant Science Centre, and Integrated Science Lab (IceLab), UMU

15.45 **Breaking the membranous refuge of *Chlamydia***
Barbara Sixt
Department of Molecular Biology, UMU and recipient of ERC Consolidator Grant

16.00 **Tracking infections through space with Bayesian phylogeographic methods**
Andrew Magee
Department of Molecular Biology, Integrated Science Lab (IceLab), The Laboratory for Molecular Infection Medicine Sweden (MIMS), UMU

16.15 **A new generation of photochromic materials**
Lars Österlund
Department of Chemistry, UMU

16.30 *Poster viewing and mingle before the dinner starts*

17.00 *Origami Workshop and Social Activity: "Dynamics unfolded"*

18.00 *Dinner*
- Announcement of the student presentation prize winners
- Announcement of the KBC Employee of the Year

DAY 2, Wednesday 11 November

SESSION 5: KEYNOTE LECTURE III and NEW FACULTY MEMBERS from KBC

Chair: Gerard Rocher Ros

9.00 **KEYNOTE LECTURE III: "The emergence of eukaryotes as an evolutionary algorithmic phase transition"**
Prof. Jordi Bascompte
Department of Evolutionary Biology and Environmental Studies, University of Zurich, Switzerland

9.45 **Regrowth after injury: Decoding the mechanisms of plant regeneration**
Abdul Kareem Valiya Kadavu
Department of Forest Genetics and Plant Physiology, Umeå Plant Science Centre, SLU

10.00 *Coffee Break*

10.00-11.00 Parallel session in Lilla hörsalen:
Outside of Academia #17: "Beyond the Bench: Building a Career Beyond Academia"
with Elena Hoffer, Co-Founder and CEO of Alma.me.

SESSION 6: RESEARCH INFRASTRUCTURE INFORMATION

Chair: Andre Mateus

10.30 **Overview of KBC Infrastructure**
Marta Bally
Chair of The Faculty of Medicine's Council for Research Infrastructure (M-RIS), UMU

Tandem Talks: Researcher - Infrastructure Case Studies

10.45 **Tandem Talk 1: Can Nordic microalgae help tackle micro- and nanoplastic pollution? Investigating tolerance and bioremediation with VISP and BAP**
Saumita Chakravarty, *Department of Chemistry, UMU*
Junko Takahashi-Schmidt, *Biopolymer Analytical Platform (BAP)*
Andras Gorzsas, *Vibrational Spectroscopy Core Facility (ViSp)*

DAY 2, Wednesday 11 November

11.10 **Tandem Talk 2: Proteome-wide effects of drugs in representative species of the human gut microbiome: insights from UPP and UCEM**

Lucia Perez Jimenez, *Department of Molecular Biology, UMU*

Andre Mateus, *Umeå Proteomics Platform (UPP)*

Sara Henrikson, *Umeå Centre for Electron Microscopy (UCEM)*

11.35 **Tandem Talk 3: Improving light-emitting electrochemical cells through nanoscale fabrication with NanoLab and UCEM**

Ajay Kumar Poonia, *Department of Physics, UMU*

Roushdey Salh, *NanoLab*

Nils Hauff, *Umeå Centre for Electron Microscopy (UCEM)*

11.00-12.00 Parallel session in Lilla hörsalen:
Outside of Academia #17: "Beyond the Bench: Building a Career Beyond Academia"
with Elena Hoffer, Co-Founder and CEO of Alma.me.

INTERACTION SESSION

12.00 *Standing Lunch*

Activities during lunch break:
- Visit infrastructure representatives by their posters at KBC Ljusgården
- Drop-in to Glasburen for Lunch pitch talks by Innovation Office: Beyond Research

Lunch pitch talks: Beyond Research:
Join us over lunch for two 10-minute talks exploring how research can move beyond academia and what to consider along the way. Drop in, listen and bring your questions!
12.30–12.40 | From research to use
How can research findings make a difference beyond academia? Get a quick introduction to research utilisation and explore different ways research can be developed, applied and put into use.
13.00–13.10 | Intellectual property in research
What is worth knowing about intellectual property as a researcher? Get an introduction to IP and how it connects to research results, ideas and opportunities for further development.
Speaker: Johan Nordlund, *Innovation Office*

DAY 2, Wednesday 11 November

SESSION 7: UMEÅ POSTDOC SOCIETY (UPS)

Chair: Iryna Yakovenko

Programme organised by UPS:

13.30 **Beyond Academia - making the transition as a Postdoc**
Elena Hoffer
Co-founder and CEO of Alma.se

14.30 *Short break*

14.40 **Flash Talks** *(3 min each)*

Danhong Li, *Department of Plant Physiology, Umeå Plant Science Centre, UMU*

Chaitra Shankar, *Department of Molecular Biology, UMU*

Nazar Beirag, *Department of Clinical Microbiology, UMU*

Ekaterina Chernova, *Department of Physics, UMU*

Omotayo Sindiku, *Department of Chemistry, UMU*

Ratish Raman, *Department of Medical and Translational Biology, UMU*

Basit Jabbar, *Department of Clinical Microbiology, UMU*

15.00 **Concluding remarks**
Stefan Björklund
Scientific coordinator of KBC

- Announcement of the KBC Photo Contest winner

Keynote Speaker



Prof. Dr. Claus Ropers

Director, Department of Ultrafast Dynamics, Max Planck Institute for Multidisciplinary Sciences & Georg-August University, Göttingen, Germany

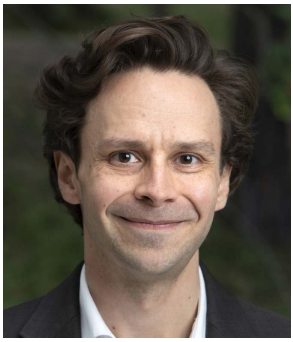
https://www.mpinat.mpg.de/ropers

Bio: After studying physics at the University of Göttingen and the University of California, Berkeley (USA), Claus Ropers worked at the Max Born Institute in Berlin and received his doctorate at the Humboldt-Universität zu Berlin in 2007. After a year as project leader at the Max Born Institute, he returned to the University of Göttingen in 2008, where he initially worked as a junior professor with tenure track, heading the research group Nano-Optics and Ultrafast Dynamics. In 2011, the University appointed him as professor at the age of only 34 years. Since 2013, he has held the professorship for Experimental Solid State Physics and has been managing director of the IV. Physical Institute – Solid State and Nanostructures since 2014. Director and Scientific Member at the Max Planck Institute for Multidisciplinary Sciences.

Claus will give a keynote lecture, **"Electron waves and light: Exploring matter in motion"** on **10 November, 9:25-10:10**.

Abstract: Electron microscopy reveals the microscopic structures underlying the properties of materials. Extending it into the time domain allows us to investigate how these structures evolve, how energy propagates, and how new states emerge. In this talk, I will introduce ultrafast electron microscopy and discuss how interactions with matter and light imprint information on electron waves that can be converted into measurable image contrast. Examples will range from light-induced structural transformations to nanoscale acoustic waves. I will also discuss how coherent interactions with light allow us to manipulate the quantum states of the probing electrons themselves, opening new possibilities for beam control and imaging.

Keynote Speaker



Prof. Ville R. I. Kaila

Department of Biochemistry and Biophysics,
Arrhenius Laboratories for Natural Sciences,
Stockholm University, Stockholm, Sweden

E-mail: ville.kaila@dbb.su.se

http://villekaila.com/

Bio: Ville R. I. Kaila received his PhD in biochemistry in 2009 from University of Helsinki. He worked as an EMBO Long-Term Fellow at the Laboratory of Chemical Physics at the National Institutes of Health (2010-2013), after which he was appointed a professorship at the Technical University of Munich. In 2019, Kaila moved with his research group to Stockholm, where he is currently professor at the Department of Biochemistry and Biophysics at Stockholm University and a Wallenberg Scholar. His research focuses on elucidating mechanistic principles of bioenergetic protein complexes by integrative biophysical approaches. Besides his passion for research, Kaila is also a classical musician and actively performs as a violinist.

Ville will give a keynote lecture, **"Molecular Mechanisms Underlying the Energy Currents of Life"**, on **10 November, 13:15-14:00**.

Abstract: Biological energy conversion is catalyzed by gigantic membrane-bound protein complexes that transduce redox or light energy into a trans-membrane proton gradient, powering the synthesis of ATP and active transport. Yet, despite significant advances, the molecular principles of these reactions remain poorly understood, and pose major scientific challenges. In this talk, I describe our integrative mechanistic exploration of bioenergetic machines – achieved by combining theory- and data-driven approaches with biochemical, spectroscopic, and cryo-electronic microscopic experiments to derive a molecular understanding of these intricate systems. I describe our recent breakthroughs in understanding intricate coupling effects in the Complex I machinery of oxidative phosphorylation, an enzyme complex that catalyzes a >200 Å redox-driven proton transfer reactions, with mutations resulting into development of severe human diseases. Our findings reveal how this enzyme machinery combines electric field effects to trigger conformational and hydration changes across the complete protein scaffold, enabling action-at-a-distance effects. I also describe how mutations linked to mitochondrial disease result in drastic perturbations in catalytic activity. On a general level, our findings suggest that bioenergetic machines employ electrostatic effects to couple catalysis with conformational dynamics, with striking similarities amongst different biological systems.

Keynote Speaker



Photo credit: Sixto Arjona

Prof. Jordi Bascompte

Department of Evolutionary Biology and Environmental Studies, University of Zurich, Switzerland

https://www.bascompte.net/

Bio: Jordi Bascompte is Professor of Ecology at the University of Zurich and Director of the PhD Program in Ecology. He is best known for having brought the interactions of mutual benefit between plants and animals into community ecology, at a time largely dominated by predation and competition. His application of network theory to the study of mutualism has identified general laws that determine the way in which species interactions shape biodiversity.

Jordi is one of the most highly-cited scientists according to Thompson Reuters. Among his distinctions are the European Young Investigator Award (2004), the Ecological Society of America's George Mercer Award (2007), the Spanish National Research Award (2011), the British Ecological Society's Marsh Book of the Year Award (2016), the Ramon Margalef Prize in Ecology (2021) and the Cozzarelli Prize of the U.S. National Academy of Sciences (2025). Recipient of an ERC's Advanced Grant, Jordi has served on the Board of Reviewing Editors of Science and has been the Ideas and Perspectives Editor at Ecology Letters. His books include Self-Organization in Complex Ecosystems (with R.V. Solé) and Mutualistic Networks (with P. Jordano), both published by Princeton University Press.

Jordi obtained a PhD in Biology at the University of Barcelona (1994), supervised by Ricard V. Solé. This was followed by a postdoctoral position in Steven Frank's laboratory at the University of California, Irvine (1996 and 1997). After that, he was awarded an independent postdoctoral fellowship at the National Center for Ecological Analysis and Synthesis (NCEAS, 1998 and 1999). In 2000, he became Associate Professor (Full Professor from 2008) at the Doñana Biological Station, a center of the Spanish Research Council, where he was based until moving to Zurich in 2015.

Keynote Speaker

Jordi will give a keynote lecture, **"The emergence of eukaryotes as an evolutionary algorithmic phase transition"** on **11 November, 9:00-9:45**

Abstract: For almost half the history of life on Earth, the complexity of all organisms was limited to that of simple prokaryotic cells such as contemporary bacteria. The process by which genes are activated was entirely regulated by proteins. This set up a limit on cellular complexity, as finding even larger proteins became computationally unfeasible. The eukaryotic cell—characterized by membrane-bound nucleus and organelles—emerged as a compromise between a conserved process of gene growth and a change in genetic regulation, which incorporated noncoding sequences. This major evolutionary event, which unlocked the path towards multicellular organisms, can be understood as an algorithmic phase transition equivalent to that of certain search algorithms.

PhD and Forskaraspirant Programme student presentation abstracts

PhD student presentation abstract

Elevator talk #1✓ **Poster #1**

From Mine Waste to Functional Clays: Redox-Driven Mineral Transformation for Sustainable Environmental Barriers

Trung Nguyen[1], Chau-Anh Duong[1], Nathan Lavauzelle[1], and Michael Holmboe[1]

[1] Department of Chemistry, Umeå University

Mining generates vast volumes of waste materials in the form of mine tailings, containing potentially hazardous minerals including sulfides, capable of producing acid mine drainage (AMD). At Aitik (Sweden), Europe's largest Cu mine, the tailings are dominated by feldspars and micas (biotite and muscovite), with approximately 1.5 wt.% sulfides [1]. Upon mine closure (around year 2045), potentially acid-generating waste (~35 wt.% sulfides) requires engineered covers with low hydraulic conductivity ($k \approx 10^{-9}$ m/s) to limit oxygen and water infiltration, typically using bentonite/smectite-amended moraine. However, the substantial bentonite demand imposes economic and material burdens. Transforming locally abundant biotite-rich tailings into swellable clay-like materials (e.g., vermiculite, smectites) could hence offer a sustainable alternative for mine waste management.

