Norsk Biovitenskapelig Selskap

The 61st Norwegian Bioscience Society Contact Meeting

STOREFJELL RESORT HOTEL

GOL, NORWAY

JANUARY 21–24, 2026

Table of Contents

Welcome!

Dear participants, speakers and exhibitors!

Welcome to the 61st NBS Contact Meeting, 21–24 January 2026, at Storefjell Resort in Gol! For more than six decades, the NBS Contact Meeting has been a place where Norwegian bioscience comes together to share new results, learn something unexpected, start new collaborations or just simply have some fun.

We have put together a program with nine outstanding plenary lecturers that covers a broad range of topics, such as bioimaging and cell biology, developmental biology, neurobiology, immunology, biochemistry, structural biology, and microbiology. As previous years the meeting will have minisymposiums and poster sessions, and a large exhibition space where companies will showcase their products. We are also excited to include Master Class sessions this year — practical sessions aimed at building skills that are useful long after you return to the lab.

We would like to thank all our sponsors and exhibitors for their support and participation. Without you, this meeting would not be possible. We encourage all participants to take a look at the sponsor page in the program and to visit the exhibition area, where companies will be showcasing new tools and technologies. You are sure to learn something new by stopping at the stands and talking to the exhibitors.

In addition to the scientific program we have planned some social highlights that make this meeting fun also in the evenings, Wednesday's quiz, Thursday's popular science event (with a taste of Kveik beer brewing traditions), and the traditional banquet on Friday. And because it's Storefjell in January: there will also be time for fresh air and skiing.

We hope you enjoy the science, the discussions, and the company. Say hello to someone new, visit the posters and the exhibition stands, and make the most of these days together with the the NBS community.

Regards,
The Organizing Committee

Organizing Committee

Svein Isungset Støve
Leader

Henriette Aksnes
Scientific Committee

Marc Niere
Co-leader & Scientific committee

Simona Chera
Scientific Committee

Pawel Burkhardt
Scientific Committee

Anita Elin-Fedøy
Economy

Valeriia Kalienkova
Exhibitors

Gloria Gamiz
Abstracts

Thomas Stevenson
Exhibitors & Sponsors

Kunwar Jung KC
Minisymposium

Lisa Reinmuth
Hotel

Alessia Caiella
Poster Session

Mary Dayne Tai
Web & Print

Practical Information

Check-in/Check-out

Check-in is possible from 13.00 on Wednesday, 21st. Rooms are guaranteed from 16.00. Luggage storage is available. Check out before 11.00 on Saturday, the 24th. Delayed check-out is possible (with an extra charge; contact reception for more details).

Meals

Breakfast is served at the hotel from 07.30-10.00 each morning. All meals are served in the hotel dining hall with a great view of the surrounding area. The lunch and dinner times are indicated in the meeting program. Drinks (both alcoholic and non-alcoholic beverages) for lunch and dinner are not included in the conference fee, except for the wine served at the banquet dinner on Friday. Your badge will serve as your meal ticket.

Reception and banquet

On Friday, a reception will be held at 19.30, in the Dance Hall (Dansesalen). Following the reception, the banquet will be held in the dining hall from 20.00, and the party will continue with a DJ in the nightclub (Nattklubb 1001). Your badge will serve as your meal ticket.

Secretariat

The secretariat is located at the reception of the conference area. You can upload your presentations for plenary sessions and minisymposia here. The secretariat is staffed at the following times:

Wednesday 21st	11.00 – 15.15
	16.30 – 17.00
	18.00 – 20.00
Thursday 22nd	08.00 – 09.00
	10.30 – 12.30
	18.00 – 19.30
Friday 23rd	08.00 – 09.00
	12.00 – 13.00

Wireless internet

Wireless Internet is available throughout the hotel (Wifi name: 1001).

Exhibition

The exhibition is open during all coffee breaks and during the periods indicated in the Program. The exhibition takes place in Storefjellhallen 1 on the -3 floor and is open as indicated in the program. We strongly encourage all participants to visit the exhibition.

Plenary sessions

All plenary lectures will take place in Nystølfjellet on floor -2. Plenary speakers can contact the support staff for help with connecting laptops. We kindly ask that you contact the support staff at least 30 min before your session to allow for testing. All plenary speakers are asked to follow the allocated times for their presentations (40 min presentation, 5 min discussion).

Minisymposia

Minisymposia will be held in parallel at 3 different locations in the conference area (Veslefjellhallen 1, 2 and 3). Each talk should last a maximum of 12 minutes. In addition, 3 minutes will be available for discussion. We kindly ask that all minisymposium speakers send their presentation by e-mail to bergennbs@gmail.com or bring a USB stick with their presentation to the Secretariat no later than 08.30 on the day of the presentation. The file should be labelled following the format: M# (see attached program) and name.

Practical Information

Poster session

The posters should be mounted on Wednesday, soon after arrival in Storefjellhall 2. All posters will be displayed until Friday evening. Authors should present their posters on: Wednesday 18.00-19.30, odd numbers (P1, P3, and so on); Thursday 18.00-19.30, even numbers (P2, P4, and so on).

Social program

There will be several opportunities for social interaction at the Contact Meeting. On Wednesday, there will be a pub quiz in the library and live music in the Piano Bar. On Thursday, there will be a popular science lecture on Kveik yeast, with the opportunity to taste traditionally brewed Kveik beer from Voss. There will also be live music in the Piano Bar and a DJ in the nightclub (Nattklubb 1001). On Friday, we will have a reception in the Dance Hall followed by the traditional NBS banquet. After the banquet, our NBS DJ will play at Nattklubb 1001, and the hotel will have live music in the Dance Hall.

Outdoor Activities

In the program for Friday, there is time for outdoor activities and relaxation. Storefjell skisenter is open from 10.00 to 13.00, and there are plenty of opportunities for cross-country skiing in the area. Trails start at the ski resort, a short walk from the Hotel. Ask at the reception for a trail map. If you are looking to avoid the cold, the hotel offers a wellness zone with swimming pools, saunas, jacuzzis, and other amenities for relaxation and comfort.

Transportation

If you need help with transport to Gol station, please contact the hotel reception desk.

Oslo-Gol Buses

Buses will depart from Oslo Airport Gardermoen and Oslo Central Station at 09.30 on Wednesday, January 21.

Buses from Gol to Oslo Airport Gardermoen and Oslo Central Station will depart at 10.00 on Saturday, January 24.

If you have not booked a ticket yet, contact Lisa Reinmuth from the organizing committee at lisa.reinmuth@uib.no.

Storefjell Hotel Map

General Assembly

Invitation to the general assembly of the Norwegian Bioscience Society

January 23, 2026
18:00-19:00, Veslefjellhallen 1, Storefjell Resort, Gol, Norway

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Agenda

- Opening of the general assembly (President).
- Approval of the invitation and agenda.
- Election of chairperson, 2 minutes secretaries and 2 persons to approve that the report for the general assembly is correct.
- Approval of the board report.
- Approval of the revised accounts of NBS, NBS-nytt and Contact Meeting
- Election of president and/or general secretary.
- Matters proposed by the board:
- Other matters received:
- Approval of the proposed budget

Orientations

- NBS-nytt: the editor informs about NBS Nytt 2025.
- Report from NBS local branches.
  - Oslo
  - Bergen
  - Trondheim
  - Tromsø
  - Ås
- Contact meeting 2027: Tromsø
- NBS Contact meeting 2028: NMBU

Trondheim December 18th, 2025
Magnus Steigedal
Secretary General NBS

NBS Contact Meeting 2026

Sponsors & Collaborators

Sponsors

01

Tannlege Olaf Aase og frues minneforelesning
Thomas Helleday
Tannlege Olaf Aase og frues legat

Tannlege Olaf Aase og Frues Stiftelse

02

EMBO

EMBO
www.embo.org

03

FEBS

FEBS
www.febs.org

04

Leica MICROSYSTEMS
Ortomedic

Leica + Ortomedic
www.ortomedic.no

05

FEBS openbio
FEBS PRESS science publishing by scientists

FEBS OpenBio
www.febs.org

06

TRIOLAB
www.triolab.com

07

communications biology

Communications Biology
www.nature.com/commsbio

08

The Research Council of Norway

NFR
www.forskningsradet.no/

Collaborators

01

NFM

Norsk Forening for Mikrobiolgi

02

CENTRE FOR DIGITAL LIFE NORWAY

DLN
www.digitallifenorway.org

03

elixir NORWAY

Elixir Norway
www.elixir.no

NBS Contact Meeting 2026

Exhibitors

01

SARSTEDT

https://www.sarstedt.com

02

Leica + Ortomedic

www.leica-microsystems.com

03

Eppendorf

www.ortomedic.no

04

Matriks

www.matriks.no

05

Mettler Toledo

www.mt.com

06

Novogene

www.novogene.com

07

ChemSupport AS

www.chemsupport.no

08

InterInstrument AS

www.interinst.no

09

BioNordika

www.bionordika.no

10

AH Diagnostics

www.ahdiagnostics.no

11

Merck
www.merck.com

12

Houm
www.houm.no

13

NMAS
www.nmas.no

14

Saveen Werner
www.swab.se

15

Berner Lab
www.bernerlab.no

16

Avantor
www.avantor.no

17

Teknolab AS
www.teknolab.no

18

BIO-RAD
www.bio-rad.com

19

TRIOLAB
www.triolab.no

20

Techtum
www.techtum.se

21

Holger Hartmann
www.holgerhartmann.no

22

Cytiva
www.cytivalifesciences.com

Programme Overview

21	22	23
	Breakfast 07:30 - 09:00	Breakfast 07:30 - 09:00
	PL IV: Timothy Lynagh 09:00 - 09:45	Outdoor Activities 09:00 - 12:30 Master Class III: Structural Biology 11:30-12:30
	PL V: Thomas Helleday 09:45 - 10:30	
	Exhibitions + Break 10:30 - 11:00	
	Minisymposia 1-3 11:00 - 12:30	
Lunch + Registration 12:00 - 14:00	Lunch 12:30 - 14:00	Lunch 12:30 - 14:15
	PL VI: Joseph A. Baur 14:00 - 14:45	Minisymposia 4-6 14:15 - 15:30
Welcome 14:45 - 15:00	PL VII: Evelien Adriaenssens 14:45 - 15:30	
PL I: Sandrine Etienne Manneville 15:00 - 15:45	Exhibitions + Break 15:30 - 16:00	Exhibitions + Break 15:30 - 16:00
PL II: Karin Lindkvist 15:45 - 16:30	NFR Panel Discussion 16:00 - 17:00	PL VIII: Paul Guichard 16:00 -16:45
Exhibitions + Break 16:30 - 17:00		PL IX: Mounia Lagha 16:45 - 17:30
PL III: Luke O' Neill 17:00 - 17:45	Master Class I: Bioinformatics Master Class II: Grant Writing 17:10 - 18:00	
Exhibitions + Poster Session I 18:00 - 19:30	Exhibitions + Poster Session II 18:00 - 19:30	NBS General Assembly 18:00 - 19:00
		Reception 19:30 - 20:00
Dinner 20:00 - 21:30	Dinner 20:00 - 21:30	Banquet 20:00
Quiz & Live Music 21:30	Kveik Beer Tasting 21:30	

Wednesday, January 21

12:00-14:00	**Registration + Lunch + Poster Mounting**	
14:45-15:00	**Welcome**	**Nystølfjellet**
15:00-15:45	**Lecture I - EMBO Lecture** Sandrine Etienne Manneville *The role of cell mechanics in glioblastoma invasion and therapeutic resistance* Chair: Henriette Aksnes	**Nystølfjellet**
15:45-16:30	**Plenary Lecture II - 2026 FEBS National Lecture** Karin Lindkvist Aquaporins in health and disease Chair: Petri Kursula	**Nystølfjellet**
16:30-17:00	**Exhibitions + Coffee Break**	**Storefjellhall 1**
17:00-17:45	**Plenary Lecture III** Luke O' Neill *How a break in mitochondrial endosymbiosis might explain the increase in inflammatory diseases* Chair: Marc Niere	**Nystølfjellet**
18:00-19:30	**Exhibitions + Poster Session I**	**Storefjellhall 2**
20:00-21:30	**Dinner**	**Spisesal**
21:30-23:00	**Social Activities - Quiz and Live Music**	**Biblioteket**

Thursday, January 22

07:30-09:00	**Breakfast**	
09:00-09:45	**Plenary Lecture IV** Timothy Lynagh *A TREEtise on ionotropic glutamate receptors* Chair: Aurora Martinez	**Nystølfjellet**
09:45-10:30	**Plenary Lecture V - Tannlege Aase og Frues Stiftelse Lecture** Thomas Helleday *Targeting DNA repair in battle of diseases* Chair: Tone Berge	**Nystølfjellet**

10:30-11:00	**Exhibitions + Coffee Break**	**Storefjellhall 1**
11:00-12:30	**Minisymposia 1-3**	**Veslefjellhallen 1-3**
12:30-14:00	**Lunch**	**Spisesal**
14:00-14:45	**Plenary Lecture VI** Joseph A. Baur *Functional consequences of mitochondrial NAD content in mammalian cells* Chair: Marc Niere	**Nystølfjellet**
14:45-15:30	**Plenary Lecture VII - Norsk Forening for Mikrobiologi Lecture** Evelien Adriaenssens *The human gut virome in health: a journey through life* Chair: Dirk Linke	**Nystølfjellet**
15:30-16:00	**Exhibitions + Coffee Break**	**Storefjellhall 1**
16:00-17:00	**Panel Discussion: Funding of biotechnology research in Norway: underfunded or underused?** **Introduction** Line Grønning-Wang *The RCN's Funding of Life Science* Panel: Line Grønning-Wang, Yamila Torres Cleuren Rein Aasland, Magnus Steigdal Chair: Trygve Brautset	**Nystølfjellet**
17:10-18:00	**Master Class I - Elixir Norway** Michael Dondrup *Population genomics done right: powers, pitfalls, and practical workflows*	**Veslefjellhallen 1**
	Master Class II - DLN Yamila Torres Cleuren *Navigating Norwegian funding: a practical guide to successful proposals*	**Veslefjellhallen 2**
18:00-19:30	**Exhibitions + Poster Session II**	**Storefjellhall 2**
20:00-21:30	**Dinner**	**Spisesal**
21:30-22:15	**Science and Social: Kveik Beer Tasting - NIBIO** Hans Geir Eiken *Kveik and the early yeast domestication in Norwegian farmhouse brewing*	**Biblioteket**
22:15	**Social Activities - Live Music + DJ**	

Friday, January 23

07:30-09:00	**Breakfast**	**Spisesal**
09:00-12:30	**Outdoor Activities**	
11:30-12:30	**Master Class III - NBS** Valeriia Kalienkova *Tips and tricks for publication-quality figures using PyMOL*	**Veslefjellhallen 1**
12:30-14:15	**Lunch**	**Spisesal**
14:15-15:30	**Minisymposium 4-6**	**Room**
15:30-16:00	**Exhibitions + Coffee Break**	**Storefjellhall 1**
16:00-16:45	**Plenary Lecture VIII - Leica + Ortomedic Lecture** Paul Guichard *Expansion Microscopy for Structural Cell Biology: From Centriole Architecture to Human Diseases* Chair: Pawel Burkhardt	**Nystølfjellet**
16:45-17:·30	**Plenary Lecture IX** Mounia Lagha *Gene expression dynamics during the awakening of the zygotic genome* Chair: Pawel Burkhardt	**Nystølfjellet**
18:00-19:00	**NBS General Assembly**	**Veslefjellhallen 1**
19:30-20:00	**Reception**	**Dansesal**
20:00	**Banquet**	**Spisesal**

Saturday, January 24

08:00-10:30	**Breakfast and Checkout**	**Spisesal**
10:00	**Bus Departure (to Oslo)**	

Plenary Speakers

01

Sandrine Etienne Manneville

Cell Biology

02

Karin Lindkvist

Structural Biology

03

Luke O' Neill

Immunometabolism

04

Timothy Lynagh

Neurobiology

05

Thomas Helleday

Biochemistry & Cancer

06

Joseph A. Baur

Biochemistry & Physiology

07

Evelien Adriaenssens

Plant Biology

08

Paul Guichard

Cell Biology

09

Mounia Lagha

Developmental Biology

January 21 | 15:00 - 15:45

PL 01

Sandrine Etienne-Manneville
National Center for Scientific Research
Institut Pasteur, Paris | FRANCE

EMBO Lecture

The role of cell mechanics in glioblastoma invasion and therapeutic resistance

Glioblastoma multiforme is the most common and aggressive malignant brain tumor, characterized by a poor prognosis and the absence of curative therapies. The intratumoral heterogeneity and invasive behavior of glioblastoma cells significantly contribute to tumor aggressiveness and therapeutic failures. Cell invasion, a hallmark of cancer, is driven by cell intrinsic mechanical properties and mechanotransduction, a multi-step cellular and gene regulatory process that governs cellular responses to mechanical stimuli. Due to their physical properties, cytoskeletal components are crucial in modulating cell mechanical and invasive properties, enabling tumor cells to respond to physical stresses encountered during cancer progression. In this presentation we will explore how variations in the expression of intermediate filament components influence tumor cell adhesion, invasion and resistance to treatment, highlighting potential therapeutic targets to improve patient outcomes.

Sandrine Etienne-Manneville is a cell biologist well-known for major discoveries in the elucidation of polarity signaling and, more recently, cytoskeletal crosstalk and its role in cell mechanics. After earning a PhD at the Institut Cochin, Paris on lymphocyte migration across the blood brain barrier and completing a postdoctoral fellowship in Pr. Alan Hall's lab in London, working on RhoGTPases in astrocyte polarization and migration, she obtained a research position at the Institut Curie in 2004. She moved in 2026 to Institut Pasteur, Paris to lead her own team. The team's focus is on the molecular mechanisms controlling themigration and invasion of normal and tumoral cells. Dr. Etienne-Manneville's research explores the regulation of cell polarity, the impact of cell-ECM and cell-cell interactions, and the role of the cytoskeleton and cytoskeletal crosstalk in cell mechanics and mechanotransduction during cell invasion through complex, mechanically challenging environments. The team was the first to demonstrate the essential role of microtubules and intermediate filaments in cellpolarization, adhesion, mechanotransduction, and directed migration, as well as in glioblastoma invasion. Currently, Dr. Etienne-Manneville investigates the mechanisms underlying glioblastoma invasion and therapeutic resistance—key factors contributing to the relapse of these incurable brain tumors affecting both children and adults.

January 21 | 15:45 - 16:30

PL 02

Karin Lindkvist
Lund University & SciLife Laboratory | SWEDEN

FEBS National Lecture

Aquaporins in health and disease

Aquaporins (AQPs) are a conserved family of transmembrane channel proteins present across all kingdoms of life and are essential for regulating the movement of water and small solutes across biological membranes. In humans, 13 aquaporins (AQP0–12) have been identified and are broadly classified into orthodox aquaporins, which selectively facilitate water transport, and aquaglyceroporins, which additionally conduct glycerol and other small molecules such as hydrogen peroxide (H_2O_2). Among the aquaglyceroporins, AQP3 and AQP7 play critical roles in cellular metabolism and signalling. Using single-particle cryo-electron microscopy, distinct functional and structural properties of these channels have been elucidated.

Human AQP3 was captured in both open and closed conformations, revealing a pH- and substrate-dependent gating mechanism. At neutral pH, AQP3 adopts an open state that permits glycerol and H_2O_2 permeation, whereas acidic conditions or elevated H_2O_2 concentrations induce a closed conformation driven by a pronounced rearrangement of loop E. This structural transition provides a molecular basis for concentration-dependent autoregulation of H_2O_2 flux and highlights AQP3 as a key regulator of cellular redox homeostasis. Similarly, high-resolution cryo-EM analysis of AQP7 revealed a unique supramolecular organization in which two tetramers adhere via extracellular loop interactions, forming an octameric assembly. The central pore formed between the four monomers contains defined densities constrained by two leucine filters. Mass spectrometry confirmed the presence of glycerol 3-phosphate within the purified protein, consistent with the observed central pore features. Notably, AQP7 is highly expressed in human pancreatic α- and β-cells, suggesting that beyond its established role in glycerol transport, the octameric AQP7 assembly may function as a junctional protein within the endocrine pancreas, linking membrane permeability to metabolic regulation.

Lindkvist belongs to the Department of Experimental Medical Science at Lund University. Lindkvist received her PhD in 2003 and spend her postdoctoral time at Stanford University. Professor Lindkvist was recruited to Lund University in 2010 in an effort to strategically build up prioritized research area of structural biology. For Lindkvist this was a strategic move to be able to combine structural biology withmicroscopy on clinical samples. Lindkvist is heading a group in medical structural biology combining high resolution microscopy with X-ray methods and single particle cryo-EM. Lindkvist offers exceptional know-how in structural biology, and has already made significant contributions to the discipline, providing several milestone structures with 40 unique entries in the protein data bank. At the Faculty of Medicine at Lund University, Lindkvist is the sole PI performing these types of studies, thus Lindkvist research line is unique and very successful and have resulted in several high impact publications.

January 21 | 17:00 - 17:45

PL 03

Luke O'Neill
Trinity College Dublin | IRELAND

How a break in mitochondrial endosymbiosis might explain the increase in inflammatory diseases

Mitochondrial disturbance is a feature of inflammatory cells, and we have been analysing mitochondrial metabolites, notably itaconate and fumarate in inflammatory macrophages. Itaconate derivatives are anti-inflammatory and have potential for the treatment of immune and inflammatory diseases. We have found that the cytokine GDF-15 is a key signal being driven by itaconate and fumarate, as well as general disturbance of mitochondria. It has anti-inflammatory effects, can limit food intake and thereby control obesity, and may act to take the pressure off damaged mitochondria in inflammation. Overall evidence is growing that a break in mitochondrial endosymbiosis might be a reason for the increasing incidence of autoimmune and inflammatory diseases. NLRP3 is an important target that becomes activated and there are over 20 inhibitors currently in development for a range of inflmamtory diseases. Other targets outside mitochondria include the enzyme PKM2 which is key to the Warburg metabolism that defines inflammation and is also being targeted in the clinic. These insights are providing a new view of metabolism in immunity and inflammation and might indicate new therapeutic approaches.

Luke O'Neill is Professor of Biochemistry in the School of Biochemistry and Immunology, Trinity Biomedical Sciences Institute at Trinity College Dublin, Ireland. He is a world expert on innate immunity and inflammation. He is listed by Thompson Reuters/ Clarivates in the top 1% of immunologists in the world, based on citations per paper.

Professor O'Neill is co-founder of Sitryx, which aims to develop new medicines for inflammatory diseases. Another company he co-founded, Inflazome was acquired by Roche in 2020 and is carrying out trials in Parkinson's Disease, Severe Asthma and Heart disease using new therapeutics based on his work. He was awarded the Royal Dublin Society / Irish Times Boyle Medal for scientific excellence, the Royal Irish Academy Gold Medal for Life Sciences, the European Federation of Immunology Societies Medal and the Landsteiner Award from the Austrian Academy of Sciences. He is a member of the Royal Irish Academy, EMBO (European Molecular Biology Organisation) a Fellow of the Royal Society and holds Honorary Degrees from the Universities of Massachusetts and Bath.

January 22 | 09:00 - 09:45

PL 04

Timothy Lynagh
Michael Sars Centre, University of Bergen | NORWAY

A TREEtise on ionotropic glutamate receptors

We tend to divide ionotropic glutamate receptors into fast synaptic detectors (AMPA receptors), multimodal modifiers (NMDA receptors), or strange cousins (delta receptors). But this view belies substantial variation in their functional repertoires, is difficult to project onto classical experimental models that have vastly different genes, and leaves several biophysical and physiological mysteries unsolved. We have explored the evolution of ionotropic glutamate receptors using phylogenetics and functional characterization of receptors from diverse animals. We find that AMPA receptors repeatedly evolve complexity and diversity in different types of animals yet converge on remarkably similar biophysical function. We find that NMDA receptors have vastly different functional properties in certain invertebrates, which in turn uncovers mechanisms behind mammalian NMDA receptors' requirement for multiple transmitters. And it turns out that delta receptors in most animals are on one hand much more normal than expected, but on another hand much weirder – they appear to be excitatory GABA receptors!

Tim is a group leader at the Michael Sars Centre at UiB, where his group analyses the evolution of ionotropic receptors to dissect the biophysical basis of their function. He received his PhD from UQ Australia, and did postdocs in Darmstadt and Copenhagen, before starting in Bergen in 2019 with an ERC Starting Grant. Work from his group has, for example, established how neuropeptides activate excitatory channels in various invertebrates, dissected the molecular evolution of NMDA receptors and AMPA receptors in complex animals, and uncovered why delta-type glutamate receptors in humans are relatively inactive. His lab also uses these discoveries to engineer novel chemogenetic tools for turning neurons on and off.

January 22 | 09:45 - 10:30

PL 05

Thomas Helleday
Karolinska Institute & SciLife Laboratory | SWEDEN

Tannlege Olaf Aase og Frues Stiftelse Lecture

Targeting DNA repair in battle of diseases

Thomas Helleday, PhD obtained a lectureship a t the Institute for Cancer Studies, University of Sheffield, UK, in 2000 where he research basic mechanisms of DNA damage response and repair and made the discovery of the PARP inhibitor treatment in BRCA mutated cancers. Dr. Helleday became professor at both University of Sheffield and Stockholm University in 2006, prior to being recruited as MRC Professor of Cancer Therapeutics a t the MRC/CRUK Gray Institute for Radiation Oncology and Biology at the University of Oxford. In 2012, he was called to the Söderberg Professor of Translational Medicine and Chemical Biology at the Karolinska Institutet in Stockholm. In 2018, he returned to University of Sheffield to direct the Weston Park Cancer Centre. Following the corona pandemic, he returned to Karolinska Institutet in 2020 to focus on translational research in his group. The focus of the research in the Helleday lab has been basic DNA repair research translated into novel treatments. Dr. Helleday has received numerous international awards and prizes such as the Eppendorf-Nature Young European Investigator Award 2005, the European Association for Cancer Research Young Cancer Researchers Award 2007, the Swiss Bridge Award 2008, the Svedberg Award 2008, Carcinogenesis Young Investigator Award 2010 and ERC Advanced Grant Awards (2010 and 2016).

January 22 | 14:00 - 14:45

PL 06

Joseph A. Baur
University of Pennsylvania | USA

Functional consequences of mitochondrial NAD content in mammalian cells

Nicotinamide adenine dinucleotide (NAD) is a redox cofactor essential to all living organisms. Its concentration declines in certain disease states and over the course of natural aging, and is increased by exercise or caloric restriction. These observations have heightened interest in the therapeutic potential of supplemental NAD precursors. The precursors nicotinamide riboside and nicotinamide mononucleotide have a variety of benefits in rodent models, including improvements in insulin sensitivity, heart function, and cognition. In human trials, both compounds have effectively boosted blood NAD levels, appeared safe over the time frames of the studies, and have shown promise in certain disease states. However, many of the specific health benefits observed in rodents have been modest or absent in humans. This disconnect raises questions including the optimal dosing strategy, species differences, relevant target cells or tissues, and subcellular compartmentalization of NAD. We report preliminary studies supporting the potential of NAD precursors to improve the course of heart failure in a large animal model (swine), as well as genetic studies in mice to understand the consequences of NAD deficiency restricted to cardiomyocytes. In parallel, we have targeted the carrier SLC25A51 to examine the consequences of mitochondria-specific NAD manipulations in hepatocytes. The use of genetic models to selectively alter specific pools of NAD can provide critical mechanistic insights that are missed in the context of complex diseases or systemic approaches to supplement or restrict NAD availability.

Joe Baur is a Professor in the Department of Physiology and the Institute for Diabetes, Obesity, and Metabolism at Perelman School of Medicine, University of Pennsylvania, as well as Director of the RodentMetabolic Phenotyping Core. His long-term interest is in the basic mechanisms that lead to aging, which is a critical risk factor for the major causes of morbidity and mortality in the western world, includingcardiovascular disease, diabetes, cancer, and neurodegenerative disorders. The Baur lab is currently focused on the use of small molecules to understand and mimic the health-promoting effects of dietarymanipulations in rodents, with a particular focus on nicotinamide adenine dinucleotide (NAD+) metabolism. He grew up near Halifax, Nova Scotia, Canada, and attended Acadia University before moving to UT Southwestern in Dallas, Texas, to pursue his PhD studies on human telomere biology. For his postdoctoral studies, he moved to Harvard Medical School to study sirtuin enzymes, which use NAD+ to alter post-translational modifications and have been hypothesized to play a role in aging. He opened his own lab at Penn at the end of 2008, where he has explored the role of NAD+ in cellular metabolism beyond sirtuins.

PL 07

January 22 | 14:45- 15:30

Evelien Adriaenssens
Quadram Institute, Norwich | UK

Norsk Forening for Mikrobiolgi (NFM) Lecture

The human gut virome in health: a journey through life

Having a diverse gut microbiome is crucial for a healthy life. One often neglected component of the microbiome is the virome, consisting of a complex community of viruses including bacterial, archaeal and fungal viruses that infect gut commensals, eukaryotic viruses that could cause infections in humans and transiently detected viruses associated with our diet. A main area of research in my lab is increasing our understanding of the virome in establishing and maintaining health across life.

We have investigated the establishment of gut-associated viruses in the first two years of life, focusing on maternal influence. Using viromics approaches, we identify persistent and transient virus communities, as well as viruses shared between mothers and infants. Across life, we show a dynamic interplay between prophages – phages integrated in the bacterial genomes – and health-associated commensal bacterial hosts. In an ageing population, we are investigating the link between the virome and cognition.

I am a molecular and computational microbiologist with a passion for everything viral. I started my research career at the University of Leuven (KU Leuven, Belgium) investigating the use of bacteriophages (viruses of bacteria) as a biological control agent in potato plant production. As part of this project, co-funded by the Institute for Agricultural and Fisheries Research Flanders (ILVO), I isolated novel phages which I extensively characterised for commercial suitability, including genomics, production optimisation and in planta trials. During my time as a postdoc, I specialised in viromics or viral metagenomics, to elucidate viral community diversity in a range of habitats. At the University of Pretoria (South Africa), I conducted research on extreme environments, such as the Namib Desert and the Antarctic Dry Valleys, where I studied several niche habitats such as hypoliths, hyperarid soil and saline springs. Using this expertise, at the University of Liverpool (UK) I used viromics approaches to investigate the spread of pathogenic viruses from wastewater effluent into a river catchment area in the North of Wales and determine the potential for food- and waterborne illness. I joined the Quadram Institute in Norwich (UK) in January 2019 where my group is investigating the role of viruses, in particular bacteriophages, in the human gut and the environment, and how we can exploit some of these viruses to improve environmental and human health, and treat disease. My group specialises in sequencing-based approaches to understand phages, including genomics, functional genomics, viromics and metagenomics, as well as classical phage biology. I am the Vice President of the International Committee on Taxonomy of Viruses (ICTV).