In this research project, we investigate the oxidative alteration of biotite through coupled Fe^{2+} oxidation and interlayer K^+-Na^+ exchange to promote structural transformation toward swellable clay minerals. Experiments were conducted on well-characterized biotite [2] and Aitik tailings using H_2O_2 in Na^+-bearing solutions. Mineralogical and physicochemical changes were characterized using X-ray diffraction (XRD), UV-Vis spectroscopy, ICP-OES, and complementary analytical techniques to study the relationships between redox reactions, structural evolution, and water-sorption properties.

Following oxidative treatments, the biotite in Aitik tailings exhibited basal spacing expansion from 10 Å to approximately 12.2 Å under dry conditions and up to 15 Å upon hydration, indicating vermiculite-like swelling behavior. Notably, a small fraction of treated tailings exhibited further expansion to approximately 18 Å under extreme pH conditions, approaching smectite-like swelling behavior. ICP-OES confirmed substantial interlayer K^+ release and mobilization of structural cations, consistent with cation exchange and structural reorganization.

These findings indicate the potential of redox-driven mineral transformations to convert non-swellable biotite into more clay-like materials with enhanced hydration properties. By linking molecular-scale geochemical processes to material functionality, this study provides a foundation for developing sustainable clay-based environmental barriers from locally available mine waste.

[1] Forsberg, Lovisa (2008), PhD thesis
[2] Malmström, Maria, et al. (1996), Journal of Contaminant Hydrology, 21(1): p. 201-213.

Forskaraspirant student presentation abstract

Elevator talk #2✓ **Poster #2**

The ageing paradox: Increasing heat resistance despite decline in protein quality control

Sofia Morney[1], Mostafa Basiony[1,2], Verena Kohler[1,2]

[1] Department of Molecular Biology, Umeå University
[2] Umeå Centre for Microbial Research (UCMR), Umeå University

A hallmark of ageing is the decline in protein quality control, a system which controls protein function and cellular health. The decline of protein quality control can lead to accumulation of misfolded proteins which can be detrimental to the cell.

Given the importance of protein quality control during stress, aged yeast cells would be expected to exhibit reduced resistance to heat stress than young cells. Surprisingly, aged yeast cells were more heat stress resistant than young cells. In contrast, we observed that older cells accumulate more misfolded proteins in protein aggregates compared to young cells, supporting the notion that protein quality control is impaired with ageing.

Together, these observations reveal an ageing paradox where aged cells, despite declining protein quality control, were more heat resistant than young cells. Therefore, we wanted to identify mechanisms that give aged cells increased heat resistance despite impaired protein quality control. We performed a genome-wide depletion screen comparing strain fitness under acute heat stress with native condition in young versus old cells. Using bioinformatic clustering analysis we grouped the hits in distinct metabolic and signaling pathways. We identified several candidate pathways that may contribute to the observed heat stress resistance in ageing yeast.

Together, the identified pathways may represent compensatory mechanisms that contribute to the heat stress resistance in ageing yeast. Future characterization of these pathways will elucidate how aged cells become increasingly heat stress tolerant despite protein quality control dysfunction.

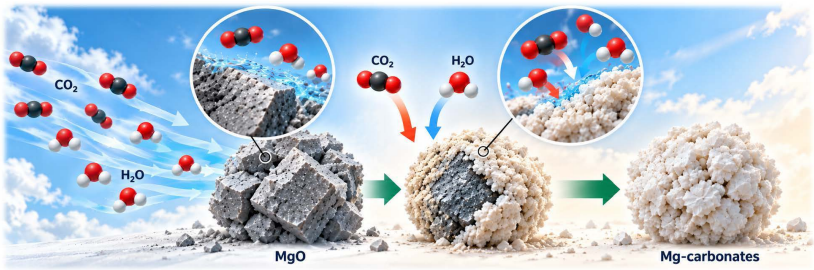
PhD student presentation abstract

Elevator talk #3✓ **Poster #3**

From Air to Minerals: The Interplay of Chemistry and Material Properties in CO_2 Capture

Romana V. Szakal[1], Jean-François Boily[1]

[1] *Umeå University, Sweden*



In recent decades, there has been an increasing concern about rising global temperatures on Earth. The main reason for global warming is the excessive emission of anthropogenic CO_2 trapped in Earth's atmosphere. It is thus important to remove this surplus CO_2 from the atmosphere on human timescales, while - ideally - ensuring its stable storage over geologic timescales. Based on CO_2 storage capacities across various methods, carbonated minerals have been identified as some of the most promising candidates. Previous research suggests that certain ultramafic rocks, rich in magnesium-bearing minerals, can naturally bind atmospheric CO_2 through weathering induced carbonation. This process can be represented by the following simplified reaction: Mg-bearing mineral + CO_2 + H_2O → hydrated Mg-carbonates + residual mineral. This knowledge has sparked interest in exploring the CO_2-binding capacity of a mineral widely used in industrial processes: periclase (MgO), more commonly known as "magnesia".

However, variabilities in reaction kinetics and carbonation efficiency have been observed across different periclase samples. This has been attributed to material-specific characteristics, such as crystallite size and morphology. These reactions occur in the presence of nanometrically thick water films at particle surfaces, which serve as reactive solvation environments that can drive phase transformation reactions. Although periclase is a highly hydrophilic mineral and, in the presence of water, hydroxylates into a structurally related phase (brucite, $Mg(OH)_2$), the formation of amorphous magnesium carbonate (AMC) may be a more favorable process than brucite formation, depending on relative humidities and CO_2 loadings. While brucite can also undergo carbonation, its formation as an intermediate phase may slow down the overall carbonation process and alter reaction kinetics compared to carbonation proceeding directly from MgO.

An additional limitation arises from the formation of a carbonate-rich product layer (shell) around the particles which may hinder further carbonation by restricting the transport of CO_2 and water to reactive surfaces. To this end, this work aims to identify the controlling parameters affecting CO_2 capture by MgO-bearing materials.

PhD student presentation abstract

Elevator talk #4✓ **Poster #4**

Human *in vivo* genetic screening for novel CAR T cell design

Florian Albrecht[1,3,4], Laura M. Carroll[2,3,4], Johan Henriksson[1,3,4]

[1] Department of Molecular Biology, SciLifeLab, Umeå University, [2] Department of Clinical Microbiology, SciLifeLab, Umeå University, [3] Umeå Centre for Microbial Research (UCMR), Umeå University, [4] Integrated Science Lab (IceLab), Umeå University

CAR T-cell therapy can produce durable responses in cancer patient. However, treatment is expensive, due to having to manage side-effects such as broad inflammatory responses, and largely limited to types of blood cancer. This highlights the need to identify genetic programs that improve therapeutic effects of CAR T-cells and allow them to be used in other types of cancer as well. Animal models incompletely reproduce human disease, limiting the translation of discoveries into clinical benefit for diseases like cancer, which interact with the immune system in complex ways. This project aims to develop a genetic screening platform that studies CAR T-cells directly in patients, linking genetic variation occurring during CAR T-cell production to cell states associated with therapeutic performance.

Experimental approaches such as Perturb-seq combine CRISPR-mediated gene perturbation with single cell transcriptomics to identify gene functions at scale. However, introducing random gene disruptions into therapeutic cells poses unacceptable risks to patients. We plan to exploit an existing feature of CAR T-cell manufacturing: Lentiviral integration into the genome, which is used to reprogramme a normal T-cell into a CAR T-cell, can alter or disrupt native gene expression. Mapping the location of integration events on the genome (and thus, which genes are disrupted by integration) alongside the transcriptome of the CAR T-cell, *after* it has been in a patient for therapeutic purposes, could reveal genetic changes associated with CAR T-cell persistence, proliferation or beneficial activity.

We use Atrandi's semi-permeable microfluidic capsules as single-cell isolation platform, which enables complex sequences of assays on the same cell. Specifically, we are developing a combined workflow comprising inverse PCR to identify lentiviral integration sites and RNA sequencing to characterize the corresponding transcriptional state. These measurements will be integrated using our computational pipeline for single-cell genome analysis to identify candidate relationships between integration sites and cellular phenotypes.

By turning existing integration events into opportunities for discovery, this project seeks to establish a human in vivo screening strategy that complements animal studies and prioritizes genetic targets for subsequent functional validation. Ultimately, the findings could guide the development of more effective CAR T-cell therapies and shorten the path from discovery to clinical application.

PhD student presentation abstract

Elevator talk #5✓

From serum to structure: sequencing antibodies with mass spectrometry

Léa MAHEUX[1], Martin Rosvall[1], Mattias Forsell[2], and Johan Normark[2]

[1] IceLab, Department of Physic, [2] Department of Clinical Microbiology, Umeå University

Influenza causes millions of severe cases and hundreds of thousands of deaths every year, and the seasonal vaccine protects only around 60% of young adults, and less in at-risk groups such as infants and the elderly (1). Protection largely comes from antibodies, proteins that each recognise one target with great precision. Yet people respond very differently to the same vaccine, and standard blood tests give one number for all antibodies together, without telling us which ones matter (1). Knowing exactly which antibodies a person carries would show how well their immune system responded and give new candidates for vaccines and therapies (2).

Today we can read antibody genes from B cells, but it is the antibodies circulating in serum that protect, and the B cell repertoire does not directly tell us which antibodies circulate in serum (1). Mass spectrometry measures the serum antibodies themselves (3). The analysis is hard for three reasons. Every person carries their own repertoire, so there is no single reference to compare against. Unlike DNA, proteins cannot be copied to amplify a faint signal. And related antibodies share most of their sequence and differ only in short stretches, so one measured fragment can fit several candidates. As a result, methods can report sequences with more confidence than they deserve. In a recent benchmark with antibodies of known sequence, 15 to 24% of the identified peptides were assigned to an antibody that was not in the sample, although the search was set to a 1% error rate (4).

My project asks how to make antibody sequencing from serum trustworthy, with an error rate that we can actually measure. The long-term goal is to go from sequence to three-dimensional structure and see what each antibody targets, which in turn could help design better vaccines.

References
1. Lee J., Boutz D.R., Chromikova V., et al. Nat. Med. 22, 1456-1464 (2016). doi:10.1038/nm.4224
2. Snapkov I., Chernigovskaya M., Sinitcyn P., Lê Quý K., Nyman T.A., Greiff V. Trends Biotechnol. 40, 463-481 (2022). doi:10.1016/j.tibtech.2021.08.006
3. Boutz D.R., Horton A.P., Wine Y., Lavinder J.J., Georgiou G., Marcotte E.M. Anal. Chem. 86, 4758-4766 (2014). doi:10.1021/ac4037679
4. Chernigovskaya M., Lê Quý K., et al. Cell Syst. 16, 101449 (2025). doi:10.1016/j.cels.2025.101449

PhD student presentation abstract

Elevator talk #6✓ **Poster #6**

Neutrophils, NETs and IL-18 in the world of COVID-19

Emelie Backman[1, 2], Remigius Gröning[1, 2], Alicia Edin[2, 3], Christoffer Granvik[1], Hinnerk Eilers[4], Anna Lange[5], Clas Ahlm[1, 2], Sara Cajander[5], Mattias N. E. Forsell[1, 2], Johan Normark[1] and Constantin F. Urban[1, 2]

[1]Department of Clinical Microbiology, Umeå University, Umeå, Sweden
[2]Umeå Centre for Microbial Research (UCMR), Umeå University, Umeå, Sweden
[3]Department of Diagnostics and Intervention, Umeå University, Umeå, Sweden
[4]Laboratory Medicine, Region Västerbotten, Norrland University Hospital, Umeå, Sweden
[5]Department of Infectious Diseases, Faculty of Medicine and Health, Örebro University, Örebro, Sweden

The novelty of Coronavirus Disease 2019 (COVID-19) leaves us with considerable knowledge gaps and central questions are what factors determine mild from severe disease and how we can predict disease progression. Severe disease is a result of an overreacting immune response where excessive release of neutrophil extracellular traps (NETs) contributes to this hyper-inflammatory state with life-threatening symptoms. We have combined clinical and pre-clinical research to investigate NETs as one of the driving forces behind severe disease. We used a sandwich ELISA to detect NET components in blood plasma collected from COVID-19 patients with clinically confirmed disease severity ranging from mild to moderate, to severe. We found increased amounts of NETs in patients and the highest levels were found in men with severe disease. Additionally, we used immunofluorescent microscopy to quantify the release of NETs from neutrophils in response to patient plasma. We found that plasma from COVID-19 patients can stimulate neutrophils from healthy donors to release NETs in levels increasing with disease severity. Intriguingly, we found elevated levels of the cytokine IL-18, known to induce NETs, in men with severe disease compared to women suggesting that IL-18 could be involved in disease progression.

PhD student presentation abstract

Poster #7

DON'T EAT THAT! Can archived air filters give early warning of threats to crops and livestock?