January 23 | 16:00 - 16:45

PL 08

Paul Guichard
University of Geneva | SWITZERLAND

Leica + Ortomedic Lecture

Expansion Microscopy for Structural Cell Biology: From Centriole Architecture to Human Diseases

The centriole, also known as the basal body, is an evolutionarily conserved organelle that coordinates essential cellular processes, including cell division, signalling, and motility through cilia and flagella. Despite its small size (500 nm in length and 250 nm in diameter) and a composition of roughly one hundred distinct proteins, the precise molecular organization of the centriole and the mechanisms by which its dysfunction leads to disease remain poorly understood. In this talk, I will present recent work from my laboratory addressing these fundamental questions in structural cell biology using a combination of cryo-electron tomography, cell biology, and ultrastructure expansion microscopy (U-ExM). These approaches allow us to visualize centriolar architecture with unprecedented molecular detail directly in cells. I will highlight how these methods have revealed new insights into the organization and assembly of centriolar substructures, and how mutations in centriolar and ciliary proteins contribute to human pathologies, with a particular focus on retinal ciliopathies such as retinitis pigmentosa. In addition, I will present examples of our work in diverse planktonic and non-canonical model organisms, which provide unique evolutionary perspectives on cell architecture and uncover conserved and divergent structural principles across eukaryotes. Together, these studies illustrate how integrating advanced imaging with evolutionary and disease-relevant models can bridge molecular architecture to cellular function and human disease.

Paul Guichard is an Associate Professor in the Department of Molecular and Cellular Biology at the University of Geneva (UNIGE), where he co-leads the Guichard-Hamel Laboratory with Virginie Hamel. Theirteam investigates the molecular architecture and assembly mechanisms of centrioles using cutting-edge methods such as Cryo-electron microscopy and Expansion Microscopy. Paul Guichard earned his PhDin structural cell biology at Institut Curie (2007–2010) and pursued postdoctoral research at EPFL (2011–2015). In 2015, he joined UNIGE as Assistant Professor, becoming Associate Professor in 2021. Togetherwith Virginie Hamel, he has received prestigious recognitions including an EMBO Young Investigator Award (2020), the Friedrich Miescher Award (2022),ERC Starting and Consolidator Grants (2017, 2022), and the Cloëtta Prize (2025), for groundbreaking contributions to centriole biology and Ultrastructure Expansion Microscopy (U-ExM). Their collaborative work continues to shed light on fundamental cellular processes with implications for developmental biology and disease research.

January 23 | 16:45 - 17:30

PL 09

Mounia Lagha
National Center for Scientific Research
Institute of Molecular Genetics, Montpellier | FRANCE

Gene expression dynamics during the awakening of the zygotic genome

A fundamental question in biology is how cellular processes are so reproducible despite the inherent variations in the chemical reactions governing them. During development of a multicellular organism, precise control of gene expression allows the reproducible establishment of patterns. Our goal is to elucidate the mechanisms responsible for precision in gene expression and to link them to accuracy in cell fate decisions. My team tackles this question using the early development of Drosophila as a model system, during the maternal to zygotic transition. During this critical developmental window, patterns of gene expression are rapidly established with remarkable reproducibility and accuracy. We use quantitative imaging, genetic manipulations, biophysics and mathematical modeling to integrate the dynamic aspects of transcription and translation. I will present our recent efforts to deploy quantitative imaging methods to monitor the dynamics of the central dogma in living embryos. Using snail and twist genes as a paradigm, we unravel how transcriptional attenuation, mechanical forces, mRNA localization and spatial control of translation contribute to sharp pattern formation and to morphogenesis.

I am a researcher in Developmental Biology and my main interest is how gene expression is precisely established during embryogenesis. My initial training was on mouse myogenesis (PhD obtained in 2008 at the Pasteur Institute in Paris under the supervision of Pr M.Buckingham and F.Relaix). For my post-doc, in order to obtain more mechanisticinsights, I changed model organism and studied transcriptional regulation during Drosophila development at UC Berkeley in the lab of Pr M.Levine (2010-2014). My postdoctoral work revealed the importance ofpaused polymerase for the coordination of cell fate decisions during gastrulation. Since 2015, I am directing a group at IGMM in Montpellier where we study mechanisms of transcriptional regulation in living Drosophila embryos. Our current research focuses on the role ofpromoters and enhancers on the dynamic aspects of transcription (transcriptional synchrony, bursting and memory). Recently we started also investigating translational control during early development. Weuse a variety of approaches ranging from classical genetics, molecular biology to quantitative live imaging and biophysical techniques. We constantly collaborate with physicists and mathematicians to developtheoretical frameworks for a better understanding of our quantitative biological data.

Panel Discussion

January 22 | 16:00 - 17:00

Room – Nystølfjellet

Funding of biotechnology research in Norway: underfunded or underused?

Research funding is important and of high interest for researchers, and many in academia argue that overall governmental funding is too low, especially for basic research. Rresearch funding from the Research Council of Norway (RCN) for biotechnology has previously been organised through large, long-term programmes (e.g., FUGE and Biotech 2021). Today, biotechnology is spread across several portfolio areas. This session will begin with an introduction from Line Marian Grønning-Wang from RCN on the current organisation of funding and the opportunities available for biotechnology research, and afterwards, she will participate in a panel discussion regarding research funding in Norway.

The Research Council's Funding of Life Sciences

16:00 - 16:20

Line Grønning-Wang
The Research Council Norway
www.forskningsradet.no

Line Grønning-Wang is a Special Adviser at the Research Council of Norway, with broad experience in strategic work related to research infrastructure, research data, and life sciences. She previously worked at the University of Oslo as a researcher and research group leader in medical biosciences. She also represents Norway as a delegate to the EMBL Council, contributing to international collaboration and governance in European molecular biology.

The panel discussion will aim to address key questions: Have funding opportunities for biotechnology in Norway decreased compared with earlier years? Do biotechnology researchers utilize the funding possibilities of RCN sufficiently? In the EU, industry participation is expected to become even more important in the next framework programme, will this be similar in Norway? And, are Norwegian researchers and industry prepared for this development? The panel debate will be lead by Prof. Trygve Brautaset (NTNU and Digital Life Norway).

Meet the Panel

16:20 - 17:00

Trygve Brautaset is a Professor of Synthetic Biology at NTNU and the Scientific director of Digital Life Norway. He has coordinated multiple international ERA/EU projects as well as several national research projects.

Yamila Torres Cleuren holds a PhD in molecular biology and bioinformatics from the University of Auckland, and is currently the Managing Director of Neuro-SysMed research centre at UiB and Helse Bergen. She leads the innovation work of a recently funded SFI centre "ICoN", driving translation, industry collaboration, and long-term impact in neurodegenerative disease research.

Rein Aasland is a Professor at the Department of Biosciences, UiO. He was Head of Department at both the Department of Molecular Biology, UiB, and Department of Bioscience, UiO. His research focuses on gene regulation and epigenetics, using biochemical, bioinformatics, and molecular biology approaches.

Magnus Steigedal is Head of the Department of Clinical and Molecular Medicine at NTNU, focusing on microbial infections and new antibiotic targets, especially for tuberculosis. He previously directed NTNU's Health, Welfare and Technology area and is Secretary General of NBS.

Master Classes

Dive into dynamic, hands-on sessions to supercharge your bioinformatics skills, ace grant writing, or craft stunning publication-ready figures. These master classes are packed with essential tools and insights for scientists at every level, from budding master's students to seasoned principal investigators.

Master Class 1

Bioinformatics

Population genomics done right: Powers, Pitfalls, and Practical Workflows

Gain insights into reproducible workflows for population genomics

Get an overview of tools for analysis and stimulation

No prior knowledge required

Michael Dondrup
Researcher
University of Bergen

Master Class 2

Grant Writing

Navigating Norwegian funding: A practical guide to successful proposals

Learn what makes a proposal fundable

Turn your idea into a clear, feasible project

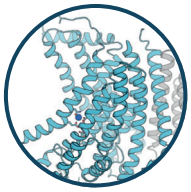
Avoid common pitfalls when writing your applications

Yamila Torres Cleuren
Managing Director
Neuro-SysMed

Master Class 3

Structural Biology

Tips and tricks to creating publication-quality figures using PyMOL.



Gain experience in basic scripting in PyMOL

No prior experience required

A laptop is required for this workshop

Limited spots!

Valeriia Kalienkova
Group Leader
University of Bergen

Elixir Norway

Centre for Digital Life Norway

Norwegian Bioscience Society

Minisymposium 1 Microbiology

Veslefjellhallen 1

Chair: Dirk Linke

11:00-11:15	**M01 | Aikaterini Katirtzoglou** *Disentangling genetic and dietary impacts on the pig gut microbiome*
11:15-11:30	**M02 | Dave Edison Rojas Calderón** *A deep dive into the genome of bacterial isolates from salmon fry*
11:30-11:45	**M03 | Gustav Vaaje-Kolstad** *Decoding the Degradation of Gram-Positive Polysaccharides*
11:45-12:00	**M04 | Mari Kaarbø** *"The Oslo Patient" : Sustained HIV Remission Five Years After CCR5Δ32/Δ32 Sibling Hematopoietic Stem Cell Transplantation*
12:00-12:15	**M05 | Sabina Leanti La Rosa** *Mind the substrate: Microbial degradation of a widely used model polyethylene is restricted to alkanes and their oxidized derivatives*
12:15-12:30	**M06 | Dirk Linke** *A dual-loop chemostat to investigate multi-species biofilms on different materials under adjustable flow conditions*

Minisymposium 2 Structural Biology

Veslefjellhallen 2

Chair: Inari Kursula

11:00-11:15	**M07 | Lisa Reinmuth** *Structural characterization of Collapsin response mediator protein 2 (CRMP2) mutants and their effects on protein dynamics*
11:15-11:30	**M08 | Jin Chuan Zhou** *The schizophrenia associated protein DISC1 is a multivalent tetrameric hub of conserved ancient fold*
11:30-11:45	**M09 | Marta Hammerstad** *The methyltransferase NmbA methylates the low-molecular weight thiol bacillithiol, and displays a specific structural architecture*
11:45-12:00	**M10 | Natalia Mojica** *Why is cholera toxin more toxic than heat-labile enterotoxin? Insights from protein crystallography and MD simulations*
12:00-12:15	**M11 | Ute Krengel** *Allosteric regulation of chorismate mutase*
12:15-12:30	**M12 | Inari Kursula** *Targeting malaria parasite motility by modulating the profilin–actin interaction*

Minisymposium 3 Biochemistry & Molecular Biology

Veslefjellhallen 3 Chair: Aurora Martinez

11:00-11:15	**M13 | Marko Sankala (Merck Life Science)** *Detection of Biomarkers with the Next-Gen FemtoQuest™ System*
11:15-11:30	**M14 | Carine Le Goff** *Reconstructing the evolutionary origins of gap junctions*
11:30-11:45	**M15 | Karl Martin Forbord** *Tankyrase inhibition demonstrates anti-fibrotic effects in preclinical pulmonary fibrosis models*
11:45-12:00	**M16 | Vincenzo Perria** *Recurring roles of BMP-FGF crosstalk in Ciona cardiac development*
12:00-12:15	**M17 | Gloria Gamiz** *Stabilizing Protein Complexes with Pharmacological Chaperones*
12:15-12:30	**M18 | Trond-André Kråkenes** *Mechanistic insights into a pharmacological chaperone targeting phenylalanine hydroxylase disease variants*

Minisymposium 4 Biotechnology, Bioinformatics & Food Science

Veslefjellhallen 1 Chair: Marc Niere

14:15-14:30	**M19 | Marita Gustavsen (Holger Hartmann AS)** *Redefining Imaging Performance: Evident's Next Generation Microscopy Platforms*
14:30-15:45	**M20 | Dominik Frei (Inter Instrument AS)** *ibidi - Tailored Solutions for Cellular Microscopy and Cell-based Assays in 2D and 3D*
15:45-15:00	**M21 | Veronica Quarato** *OmniCorr: A multi-omics integration tool for exploring host-microbiome interactions*
15:00-15:15	**M22 | Veronica F. Blihovde** *Paecilomyces variotii (PEKILO®) in novel feeds for Atlantic Salmon*
15:15-15:30	**M23 | Ana Lucia Campaña Perilla** *Microbial Synthesis of Precious Metal Nanoparticles: mechanisms, characterization, and practical application challenges*

Minisymposium 5 Genetics, Genomics & Immunology

Veslefjellhallen 2

Chair: Valeriia Kalienkova

14:15-14:30	**M24 | Dorota Jaskula** *Genotyping Structural Variants in Regulatory Regions of SIX6, a Major Maturation Gene in Atlantic Salmon*
14:30-15:45	**M25 | Mariel Wictoria Holmen** *Population structure and genomic diversity of semi-domesticated reindeer herds: Implications for breeding strategies to enhance CWD resistance*
15:45-15:00	**M26 | Thea Johanna Hettasch** *Haplotype-resolved genome assemblies for Norwegian Red cattle*
15:00-15:15	**M27 | Ole Kristian Greiner-Tollersrud** *A novel model on the etiology of the autoinflammatory disease DADA2 reveals a role of lysosomal metabolism of macrophages*
15:15-15:30	**M28 | Eirik Sandvik Gulbrandsen** *Changes in the Methylome Following Cladribine and Rituximab Treatment in People with Multiple Sclerosis*

Minisymposium 6 Cancer Biology & Cell Biology

Veslefjellhallen 3

Chair: Pawel Burkhardt

14:15-14:30	**M29 | Deo Pandey** *CDK12/CDK13 inhibition disrupts transcriptional elongation and replication fork progression in glioblastoma*
14:30-15:45	**M30 | Lilith Sian Lee** *The elusive cancer feeder: the intestinal smooth muscle tissue*
15:45-15:00	**M31 | Ole Vidhammer Bjørnstad** *Tankyrase Inhibition Reprograms Melanoma Metastases to Overcome Resistance to PD-1 Blockade*
15:00-15:15	**M32 | Austin James Rayford** *Targeting AXL-mediated immunotherapy resistance mechanisms in the lung tumor microenvironment*
15:15-15:30	**M33 | Henriette Aksnes** *Molecular mechanisms of brain calcification*

M01

Disentangling genetic and dietary impacts on the pig gut microbiome

Aikaterini Katirtzoglou (1), Jorge Langa (2), Nanna Gaun (2), Antton Alberdi (2), Torgeir R Hvidsten (1), Phillip Pope (1,3) and Sabina Leanti La Rosa(1)*

(1) Faculty of Chemistry, Biotechnology and Food Science, Norwegian University of Life Sciences, Ås, Norway.
(2) Center for Evolutionary Hologenomics, Globe Institute, University of Copenhagen, Copenhagen, Denmark
(3) Centre for Microbiome Research, Queensland University of Technology, Brisbane, Australia

Boosting Protein Efficiency (PE) plays a critical role in making swine production more cost-effective while minimizing its environmental footprint. Current strategies to enhance PE focus on amino-acid balancing in feeds and genomic selection of pigs. Given the pivotal role of gut microbiota in modulating nutrient digestibility and overall metabolism in pigs, there is increasing interest in understanding if host genetics influences the gut microbiome, aiming to select pigs that harbor microbiomes conducive to improved efficiency and performance. In this study, we employed shotgun metagenomics to explore the gut microbiome of 48 pigs from high and low estimated breeding value groups (HEBV and LEBV, respectively), which received two diets differing in Standardized Ileal Digestible (SID) Lysine levels (high or low). We reconstructed 1,128 MAGs, encompassing 14 phyla and 300 potentially novel species. Although ordination analyses revealed no clear separation at the broader microbiome level between genetic or diet groups, differential abundance analysis identified 220 and 150 MAGs differing between genetic and diet groups respectively. Functional annotation of the differentially abundant MAGs between LEBV and HEBV pigs highlighted differences in the presence of carbohydrate active enzymes. Co-expression network of differentially abundant MAGs between genetic groups showed three main hubs: a conserved Prevotella-dominated hub, an LEBV-specific Eubacterium-dominated hub, and a HEBV-specific hub with Lachnospirales species. Together, these patterns suggest that pigs with different breeding values may harbor some distinct community types while still sharing a conserved core microbiome structure. This work highlights that host genetics potentially have a pronounced effect in shaping gut microbiome and provides insight that could guide breeding decisions considering both host and microbiome as a single unit.