Anton Sandström[1], Daniel Svensson[1], José Lozano Villegas[1], Anna-Mia Johansson[1], Anna Berlin[2], Anders Kvarnheden[2], Siamak Zohari[3], Eric Capo[1], and Per Stenberg[1,2]

[1] Department of Ecology, Environment and Geoscience, Umeå University, [2] Swedish University of Agricultural Sciences, [3] Swedish Veterinary Agency, [4] Swedish Defence Research Agency

Food production is a critical societal function. Vulnerable global supply chains and rising geopolitical tension create an urgent need for preparedness against deliberate threats to the food system, which can be used in both war and peacetime to cause disruption or gain strategic advantage.

To address this, the Formas-funded Food Defense Research Centre [1] aims to develop new methods and strengthen the operational capacity of key food system stakeholders to detect and counter deliberate chemical and biological threats, while raising awareness and managing the interconnected challenges of economic disruption and information warfare. The centre is organized into four different tracks: Biological, chemical, economic and information warfare.

The biological track has three aims: to establish natural profiles of pathogens, to predict their future impact, and to detect non-natural incidents as deviations from natural patterns. Air filters from Ljungbyhed, Sweden, originally designed to detect radioactive fallout, have yielded weekly environmental DNA (eDNA) samples from 2013–2022, covering organisms across the tree of life [2]. From this time series we have estimated relative abundances, modelled long-term trends and seasonal variation using generalized additive models (GAMs), and modelled aerosol transport to infer where the eDNA originates.

My work addresses the first two aims. Using this metagenomic dataset, I study crop and livestock pathogens, from bacteria and fungi to parasites and pests, and ask: Which pathogens can be detected, and how often? How do detections compare with other surveillance data? Which pathogens are missed, and why? In a later stage, I will focus on selected pathogens and test whether fluctuations in their abundance are linked to environmental change, to improve prediction and targeted mitigation.

Together, this work aims to establish archived air filters as a tool for biosurveillance and early warning in the food system.

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PhD student presentation abstract

Poster #8

Exploring Swedish clay occurrences as natural analogues for the engineered barrier in deep nuclear waste disposal

Tom Falentin[1] and Michael Holmboe[1]

[1] Department of Chemistry, Umeå University

After more than 30 years of intermediate storage for the long-term and most radioactive nuclear waste of Sweden, the study of a definitive disposal is ongoing. This project is based on the observation of natural systems like the natural nuclear reactors in Oklo, Gabon (which remained stable and harmless for the surrounding ecosystem for millions of years) and consist of a multilayer barrier, deeply buried in a remarkably stable geological area. The outer protection layer is notably made of compacted bentonite (smectite-rich material) for its ability to adsorb cations and swelling properties, which maintain the water sealing and could fill potential fractures in the worst scenario.

The study of smectite minerals in such condition, responsible for the above-mentioned properties, was previously carried out in two different ways. Short term laboratory or multi-year *in-situ* experiments and simulations were performed to evaluate the impact of different factors like water erosion, contact with iron canister alteration products or microbiological activity. However, real long-term stability can only be accessed through the study of natural analogues with similar conditions to the waste disposal itself. This aspect is the most important given that the repository is designed to last more than 100,000 years.

Considering that previous studies mainly focused on a few localities, namely Kirunavaara and Malmberget, and the study of Swedish clay occurrences is of a few extents, a first step is to identify and localize new smectite occurrences with relevant geological context[1-3]. We aim to base our research on the digital core library provided by the Geological Survey of Sweden (SGU) to identify locations that stayed under the radar, through their large set of hyperspectral data. The objective is to use Multivariate Curve Resolution – Alternating Least Squares (MCR-ALS) method to recover the mineralogy and potentially take advantage of the large amount of data to build an AI agent that help resolving it. Finally, our objective is to better understand the formation of these Swedish smectite occurrences and the factors making them stable over the long term.

References:
[1] Geology of deep clay alteration zones in the Kiirunavaara and other iron ore deposits, northern Norrbotten, Sweden, Gilg H. Andersson, 2020.
[2] Kiruna Natural Analogue project, Alexander W Russell et Al., 2024.
[3] Low-temperature alteration in the iron ore deposit of Norrbotten, Sweden, Phillip Rieger, 2017.

PhD student presentation abstract

Poster #9

Structural insights into non-exonuclease domain Pol ε variants in cancer

Joel G Markgren[1], Joanna Hansson[1], Klara Yngvesson[1], Kamal Asalya[1], Vimal Parkash[1], Göran Bylund[1], Erik Johansson[1]

[1] Department of Medical Biochemistry and Biophysics, Umeå University

Specific substitutions in the exonuclease domain of DNA polymerase ε (Pol ε) are established oncogenic drivers associated with an ultramutator phenotype. While several of these variants have been structurally characterised, the mechanisms of cancer-associated variants outside the exonuclease domain remain less well understood.

Pol ε variants can reduce replication fidelity through multiple mechanisms, including impaired proofreading and increased mismatch extension. Mutational signatures and biochemical studies suggest that no single mechanism fully explains the effects of different cancer-associated variants.

Here, we determined structures of yeast Pol ε variants orthologous to human variants found in tumors with high mutation burden. Combined with biochemical characterisation, these structures reveal how mutations outside the exonuclease domain can alter the polymerase structure and function, providing new mechanistic insight into their potential role in tumorigenesis.

PhD student presentation abstract

Poster #10

Drug resistance mechanisms in gut microbiome species

Annika Druy[1], Lucía Pérez Jiménez[2], André Mateus[1,3,4]

[1] Department of Chemistry, Umeå University, [2] Department of Molecular Biology, Umeå University, [3] The Laboratory for Molecular Infection Medicine Sweden (MIMS), Umeå University, [4] Umeå Center for Microbial Research (UCMR), Umeå University

The composition of the gut microbiome has been associated with multiple diseases. This composition can be affected by both antibiotics and non-antibiotic drugs. Our lab is currently using proteomics approaches to identify which cellular processes are affected by drugs in these organisms. By uncovering the mechanisms of action of multiple drugs, we hope to be able to identify compounds to target the growth of specific species, and to enable measuring a direct impact on health.

During this endeavor, we have identified multiple proteins associated with drug resistance that change in their levels in the presence of specific drugs. However, exactly which drugs these proteins confer resistance to is currently unknown.

We have observed that multiple drug resistance-associated proteins have increased levels in the presence of different drugs. Therefore, we first want to identify which drugs are affected by the different resistance mechanisms that are upregulated in gut microbiome species. Currently, we are investigating drug-drug interactions to see if the upregulation of resistance mechanisms by one drug provides protection against another. Later, we want to characterize the regulation of expression of these different resistance mechanisms, to hopefully provide a potential point of therapeutic intervention.

In this project, we will use a combination of molecular biology, biochemistry, metabolomics, and computational biology approaches to identify how these proteins impact the effect of drugs. The results of this project provide the basis to better understand how drugs affect the growth of microbiome species and how they may affect resistance formation.

PhD student presentation abstract

Poster #11

Adenosine A_3 Receptor Signalling Regulates *Candida albicans* Induced NET Formation

William Björk[1], Ava Hosseinzadeh[1,2], Nadeem Ullah[1], Emelie Backman[1] and Constantin F. Urban[1]

[1]Deparment of Clinical Microbiology, [2] Umeå Centre for Microbial Research

Candida albicans is an opportunistic fungal pathogen and part of the natural human microbiota. It colonizes our mucosal surfaces, where it is most abundant the gastrointestinal tract (GI-tract).

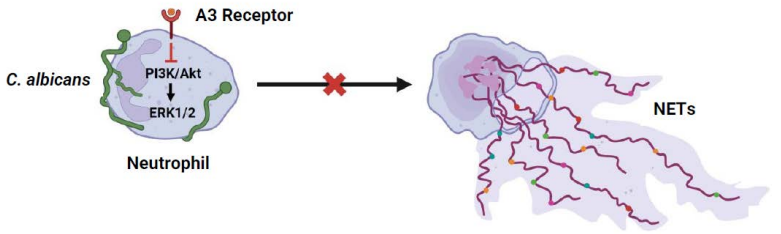
C. albicans causes, most commonly, local infections of the oral and vaginal mucosa. Even though these infections can be uncomfortable and cause discomfort/pain, it is treatable with commercially available antifungal drugs. However, individuals who are for example immunocompromised (a growing risk group), where the natural defences in the GI-tract are disrupted, *C. albicans* can cause invasive candidiasis/candidemia. This infection is systemic and is caused when *C. albicans* enters the bloodstream. Invasive candidiasis is associated with relatively high mortality, while at the same time both diagnostic and treatment tools/drugs are lagging behind.

Our group aims to understand the interactions between *C. albicans* and neutrophils, an innate immune cell which make up the first line of defence against fungal infections. *C. albicans* is a known potent activator of neutrophils and strongly induce the formation of neutrophil extracellular traps (NETs). While NETs contribute to antimicrobial defence, we hypothesize that excessive NET formation and subsequent accumulation might, during invasive candidiasis, contribute to excessive inflammation and tissue damage.

Despite their abundance and central role in host defence, the mechanisms regulating neutrophil responses to fungal pathogens are poorly understood.

One mechanism through which neutrophil responses can be regulated is extracellular adenosine signalling. Adenosine, a structural component of ATP, acts as a short-lived signalling molecule through four adenosine receptors (A1, A2a, A2b and A3) present on neutrophils.

Based on our observation of elevated plasma adenosine levels during experimental C. albicans infection in mice, we investigated whether adenosine signalling could alter the neutrophil response to *C. albicans in vitro*. We found that activation of the A3 adenosine receptor inhibits NET formation in *C. albicans* stimulated neutrophils.



PhD student presentation abstract

Poster #12

Within and Between Stand Genetic Dynamics in Norway Spruce

Vasilina Akulova[1], Lucyna Slusarz[2], Kelly Swarts[1]

[1] Umeå Plant Science Centre (UPSC), Department of Forest Genetics and Plant Physiology, Swedish University of Agricultural Sciences, [2]Gregor Mendel Institute, Austrian Academy of Sciences, Vienna BioCenter, Vienna, Austria

Climate change is reshaping forest ecosystems, with serious consequences for long-lived tree species that form major global carbon sinks. Picea abies occupies a wide ecological range across Europe, making it an ideal system to investigate how genetic structure and demographic processes vary across spatial scales.

Here, we use an extensive sampling design including more than 5,000 trees distributed across plots, stands (sites), and continental-scale regions, in both managed and natural populations in European mountain environments including Fennoscandia, the Alps and the Carpathians. This multi-scale framework allows us to disentangle within and between stand genetic dynamics and assess how patterns of genetic structure and demography change with spatial scale.

Genome-wide variation was characterized using high-density SNP data (>2 million SNPs, GBS-based approach), enabling fine-scale resolution of population structure and demographic patterns. We examine how genetic diversity is partitioned within plots and stands, how stands are differentiated across regions, and how these patterns reflect potential signals of selection.

By integrating sampling scale into our analyses, this study provides new insights into the spatial organization of genetic variation in a long-lived conifer with a large effective population size. These results contribute to a better understanding of forest population dynamics and provide a foundation for future quantitative genetic and genome-wide studies of climate adaptation.

PhD student presentation abstract

Poster #13

NheABC is a pH-dependent cytotoxin that targets cholesterol in the cell membrane and contributes to the virulence of *Bacillus cereus* in wound infections

Abdelbasset Yabrag[1,2], Anne Yska[1,2], Naeem Ullah[1,2], Toril Lindbäck[3], Manoj Puthia[4], and Aftab Nadeem[1,2]

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Members of the *Bacillus cereus* group are Gram-positive, spore-forming, facultative anaerobic bacteria widely distributed in the environment. Pathogenic *B. cereus* group strains have been linked to a range of illnesses and infections, including severe non-gastrointestinal infections, such as wound infections. In the present study, we show that NheABC exhibits potent cell membrane permeability in 2D epithelial cell cultures as well as in 3D spheroids and intestinal organoids, with prominent effects on the cell membrane. Functional analysis using liposome leakage assays demonstrated that cholesterol promoted NheABC-mediated membrane permeabilization, suggesting that cell membrane lipid composition contributes to NheABC activity. Moreover, using epithelial cells and liposomes as model systems, we further demonstrated that the cytolytic activity of NheABC is pH-dependent and is markedly reduced under acidic conditions (pH 5.5). Importantly, NheABC enhanced bacterial colonization and the local inflammatory response in a murine model of wound infection. Overall, our study highlights the critical role of cholesterol and pH in regulating NheABC-mediated cytolytic activity in mammalian cells, which may lead to the development of novel therapeutic strategies for managing *B. cereus* group-related gastrointestinal and non-gastrointestinal infections.

PhD student presentation abstract

Poster #14

Investigating the role of 6-PTPS in *Plasmodium berghei* oocyst development and transmission

Arabela Vivar Morón[1], Oliver Billker[1]

[1] Department of Molecular Biology, Umeå University, Sweden

The folate pathway supplies essential cofactors for DNA synthesis, replication, and amino acid metabolism. While mammals depend on dietary folate, malaria parasites can also synthesize their folates *de novo*, with both routes contributing to optimal parasite growth and propagation. Although the downstream enzymes DHPS and DHFR are established antimalarial drug targets, upstream biosynthetic enzymes remain poorly studied, particularly during mosquito stages, when oocyst extensive DNA replication and development generates the sporozoites required for transmission to the mammalian host.