M02

A deep dive into the genome of bacterial isolates from salmon fry

Dave Rojas Calderon (1), Ronja Marlonsdotter Sandholm (1), Thea Samskott (1), Mia Tiller Mjøs (2,3), Eirik Degré Lorentsen (2), Åsmund Røhr Kjendseth (1), Ingrid Bakke (2) and Sabina Leanti La Rosa (1)

(1) Faculty of Chemistry, Biotechnology and Food Science, Norwegian University of Life Sciences, Ås, Norway.
(2) The Norwegian University of Science and Technology (NTNU), Department of Biotechnology and Food Science, Trondheim, Norway.
(3) Brynsløkken AS, Delitoppen 3, 1540 Vestby.

With the human population expected to reach 9.8 billion by 2050, global seafood demand is predicted to double. In response, aquaculture is quickly expanding, with Atlantic salmon among the most intensively farmed species. While the gut microbiota is known to play an important role in health and growth of some fish, yet its functional role in salmon, particularly in juvenile stages, remains underexplored. This knowledge gap limits the understanding of salmon-microbiota interactions that could otherwise be leveraged in the development of new strategies to enhance salmon well-being and performance. In this study, we isolated and genotypically characterized 11 bacterial strains from the gut of Atlantic salmon fry. Whole-genome sequencing followed by functional annotation showed the broad metabolic versatility of these isolates, including their potential to produce carbohydrate active enzymes, proteases, lipases, and (poly)phenol-degrading enzymes, supporting metabolism of feed component. All isolates carried genes for production of beneficial metabolites, such as short-chain fatty acids (acetate, propionate, lactate), B vitamins, and vitamin K2. Genes encoding bacteriocins and other secondary metabolites were identified, suggesting niche competitiveness against intestinal pathogens. Among them, we show that Lactococcus raffinolactis ASF-5 can metabolize raffinose, an anti-nutrient often found in plant-based feeds derived from legumes, through the activity of a GH36 a-galactosidase and two GH32 sucrases. Safety assessment indicated susceptibility to tested antibiotics and absence of hemolytic activity, supporting its potential as feed supplement. Overall, these findings expand the understanding of how gut bacteria in juvenile salmon may interact with dietary components and their functions that can contribute to salmon health and nutrition. This knowledge could inform microbe-based approaches to improve salmon well-being and resilience in farming systems.

M03

Decoding the Degradation of Gram-Positive Polysaccharides

Gordon Jakob Boehlich, Pascal Mrozek, Ahmad Tsjokajev, Victor Daisuke Kietzmann, Cornelia Rognstad Karlsen, Synnøve Sætervik, Hanna Kristine Hallgren, Emily Catherine Raw Kverndal, Marika Kulseth, Svein Horn, Bjørge Westereng and Gustav Vaaje-Kolstad

Norwegian University of Life Sciences, Faculty of Chemistry, Biotechnology and Food Science, 1433 Ås, Norway

Bacteria produce a wide variety of extracellular and cell-associated polysaccharides that are critical for survival in fluctuating environments. Exopolysaccharides support biofilm formation, water retention, and surface adhesion, while capsular polysaccharides provide protection against immune defenses and physical stress. In Gram-positive bacteria, peptidoglycan together with diverse cell wall polysaccharides, and teichoic acid glycopolymers, form a robust yet dynamic envelope. New structural and functional features of these polymers continue to emerge, but their ecological turnover remains poorly understood. In particular, little is known about how these biopolymers are degraded in natural microbial communities or how such degradation influences e.g. gut or soil microbiota.
Here, we describe the extraction, purification, and structural characterization of exopolysaccharides, cell wall polysaccharides, and wall teichoic acids from Gram-positive bacteria, many of which have not been described before. Using targeted microbial enrichment strategies, we have isolated bacteria capable of degrading these polymers and applied genomic and proteomic analyses to identify candidate pathways and enzyme systems involved in their deconstruction. Functional expression and biochemical characterization of selected enzymes revealed novel hydrolases and lyases mediating both endo- and exo-acting depolymerization. These enzymes enabled the production of structurally defined oligosaccharides for kinetic analysis and glyco-conjugation chemistry. The latter, enabled generation of fluorescently labeled oligosaccharides that allowed visualization of carbohydrate uptake and metabolism in bacterial isolates. Collectively, our findings advance understanding of the structural diversity and ecological fate of Gram-positive polysaccharides and glycopolymers and provide new enzymatic tools for glycobiology and microbiological research.

M04

"The Oslo Patient": Sustained HIV Remission Five Years After CCR5Δ32/Δ32 Sibling Hematopoietic Stem Cell Transplantation

Anders Eivind Myhre (1), Malin Holm Meyer-Myklestad (2,3), Hanne Hestdal Gullaksen (3,4), Ole S. Søgaard (5,6), Martin Tolstrup (5,6), Maria Salgado (7,8,9), Javier Martinez-Picado (7,8,9,10,11), Anne-Marte Bakken Kran (2,12), Dag Henrik Reikvam (3,4), Pål Aukrust (4,13,14), Tobias Gedde-Dahl(1,4), Tuva Børresdatter Dahl(13), Marius Trøseid (4,13,14), and Mari Kaarbø (2)

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(2) Department of Microbiology, Oslo University Hospital, Oslo, Norway.
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(4) Institute of Clinical Medicine, University of Oslo, Oslo, Norway.
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(6) Department of Clinical Medicine, Aarhus University, Aarhus, Denmark.
(7) IrsiCaixa, Badalona, Barcelona, Spain.
(8) Germans Trias i Pujol Research Institute, Badalona, Barcelona, Spain.
(9) CIBERINFEC, Instituto de Salud Carlos III, Madrid, Spain.
(10) University of Vic–Central University of Catalonia (uVic-UCC), Vic, Spain.
(11) Catalan Institution for Research and Advanced Studies (ICREA), Barcelona, Spain.
(12) Norwegian Institute of Public Health, Oslo, Norway.
(13) Research Institute of Internal Medicine, Oslo University Hospital, Oslo, Norway.
(14) Section of Clinical Immunology and Infectious Diseases, Department of Rheumatology, Dermatology and Infectious Diseases, Oslo University Hospital, Oslo, Norway.

A small number of allogeneic hematopoietic stem cell transplants (allogeneic HSCT) from donors who are homozygous for the CCR5Δ32 mutation (CCR5Δ32/Δ32) have led to sustained remission of HIV. We report a new addition to this group: “the Oslo patient”, a man over 60 who remains in HIV remission five years after receiving an allogeneic HSCT from his human leukocyte antigen–identical (HLA-identical) CCR5Δ32/Δ32 sibling donor. Transplanted for myelodysplastic syndrome, he achieved rapid and complete donor chimerism in peripheral blood and, importantly, full replacement of gut-associated lymphoid tissue (GALT)—the primary site of persistent HIV. After developing severe graft-versus-host disease (GvHD) of the gut and skin, he discontinued antiretroviral therapy (ART) 24 months post-transplant. During a subsequent 24-month analytical treatment interruption (ATI), plasma HIV RNA remained undetectable. Extensive virologic and immunologic assessments—including the intact proviral DNA assay (IPDA) and droplet digital PCR (ddPCR) of blood and gut samples, quantitative viral outgrowth assays (qVOA) using 65 million CD4-positive T cells, and serial measurements of HIV-specific T-cell and antibody responses—showed no intact proviruses, no replication-competent virus, and a steady decline in HIV-specific immunity. This represents the first known case of HIV remission following allogeneic HSCT from a sibling donor in someone of this age and is among the most comprehensively studied to date. The convergence of a CCR5-null donor graft, deep donor chimerism within GALT, prolonged GvHD activity, and possible reservoir-modulating effects of Janus kinase inhibitor (JAK inhibitor) therapy provides compelling new evidence for mechanisms that may underpin durable HIV cure.

M05

Mind the substrate: Microbial degradation of a widely used model polyethylene is restricted to alkanes and their oxidized derivatives

Ronja Marlonsdotter Sandholm (1), Gordon Jacob Boehlich (1), Ørjan Dahl (1), Ravindra R. Chowreddy (2), Anton Stepnov (1), Gustav Vaaje-Kolstad (1) and Sabina Leanti La Rosa (1)

(1) Faculty of Chemistry, Biotechnology and Food Science, Norwegian University of Life Sciences, Ås, Norway
(2) Norner Research AS, Porsgrunn, Norway

Plastics are among the most extensively utilized materials worldwide, yet their inherent chemical stability limits biodegradation, contributing to escalating global pollution. To address this challenge, plastic-degrading microorganisms and their enzymes offer promising avenues for the development of biotechnological recycling strategies. In this context, soils contaminated with plastic waste may serve as rich reservoirs of yet-undiscovered plastic-transforming microorganisms. In this study, we enriched two microbial communities from soil collected at a plastic-polluted site in Flisa (Norway) to select for bacteria involved in the degradation of a widely used model polyethylene (low-molecular-weight polyethylene, LMWPE). Using genome-resolved metatranscriptomics, we identified metabolically active populations related to Acinetobacter guillouiae and Pseudomonas sp., which exhibited upregulation of genes encoding alkane 1-monooxygenases, Baeyer–Villiger monooxygenases, and cytochrome P450 monooxygenases with functions compatible with degradation of medium- and long-chain hydrocarbons and their oxidized derivatives. Unexpectedly, in-depth spectroscopic, spectrometric, and chromatographic analyses revealed that the LMWPE substrate contained medium (C10–16) and long-chain (C17–34) alkanes and 2-ketones, preventing misinterpretation that the polymer itself was being degraded by the microbial consortia. Consistent with this finding, an A. guillouiae isolate selectively degraded alkanes and ketones ranging from C10–27, as confirmed by proteomics and substrate characterization post-growth. Beyond expanding our understanding of the enzymatic repertoire of soil microbes for processing alkanes and ketones, likely originating from abiotic oxidation of LMWPE, this work provides a refined compositional analysis of a widely used substrate and delivers critical insights for future efforts aimed at conclusively identifying organisms and enzymes involved in polyethylene transformation.

M06

A dual-loop chemostat to investigate multi-species biofilms on different materials under adjustable flow conditions

Jan-Ole Reese (1), Ingrid Maria Castro Lund (1), Håvard Jostein Haugen (2,3), Athanasios Saragliadis (1), Ståle Petter Lyngstadaas (2,3) and Dirk Linke (1)

(1) Department of Biosciences, UiO
(2) Department of Biomaterials, UiO
(3) Corticalis AS

Natural biofilms are typically composed of a mix of different microbial species and are often exposed to strong shear forces resulting from liquid flow. Simple biofilm models that attempt to study biofilms are based on a single species and on static growth conditions. To overcome these limitations, we developed a modular dual-loop reactor that decouples bacterial cultivation from hydrodynamic exposure, enabling independent control of nutrient availability (and thus, cell density) and flow rate (and thus, shear stress). Importantly, the system allows for testing different surface materials in a systematic manner.

To validate our setup, we used a community of six keystone members of oral biofilms in conjunction with titanium materials of defined roughness that mimic dental implant surfaces. We found that biofilm mass, robustness, and species distribution not only differ significantly between static and dynamic growth conditions, but also vary strongly with different flow velocities. The biofilms formed under flow could be separated into two fractions, one that washed away very easily, and a more robust, basal layer. At low shear forces, overall biofilm mass was the highest, but at the expense of biofilm robustness. At medium shear forces, the robust fraction of the biofilm had the highest relative content of extracellular matrix. At the highest flow rates, the biofilm mass was low, but late colonisers (represented by the oral pathogens Porphyromonas gingivalis and Aggregatibacter actinomycetemcomitans) had the lowest relative abundance. This is in accordance with the concept that high flow of saliva reduces the risk of oral disease. Future applications of our system will include the systematic testing of antimicrobial coatings or surface design effects under defined flow regimes, opening the path towards better medical implants.

References: Reese at al, submitted
Funding: RCN Projects MISFAITH and DEBRIGEL (to HH, SPL, DL)
Advanced characterization techniques, including TEM, EDX, AFM, TGA, and FTIR, were employed to analyze NP composition, morphology, size distribution, and surface properties. Based on these analyses, comparative studies demonstrated that genetic modifications influence metal uptake and enhance the efficiency and selectivity of NP synthesis. In addition, catalytic activity tests showed that biosynthesized palladium NPs exhibited performance comparable to commercial nanocatalysts. Building on these results, purification strategies to remove residual biological molecules were also evaluated, highlighting practical challenges for industrial and biomedical applications.
Overall, these findings underscore the potential of microbial systems as a sustainable platform for the synthesis of metal NPs with high catalytic efficiency, paving the way for scalable production and their use in diverse industries.

M07

Structural characterization of Collapsin response mediator protein 2 (CRMP2) mutants and their effects on protein dynamics

Lisa Reinmuth (1), Anne Baumann (1), Petri Kursula (1)

(1) Department of Biomedicine, University of Bergen, Norway

Collapsin response mediator protein 2 (CRMP2) is an important scaffolding protein involved in neuronal growth and excitability. Several post-translational modifications are associated with a variety neurological disorders, including Alzheimer's, Bipolar disorder and Epilepsy. To study disease mechanisms and develop targeted treatment options, understanding of protein behaviour is important.

In this project, I created a set of mutants to study protein oligomerization and post-translational modification mimicries, looking at structural integrity and potential drug interactions. This platform should help overcome discrepancies arising from the transfer between complex cells and organisms to a simplified system. It allows selected targeting of important protein states. The structural characterization highlighted distinctive effects of two phospho-mimicking mutants. Additionally, a protein segment of about 10 amino acids could be identified, which is crucial for the self-interaction behaviour. This has a strong effect on the availability of binding sites for protein protein or drug interactions. Thus, further steps include utilizing this set of mutants in small molecule and peptide development.

M08

The schizophrenia associated protein DISC1 is a multivalent tetrameric hub of conserved ancient fold

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Disrupted in Schizophrenia 1 (DISC1) is a pleiotropic protein that plays essential roles in neuronal proliferation and migration, intracellular signalling and cargo transport. In these contexts, DISC1 associates with a wide range of partner molecules. Mutations at the DISC1 locus are strongly linked to a spectrum of mental illnesses, including schizophrenia and depression. Despite its clinical relevance, the molecular architecture and function of DISC1 have remained poorly understood for decades.

Here, we present an unpublished cryo-electron microscopy structure of the entire conserved core region of DISC1. The structure reveals an intricate homotetrameric assembly centered on four copies of conserved, bacteria-derived UVR domains. These domains exhibit a strikingly conserved dimerization function that extends beyond the prokaryotic kingdom. Supporting this notion, our combined structural and biochemical analysis highlight the critical contribution of UVR dimers to complex stability in metazoan DISC1.