A previous genetic screen in *Plasmodium berghei* identified 6-PTPS, enzyme catalyzing the second reaction in the parasite's de novo folate biosynthesis pathway, as a potential candidate involved in oocyst development. To investigate its role, homozygous knockout parasites were generated using PlasmoGEM vectors. Endogenously GFP-expressing parasites were used to assess oocyst development at 16- and 24-days post-infection (dpi) and quantify sporozoites that had reached the mosquito salivary glands.

Preliminary results suggest delayed oocyst development and possible increased degeneration at 16dpi, accompanied by reduced salivary gland sporozoite numbers and infectivity in mice at 24dpi. These findings indicate that 6-PTPS may contribute to efficient sporogony and the production of infectious sporozoites, potentially affecting transmission success.

Further experiments will validate these phenotypes, assess competitive fitness against wild-type parasites, and investigate the effects of para-aminobenzoic acid, a main precursor of folate cofactors, availability and potential 6-PTPS inhibition. Characterizing the role of 6-PTPS during mosquito-stage development could reveal new vulnerabilities for transmission-blocking antimalarial interventions.

PhD student presentation abstract

Poster #15

Elucidating the role of O4 channel in substrate water delivery in Photosystem II

Arshed N.M.A[1], Messinger J.[1], Li D.H.[1], Aydin O.A.[1]

[1] *Umeå Plant Science Centre, Umeå University*

Photosystem II (PSII) is a membrane protein complex found in plants, algae and cyanobacteria that catalyzes the light driven water oxidation while releasing molecular oxygen, protons and electrons. These reactions take place in the oxygen evolving complex (OEC) that contains Mn_4CaO_5 cluster, which is the active site of water oxidation. Efficient water oxidation depends on the substrate water delivery towards the OEC, and the removal of protons generated during the reaction. Three water-filled channels, O1, O4 and Cl1, connect the OEC to the lumen and are thought to participate in the delivery of the water and the egress of protons, but their individual roles are still under investigation [1].

The O1 channel, which opens near to the O_1 atom in Mn_4CaO_5 cluster, has been proposed as the main pathway to deliver the substrate water [2]. In contrast, recent studies support that the Cl1 channel, which is located near to the Cl1 atom, is involved mainly in proton egress [3]. The role of the O4 channel, which is also known as narrow channel, that connects to the OEC near the O4 atom of the Mn_4CaO_5 is still under investigation. The structural and computational analyses indicate that it forms a hydrogen-bonded water network extending from the OEC toward the lumen and may contribute to either substrate water delivery or proton egress during specific S-state transitions [4].

This research project focuses on investigating the role of the O4 channels using complementary functional and structural approaches. The strategy involves introducing single site mutation on specific amino acids lining the O4 channel. We focus especially on those in bottleneck regions of the channel as they may be involved in controlling the substrate water delivery. The structures of the mutants will be determined by single particle cryoEM and their functional consequences will be evaluated by measuring substrate-water exchange kinetics using time resolved membrane inlet mass spectrometry (TR-MIMS) as well as complementary EPR and fluorescence experiments. Specific changes in the substrate water exchange kinetics would provide direct evidence for the involvement of the O4 channel in substrate water delivery.

References

1. Umena, Y., Kawakami, K., Shen, JR. et al. Crystal structure of oxygen-evolving photosystem II at a resolution of 1.9 Å. Nature 473, 55–60 (2011). https://doi.org/10.1038/nature09913.
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PhD student presentation abstract

Poster #16

Keeping proteins in check: Age-dependent changes in compartmental protein quality control

Mostafa Basiony[1,2], Verena Kohler[1,2]

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[2] Umeå Centre for Microbial Research (UCMR), Umeå University, Umeå, Sweden

Cells maintain the functionality of their proteins through specialized protein quality control systems in different cellular compartments. Ageing progressively impairs these systems, leading to the accumulation of damaged proteins and decline in cellular fitness. While these systems have been extensively studied in young cells, much less is known about how they change during ageing.

To address this question, we combined genome-wide yeast library screening with protein interaction studies in baker's yeast. The library screening approach was used to identify proteins whose abundance changes during ageing. In parallel, protein interaction studies were used to investigate age-dependent changes in the interaction network of key protein quality control factors.

Our analysis reveals broad age-dependent changes in protein quality control systems. While the abundance of many proteins decreases with age, several protein quality control factors, including those involved in the clearance of damaged proteins, become increasingly abundant in older cells. In addition, we examined key protein quality control factors essential in maintaining protein function in the cytosol, nucleus and mitochondria, and found that their interaction networks are progressively remodelled throughout the lifespan, indicating that the composition of these protein quality control systems changes during ageing.

Together, these findings demonstrate that compartmental protein quality control systems are dynamic throughout the lifespan and undergo substantial age-dependent changes in composition.


Information from Research
Infrastructures

BAF - The Biogeochemical Analytical Facility

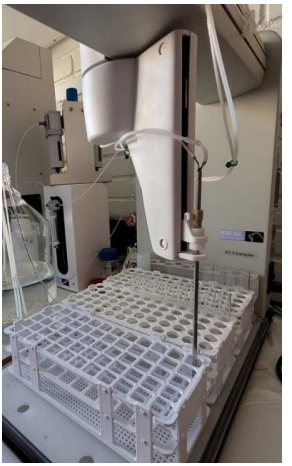
The infrastructure provides instruments for analysis of key chemical parameters in terrestrial and aquatic biogeochemical and ecological research and as such is of major interest for a large range of research groups.

BAF act as a core analytical facility for several major research projects run by researchers at EMG together with their collaborators and is also open for other users at Umeå and other universities.

INSTRUMENTS

The facility covers a scope of different instruments including:

- Gas chromatograph
- TOC/TN analyzer
  - Skalar, Formacs HTI
- Nutrient analyzer (NO_3+NO_2, NH_4, PO_4, TN, TP)
  - Seal Analytical, QuAAtro -39
- Elemental analyzer, for analyses of C/N/H/S on solids and glass fibers
  -Elementar, Unicube
- Fluorometer - Perkin Elmer, LS55
- Respicond facility (to measure respiration)
- Inverted microscope also with epifluorescence and cameras - Nikon, Eclipse TE 2000 and Eclipse T*i*



CONTACT

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MORE INFORMATION

https://www.umu.se/en/research/infrastructure/baf/

Posters I-1 a,b

BAP - Biopolymer Analytical Platform

The Biopolymer Analytical Platform (BAP) is dedicated to support research among KBC groups on cell walls of terrestrial and aquatic plants, biopolymer and environmental materials. Our competence lies in applying a large range of standard and advanced methods for the analysis of lignocellulose, as well as in fine detection of soluble sugars and starch. The instrumental backbone for many of those methods is gas chromatography/mass spectrometry (GC/MS). Pyrolysis-GC/ MS is one of the most important analytical devices that quickly yields highly reproducible and comprehensive chemical fingerprinting of carbohydrate and lignin types in samples in the lower microgram range. Pyrolysis-GC/MS can be also used for identification and quantification of microplastics and PFAS in environmental materials.

Postdocs, PhD students or project students with good lab work skills are required to do sample preparation in the BAP lab. We also provide an option to hire a professional staff hourly, in case your group has a lack of lab workers for sample preparation. It is possible to try a new method with us in the form of a project.

EXAMPLES FOR APPLICATIONS

- Pyrolysis-GC/MS for carbohydrate and lignin (G, S and H types) content estimation and for identification of organic compounds in soil/sediment and water
- TMS/Alditol acetate sugar-GC/MS for monosaccharide composition analysis
- Updegraff cellulose/anthrone assay for crystalline cellulose determination
- Klason and acetyl bromide lignin assay for lignin determination
- Enzymatic assays for soluble sugars and starch detection
- Size exclusion chromatography (SEC) for determination of MW, DP etc. of lignocellulose polymers
- Sample preparation and extraction using accelerated solvent extractor (ASE) 350

STEERING COMMITTEE

Totte Niittylä (Director), Dept. of Forest Genetics and Plant Physiology, SLU
Hannele Tuominen, Dept. of Forest Genetics and Plant Physiology, SLU
Leif Jönsson, Dept. of Chemistry, UMU
Ola Sundman, Dept. of Chemistry, UMU
Stéphane Verger, Dept. of Plant Physiology, UMU
Junko Takahashi-Schmidt, Dept. of Forest Genetics and Plant Physiology, SLU

CONTACT

First contact for the customer: Platform manager, Junko Takahashi-Schmidt (Junko.TS@slu.se). We are in KBC G5.

BAP Biopolymer Analytical Platform

MORE INFORMATION

https://www.upsc.se/platforms/cell-wall-analysis/4845-biopolymer-analytical-platform.html

Posters I-2 a,b,c

BICU - The Biochemical Imaging Centre Umeå

The Biochemical Imaging Centre Umeå (BICU) provides state-of-the-art imaging technology including advanced light microscopy and atomic force microscopy. BICU is an open-access imaging centre that offers cutting-edge technologies to researchers all over Sweden. Detailed information regarding our imaging centre organization and user fees can be found on our webpage.

We provide access and training to wide range of instruments including widefield, confocal and Tirf microscopy, FLIM, FLIM-FRET, FRAP, super-resolution (SIM and SMLM) and live cell imaging for an optimal spatial and temporal resolution. Furthermore, the centre provides access to Atomic Force Microscopy (AFM) to generate high resolution 3D topographical images and measure mechanical properties such as adhesion, stiffness and deformation of samples ranging from metal, glass, and surfaces coated with biomolecules to live cell under their physiological environment.

Apart from providing microscopy services we also actively take part in programs aimed at training young researchers in the use of the basic as well as advanced microscopy techniques and basic image analysis.

BICU is part of a National Microscopy Infrastructure (NMI): a Swedish infrastructure for the use and support of advanced microscopy in life science. The mission of NMI is to provide faster access to innovative technology and competence in microscopy for the life science research community. NMI also coordinates national and international knowledge exchange programs in microscopy. NMI in Umeå is the node specialized for advanced correlative imaging techniques. Hereby, BICU closely collaborates with Umeå Centre for Electron Microscopy (UCEM) to provide accessibility to various correlative light and electron microscopy (CLEM) techniques both in room temperature and cryo.

CONTACT

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Facility Manager: Irene Martinez Carrasco, irene.martinez@umu.se
Staff Scientist for CLEM: Sebastian Rönfeldt, sebastian.ronfeldt@umu.se
Staff Scientist for AFM: Fouzia Bano, fouzia.bano@umu.se

BICU

MORE INFORMATION

https://www.umu.se/en/research/infrastructure/biochemical-imaging-centre-umea-bicu/

Research Infrastructures

Posters I-3 a,b,c,d

BMCU - BioMolecular Characterization Unit

Research Infrastructure BMCU is an interdisciplinary facility that provides access to state of-the-art instrumentation allowing for the measurement of biomolecular interactions, including affinities and for the characterization of biomolecules and nanoparticles.

To characterize biomolecular interactions, BMCU currently provides access to several biosensing techniques, including optical (surface plasmon resonance, SPR) and gravimetric (quartz crystal microbalance with dissipation, QCM-D), as well as fully automated and a manual isothermal calorimetry (ITC) instrument. All these methods allow researchers to characterise interactions of proteins with other proteins, RNA, lipids, carbohydrates or small molecules, and much more.

To characterize biomolecules and nanoparticles. BMCU provides access to circular dichroism that is used to study protein conformations, and mass photometry that allows easy and fast determination of the size of biomolecules or of biomolecular assemblies. For the characterization of larger molecular aggregates, including nanoparticles, the users have access to a nanoparticle tracking analysis (NTA) instrument which provides quantitative information on sizes and concentrations and a dynamic light scattering (DLS) instrument for size determination.

CONTACT

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BMCU

MORE INFORMATION

https://www.umu.se/en/research/infrastructure/biomolecular-characterization-umea-/

CASP - Computational Analytics Support Platform

The Computational Analytics Support Platform (CASP) is a data analytics service at Umeå University (UmU), launched during 2021, within the framework of the Computational Life Science Cluster. CASP is a local co-funded KBC infrastructure that primarily supports, but also trains life scientists in the analysis of experimental data using data-driven tools and strategies. We focus on the analysis of data from a wide range of technologies, with a particular focus on downstream omics (metabolomics/ proteomics).

Our aim is to help bridge the existing gap in data-driven life science, allowing researchers to convert complex data into meaningful biological and chemical interpretations via the use of advanced data-driven tools and strategies. Combined, the group have strong expertise in data-driven life science, in addition to wide domain expert knowledge arising from active engagement with multiple projects in the 'omics' area and beyond. This allows a full understanding of the researcher's needs, not only in terms of the data analysis, but also in how the data was generated and equally important, the interpretation of the biology behind the project.