Notably, this oligomerization capacity is strongly predicted to be conserved across DISC1 homologues, including those found in simple flagellated organisms such as Monosiga brevicollis and Trypanosoma brucei. Consistent with the role of DISC1 as a cytoskeletal regulator, mutational analysis demonstrate that the tetrameric architecture enables DISC1 to simultaneously coordinate multiple copies of the centrosomal protein NDE1. Importantly, tetramerization and partner binding represent structurally independent functions of DISC1.
Together, our findings provide key structural evidence supporting an ancient evolutionary origin and a conserved scaffolding function for this mammalian protein implicated in schizoaffective disorders.

M09

The methyltransferase NmbA methylates the low-molecular weight thiol bacillithiol, and displays a specific structural architecture

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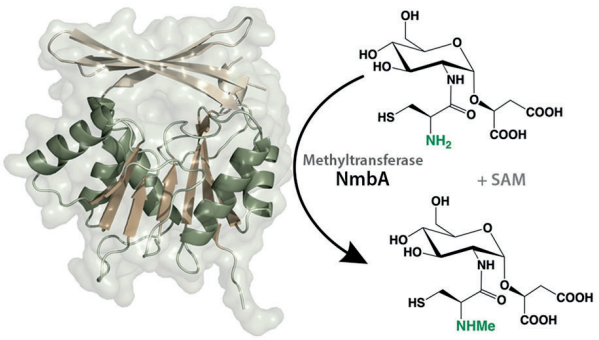
Low-molecular-weight (LMW) thiols maintain the cellular redox balance and protect cells against reactive species, heavy metals, toxins, and antibiotics. Despite having similar metabolic functions, structurally distinct LMW thiols are widespread in nature, with bacillithiol (BSH) being the predominant LMW thiol in bacteria. The LMW thiol N-methyl-BSH (N-Me-BSH) has been identified in the green sulfur bacterium Chlorobaculum tepidum, revealing the presence of a putative S-adenosyl-l-methionine (SAM)-dependent methyltransferase (MT), NmbA, which could catalyze the final biosynthetic step of N-Me-BSH. In this study, we report biochemical evidence for NmbA´s specific function as an MT of the N-atom of the BSH cysteine moiety. We also present the crystal structure of NmbA, confirming that NmbA is a Class I SAM-dependent MT, however, displaying a unique three-dimensional architecture that differs from those of other natural product MTs (NPMTs). The NmbA active site has a narrow molecular basket structure resulting from an unusual organization of the variable Cap domain, and our docking calculations suggests that it can specifically accommodate the BSH substrate. Our research provides a valuable overview of the phylogenetic distribution of N-Me-BSH in bacteria, alongside essential functional and structural insight into a new class of N-directed NPMTs. These findings contribute to the field of SAM-dependent MTs and may allow for targeting distinct bacterial defense mechanisms involving LMW thiols with potential environmental, biotechnological, and medical implications.



M10

Why is cholera toxin more toxic than heat-labile enterotoxin? Insights from protein crystallography and MD simulations

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Cholera toxin (CT) and heat-labile enterotoxin (LT) are two similar AB_5 toxins responsible for the diarrhea characteristic of Vibrio cholerae and enterotoxigenic Escherichia coli (ETEC) infections. They consist of a catalytically active A1 subunit, an A2 linker, and a pentamer of cell-binding B-subunits[1]. Both toxins bind to the same receptor on the host cells and have similar levels of enzymatic activity, yet CT is more potent than LT, making cholera the more severe disease. The difference in toxicity has been attributed to structural differences near the C-terminus of the A2 linker (amino acid residues 226-236)[2], but the underlying molecular mechanism remains unknown. Recently, we showed that toxin disassembly by protein disulfide isomerase (PDI), which is a key event in the intoxication process, is more efficient for CT than for LT[3].

Here, we investigated how substitutions in the critical A2 linker region affect toxin potency and PDI-driven disassembly. We obtained the crystal structures of two CT variants, where either one or four residues in the A2 region were substituted for the corresponding residues in LT, and carried out molecular dynamics (MD) simulations. Our results suggest that characteristic A2 residues affect the flexibility of the toxins, which may play an important role in their resulting toxicity.

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M11

Allosteric regulation of chorismate mutase

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Chorismate mutase (CM) is a model enzyme, which I have been investigating together with the group of Dr. Peter Kast (ETH Zurich) for over 25 years. CM is a central enzyme of the shikimate pathway, which directs the synthesis of aromatic amino acids towards Tyr and Phe (and away from Trp). There are two major CM families, AroQ and AroH, with several subfamilies and distinct structures. Especially intriguing is the $AroQ_{delta}$ CM family, which has low activity on its own, but can be boosted to full activity by DAHP synthase (DS), a partner enzyme in the same pathway.[1] Even more intriguing is the fact that these CMs are feedback-regulated by aromatic residues binding on DS – far away from CM – by inter-enzyme allostery.[2,3] (Fig. 1; credit: Joel Heim). The low natural activity of $AroQ_{delta}$ CMs provided a unique chance to enhance their performance by directed evolution.[4] Here, I will present our latest results of this SNF-funded project.

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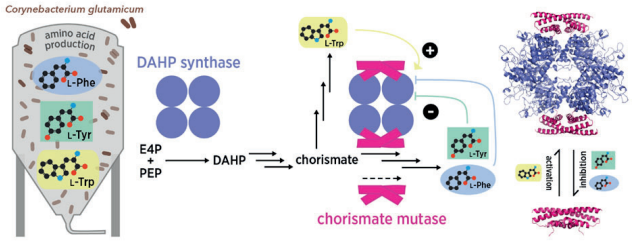

M12

Targeting malaria parasite motility by modulating the profilin–actin interaction

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Motility is essential for malaria parasite survival and pathogenicity, enabling host cell invasion and transmission between hosts. Compared to most other eukaryotes, malaria parasites rely on a highly reduced and divergent actin cytoskeleton, supported by an unusually limited set of actin regulatory proteins. This streamlined system provides a unique opportunity to dissect fundamental mechanisms of actin-based motility while simultaneously identifying parasite-specific vulnerabilities.

Here, I will focus on profilin, a central regulator of actin dynamics and one of the earliest characterized components of the malaria parasite actin regulatory machinery. Nearly two decades of work have revealed how parasite profilin differs structurally and functionally from its human counterpart, how it interacts with parasite actin, and how this interaction underpins force generation during gliding motility. Recently, we have explored the profilin–actin interface as a potential drug target. Small-molecule compounds from the Medicines for Malaria Venture (MMV) collection selectively modulate the parasite profilin–actin interaction, impairing actin polymerization and parasite motility without affecting the human system. By combining structural biology, biochemical assays, resistance mutation analysis, and fragment-based screening, we are beginning to define the molecular basis of compound action and resistance.

Our work illustrates how fundamental studies on parasite cytoskeletal biology can inform drug design strategies. Modulating the profilin–actin interaction emerges as a promising approach for selectively targeting malaria parasite motility and host cell invasion, highlighting actin regulation as a viable avenue for antimalarial drug development.

M13

Detection of Biomarkers with the Next-Gen FemtoQuest™ System

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FemtoQuest™, powered by SMC® technology, offers femtogram-level sensitivity for protein detection, enabling earlier disease detection, enhanced biomarker validation, and improved cohort differentiation. Its dual-plex capability reduces sample requirements while delivering reliable and reproducible results. The AAW™ workstation integrates seamlessly with FemtoQuest™, automating workflows to improve precision, scalability, and consistency, while minimizing hands-on time. With over 50 validated kits across key research areas such as neuroscience, inflammation, and cardiovascular research, FemtoQuest™ sets a new benchmark for sensitivity, efficiency, and versatility in biomarker research

M14

Reconstructing the evolutionary origins of gap junctions

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Cell-cell communication is a fundamental feature in multicellular organisms, enabling coordination and integration of physiological processes. In addition to chemical synapses, electrical synapses mediated by gap junctions play a key role in rapid signal transmission and cellular synchronization. Gap junctions are clusters of intercellular channels that permit direct cytoplasmic exchange of ions and small molecules between adjacent cells. While the structure, expression and function of gap junctions are well-characterized in many metazoans, their evolutionary origin, molecular composition and functional roles remain poorly understood. Using multiplexed Hybridization Chain Reaction (HCR) and immunostaining, we analyzed the full complement of innexins responsible for forming gap junctions in an early diverging animal lineage. We characterized the spatial and temporal expression patterns across multiple developmental stages of the ctenophore Mnemiopsis leidyi. We found that two innexins are broadly expressed in the whole organism, whereas others exhibit highly restricted cell-type specific expression. Notably, we characterized innexins expression in the aboral organ, a major integration center, and in the comb cells involved in locomotion. Moreover, two innexins are highly specific to the nervous system. In parallel, we predicted post-translational modifications, such as glycosylation, that may prevent gap junction formations. These findings allow us to predict which innexins are likely to function as hemichannels or as gap junctions. Our results provide key insights into the intercellular communication and neural circuitry in ctenophores, and provide novel information about the nervous system origins.

M15

Tankyrase inhibition demonstrates anti-fibrotic effects in preclinical pulmonary fibrosis models

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Idiopathic pulmonary fibrosis (IPF) is a progressive and fatal lung disease with limited therapeutic options. Although transforming growth factor beta 1 (TGFB1, TGFβ) is a central driver of fibrosis, additional pathways, including Wingless/INT-1 (WNT)/β-catenin and yes-associated protein 1 (YAP), contribute to IPF pathogenesis, and inhibition of TGFβ alone has shown limited efficacy. Tankyrase (TNKS) 1 and 2, post-translational regulators of WNT/β-catenin and YAP signaling, therefore represent promising antifibrotic targets. OM-153, a potent and selective TNKS inhibitor, was evaluated across primary human lung fibroblasts, Scar-in-a-Jar assays, lung-on-a-chip models, and precision-cut lung slices (PCLS) stimulated with an IPF-relevant cytokine cocktail or TGFβ, as well as in bleomycin-challenged mice and PCLS from end-stage pulmonary fibrosis donors. OM-153 stabilized the TNKS substrates axin 1 (AXIN1) and angiomotin-like 1 (AMOTL1), suppressed WNT/β-catenin and YAP signaling, and reduced profibrotic extracellular matrix synthesis and deposition in vitro, in vivo, and ex vivo. These findings support selective TNKS inhibition as a mechanistically distinct antifibrotic strategy with translational potential for IPF.

M16

Recurring roles of BMP-FGF crosstalk in Ciona cardiac development

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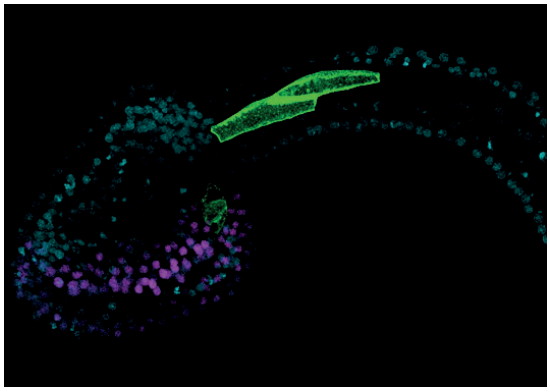
Heart development requires precise coordination between cell fate specification and cellular behaviours such as migration and oriented cell division. BMP and FGF signalling are central to cardiogenesis across species, yet how their interaction governs these processes at successive stages remains poorly understood.

The cardiopharyngeal lineage of Ciona offers a versatile model to address this question with single-cell resolution. The lineage arises from two founder cells per side, which undergo successive asymmetric divisions and collective migration, giving rise to heart and pharyngeal muscle.
We find evidence that BMP-SMAD signalling acts recurrently within this lineage, alternating between cell-autonomous and non-cell-autonomous modes, and between antagonistic and permissive relationships with FGF-MAPK.

Following founder cell asymmetric division, the rostral daughter cells are induced by FGF-MAPK into cardiac progenitor fate while sister cells adopt tail muscle identity. Here, BMP appears to act cell-autonomously, likely dampening FGF-mediated transcriptional responses: BMP inhibition via Noggin or Smad6 produces supernumerary cardiac progenitors at the expense of tail muscle.

Cardiac progenitors migrate collectively as polarised leader-trailer pairs toward the ventral midline. During migration, FGF-MAPK activity likely suppresses BMP-SMAD signalling, maintaining multipotency. Concurrently, BMP plays a non-cell-autonomous role in orienting migration: Noggin or DMH1 disrupts pair alignment and ventral convergence, whereas Smad6 does not, suggesting an extrinsic BMP cue. After migration, progenitors divide again: lateral daughters receive FGF-MAPK and remain multipotent, while medial daughters, lacking FGF, activate cardiac genes in a BMP-permissive context.

Our findings highlight the context-dependent, recurring roles of BMP-SMAD signalling, offering a framework for understanding how BMP-FGF crosstalk coordinates cardiac development.



M17

Stabilizing Protein Complexes with Pharmacological Chaperones

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Protein-protein interactions are essential for numerous cellular processes, yet many diseases arise from misfolding or instability of one or more of the proteins in the formed complexes. Pharmacological chaperones are small molecules that selectively bind to and stabilize target proteins, helping them achieve or maintain their correct conformation. This approach offers a promising strategy to restore the function of destabilized protein complexes implicated in several disorders. In this study, we used a high-throughput screening to identify pharmacological chaperones that stabilize the interaction between Tyrosine Hydroxylase (TH) and DNAJC12 (TH:DNAJC12 complex). TH is the rate-limiting enzyme in the synthesis of dopamine and mutations in TH produce TH deficiency (THD), a rare genetic disorder characterized by severely low dopamine levels. Patients with THD present a wide spectrum of symptoms, from dopa-responsive dystonia and parkinsonism to severe encephalopathy. The HSP40 cochaperone protein DNAJC12 has recently been shown to preserve the stability of TH in vitro and in vivo, and is also linked to parkinsonism when mutated. We therefore hypothesized that the loss conformational integrity of TH might be compensated by stabilizing the TH:DNAJC12 complex, positioning this interaction as a promising and innovative therapeutic target for the development of mechanistic treatments for parkinsonisms, Through the compound screening and concentration-dependent stability and activity analyses, as well as experimental and computational structural characterizations, we identified diflunisal as a pharmacological chaperone that stabilizes the TH:DNAJC12 complex, prevents TH aggregation, and preserves TH enzymatic activity and regulation, making it a promising candidate in THD and related disorders. This approach may also be adapted to other diseases associated with protein misfolding and proteostasis dysregulation.

M18

Mechanistic insights into a pharmacological chaperone targeting phenylalanine hydroxylase disease variants

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Phenylketonuria (PKU) is an inborn metabolic disorder caused by variants in phenylalanine hydroxylase (PAH), leading to neurotoxic accumulation of L-phenylalanine (Phe) and neurocognitive impairment if left untreated. Current therapy relies on strict dietary restrictions and limited pharmacological options, highlighting the need for disease-modifying strategies. Hit1, a lead pharmacological chaperone in preclinical evaluation, lowers Phe levels in human cell lines expressing PAH missense variants. The effect of Hit1 was further assessed in a mouse model homozygote for the second most frequent PAH missense variant PAH-p.R261Q, which confers approximately 15% residual enzyme activity and results in a moderate to severe PKU phenotype. Hit1 was nominated as our lead candidate after demonstrating significant Phe-lowering effect in this mouse model. To advance the mechanistic understanding of PAH proteostatic regulation by Hit1, we characterized its binding mode and stabilizing effect using biophysical and computational approaches. Our results indicate that Hit1 binds interdomain sites within the PAH tetramer and stabilizes the protein structure, consistent with increased PAH protein levels and enzymatic activity observed in cellular and animal models. Together, these findings highlight Hit1 as a promising pharmacological chaperone for PKU therapy.

M19

Redefining Imaging Performance: Evident's Next Generation Microscopy Platforms

Marita Gustavsen

Holger Hartmann AS, Langhus, Norway

Recent advances in microscopy are redefining what is possible in biological imaging. This presentation introduces Evident's (former Olympus) next-generation microscope systems — highlighting how new optical designs, speed and system flexibility enable more robust, quantitative and dynamic life science research.

M20

ibidi - Tailored Solutions for Cellular Microscopy and Cell-based Assays in 2D and 3D

Dominik Frei

Inter Instrument AS

Advanced cellular microscopy and cell-based assays increasingly demand experimental systems that are physiologically relevant, reproducible, and compatible with high-resolution imaging. ibidi develops and manufactures precision-engineered labware designed to meet these challenges, offering tailored solutions for cell culture, live-cell microscopy, and quantitative analysis in both 2D and 3D environments. This presentation will highlight how ibidi's standardized yet flexible platforms—ranging from imaging chambers and microfluidic systems to 3D culture and organoid formats—enable controlled experimental conditions, improved data quality, and seamless integration with modern microscopy techniques. Selected application examples will illustrate how these tools support studies of cell growth, migration, and tissue-like organization, helping bridge the gap between in vitro models and physiological relevance.

M21

OmniCorr: A multi-omics integration tool for exploring host-microbiome interactions

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Despite growing evidence that host-microbiome interactions shape key traits, animals and their microbiomes are not yet routinely considered as integrated biological units. Hologenomics, the combined analysis of host and microbial genetic features, offers a promising approach to study these systems more holistically. In line with this, holo-omics uses multiple omics datasets to explore interactions between hosts and their microbiomes. Although the generation of host and microbiome omics data is rapidly increasing, there remains a lack of computational tools for integrating and visualizing these data in ways that facilitate the prediction and interpretation of host-microbiome interactions. To address this gap, we developed OmniCorr, an R package for multi-omics data integration. OmniCorr manages the complexity of omics data by grouping co-varying features such as genes, proteins, and metabolites into biologically meaningful modules, and explores correlations among these modules across different omics layers, host-microbiome interfaces, and associated metadata, while also highlighting statistically significant associations that may reflect underlying host-microbiome interactions. We demonstrate the utility of OmniCorr using two datasets from distinct biological systems: a cattle dataset that links host proteomics with metaproteomics to investigate methane emission variability, and a pig dataset combining metabolomics and metagenomics to examine how dietary lysine levels influence growth in animals with differing genetic potentials for nitrogen efficiency.

OmniCorr is freely available at GitHub: https://github.com/shashank-KU/OmniCorr.

M22

Paecilomyces variotii (PEKILO®) in novel feeds for Atlantic Salmon

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Globally, aquaculture is the fastest growing food-producing sector and an important contributor to food security. Norway is one of the world's leading producers of farmed fish, with salmon farming being Norway's second largest export industry. The rapid development of the aquaculture industry has increased the need to focus on the socio-economic impact, circularity, and sustainability of aquafeeds.

This increased requirement for sustainable alternative feed ingredients has led us to research on microbial ingredients, such as bacteria, yeast, microalgae, and fungi, which are showing promise in salmon feeds. Microbial ingredients have the capacity to convert low-value, non-food organic waste streams from forestry, agriculture, and food manufacturing industries into high-value nutrients with a low carbon footprint and with less dependency on arable land, water, and changing climatic conditions than plant-based protein sources. The mycoprotein Paecilomyces variotii (PEKILO®) is based on residual raw material from spruce trees, and has a high crude protein content (approx. 65%), and a beneficial amino acid composition for Atlantic salmon.

Our experiments show that dietary inclusion of P. variotii, replacing 5% to 20% of the crude protein content, in feeds for Atlantic salmon reared in freshwater for a 9-week period, gives a high feed intake, good growth and better feed utilization, in addition to a lower climate footprint and positive effects on fish health. Analysis of the distal intestine shows that dietary inclusion of P. variotii improves gut health and suggests both activation and control of the inflammatory response through significant upregulation of several cytokines (ifng, il10, and tgfb), effector molecules (inos, arg1, sod) and transcription factors (irf4) in this key mucosa-associated lymphoid tissue. Thus, P. variotii is a promising alternative ingredient in salmonoid aquafeeds with both beneficial effects on fish performance and health.

M23

Microbial Synthesis of Precious Metal Nanoparticles: mechanisms, characterization, and practical application challenges

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Bacteria possess sophisticated mechanisms that enable the reduction of toxic metal ions into nanoparticles (NPs), providing a sustainable alternative to conventional chemical and physical synthesis methods. In this context, microbial-metal interactions offer a versatile platform for eco-friendly production of precious metal NPs, including palladium and alloys containing iron, gold, platinum, copper, and silver. Here, we explore the microbial synthesis of metal NPs using wild-type and genetically engineered Escherichia coli strains to optimize the production for industrial-scale applications through process refinement, while simultaneously elucidating the mechanisms underlying bacterial metal reduction. When exposed to metal ion solutions, the cells produced NPs localized across different cellular regions, typically under 5 nm in size.

Advanced characterization techniques, including TEM, EDX, AFM, TGA, and FTIR, were employed to analyze NP composition, morphology, size distribution, and surface properties. Based on these analyses, comparative studies demonstrated that genetic modifications influence metal uptake and enhance the efficiency and selectivity of NP synthesis. In addition, catalytic activity tests showed that biosynthesized palladium NPs exhibited performance comparable to commercial nanocatalysts. Building on these results, purification strategies to remove residual biological molecules were also evaluated, highlighting practical challenges for industrial and biomedical applications.

Overall, these findings underscore the potential of microbial systems as a sustainable platform for the synthesis of metal NPs with high catalytic efficiency, paving the way for scalable production and their use in diverse industries.

M24

Genotyping Structural Variants in Regulatory Regions of SIX6, a Major Maturation Gene in Atlantic Salmon

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Maturation is a pivotal event in the life history of Atlantic salmon (Salmo salar) regulating the timing of migration from the sea to freshwater rivers for spawning. This trait shows marked variation; genome wide association studies (GWAS) identified two major loci, one of which fine mapped to a region on chromosome 9 containing the SIX6 gene. Associated SNPs are either synonymous in CDS or in regulatory regions outside SIX6, making them unlikely to be causal. Structural variants (SVs) are known to alter regulatory architecture, often occurring in high linkage disequilibrium with tag SNPs, motivating our search for SVs in the regulatory regions of SIX6. Further, we sought to identify effective methods for genotyping variation that account for historical whole-genome duplications in the Atlantic salmon genome. Using genome assemblies of individuals with known genotypes at associated loci, we identified three SVs, two deletions and one insertion, overlapping a CpG island located upstream of SIX6. Assembly of 16 phased regional contigs confirmed the initial detection of both a deletion and nearby insertion linked with tag SNPs from the GWAS. To explore population-level frequencies of these SVs and the haplotype structure we constructed a regional genome graph and performed short-read genotyping in an aquaculture population, offering initial insight into haplotype diversity and method feasibility. In parallel, we developed a PCR-based assay targeting these SVs in individuals with known genotypes. Preliminary results demonstrate clear genotype-specific size differences on agarose gels, validating the concept for further genotyping. These findings suggest that SVs linked to SIX6 may contribute to the regulation of maturation timing and provide a foundation for downstream identification of causal variants. Ongoing work will refine graph-based genotyping and expand PCR assays, laying the groundwork for mechanistic and functional studies of these potentially causal variants.

M25

Population structure and genomic diversity of semi-domesticated reindeer herds: Implications for breeding strategies to enhance CWD resistance

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The first European case of Chronic wasting disease (CWD) was confirmed in a wild reindeer (Rangifer tarandus tarandus) in Norway in 2016. Since then, 20 more cases have been reported in wild reindeer. The potential expansion of CWD in wild populations and transmission to semi-domesticated reindeer is a major concern. Specific genetic variants in the prion protein gene reduce an individual's CWD susceptibility. This study aims to investigate the potential of breeding for CWD resistance in semi-domesticated reindeer herds to enhance herd resilience. Selection for resistance may reduce overall genetic variation, a critical first step is therefore to evaluate the existing genetic diversity within and across herds. A high-quality reference genome was assembled using whole-genome sequencing data generated with Oxford Nanopore technology. To explore population-level variation, 177 semi-domesticated reindeer representing five different herds were whole-genome re-sequenced using Illumina short-read technology. These sequences were aligned to the newly assembled reference and used to genotype genetic variants. We found 17 million single nucleotide polymorphisms and short indels. Multidimensional scaling analysis revealed clear population structure across herds, with all herds showing significant clustering (PERMANOVA $p<0.001$). However, there was low genetic differentiation between herds (F_{ST} <0.01). Heterozygosity analysis revealed no indications of population substructure or non-random mating within herds, and runs of homozygosity revealed no significant recent inbreeding. Together these analysis shows small genetic differentiation among five semi-domesticated reindeer herds. Nevertheless, they are genetically distinct and display little signs of inbreeding which may indicate that selective breeding for CWD resistance is possible without reducing overall fitness.

M26

Haplotype-resolved genome assemblies for Norwegian Red cattle

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Norwegian Red (NR) cattle are the main dairy breed in Norway, bred according to a broad breeding goal including health and fertility since the 1970s. Genomic studies on NR cattle have relied on the public cattle reference, which is based on the Hereford breed, thus increasing the risk of missing or misrepresenting NR breed-specific variation. Moreover, the public cattle reference is a pseudohaploid assembly, representing homologous chromosomes in a collapsed manner, which results in loss of haplotype-specific alleles and misrepresentation of complex variants. To develop more refined NR specific resources, we utilised long-read sequencing (PacBio HiFi + ONT) and trio-binning to construct six new haplotype-resolved assemblies representing NR genomes. All six haplotypes show high contiguity (N50 > 73 Mbp) and completeness (BUSCO > 95%). Counting the number of haplotype-specific k-mers in the final assemblies shows that only a small fraction [0.46 – 2.52%] are found in the wrong haplotype, suggesting successful separation of offspring sequences into haplotypes. Most autosomes have been assembled to include the acrocentric centromeres, and mapping of bovine satellite sequences reveal distinct organisational patterns of different satellite units across these highly repetitive regions. The NR2025 assemblies can be further combined into an NR pangenome, providing a valuable resource for identification of novel variants and haplotypes in the NR population. The NR pangenome will enable more accurate association studies of genotype-to-phenotype relations and genomic predictions in NR cattle, ultimately enhancing the efficacy of selection for desirable traits.

M27

A novel model on the etiology of the autoinflammatory disease DADA2 reveals a role of lysosomal metabolism of macrophages

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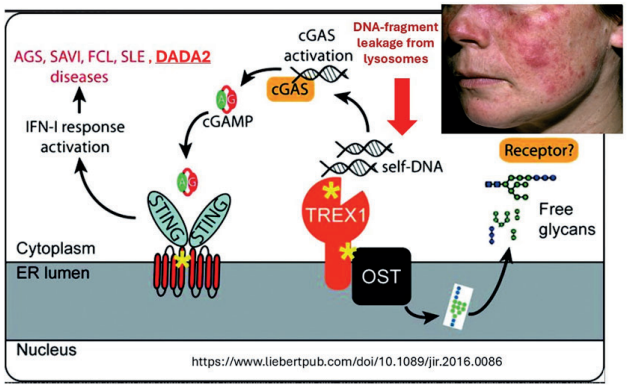
In bioscience today there is a general assumption that basic knowledge and principles have been achieved. Further research should focus on using the knowledge as a fundament for basic science and in developing diagnostics and therapy to combat diseases, thus improving the quality of life and life span in an increasingly older human population. Although funding agencies often emphasize prioritizing "groundbreaking", "risky" and "gamechanging" projects the reality is that funding is skewed towards already established projects and ideas. In the research of the etiology of the autoinflammatory disease DADA2 (Deficiency of Adenosine DeAminase 2) the acclaimed and published models are built on established knowledge. Nevertheless, none of these models can explain adequately the spectra of clinical phenotypes in DADA2 patients. My research has shown that a novel model that breaks with current knowledge is the only way to unravel the etiology of DADA2. This involves 1) changing the location and physiological function of ADA2 from blood plasma to macrophage lysosomes. 2) changing the physiological function of ADA2 from deamination of free adenosine to DNA binding and modification 3) a novel mechanism of inflammation initiation in macrophages by the leakage of DNA fragments through the lysosomal membrane. This model has profound implications on the role of lysosomal metabolism in inflammation initiation, and thus our understanding of the etiologies of several inflammatory diseases.



M28

Changes in the Methylome Following Cladribine and Rituximab Treatment in People with Multiple Sclerosis

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Background: The prognosis of multiple sclerosis (MS) has improved substantially over the past two decades due to high-efficacy therapies such as rituximab and cladribine. Although these treatments have been extensively studied clinically, their potential epigenetic effects in MS remain unexplored. We sought to characterize and compare DNA methylation (DNAm) changes associated with rituximab and cladribine in people with MS.

Methods: Whole blood samples were obtained from patients enrolled in the clinical NOR-MS trail at baseline and at 8 and 96 weeks after initiating rituximab (n=119) or cladribine (n=126). Genome-wide DNAm was profiled using the EPICv2 array. Associations were tested using fixed-effects linear models with empirical Bayes shrinkage as implemented in the LIMMA package.

Results: At 8 weeks, 128 and 65 CpG sites were differentially methylated relative to baseline in the cladribine- and rituximab-treated groups, respectively. At 96 weeks, the number of differentially methylated sites increased markedly in the cladribine group (n=16,803 CpGs), compared with baseline. In contrast, only a modest increase was observed in the rituximab group (n=191 CpGs). A total of 47 CpG sites were overlapping between therapies in at least one time-point comparison, indicating overlapping epigenetic responses arising from either shared treatment mechanisms or underlying MS disease activity.

Conclusions: This study provides the first systematic characterization of DNAm changes associated with rituximab and cladribine therapy in people with MS, offering novel insights into the molecular consequences of high-efficacy MS treatments. Cladribine was associated with substantially more widespread epigenetic remodeling in whole blood then Rituximab. Our findings indicate that cladribine induces broader DNAm alterations beyond the mechanisms related to B-cell depletion. These results might help inform treatment preference in the future.

M29

CDK12/CDK13 inhibition disrupts transcriptional elongation and replication fork progression in glioblastoma

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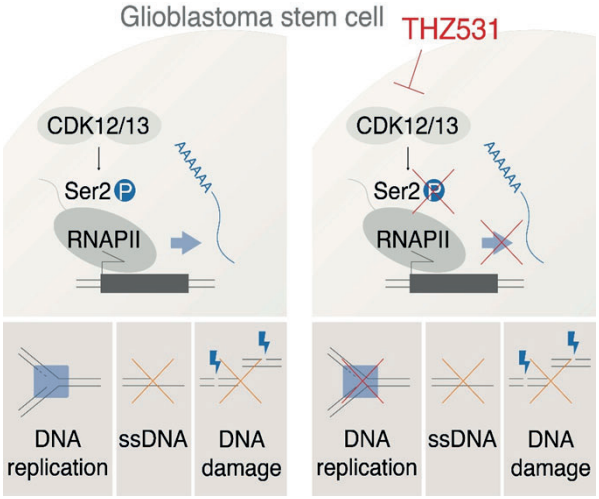
Glioblastomas are the most prevalent and aggressive malignant brain tumors, characterized by hypertranscription and dependence on neurodevelopmental transcription factors. The transcriptional cycle is regulated by phosphorylation of the C-terminal domain (CTD) of RNA polymerase II (RNAPII) by transcriptional cyclin-dependent kinases (tCDK), including CDK7, CDK9, CDK12, and CDK13. Here we find that glioblastoma stem cells (GSC) are selectively sensitive to CDK12/CDK13 inhibition, whereas CDK7 and CDK9 inhibition cause non-specific cytotoxicity. This selective targeting halts GSC and organoid proliferation, curtails GSC invasion and suppresses tumor growth in a xenograft mouse model. In GSCs, CDK12/CDK13 inhibition leads to a rapid and genome-wide loss of serine-2 phosphorylation (pSer2) of the RNAPII CTD, abolishing transcriptional elongation and a transcriptional program sustained by key neurodevelopmental transcription factors. CDK12/CDK13 inhibition unexpectedly arrests DNA replication and fork progression in a manner distinct from the effect of inhibiting other tCDKs. This dramatic arrest precedes DNA damage response activation and cell cycle arrest, directly linking RNAPII elongation to fork dynamics and revealing a previously unrecognized dependence of DNA replication on CDK12/CDK13-RNAPII regulation.