Support packages we provide

- Packaged and customer-specific data analytics projects
- One-to-one consultations for data analysis support
- Personalised tutorials including theoretical knowledge and hands-on experience using data analysis and processing software
- Extended data analytics support for high-throughput experimental platforms including the Swedish Metabolomics Centre

Services we provide

- Statistical experimental design
- Multivariate data analysis
- Machine learning
- Pathway analysis and interpretation
- Publishing

CONTACT

Please contact the Platform Manager Kate Bennett (katie.bennett@umu.se). We can help with the analysis of many different data types so please feel free to contact us and we will be happy to answer your questions.
We look forward to supporting you in your projects!

MORE INFORMATION

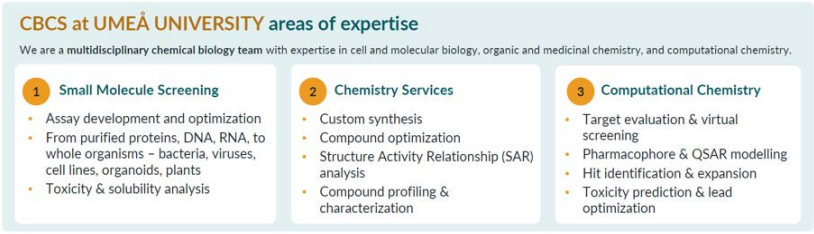
https://www.umu.se/en/research/infrastructure/computational-analytics-support-platform-casp/

Poster I-4

CBCS - Chemical Biology Consortium Sweden

Our mission is to identify, validate, and utilize small molecules for biological exploration, in collaboration with research groups.

CBCS is a national VR-funded SciLifeLab research infrastructure that enables the identification and development of small molecules for investigating biological systems. These chemical tools provide powerful means to decipher biological pathway functions and generate leads for drug discovery.



Compound Collections

- >350,000 compounds available for small molecule screening
- AstraZeneca collaboration providing access to 14,000 annotated compounds targeting 1,700+ human proteins

Access to CBCS Services

- *Quick access:* Consultations and small service projects (first-come, first-served)
- *Project-based:* Extensive screening and chemistry projects (peer-reviewed, prioritized by scientific merit, impact, and feasibility)
- *Equipment access:* Collaborative agreements or user arrangements

Core Equipment at UMU

Screening & Detection

- Plate readers: Biotek Synergy H4, BMG ClarioStar
- High-content screening: Molecular Devices ImageXpress
- High-throughput flow cytometry: Sartorius iQUE3

Automation & Chemistry

- Multiwell liquid dispensers: Biomek i5, NxP, Assist Plus, WellJet
- HPLC systems: Gilson & Shimadzu
- Fully equipped organic chemistry laboratories

Training

Online course (Spring 2027): *Exploring biology with small molecules: screening tools and strategies*

Additional Services

CBCS has nodes at all six partner universities, offering a range of services including fragment-based screening with NMR, screening in BSL-3 environments, cell painting, functional precision medicine, and assessment of compound cardiotoxicity – all accessible to researchers nationwide.

CONTACT

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MORE INFORMATION

www.cbcs.se ; www.scilifelab.se/units/cbcs;
www.umu.se/en/research/infrastructure/cbcs

CBCS UMU Web

Poster I-5

C-Trap Facility

The C-Trap facility provides access to a dual-trap C-Trap dymo 300 instrument, which combines optical tweezers, multichannel microfluidics, and confocal fluorescence microscopy into a single, fully synchronized system.

This setup enables real-time visualization of biomolecular interactions and dynamic processes at single-molecule resolution, while simultaneously allowing correlated force measurements.

Facility users receive support and guidance in experimental design, sample preparation, data collection, and analysis. Applications include studies of DNA/RNA–protein binding events, biomolecular conformational changes, motor proteins dynamics, receptor-ligand interactions, and the biomechanical properties of molecules, membranes, cell walls and soft nanomaterials.

The C-Trap was funded by Kempestiftelserna, the Faculty of Science and Technology, the Faculty of Medicine, and the Department of Plant Physiology at Umeå Plant Science Centre (UPSC). The facility is hosted by UPSC and is also part of the Chemical Biological Centre (KBC).

Examples of research at the C-Trap

- **DNA/RNA-protein interactions**
  - Direct visualization and kinetics of single-protein binding events
  - Force spectroscopy of protein–nucleic acid complexes
- **Conformational changes in biomolecules**
  - Single-protein folding/unfolding behaviour
  - DNA or RNA secondary/tertiary structure dynamics
- **Visualization and manipulation of dynamic molecular events in real time**
  - Motor proteins (polymerases, helicases)
  - Transcription and translation
  - DNA repair mechanisms
  - Phase separation and biomolecular condensates
- **Biomechanical properties of molecules and cell membranes/walls**
  - Mechanical properties of biomolecules under varying conditions
  - Chromatin compaction and remodelling
  - Cell wall-cell membrane interactions
  - Ligand-cell surface receptor interactions
- **And more… come to us with your project/ideas!**

CONTACT

Rubén Casanova Sáez, C-Trap manager, Dept. of Plant Physiology, Umeå University: ruben.casanova-saez@umu.se

MORE INFORMATION

https://www.upsc.se/platforms/c-trap-facility.html

Research Infrastructures

Poster I-6 a,b
HPC2N - High Performance Computing Center North

High Performance Computing Center North (HPC2N) is a national center for Scientific and Parallel Computing as we are a branch of the National Academic Infrastructure for Supercomputing in Sweden (NAISS). HPC2N is a National Data Science Node in ”Epidemiology and Biology of Infections” (DDLS)..

HPC2N is also a local/regional resource for researchers at HPC2N's partners (IRF, LTU, Mittuniversitetet, SLU and UmU). Our Director of HPC2N is Professor Paolo Bientinesi from the Computing Science Department.

We offer different types or hardware for computing and visualization including standard CPUs and Graphical Processing Units (GPU)s. Most common packages for Scientific Research are installed on our cluster for instance GROMACS, VASP, MATLAB, R/ Rstudio, among others.

To get started with our system, we offer different types of training courses including introductory courses, and more specialized courses in topics such as Molecular Dynamics, QM/MM, Git, R, Machine Learning, MPI, Julia, and OpenMP.

We provide a general support through a ticket system and a more advanced support for specific questions from researchers on-demand.

CONTACT
General questions: info@hpc2n.umu.se
More specific questions: support@hpc2n.umu.se

Visiting address:
Umeå University
MIT-building
HPC2N
Campustorget 5, 4th
S-907 36 Umeå
Sweden

HPC2N

MORE INFORMATION
https://www.hpc2n.umu.se/

Poster I-7

InfraVis

InfraVis is a national research infrastructure for data visualization. We help researchers make sense of complex data through visualization and visual analytics. Our experts collaborate with researchers at different stages of their work, from structuring and visualizing raw data to supporting further analysis and communicating research findings to other scholars and wider society.

We create both static and interactive visualizations of different sizes and scopes, from simple infographics and visual abstracts for research papers to tailored software for data analysis. We work across all research disciplines and welcome new collaborations. Our team brings together a broad range of skills, including programming in a variety of languages, geographic information systems (GIS), 3D and AR visualization and game development.

We are always open to new projects. Researchers can apply for support directly through the InfraVis website for smaller projects, or through our annual Open Call in the autumn each year for larger projects that require more extensive support.

At KBC DAYS we will present some of the projects relevant for the research field, for example the interactive app showing the availability of care diagnostics in Western Uganda. Another project is visualization showing how griffon vultures (*Gyps fulvus*) use a collaborative strategy when looking for carcasses of dead animals in open landscape

CONTACT

Karin Danielsson, Director of Humlab at the Faculty of Arts and Humanities,
karin.danielsson@umu.se

MORE INFORMATION

https://infravis.se

Poster I-8

LLUm - Laserlab Umeå

Laserlab Umeå (LLUm) is part of Laserlab Sweden, a distributed national research infrastructure. LLUm brings together laboratories employing advanced laser technologies and laser-based techniques across a wide range of scientific disciplines. The infrastructure encompasses eight research groups with complementary expertise in laser physics, attosecond science, spectroscopy, nanophotonics, biophysics, and related fields.

Laserlab Umeå comprises **the following research groups and laboratories**:

- Relativistic Attosecond Physics Laboratory (REAL, Laszlo Veisz)
- High-precision Laser Spectroscopy and Refractometry Laboratory (Ove Axner)
- Optical Frequency Comb Spectroscopy Group (Aleksandra Foltynowicz Matyba)
- Applied Laser Spectroscopy Group (Florian Schmidt)
- Biophysics and Biophotonics Group (Magnus Andersson)
- Ultrafast Nanophotonics Group (Nicolò Maccaferri)
- Microphotonics Group (Max Yan)
- Ultrafast Quantum Electronics Group (Markus Ludwig)

Together, these laboratories offer scientific and industrial users access to a broad range of advanced laser systems and experimental techniques. Their capabilities span from ultrahigh-intensity, few-cycle laser systems with peak powers reaching 100 TW and attosecond light sources to femtosecond lasers, optical frequency combs, narrow-linewidth lasers, systems for high-precision spectroscopy and optical manipulation, and high-energy picosecond-to-nanosecond lasers for general-purpose applications. Dedicated experimental platforms and beamlines expand the capabilities, to provide unique opportunities for interdisciplinary research, advanced laser-based experiments, and scientific and industrial collaborations.

External users can benefit from the combination of advanced laser technologies, specialized experimental infrastructure, and the scientific expertise of the participating research groups.

CONTACT

László Veisz, Head of the REAL facility, Dept. of Physics, Umeå University:

laszlo.veisz@umu.se

MORE INFORMATION

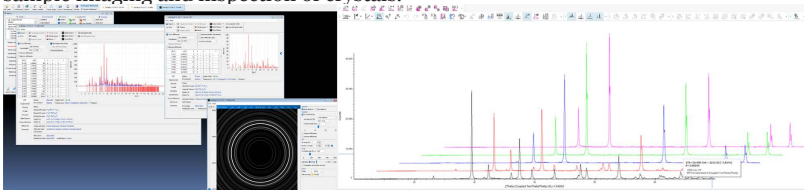
https://www.umu.se/en/department-of-physics/research/laserlab-umea/

Poster I-20

MAXS - Multi-purpose Adaptive X-ray Scattering platform

Research infrastructure MAXS offers state-of-the-art X-ray diffraction, total X-ray scattering, and X-ray reflectometry with several sample environments for advanced material characterization to users from academy, industry, or public sectors. The platform also offers a comprehensive data evaluation environment with access to extensive reference databases for data collected at MAXS or elsewhere, including compatibility with data from synchrotron light sources.

The instruments at MAXS are two independent Bruker D8Advance systems with the possibility to choose from three X-ray wavelengths (Cr, Cu, and Mo), line or point X-ray profiles, variable detector configuration with two detector types, and a broad selection of sample stages to match the needs of an experiment. The users can define what they need from an experiment and the instrument can be configured accordingly. An important feature is the automatic sample changer, increasing the sample throughput. This is complemented by stereomicroscopy with imaging capabilities which enables sample imaging and inspection of crystals.



Data evaluation environment is provided locally at MAXS at two workstations with the comprehensive PDF-5+ database, but also via network for internal users permitting local installation within Umeå University with local COD database. Up to 20 users can simultaneously use the evaluation software with local installations of the crystallographic open database (COD) making it readily accessible for both research and education.

COURSES

MAXS hosts a user training course (1.5 ECTS) which includes a basic radiation safety traning module. We will open a longer course in powder X-ray diffraction (7.5 ECTS) in winter 2025/2026 which goes into details about diffraction and different strategies for data analysis.

CONTACT

The managing team consists of Nils Skoglund (manager), Charlie Ma, Markus Carlborg, and Marjan Bozaghian Bäckman. Please contact us at maxs@o365.umu.se if you are interested. We are located in room B6-39-07.



MORE INFORMATION

https://www.umu.se/en/research/infrastructure/multi-purpose-adaptive-x-ray-scattering-platform-maxs/

Poster I-9

NanoLab

NanoLab is an open-access infrastructure located at the Department of Physics.

It is mainly a classified Class 100 cleanroom which comprises a variety of advanced fabrication and characterization/analysis instruments, including;

- Kurt J. Lesker PVD75 Thermal Evaporator
- Obducat NIL 2.5 Nanoimprinter
- Atomic force microscope (Park NX-Hivac)
- Plasma cleaning system ATTO (power 0-50W)
- Plasma cleaning/etching system PE-100 (power 0-300W)
- Karl Süss Mask Aligner MJB3
- Olympus BX51 Optical Microscope
- PANalytical Xpert3 Powder XRD
- ARL QUANT'X Benchtop EDXRF Analyzer
- Theta OneAttension Contact Angle Meter
- SPIN150-NPP Spin Coater
- Four-Point Probe system
- Vacuum Chamber Furnace - VBF-1200X-H8
- Filmetrics F10-RT-UVX
- SENTECH SENresearch 4.0 Spectroscopic Ellipsometer
- FLS1000 Photoluminescence Spectrometer

NanoLab offers many other standard lab instruments too, such as vacuum ovens, hotplates, UV- curing boxes, analytical scales, etc. Visit NanoLabs website for more details and specific parameters of each individual instrument.

NanoLab is available for all scientists at Umeå University, as well as external institutions. Important to know, that NanoLab offers space for user's own experiments inside the cleanroom. Users have access to fume hoods and central gases and vacuum in each working station.

COURSES

NanoLab is used for both research and in advanced level ground education courses. Training courses (1.5 ECTS) are offered annually for PhD and Postdoc users, besides lab parts in several technical physics courses (7.5 hp).

CONTACT

Director of NanoLab: Dr. Roushdey Salh, roushdey.salh@physics.umu.se

MORE INFORMATION

https://www.umu.se/en/research/infrastructure/nanolab/

Poster I-10

NBIS - National Bioinformatics Infrastructure Sweden

NBIS, National Bioinformatics Infrastructure Sweden, is a distributed national research infrastructure. We are the SciLifeLab bioinformatics platform and the Swedish node in Elixir, a European intergovernmental organisation bringing together life science resources from across Europe. With over a hundred staff members, we work with bioinformatics support, infrastructure and training.

NBIS has staff at six sites: Umeå, Uppsala, Stockholm, Linköping and Lund. We provide expertise in most areas of bioinformatics, including omics analysis, genome assembly/annotation, image analysis and biostatistics. We also offer support in systems development, such as interactive websites and data processing pipelines.

NBIS is mainly funded by the Swedish Research Council, SciLifeLab, the Knut and Alice Wallenberg Foundation, and Swedish universities.

We provide:

- Weekly online drop-in sessions, Tuesdays at 14:00; http://meet.nbis.se/dropin. Join to discuss study design, data analysis or other bioinformatics-related questions.
- Free consultation meetings to discuss study design.
- Hands-on project support, ranging from assistance with smaller tasks to long-term engagement.
- Free, extensive hands-on support to a limited set of projects selected in a peer review process (enabled by a grant from Knut and Alice Wallenberg Foundation).
- Tools, data management, systems development and guidelines for the life science community.
- Introductory and advanced training events, such as workshops in RNAseq data analysis, epigenomics data analysis, tools for reproducible research, python programming, and many other bioinformatics related topics.
- The Swedish Bioinformatics Advisory program - A mentorship program for PhD students interested in guidance from a bioinformatics expert.

CONTACT

For general questions: info@nbis.se
Local contact in Umeå:
Jeanette Tångrot, jeanette.tangrot@umu.se

NBIS
NATIONAL BIOINFORMATICS INFRASTRUCTURE SWEDEN

MORE INFORMATION

https://www.nbis.se

Poster I-11

µNiSCH - µNordic Single Cell Hub

µNiSCH (µNordic Single Cell Hub) is a cutting-edge infrastructure dedicated to advancing single cell biology at Umeå University. Our facility focuses on consolidating and expanding research in this dynamic field. We are also at the forefront of developing innovative molecular tools for single cell transcriptomics and genomics, with a special emphasis on microbial studies. The facility is located within the Department of Molecular Biology.

Both the advanced equipment and specialized expertise are open to all research groups interested in single cell biology applications on eukaryotic and prokaryotic cells, including:

- Single cell transcriptomics
- Single cell genomics
- Cell-based phenotypic screening assays
- Multi-step biological workflows in single cells
- Spatial distribution of gene expression
- Characterization of tissue microenvironment

Currently, we can offer expertise and access to the following equipment:

Onyx Microfluidics Platform, a microfluidic platform designed to generate and manipulate water-in-oil droplets or semi-permeable capsules for high-throughput single-cell and single-molecule analysis.

Chromium Single Cell Gene Expression system, a cutting-edge platform designed to analyze gene expression at the single-cell level.

BD Rhapsody HT Xpress System, a high-throughput microwell-based technology for advanced single-cell analysis.

The OT-2 multi-well pipetting robot, an automated liquid-handling system designed to streamline and enhance laboratory workflows.

The Pannoramic Midi II, an automatic digital slide scanner for high-throughput microscopy imaging, offering precision and efficiency in pathology and research applications.

LabSat Multiplex immunostaining system, an advanced automated platform designed for rapid and precise immunohistochemistry and immunofluorescence staining, particularly in research and clinical settings.

Celsee Genesis system, enable the capture of cells from liquid biopsies and other sample types. After capture, the enriched cells can be recovered for downstream analysis such as single-cell genomics, digital PCR, or culture.

Mantis Rapid Dispenser System, liquid handling platform designed to streamline and enhance precision in laboratory workflows.

CONTACT

For requests or questions, please contact:
Staff Scientist Dr. Tugrul Doruk (tugrul.doruk@umu.se)
Director of Facility Dr. Kemal Avican (kemal.avican@umu.se)

MORE INFORMATION

https://www.umu.se/en/research/infrastructure/micro-nordic-single-cell-hub/

Poster I-12

NMR - Nuclear Magnetic Resonance

The KBC NMR Core facility provides access to state-of-the-art NMR equipment and expertise for all researchers in the KBC and Campus environment. This facility is part of the national infrastructures SwedNMR funded by VR RFI and SciLifeLab and it is operated by the Swedish NMR Centre at the University of Gothenburg and Umeå University. As a national service infrastructure, we grant access to academic and industrial researchers across Sweden.

The NMR facility offers access to powerful liquid and solid-state NMR infrastructure with spectrometers ranging from 400 to 850 MHz. Our ultrafast magic angle spinning probe and cryo-MAS probe are unique for the Nordic countries, enabling high-resolution spectra of proteins and studies and complex biological samples in the solid-state. High-field instruments are equipped with cryo-probes for optimal sensitivity for biomolecular solution NMR and environmental NMR. Robotic sample preparation and sample changers are available for high-throughput applications such as metabolomics and fragment- based screening (FBS).

SERVICE PROVIDED BY THE INFRASTRUCTURE

The NMR core facility offers nation-wide NMR access in four areas: Liquid- and solid-state structure analysis, materials science, metabolite studies and chemical biology. In addition, our personnel provide expertise according to the users need in all areas, from experimental design and sample preparation to data analysis.

Three-dimensional structures can be determined for soluble proteins, solid and membrane-bound proteins, nucleic acids and biomolecular complexes.

Metabolomics can be carried out on liquid and solid samples, including temperature-sensitive biological specimen. Advanced support of the entire process is provided, including bioinformatics data analysis support. Through collaboration with the Swedish Metabolomics Centre, we offer combined NMR- and MS-based metabolomics.

Our solid-state NMR equipment allows structural studies of insoluble protein aggregates such as amyloid fibrils and membrane proteins in their functional lipid environment.

FBS is performed using substance libraries from - and in interaction with - Chemical Biology Consortium Sweden (CBCS).

PERSONNEL

Gerhard Gröbner, prof., Platform Director, Dept of Chemistry
Jürgen Schleucher, prof., Platform Director,
Dept of Med Biochemistry and Biophysics
Mattias Hedenström, Staff Scientist, Dept of Chemistry
Tobias Sparrman, Staff Scientist, Dept of Chemistry
Ilona Dudka, Staff Scientist, Dept of Chemistry
João Figueira, Staff Scientist, Dept of Chemistry

MORE INFORMATION

https://www.umu.se/en/research/infrastructure/nmr/
https://www.scilifelab.se/units/swedish-nmr-centre/
https://www.swednmr.se

Poster I-21

PEP - Protein Expertise Platform

The Protein Expertise Platform (PEP) is a core facility at the Chemical Biological Center (KBC) and a module of the national infrastructure **Protein Production Sweden (PPS)**.

Proteins are essential for life's processes and the Protein Expertise Platform (PEP) at Umeå University provides custom production of recombinant proteins in *E. coli*, *Lactococcus* and Plant Cell Suspensions. The PEP is a module of the Protein Production Sweden (PPS) national research infrastructure and received continuous funding from VR and the local Universities during 2027 - 2030. The PPS provides expert competence in a variety of expression systems, including *E. coli*, mammalian cells, insect cells, the yeast *P. pastoris*, plant cells and in a cell-free system, as well as in gene and vector design, production and purification of proteins and quality control.

PPS can also produce proteins with different labels (^{13}C, ^{15}N, SeMet, ...) and with inbuilt non-natural amino acids.

Researchers can apply for project support through a common application portal found on the PPS website (www.gu.se/pps).

CONTACT

For Project request or questions regarding our services:

Uwe Sauer uwe.sauer@umu.se
Phone: 090-786 5930

MORE INFORMATION

https://www.umu.se/en/research/infrastructure/pep/

Poster I-13

SMC - Swedish Metabolomics Centre

Swedish Metabolomics Centre (SMC) is a national research infrastructure launched in 2013 through an infrastructure grant from the Knut & Alice Wallenberg Foundation, with co-funding from Umeå University and the Swedish University of Agricultural Sciences. Since 2016, SMC has been part of SciLifeLab.

SMC provides access to advanced mass spectrometry-based analyses of small molecules, lipids, and metabolites in biological tissues and fluids. The centre's aim is to support researchers at Swedish universities in conducting high-quality metabolomics studies, while also serving as a knowledge hub in metabolomics and related areas.

SERVICES

All service requests begin with a discussion between the researcher and SMC staff to define the research question and determine the most appropriate analytical strategy. In addition to full-service analyses, SMC offers an Open Access Program (OAP), allowing trained researchers to perform their own analyses using SMC instruments.

- Untargeted metabolite profiling (metabolomics)
- Targeted metabolite profiling (e.g. amino acids, sugars, fatty acids, plant hormones, steroidal hormones)
- Lipid profiling
- Method development
- Basic statistics
- Open lab access services

EQUIPMENT

Mass spectrometers

- Leco Pegasus BT, GCTOFMS
- Leco Pegasus HT, GCTOFMS
- Agilent 7000C, GCQqQMSMS
- Agilent UHPLC-QqQMSMS 6495A
- Agilent UHPLC-QqQMSMS, 6495D (2)
- Agilent 6546 Accurate-Mass UHPLC-QTOFMSMS (2)
- Agilent 6560 Ion Mobility UHPLC-QTOFMSMS

CONTACT

For service requests or questions please contact:
info@swedishmetabolomicscentre.se
Head of Unit: Dr. Annika Johansson
(annika.johansson01@umu.se), +46722445254

Swedish Metabolomics Centre

MORE INFORMATION

https://www.umu.se/en/research/infrastructure/metabolomics/
https://www.swedishmetabolomicscentre.se/

Poster I-14 a,b,c,d,e

UCEM - Umeå Centre for Electron Microscopy

UCEM provides instruments and methods in Transmission Electron Microscopy (TEM) and Scanning Electron Microscopy (SEM). The Centre operates as an interdisciplinary University core facility for Electron Microscopy (EM), and as a national and international research infrastructure for Cryo-EM, electron tomography, EM volume imaging and correlative microscopy methods. UCEM offer service at seven EM instruments, diverse sample preparation equipment as well as computer infrastructure and software for image processing. The facility team provides service and training for EM users. Students and researchers have access to advanced sample preparation, imaging and image analyses at UCEM.

SEM instruments, Merlin and Evo, offer high-resolution surface imaging, with multiple detector systems. The Scios DualBeam is an instrument combining SEM with a Focused Ion Beam (FIB) volume imaging, Ga-ion and electron beam lithography. Aquilos 2 FIB-SEM is used for thin cryo-lamella preparation, cryo-lift-out, and cryoSEM imaging, with possibilities to combine lamella preparation with subsequent TEM or cryo electron tomography analyses. Service at UCEM also includes cell culture facilities, BSL2 accommodated labs, cell and tissue fixation, resin embedding, ultramicrotome sectioning, Tokuyasu sectioning, immunolabeling and staining techniques. TEM instruments Talos L120 offer ideal TEM solutions for entry level and sample screening, negative staining, studies of cell and tissue morphology. Cryo-EM is the method of choice for structure biology and visualization of hydrated proteins, viruses, cells and small organisms. For cryo-EM samples are plunge frozen in liquid ethane, preserved in amorphous ice and imaged under cryo condition. Glacios 200 kV and Titan Krios 300 kV are equipped with autoloaders for cryo samples and equipped with direct electron detectors, Falcon 4i, including a Selectris energy filter for contrast enhancement. The method single particle analysis (SPA) is used for 3D reconstruction of proteins and complexes in structural studies and cryo-electron tomography is used to study e.g. subcellular volumes or microorganisms in 3D. The same instrument configuration, is also use for electron diffraction of nano-to-micro-meter crystals for atomic structural reconstruction of proteins and chemical compounds, the method is called MicroED. Correlative Light and Electron Microscopy (CLEM, collaboration with BICU) solutions enable localisartion of proteins or structures of interest, for subsequent high-resolution EM analysis. Micropatterning on grids and imaging with a cryo-stage fluorescence microscopy are avalible. UCEM supports sample preparation for other open facilities for example MAX IV microscopy beamlines.