M30

The elusive cancer feeder: the intestinal smooth muscle tissue

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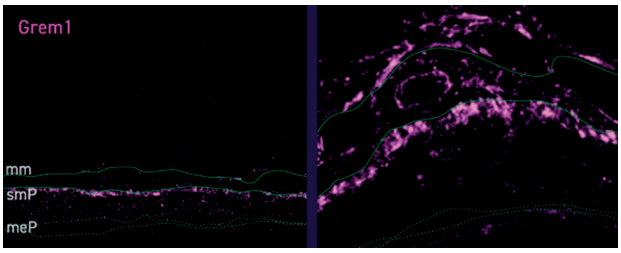
Colorectal cancer (CRC) is one of the deadliest cancers with increasing global incidence and challenging management in the past decades. Interplay between cancer cells and tissue resident cells leads to the remodelling of the local environment into the tumour microenvironment (TME), which supports tumour growth. The intestinal smooth muscle tissue (SMT) makes up a large part of the intestinal wall and has been widely known for its peristalsis function, however it is hardly studied under the context of the TME.

In this study, the SMT participation in the TME from the early stage of tumour development before metastasis in a multiple intestinal neoplasia mouse model was investigated. Our immunohistochemistry and RNA in-situ hybridisation results showed that BMP antagonists—normally function as regulatory proteins that maintain cell stemness and thereby support cell proliferation—were up-regulated in the SMT underneath mouse adenomas. In addition, single-cell RNA comparison analysis of the SMT underneath adenomas and healthy epithelial lining revealed changes in cell-type-specific RNA profiles and cell populations; the results also imply the interplay between different cell populations that may promote tumour growth. Preliminary immunohistochemistry results of human CRC tissue also showed the SMT remodelling before tumour metastasis. This suggests that the SMT may support tumour development as part of the TME early on in CRC.



M31

Tankyrase Inhibition Reprograms Melanoma Metastases to Overcome Resistance to PD-1 Blockade

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Immune checkpoint inhibitors targeting programmed cell death protein 1 (PD-1) have transformed melanoma treatment, but many tumors remain non-responsive, in part due to immune exclusion driven by canonical WNT/β-catenin signaling. To overcome this resistance, we evaluated the tankyrase 1/2 inhibitor OM-153, which suppresses WNT/β-catenin and Yes-associated protein (YAP) signaling, in combination with anti-PD-1 in immunocompetent melanoma models.

Melanoma lung metastases were established in a syngeneic in vivo model using the B16-F10 cell line and treated with anti-PD-1, OM-153 or combination. Bioluminescence imaging showed a significant reduction in tumor burden only in the combination group compared to control. To explore underlying mechanisms, single-cell RNA sequencing revealed altered differentiation states of melanoma metastases in the OM-153 and combination treatment groups. Consistent with these findings, we observed upregulation of microphthalmia-associated transcription factor (MITF) in OM-153-treated groups. MITF stabilization has previously been linked to altered antigen presentation, cytokine release, enhanced CD8+ T cell cytotoxicity, and increased sensitivity to immune checkpoint inhibition.

To define OM-153-specific effects, B16-F10 cells were treated in vitro and analyzed by bulk RNA sequencing and quantitative proteomics. OM-153 induced broad transcriptional and proteomic remodeling of pathways associated with WNT/β-catenin and Hippo signaling. Notably, OM-153 enhanced signaling driven by MITF, and complementary experiments demonstrated increased nuclear MITF localization.Using the B16F10-OVA model, we observed enhanced CD8+ T-cell-mediated killing by OT-1 T cells of OM153-treated target cells compared with untreated controls. Together, these findings suggest that tankyrase inhibition can reprogram melanoma cells and the tumor microenvironment to overcome checkpoint inhibitor resistance and position OM-153 as a targeted partner for PD-1 blockade.

M32

Targeting AXL-mediated immunotherapy resistance mechanisms in the lung tumor microenvironment

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AXL, a receptor tyrosine kinase, is upregulated by normal and malignant cells in many tissues during chronic inflammation and wound-healing, and is also a central negative feedback regulator of innate immunity. Although many studies have implicated AXL in both tumor-intrinsic and immune-mediated mechanisms of immune checkpoint inhibitor (ICI) resistance, current data on AXL expression in tumor and immune cells in clinical cancer specimens is lacking, while its prognostic and predictive role in the context of ICI treatment and the ability of AXL-inhibiting drugs to potentiate ICI efficacy remains elusive.

In this work, we first showed that AXL expression in tumor cells was associated with aggressive phenotypic features, an immunosuppressive tumor microenvironment and poor survival in a real-world cohort of non-small cell lung cancer (NSCLC) patients treated with ICI monotherapy. We then demonstrated that addition of bemcentinib, a selective small-molecule AXL inhibitor, to ICI therapy in a multi-national clinical trial of advanced pretreated NSCLC patients resulted in improved clinical benefit compared to standard-of-care treatments, particularly within subgroups with AXL-positive and STK11-inactivated tumors expected to have the worst prognosis. In murine models, bemcentinib sensitized STK11-mutant NSCLC tumors to ICI treatment via AXL-targeting in dendritic cells, suggesting an additional tumor-cell extrinsic mechanism that supports the efficacy of bemcentinib-ICI treatment observed in patients with STK11-loss. Taken together, these findings provide a strong scientific rationale for current and future clinical trials incorporating AXL inhibitors with ICI therapy to improve NSCLC patient outcomes.

M33

Molecular mechanisms of brain calcification

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Brain calcification remains a relatively underexplored phenomenon despite its potential to reveal novel disease mechanisms and treatments for neurodegenerative conditions. Hereditary brain calcification, such as primary brain calcification (PBC), offers a powerful model for studying the molecular and cellular processes that drive calcification processes in the brain. Over the past decade, neurogenetic research has established a set of seven genes whose pathogenic variants cause PBC. Thus, mutations in these genes, interestingly, converge on the same clinical diagnosis. While a majority of these are membrane proteins, knowledge about potential functional connections between the PBC proteins, are however scarce and the molecular disease pathway is unknown. Recent advances, including our identification of NAA60 as the seventh brain calcification gene[1], have offered an opportunity to understand brain calcification via N-terminal acetylation at the Golgi apparatus[2]. Our work in the newly formed research group MemBrain use molecular cell biological approaches to connect the protein modifier NAA60 to the other PBC proteins, whose functions span ion transport, cellular signalling, and glycan modification.

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1. Chelban V & Aksnes H, et al. Nature communications 2024, PMID: 38480682.
2. Siggervåg A, et al. Brain 2025, PMID: 40344186
3. Bekkelund ÅK, et al. Trends Mol Med. 2025, PMID: 39755442.

Poster Session Overview

P01	Anette Siggervåg	*Disrupted function of the secretory pathway – a potential disease mechanism of NAA60-causative primary brain calcification*
P02	Alessia Caiella	*Identification of substrates and cellular functions of NatB by proteomics of knockout cells*
P03	Cheryl Oortwijn	*A modification-specific antibody to determine the N-terminal acetylation status of α-synuclein*
P04	Chiara Cappelletti	*Molecular signatures from extracellular vesicles for improved decision-making and treatment response in people with multiple sclerosis*
P05	Esteban Lopez Tavera	*Discovery and characterization of bacterial unspecific peroxygenase-like heme-thiolate enzymes*
P06	Evgeny Onishchenko	*Age-based analytical framework to characterise dynamics of cellular processes*
P07	Hanne Øye	*Actin's N-terminal acetyltransferase NAA80 regulates cytoskeleton morphology*
P08	Helena Hradiská	*Temperature dependence of proline racemase – an EVB study*
P09	Henriette Aksnes	*Molecular mechanisms of brain calcification*
P10	Ine Kjosås	*N-terminal acetylation by NatC*
P11	Julie Elisabeth Heggelund	*Activating antibodies in Dermatitis Herpetiformis: X-ray crystal structures*
P12	Lilith Sian Lee	*The elusive cancer feeder: the intestinal smooth muscle tissue*
P13	Lisa Hubers	*Functional Impact of Nth-like DNA Glycosylase on Mitochondrial Dynamics*
P14	Lukas Michael Meyer	*The role of autotransporter adhesins in Enterobacter cloacae infections*
P15	Laurent Besnier	*Transcriptional Perturbation of DNA Replication Timing Following CDK12/13 Inhibition in Pancreatic Cancer Cells*

Poster Session Overview

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P17	Linnea Vie Løkeland	*Effects of simulated diving on inhibitory cyclic nucleotide signaling in human platelets*
P18	Malin Lundekvam	*The cytosolic enzyme NAT16 acetylates histidine potentially impacting kidney physiology*
P19	Matias Aracena-Solem	*Structures, activity and heme binding capacity of heme degrading proteins HmoA and HmoB*
P20	Md Kaykobad Hossain	*Mapping the initial effects of carcinogen-induced oncogenic transformation in the mouse bladder*
P21	Nina McTiernan	*Pathogenic NAA10 variants cause rare congenital disease in humans*
P22	Roshman James Rajkumar	*Targeting Transcriptional Vulnerabilities in Pancreatic Cancer by Integrated SLAM-seq and ATAC-seq*
P23	Sebastian Gonzalez	*Exploring the 14:3:3 gamma and tyrosine hydroxylase (TH) interaction: a biochemical and therapeutical approach*
P24	Susanne Mosler	*The influence of ERK2 autophosphorylation at threonine 188 on the embryonic development of Danio rerio*
P25	Thomas Stevenson	*FlickerPrint for Monitoring Intracellular Droplet Organelles*
P26	Yuhong Wang	*Tunable AMPA receptor function via recurrent evolution of hetero-tetramers*
P27	Zonglai Liang	*Mechanisms and Consequences of Bacterial Persistence Within Breast Cancer Cells*
P28	Karl M. Forbord	*Tankyrase inhibition demonstrates anti-fibrotic effects in preclinical pulmonary fibrosis models*
P29	Ole Vidhammer Bjørnstad	*Tankyrase Inhibition Reprograms Melanoma Metastases to Overcome Resistance to PD-1 Blockade*
P30	Mary Dayne Sia Tai	*Exploring the different conformations of hepatic transporters*

P01

Disrupted function of the secretory pathway – a potential disease mechanism of NAA60-causative primary brain calcification

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NAA60 is a Golgi-localized N-terminal acetyltransferase that modifies membrane proteins. Recently, pathogenic biallelic variants of NAA60 have been linked to an inheritable neurodegenerative disease known as primary brain calcification (PBC) [1]. This condition is characterized by bilateral calcium phosphate deposits in various brain regions, and affected individuals often present with symptoms such as ataxia, neurodegeneration, parkinsonism, and psychiatric features. PBC has previously been associated with pathogenic variants in six genes. The identification of NAA60 as the seventh causal gene provides new opportunities to understand the molecular mechanisms underlying calcification in PBC brains, which remain largely unresolved.

Although a few cellular phenotypes have been reported in NAA60-depleted cultures, its cellular and physiological role is still poorly understood. One previously described phenotype is Golgi fragmentation in NAA60 knockdown studies. This phenotype may be particularly relevant in PBC since it is shared with another PBC-causing gene [2]. We recently investigated fibroblasts isolated from NAA60 PBC-cases. Surprisingly, these showed no changes in Golgi structure, and the structural integrity of this organelle was also preserved in multiple NAA60 knockout cell lines. Next, we observed Golgi fragmentation following NAA60 knockdown in a range of cell lines. This suggested that Golgi fragmentation may be an acute effect after NAA60 depletion, potentially associated with compensatory mechanisms in systems of more long-term loss of NAA60. Next, initial assessment of Golgi functionality, revealed reduced expression of a selected secretory protein in NAA60 knockout cells. This points to a general defect in the secretory pathway in NAA60-deficient cells that we are currently investigating as a potential PBC disease mechanism.

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1. Chelban & Aksnes et al. Nat Commun. 2024. PMID: 38480682
2. Siggervåg et al. Brain. 2025. PMID: 40344186

P02

Identification of substrates and cellular functions of NatB by proteomics of knockout cells

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N-terminal acetyltransferases (NATs) are a class of enzymes responsible for acetylating 80% of the human proteome. One of the major NATs, NatB, acetylates MD-, ME-, MN- and MQ- starting proteins, which accounts for approximately 20% of the proteome. NatB is composed of two subunits, the catalytic subunit NAA20 and the ribosome-anchoring, auxiliary subunit NAA25. Previous studies using NAA20 and NAA25 depleted cells suggested a role of NatB in cytoskeletal maintenance, something that was believed to be attributed mainly by one cytoskeletal protein.

After the recent discovery of pathogenic NAA20 variants with impaired catalytic activity, the identification of high-impact NatB substrates as well as revealing the physiological role of this enzyme is increasingly relevant. Here, we analyzed NAA20 and NAA25 CRISPR knockout (KO) cell lines to investigate human cells completely lacking NatB, aiming to robustly identify targets of NatB, as well as possibly further understand the roles of this enzyme.

N-terminomics revealed consistent similarities in the degree of N-terminal acetylation between NAA20 and NAA25 KO cells. Here, we found 92 proteins that were affected by KO of either one of the NatB subunits and had at least a 10% reduction in N-terminal acetylation compared to WT cells. Shotgun proteomics and GO-term analysis additionally showed that the cytoskeleton is widely affected by the absence of NatB. We sought to substantiate these findings by immunoblotting and immunocytochemistry of F-actin and cytoskeletal proteins, in addition to live-cell microscopy to investigate cellular motility.

P03

A modification-specific antibody to determine the N-terminal acetylation status of α-synuclein

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Aggregation of alpha-synuclein (α-syn) in Lewy bodies and Lewy neurites is a key feature in the pathogenesis of Parkinson's disease and other synucleinopathies. α-syn undergoes various post-translational modifications (PTMs), including N-terminal acetylation. While many α-syn PTMs are well studied and known to affect its disease properties, N-terminal acetylation has thus far only been studied in pure biochemical in vitro experiments. These suggest that N-terminal acetylation of α-syn affects several pathological hallmarks such as aggregation, membrane binding capacity and degradation. However, limited research has been conducted in physiologically relevant models and N-terminal acetylation-deficient cell systems to support these findings. Furthermore, the assessment of the N-terminal acetylation status of α-syn in physiological samples has suffered a lack of available research tools.