UCEM was establishment by external funding from Swedish Research Council, Knut and Alice Wallenberg Foundation and Kempe Foundations. Operations and services are partly funded by SciLifeLab, KAW and UMU.

CONTACT

For general enquiries: Linda Sandblad, UCEM Director
Visiting address:
Electron Microscopy Building, KB-D, Umeå University
Mobile: +46 (0)70 932 49 36, E-mail: linda.sandblad@umu.se

UCEM
Umeå Centre For
Electron Microscopy

MORE INFORMATION

https://www.umu.se/en/research/infrastructure/umea-centre-for-electron-microscopy-ucem/

Poster I-15

UHRF - Umeå Hypoxic Research Facility

The Umeå Hypoxic Research Facility (UHRF) is a unique open-access research infrastructure at Umeå University dedicated to supporting research under precisely controlled oxygen conditions, ranging from atmospheric oxygen levels to complete anoxia. UHRF provides researchers with access to specialized equipment, technical expertise, methodological support, and training activities that enable studies that are difficult or impossible to perform in conventional laboratory environments. The facility is accessible to researchers from Umeå University, national and international academic users, and industrial partners.

UHRF currently consists of multiple oxygen-controlled workstations, including hypoxic and anoxic Don Whitley chambers, a hybrid hypoxic-anoxic refrigerated workstation, an Anoxomat system for anaerobic cultivation, a BioFlo120 chemostat for continuous culture experiments, a Bio-Rad S3 flow cytometer equipped with cell sorting capabilities, fluorescence microscopy, and additional analytical equipment. These platforms allow precise manipulation of oxygen availability while enabling real-time monitoring of cellular growth, physiology, and microbial behavior.

Beyond providing access to advanced instrumentation, UHRF offers comprehensive support throughout the research process. Users receive training, assistance with experimental design, technical guidance, and support in data analysis and interpretation. The facility also organizes workshops, courses, seminars, and international conferences to promote knowledge exchange and strengthen the scientific community working on oxygen-dependent biological processes

The infrastructure supports a broad range of research fields, including microbiology, infection biology, molecular biology, biotechnology, cancer biology, immunology, environmental sciences, plant biology, and microbial ecology. By combining controlled oxygen cultivation with modern analytical technologies, UHRF enables innovative approaches to studying microbial physiology, host-microbe interactions, cellular adaptation, and oxygen-dependent metabolic processes.

CONTACT

Dr. Emilio Bueno (Facility Manager)

Prof. Felipe Cava (Facility Director)

UHRF
Umeå Hypoxia Research Facility

MORE INFORMATION

https://www.umu.se/en/research/infrastructure/umea-hypoxic-research-facility/

UMSC - Umeå Marine Sciences Centre

Umeå Marine Sciences Center is a complete research facility with all the platforms required to conduct world-leading research. We have several research vessels, smaller boats, a hovercraft, snowmobiles, mesocosms, a diverse array of field and lab-based analytical instrumentation, a research dive team and an engineering workshop, all underpinning world-class research and innovation.

Our indoor mesocosm facility is one of the most advanced in Europe. It enables us to conduct large-scale deep-water experiments with high precision and accuracy over environmental conditions, including control of temperature, salinity, stratification, convective stirring, haloclines, ice cover, carbonate chemistry and light fields.

Mesocosm highlights:

- 12 replicated 6m deep mesocosms
- Full salinity range (2-34)
- 3 adjustable temperature depths enabling stratification and convective stirring from polar to tropical temperatures (2-30°C accuracy +/- 0.5° C)
- Carbonate chemistry control for example in multiple stressor experiments
- Advanced adjustable light sources emulating daylight spectra for any biome globally
- Control of over-chamber atmospheric air temperature down to -200 C
- Ice cover where freezing or thawing rate can be adjusted
- Intact bottom sediments can be transferred to the mesocosms

At Sea: Umeå Marine Sciences Center also has 12 transportable free-floating mesocosms, designed for experiments in extreme and icy conditions which can be used in situ, or transported to other locations.

In the Laboratory: Our facility contains two experimental halls with smaller mesocosms and aquaria including licencing for fish-based investigations. Our advanced water treatment allows experiments with environmentally hazardous chemicals and pharmaceuticals or biological agents.

A full list of our facilities is available here: https://www.umu.se/en/umea-marine-sciences-centre/infrastructure-and-services/.

Link to funding for free access: https://www.umu.se/en/umea-marine-sciences-centre/funded-infrastructure-access/.

CONTACT
Dr Regina Kolzenburg: regina.kolzenburg@umu.se

MORE INFORMATION
https://www.umu.se/en/umea-marine-sciences-centre/

Poster I-16

UPP - Umeå Proteomics Platform

The Umeå Proteomics Platform (UPP) provides state-of-the-art mass spectrometry-based proteomics services to support biological, biomedical, and clinical research. The platform enables comprehensive protein-level analyses to investigate the effects of genetic mutations, disease, environmental factors, pharmacological interventions, and other biological perturbations. UPP serves all researchers at Umeå University.

UPP offers support throughout the entire proteomics workflow, from experimental design and sample preparation to mass spectrometric analysis, bioinformatics, and statistical analysis. The infrastructure assists users in developing robust experimental strategies and delivers processed datasets together with initial data interpretation, enabling researchers to focus on biological discovery and hypothesis generation.

The platform supports a broad range of proteomics applications, including protein identification, quantitative proteome profiling, characterization of protein complexes and interaction networks, and analyses of post-translational modifications such as phosphorylation, glycosylation, ubiquitination, and SUMOylation. These capabilities make UPP a valuable resource for both hypothesis-driven and discovery-based research projects across the life sciences.

The facility is equipped with advanced high-resolution mass spectrometry instrumentation, including Orbitrap Exploris 480 mass spectrometers coupled to Vanquish Neo nanoflow liquid chromatography systems. This instrumentation enables highly sensitive and accurate analyses of complex biological samples and supports a wide range of quantitative and targeted proteomics workflows.

CONTACT

André Mateus, andre.mateus@umu.se Co-director Umeå Proteomics Platform
Iker Valle Aramburu, iker.aramburu@umu.se Co-director Umeå Proteomics Platform

MORE INFORMATION

https://www.umu.se/en/research/infrastructure/umea-proteomics-platform/

Poster I-17

UPSCb - Umeå Plant Science Centre Bioinformatics Facility

The UPSC bioinformatics facility (UPSCb) is a small group of bioinformaticians involved in supporting research, training and teaching at UPSC and outside of it.

Since its foundation in 2016, the facility has been handling a total of 300 projects for 75 different principal investigators (PIs); *i.e.* involving over 50 percent of all research and associated research groups at UPSC.

We have a strong expertise in High Throughput Sequencing (HTS) data analysis, having been involved in the genome assembly of four species and having handled several thousands of RNA-Seq samples (including single-cell sequencing), as well as ribosome profiling, transcription starting site sequencing data, methyl-seq, ATAC-seq, and others.

We offer mainly 4 types of services:

- scientific project's data analysis training: PI "contributes" a PhD / Post-doc who is to be supervised by the facility to learn doing the analyses (800 SEK / h)
- data processing as a service: the facility runs states of the art tools to process the data (800 SEK / h)
- data science teaching: the PI books us to give one or more lessons in a course they are running (500-800 SEK / h)
- data storage: we match the legal requirements by storing two copies on two different media in two locations (800 kr / TB / year)

CONTACT

While UPSC groups have priority, we also work with several groups outside of it, contact us at bioinfo-facility@upsc.se.

MORE INFORMATION

https://www.upsc.se/platforms/upsc-bioinformatics-facility.html

Posters I-18 a,b

The UPSC Microscopy Facility

The Umeå Plant Science Centre (UPSC) Microscopy Facility offers hands-on introductions, user consultation, and open-access usage following mandatory introduction based on a flat rate fee per hour for usage of equipment.

UPSC Microscopy Facility has the main focus to work with plant images and hence our confocal and multiphoton systems are tailormade for work with thick samples, have spectral detectors to adapt to autofluorescence, very sensitive HyD or GaAsP PMT detectors and long working distance objectives as well as high resolution objectives. We have sectioning equipment, motorized stages for tiling and stitching at our imaging microscopes and often both highly sensitive monochromatic cameras and color cameras. Our latest addition is a Thunder flexisystem stereo/macroscope to remove out of focus blur and thus clarify fluorescence imaging using computational clearing and adaptive deconvolution.

EQUIPMENT

- **Sectioning:** Cryostat – CryoStar NX70 equipped with CryoJane tape system, Vibratome VT1000S, Microtome Zeiss HM 350, Ultramicrotome – Power Tom XL
- **Light microscopes:** Leica DMi8 inverted fluorescence microscope, Leica 205FA epifluorescence microscope, Leica Thunder Imager Model Organism etc.
- **Fluorescence Activated Cell Sorter** (FACS) BD FACS **Aria III** Flow Cytometer and the BD FACS **Melody™** Cell Sorter (new solution eliminate manual steps and simplify your workflow with smart automation. The system is typically ready in less than 17 minutes)
- **Atomic Force Microscope** NanoWizard® 4 XP BioScience with Leica LSI HSC macroconfocal is placed on top.
- **Confocal** microscopes: Zeiss **LSM880** CLSM with airyscan, airyfast, PicoQuant FLIM, FLIM-FRET, FCS, FCCS and inverted stand; Zeiss **LSM800** CLSM with airyscan and upright stand; Leica **Stellaris 8** DIVE multiphoton with White light laser, powerful Mai-Tai multiphoton laser, Tau, Lightning and inverted stand; Nikon CrEST Cicero Spinning Disks for fast imaging and an upright stand Nikon LV100ND microscope; Zeiss **LSM980** CLSM, with black box around the system can either be operated at room temperature or with a temperature-controlled stage insert (10-40°C). **LSM990** with airyscan 2, lightfield 4D, PicoQuant FLIM, and flipped stand available as collaboration with Stephanie Yvette Robert.
- **Brillouin Microscope -** Label-free, non-invasive mechanical imaging of living plant tissues in 3D. Equipped in 780 nm fibre-coupled laser. Detection by multi-stage dispersive spectrometer with cooled 4.2 MP sCMOS camera and free spectral measurement rangerange ≥ 15 GHz. Fully integrated with Zeiss LSM 780 confocal microscope.

CONTACT

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MORE INFORMATION

https://www.upsc.se/platforms/microscopy-facility.html

ViSp - Vibrational Spectroscopy Core Facility

ViSp provides FT-IR and Raman spectroscopy and microspectroscopy services, ranging from design of experiments to measurements and data analysis. ViSp has state-of-the-art instrumentation, including two vacuum bench FTIR spectrometers, two confocal Raman microscopes with 5 laser lines (from 405 to 785 nm), a portable Raman spectrometer and a cutting-edge combined optical photothermal infrared (OPTIR) and Raman microscope. The techniques are suitable to detect and localise (at submicron resolution) chemical changes in a wide range of samples, at high speed and low cost, non-destructively and free of external agents (dyes, markers, labels). ViSp can provide both hardware and software development to adapt the techniques to the needs of the users / projects.

EXAMPLE APPLICATIONS/RESEARCH PROJECTS

Due to the exceptional versatility of the techniques, example projects cover a wide range of scientific disciplines and applications. Among the most prominent are materials sciences (nanotechnology, semiconductors), plant sciences (high-throughput chemotyping/screening, investigating the effects of gene manipulations or environmental factors), environmental sciences and biofuel applications (from microplastics, to biochars, and algae), bio/geo/chemistry (absorption on mineral surfaces, real-time, in situ monitoring of reactions, protein conformational changes) and medicine (assessing tissue compositional changes under various pathological conditions, diagnosing and monitoring disease onset and progression, drug targeting and molecular mechanistic studies, in vivo chemical compositional analysis of tissues). ViSp is primarily research driven and actively participates in projects where new methods need to be developed as well as applying existing methodologies in new areas.

TEACHING ACTIVITIES / COURSES

A User Licence Course is run twice a year, giving a basic introduction to vibrational spectroscopy in general and training users in running their own experiments at ViSp. ViSp is also involved in several courses at Umeå University and SLU.

LOCATION

Chemistry Department, Building C, floors 1 and 6.

CONTACT

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VIBRATIONAL SPECTROSCOPY CORE FACILITY

MORE INFORMATION

https://www.umu.se/en/research/infrastructure/visp/

Poster I-19
XPS - X-Ray Photoelectron Spectroscopy Platform

The X-ray photoelectron spectroscopy (XPS) platform is an open infrastructure at Umeå University enabling users both within UmU and outside to obtain analyses of the chemical composition of their sample surface. Knowledge of the elemental composition, oxidation state and spatial distribution of atoms at surfaces, near-surfaces, and interfaces is crucial to our understanding of key reactions in nature and technology. Surfaces are, after all, the interface through which materials - as small as nanoparticles and bacteria, to as big as nuclear fuel reactors and spaceships - interact with their environments. XPS, also known as Electron Spectroscopy for Chemical Analysis (ESCA), is now one of the most widely used tools in countless fields of science and engineering where advanced analyses of surfaces and interfaces is needed. The platform provides surface analysis by XPS, UPS, and LEIPS techniques. Full range of conventional XPS experiments is available including monochromatic Al Kα excitation, angle- resolved XPS, XPS imaging, and cryogenic measurements.

EQUIPMENT

AXIS Ultra DLD is an electron spectrometer manufactured by Kratos Analytical, Ltd. (UK). The instrument was installed at the Dept of Chemistry in 1999 and upgraded twice in 2004 and 2009.

The new XPS spectrometer **AXIS SUPRA+** is installed and put in operation November 2023.

SERVICES

In the outermost 10 nm of a surface (10 atomic layers), XPS provides:

- Identification of all elements (exc. H and He) present in concentrations >0.1 atomic %
- Semi quantitative determination of the elemental surface composition
- Information about the molecular environment (oxidation state, bonding atoms, etc.)
- Non-destructive elemental depth profile 10 nm into the sample and surface heterogeneity assessment
- Lateral variations in surface chemical composition (XPS imaging with spatial resolution of 1-5 µm)
- Studies on wet/hydrated (frozen) samples
- Experimental determination of band gap, work function, electron affinity and ionization energy in materials with UPS (HOMO) and LEIPS (LUMO)

The XPS platform is **the only facility for XPS analyses in Northern Sweden** (north of Uppsala). The platform supports a unique field of research, developed at the Department of Chemistry involving investigations of fast-frozen samples including mineral-aqueous solution interfaces, interfaces of biomaterials with biologically relevant media, and surface chemistry of microorganisms. The platform also supports a large range of research areas by providing state-of-the-art surface analysis in areas including ecology, chemistry, physics, archeology, molecular biology and engineering. .

STEERING BOARD

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CONTACT

Dmitry Shevela, Dept. of Chemistry, KB.C6, B6-35-07/B6-35-01 (XPS lab) & B6-01-01 (office), tel. 090-786-5293. dmitry.shevela@umu.se

MORE INFORMATION

https://www.umu.se/en/research/infrastructure/xps/

Research Infrastructures

XRDF - X-Ray Diffraction Facility

The X-Ray Diffraction Facility (XRDF) at the Dept. of Chemistry and the Chemical Biological Centre takes your project from pure protein (in collaboration with the Protein Expertise Platform, PEP) to 3D structure. The XRDF provides expert crystallographic advice and hands-on access to nano-drop crystallization robots as well as to automated crystal imaging and storage system. Collections of X-ray diffraction data is done on the state of the art X8 PEOTEUM X-Ray diffraction system providing atomic resolution 3D structures of proteins and their complexes with DNA and RNA.

XRDF Crystallization Services

- Crystallization Set-ups in 96-Well Plates (up to 288 different conditions per plate) using Commercial and Custom Crystallization Screens
- Crystal Imaging, Evaluation & Storage
- Optimization of initial crystallization conditions

X-ray Diffraction Data Collection (using in-house X-ray Generator & Synchrotron)

- From Single Crystals (Powders Diffraction also possible)
- X-Ray Crystal Structure Determination
- 3D Structure Refinement, Quality Validation & PDB data deposition

X-Ray User Training Courses

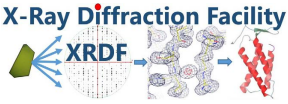
- Course in Crystallography & Crystallization
- User training for crystallization robot and crystal imager (“driver’s licences”)

Collaborations with KBC platforms (added value):

- **PEP**, UCEM, NMR, LCBU, Imaging facility, ..

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MORE INFORMATION

https://www.umu.se/en/research/infrastructure/x_ray_diffraction_facility/

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BMCU - BioMolecule Characterization Unit	johan.olofsson.edlund@umu.se	**I-3a** **I-3b** **I-3c** **I-3d**
CASP - Computantional Analytics Support Platform	katie.bennett@umu.se	
CBCS - Chemical Biology Consortium Sweden	stina.berglund.fick@umu.se gustavo.carvalho@umu.se	**I-4**
C-Trap Facility	Ruben.casanova-saez@umu.se	**I-5**
HPC2N - High Performance Computing Center North	pedro.ojeda-may@umu.se	**I-6a** **I-6b**
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LLUm - Laserlab Umeå	laszlo.veisz@umu.se	**I-8**
MAXS - Multi-purpose Adaptive X-ray Scattering platform	nils.skoglund@umu.se	**I-20**
NanoLab	roushdey.salh@umu.se	**I-9**
NBIS - National Bioinformatics Infrastructure Sweden	jeanette.tangrod@umu.se	**I-10**
µNiSCH µNordic Single Cell Hub	tugrul.doruk@umu.se	**I-11**
NMR - Nuclear Magnetic Resonance Core Facility	tobias.sparrman@umu.se	**I-12**
PEP - Protein Expertise Platform	uwe.sauer@umu.se	**I-21**
SMC - Swedish Metabolomics Centre	annika.johansson01@umu.se	**I-13**
UCEM - Umeå Centre for Electron Microscopy	linda.sandbland@umu.se	**I-14a** **I-14b** **I-14c** **I-14d** **I-14e**
UHRF - Umeå Hypoxic Research Facility	emilio.bueno@umu.se	**I-15**
UMSC - Umeå Marine Sciences Centre	regina.kolzenburg@umu.se nick.kamenos@umu.se	
UPP - Umeå Proteomics Platform	andre.mateus@umu.se iker.aramburu@umu.se	**I-16**

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Legal and Information Management Office		**I-24**
SLU Holding	maria.klintenas@slu.se	**booth**
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MORE INFORMATION ABOUT RESEARCH INFRASTRUCTURE AT KBC

https://www.umu.se/en/chemical-biological-centre/kbc-scientific-infrastructures/

Umeå University Library

Poster I-22

Open research information and the importance of persistent identifiers for scholarly communication

Theresa Kieselbach, Olivia Ekman, Amalia Juneström, and Kristoffer Lindell
Umeå University Library, Umeå University

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Two key areas of Open Science are Open Access to scholarly publications and access to research data according to the principle "as open as possible and as closed as necessary". A prerequisite for that is metadata that makes research outputs searchable and findable and show how they are related to one another.

Metadata about research has so far mainly covered publications. Scopus and Web of Science are metadata databases that many researchers use for literature searches. They do not meet the need for access to research information in Open Science because they do not cover other research outputs like research data, code and protocols. In addition, they are proprietary resources and not openly accessible.

The need for Open Access to research information was a driving force for the development of scientific knowledge graphs like OpenAlex and OpenAIRE Graph. These graphs are databases that link entities that at different sites, and they allow searches in a larger space of research outputs.

Persistent identifiers are central for scientific knowledge graphs because they are machine-readable and give an entity a unique identity. For instance, a researcher can have an ORCID, an organization a ROR-ID and a research output a DOI. We discuss the importance of unique persistent identifiers for scholarly communication to make researchers and their outputs visible in scientific knowledge graphs.

Research Support and Collaboration Office

Poster I-23

Looking for research funding or preparing an application? – Research Funding Support at Umeå University

Obtaining research funding requires more than a strong research idea. Researchers increasingly need to navigate a complex funding landscape, identify suitable opportunities, build competitive proposals, and manage funded projects. The Research Support and Collaboration Office supports researchers throughout the entire funding lifecycle. We offer access to tools, information events, and tips for identifying funding opportunities, facilitate idea development and offer feedback and guidance for proposal development, as well as offer budget support, support on how to meet formal requirements, and as support for post-award project management. Our poster also highlights opportunities to engage with the Research Support Office through newsletters, tools, workshops, and individual support, for major national and international funding schemes.

Keywords: research funding, grant applications, proposal development, budget support, post-award support, EU-funding.

MORE INFORMATION
https://www.umu.se/en/research-support-and-collaboration-office/

Support regarding research data

Poster I-24

Support regarding research data

At Umeå University, there are various ways to receive help with data management. For example, you can receive guidance on how to handle sensitive data, which services to use to store your data and how to make data accessible. You can also receive feedback on your data management plan.

The University has a university-wide, cross-functional support team for research data management that supports you with research data issues in areas such as archiving, law, IT, open data, and information security.

Umeå University offers a number of courses for staff who have contact with research data. Courses are suitable for anyone managing research data in their role as a researcher, doctoral student, administrator or manager.

MORE INFORMATION
https://www.umu.se/en/researcher/plan-and-implement/manage-research-data/support-regarding-research-data/

Coordinated Services at KBC

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SciLifeLab site Umeå	Project administrator: Ainhoa Querejeta Azurmendi, ainhoa.querejeta@umu.se
UCMR	Research Coordinator: Ingrid Söderbergh, ingrid.soderbergh@umu-se
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KBC Head of Service	Clas Wikström, clas.wikstrom@umu.se
Mechanic workshop at the Department of Physics	peter.wikstrom@umu.se isak.silander@umu.se
KBC IT-support	http://kbc-support.ad.umu.se/IT/
KBC Chem Store	https://www.umu.se/en/department-of-chemistry/chemshop/

MORE INFORMATION ABOUT COORDINATED SERVICES AT KBC

https://www.umu.se/en/chemical-biological-centre/services-kbc/


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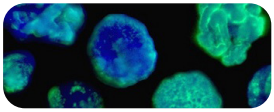
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Secondary antibodies, Tag antibodies and reagents

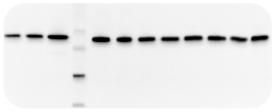
Secondary antibodies

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Tag antibodies

Biotin | CRISPR | DYKDDDDK
FITC/TRITC | GAL4/GUS/LUC/others
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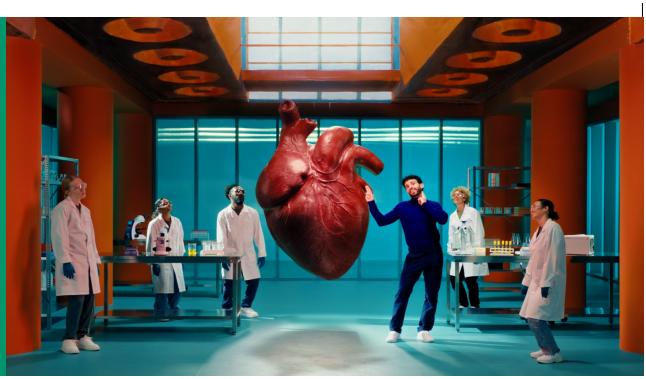
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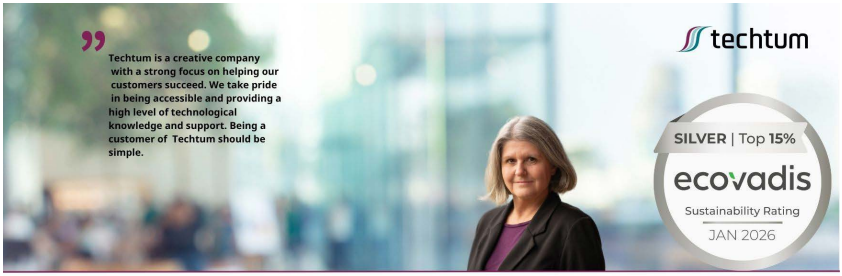
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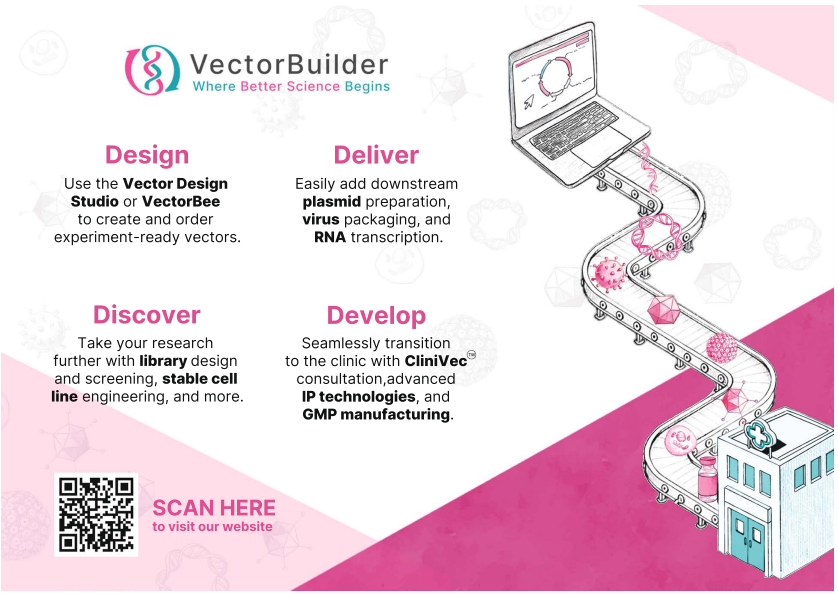
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