Here, we tested a new set of antibodies made to specifically recognize Nt-acetylated and non-Nt-acetylated α-syn. Dot blot analyses indicated that the antibodies bound exclusively to their target peptides (synthetic NtAc vs. non-NtAc α-syn). To further substantiate this finding, we conducted protein analysis on the lysates from NatB CRISPR knockout (KO) cell lines, previously determined to have reduced levels of α-syn Nt-acetylation (Caiella et al., unpublished). In agreement with this, the anti-NtAc-α-syn antibodies mainly bound to α-syn from the wildtype (WT) cell line and showed reduced intensity in NatB KO cell lines. Moreover, our results demonstrate that non-NtAc-α-syn is present in KO cell lines but absent in the WT cell line, this effect persists even with SNCA gene overexpression. This work highlights the potential of this set of modification-specific antibodies for further use in human synucleinopathy tissue samples to investigate the potential role of Nt-acetylation in disease development and progression.

P04

Molecular signatures from extracellular vesicles for improved decision-making and treatment response in people with multiple sclerosis

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Multiple sclerosis (MS) is a chronic autoimmune and neurodegenerative disease affecting more than 2.8 million people worldwide. Its marked clinical heterogeneity makes it difficult to predict disease progression and treatment response, underscoring the need for reliable and accessible biomarkers. Extracellular vesicles (EVs) are nanosized, membrane-encapsulated vesicles present in all biological fluids and carry molecular signatures that are representative of their cell of origin. Because EVs can cross the blood-brain barrier, their cargo represents a promising source of biomarkers for neurodegenerative disorders such as MS. In this study, we aim to establish a robust workflow for EV purification from cerebral spinal fluid (CSF) obtained from individuals undergoing lumbar puncture during clinical evaluation for MS at Oslo University Hospital. EVs may be used to identify proteomic biomarkers that can 1) distinguish MS from other neurological disorders and 2) predict treatment response from the timepoint of the diagnostic work-up. EVs were isolated by sequential centrifugation and characterized by Western blotting, nanoparticle tracking analysis and transmission electron microscopy. Then, quantitative proteomic profiling of EV protein cargo was performed using liquid chromatography-electrospray-tandem mass spectrometry. For this pilot phase of our study, we optimized the workflow and demonstrated that EVs can be robustly isolated from small CSF volumes and their protein content reliably quantified. Proteomic data from these pilot experiments will be presented at the NBS conference. This work establishes a foundation for the identification of EV-based biomarkers associated with MS onset and disease progression.

P05

Discovery and characterization of bacterial unspecific peroxygenase-like heme-thiolate enzymes

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Unspecific peroxygenases (UPOs, EC 1.11.2.1) are promising biocatalysts for the oxyfunctionalization of organic molecules and the synthesis of industrially relevant compounds due to their vast repertoire of catalyzed reactions. To date, thousands of putative UPO genes have been identified in eukaryotic genomes, most of them in the Ascomycota and Basidiomycota phyla, and several UPOs have been characterized. Remarkably, no related enzymes have ever been reported in prokaryotic organisms. Here, we describe the discovery of a diverse family of bacterial heme-thiolate peroxygenases through structure database mining, followed by functional characterization of selected representatives. The bacterial UPO-like proteins (BUPOs) are structurally analogous to family I (short) fungal UPOs, despite having sequence identity below 20%. Expression of one of these proteins (HydBUPO) in its native host (Hydrogenophaga sp. A37) was confirmed by proteomics. Several BUPOs were cloned and expressed in Escherichia coli. In biochemical assays, the BUPOs were able to catalyze one-electron oxidation (peroxidase activity) of ABTS and 2,6-dimethoxyphenol, as well as two-electron oxidation (peroxygenase activity) of naphthalene, indole, 3-phenyl-1-propanol, and 16-hydroxypalmitic acid, using hydrogen peroxide as a co-substrate. These enzymes thus represent a previously unknown family of bacterial heme-thiolate peroxygenases that share structural and functional features with eukaryotic UPOs, offering potential candidates for developing industrially relevant biocatalysts.

P06

Age-based analytical framework to characterise dynamics of cellular processes

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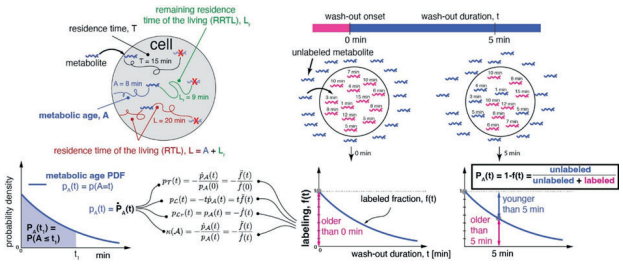
Cells continuously produce and degrade multiple small and large molecules, essential for maintaining homeostasis. The study of this dynamics has gained momentum since the development of pulse-chase and wash-in/out methods, utilizing fluorescent or isotopic labeling of cellular components to assess properties such as turnover rates or half-lives. However, standard analyzes of these experiments often depend on simplifications such as the homogeneity of analyzed molecules or their immediate labeling, which does not always hold. We have developed a rigorous analytical framework that interprets the readouts of dynamic labeling experiments as the distribution of metabolic ages, defined as the time that molecules have spent within a cell. Using age-based interpretation, we demonstrate how the experimentally observed labeling dynamics is connected to a variety of dynamic parameters including half-lives, decay rates, and residence times of analyzed molecules, and how these interpretations are affected by the conditions of delayed input or complex degradation patterns. To aid in the experimental quantification of dynamic parameters, we introduce a general compartmental model-based approach which we implement in a publicly available Python package (https://gitlab.com/elad.noor/symbolic-compartmental-model). We illustrate the practical utility of this framework by quantifying metabolic ages and determining the kinetic pool structure of budding yeast proteins at optimal and suboptimal growth temperatures, revealing distinct kinetic populations of ribosomal proteins.



P07

Actin's N-terminal acetyltransferase NAA80 regulates cytoskeleton morphology

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Actin is one of the most abundant proteins in nature and is involved in many important cellular functions, including cell division, organelle movement, cell signaling, cell migration and regulation of gene transcription. The dynamic transition between monomeric and filamentous forms is fundamental for actin's cellular activity. This transition is exquisitely regulated in cells by a large number of actin-binding and signaling proteins, as well as by several posttranslational modifications like N-terminal acetylation (Nt-Ac).

NATs (N-terminal acetyltransferases) are a family of enzymes which catalyzes the transfer of an acetyl group from acetyl-CoA to the N-terminal amino group of 80 % of the human proteome. NAA80 (N-alpha-acetyltransferase 80) or NatH is a recently discovered member of the NAT family and has been found to specifically acetylate actin`s N-terminus post-translationally. Absence of actin Nt-acetylation in HAP1 NAA80 KO cells has been found to alter cytoskeletal dynamics by displaying an increase in filopodia and lamellipodia formation and accelerated cell motility. Here, we show that actin Nt-acetylation affects cytoskeletal morphology in lung cancer cells by using a NAA80 KO cell model.

P08

Temperature dependence of proline racemase – an EVB study

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Enzyme reactions are often times studied computationally by running QM/MM simulations where the reaction centre is treated with quantum mechanics and the rest of the enzyme with molecular mechanics. Our group is choosing different approach – empirical valence bond (EVB) [1]. Here, QM calculations are run separately for the reaction in water or in a small system without the whole enzyme. Then we use the calibration from this reference reaction for the enzymatic reaction without running any more QM calculations. EVB allows us to study multiple mutants and homologs with only one calibration. We can also run MD/EVB simulations at multiple temperatures to obtain Arrhenius plot that gives us entropic and enthalpic contributions, thus we can compare thermophilic, mesophilic and cold-adapted homologs [2]. In this project, EVB is employed to study proline racemase, an enzyme that catalyses isomerisation between L- and D-proline. I'm currently working with four homologs: two bacterial from Acetoanaerobium (Clostridium) sticklandii and Pseudomonas protegens, one eucaryotic from Trypanosoma cruzi [3] and one from hyperthermophilic archaeon Thermococcus litoralis [4].

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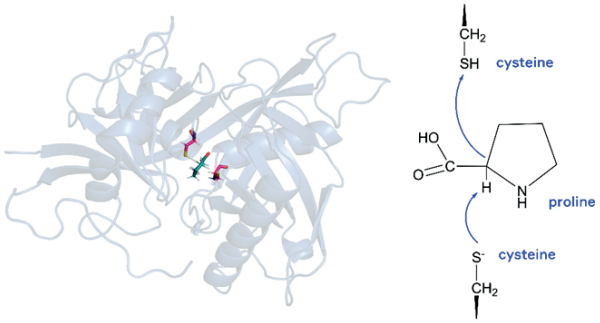

P09

Molecular mechanisms of brain calcification

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Brain calcification remains a relatively underexplored phenomenon despite its potential to reveal novel disease mechanisms and treatments for neurodegenerative conditions. Hereditary brain calcification, such as primary brain calcification (PBC), offers a powerful model for studying the molecular and cellular processes that drive calcification processes in the brain. Over the past decade, neurogenetic research has established a set of seven genes whose pathogenic variants cause PBC. Thus, mutations in these genes, interestingly, converge on the same clinical diagnosis. While a majority of these are membrane proteins, knowledge about potential functional connections between the PBC proteins, are however scarce and the molecular disease pathway is unknown. Recent advances, including our identification of NAA60 as the seventh brain calcification gene1, have offered an opportunity to understand brain calcification via N-terminal acetylation at the Golgi apparatus2. Our work in the newly formed research group MemBrain use molecular cell biological approaches to connect the protein modifier NAA60 to the other PBC proteins, whose functions span ion transport, cellular signalling, and glycan modification.

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P10

N-terminal acetylation by NatC

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N-terminal (Nt-) acetylation is a protein modification catalyzed by N-terminal acetyltransferases (NATs). Approximately 80% of all human proteins undergo acetylation at their N-terminus. This modification changes the positive charge at the N-terminus into a hydrophobic segment, which can influence crucial protein properties such as localization, folding, and turnover. However, a broader proteome function remains elusive. Seven human NATs have been identified to date: NatA - NatF and NatH. NatC, one of the major NATs, consists of the catalytic subunit NAA30 and two auxiliary subunits, NAA35 and NAA38. NatC may co-translationally acetylate the Nt-methionine if it is followed by a hydrophobic or amphipathic amino acid (Met-L/I/F/W/V/M/H/K). Despite being one of the major NATs, the biological impact of NatC is still unknown. In this study, we used HAP1 NatC knockout (KO) cells, NAA30-, NAA35-, and NAA38-KO, as the experimental model to investigate the cellular impact of abolished NatC activity. We found that NatC plays an essential cellular role in protecting substrates from proteasomal degradation by specific ubiquitin ligases, such as the UBR4-KCMF1 complex, UBR1, and UBR2. The absence of NatC activity induces proteotoxic stress in cells, among others by an increased degradation of the neddylation regulators UBE2M and UBE2F. UBE2M/F neddylates the Cullins, activating them as Ub-ligases. Therefore, the absence of NatC activity may result in reduced Ub-ligase activity of the Cullins, leading to a dysregulation of the protein turnover of Cullin substrates. Finally, we observed cellular phenotypes such as increased cellular granularity and lysosomal content. We also found that all the NatC KO cell lines exhibited changes in mitochondrial morphology. These NatC KO-mediated phenotypes are linked to NatC's role in protecting proteins from degradation, since all observed phenotypes were partially reversed when knocking down the Ubiquitin E3 ligases UBR4, UBR2, and UBR1.

P11

Activating antibodies in Dermatitis Herpetiformis: X-ray crystal structures

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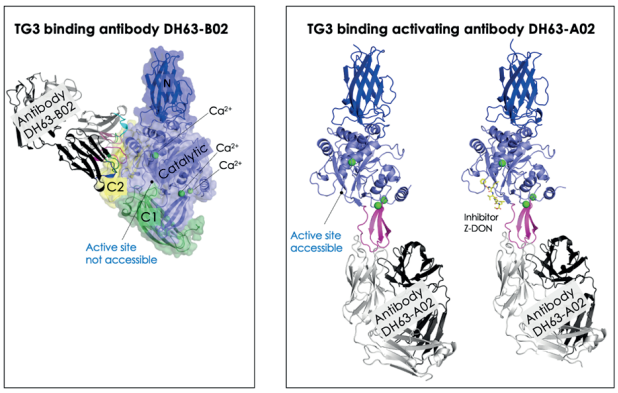
Dermatitis herpetiformis (DH), a skin manifestation of the gluten-sensitive condition celiac disease, is hallmarked by autoantibody production to transglutaminase 3 (TG3). TG3 is a calcium dependent enzyme that targets glutamine residues in polypeptides for either transamidation or deamidation modifications. TG3 has four domains (N-terminal, catalytic core and two C-terminal b-barrels: C1C2). To become catalytically active the enzyme needs a proteolytic cleavage between the core domain and C1C2, in addition to binding calcium ions.

In a recently published paper in Nature Communications, we present two X-ray crystal structures showing how a Fab fragment of a DH patient derived antibody promotes the active conformation of TG3.

We demonstrate that TG3, upon binding of the autoantibody, undergoes a large conformational change as a b-sheet in the catalytic core domain moves and C1C2 detaches. The findings support a model where B-cell receptors of TG3-specific B cells bind and internalize TG3-gluten enzyme-substrate complexes thereby facilitating gluten-antigen presentation, T-cell help and autoantibody production. The promotion of the active conformation translates into increased gluten presentation to T cells when such antibodies are expressed as BCRs.



P12

The elusive cancer feeder: the intestinal smooth muscle tissue

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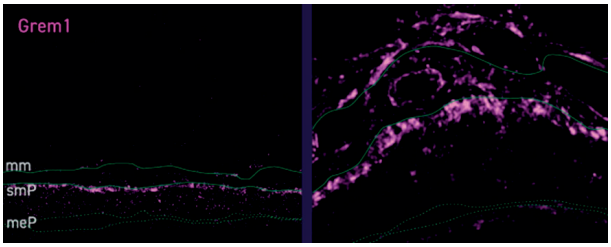
Colorectal cancer (CRC) is one of the deadliest cancers with increasing global incidence and challenging management in the past decades. Interplay between cancer cells and tissue resident cells leads to the remodelling of the local environment into the tumour microenvironment (TME), which supports tumour growth. The intestinal smooth muscle tissue (SMT) makes up a large part of the intestinal wall and has been widely known for its peristalsis function, however it is hardly studied under the context of the TME.

In this study, the SMT participation in the TME from the early stage of tumour development before metastasis in a multiple intestinal neoplasia mouse model was investigated. Our immunohistochemistry and RNA in-situ hybridisation results showed that BMP antagonists—normally function as regulatory proteins that maintain cell stemness and thereby support cell proliferation—were up-regulated in the SMT underneath mouse adenomas. In addition, single-cell RNA comparison analysis of the SMT underneath adenomas and healthy epithelial lining revealed changes in cell-type-specific RNA profiles and cell populations; the results also imply the interplay between different cell populations that may promote tumour growth. Preliminary immunohistochemistry results of human CRC tissue also showed the SMT remodelling before tumour metastasis. This suggests that the SMT may support tumour development as part of the TME early on in CRC.



P13

Functional Impact of Nth-like DNA Glycosylase on Mitochondrial Dynamics

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DNA instability is a hallmark of aging and is linked to neurodegeneration. NTH-like DNA glycosylase (NTHL1) is a key enzyme of the base excision repair (BER) pathway which is essential for maintaining nuclear and mitochondrial genome integrity.

Here, we investigate the consequence of NTHL1 loss on mitochondrial DNA (mtDNA) stability and function in a cellular model. Our results challenge the conventional view that loss of DNA repair is invariably detrimental, revealing that NTHL1 deficiency can confer a beneficial mitochondrial phenotype. NTHL1 knockout in human cells led to a significant accumulation of mtDNA lesions, which was surprisingly accompanied by a marked increase in mtDNA copy number, elevated oxidative phosphorylation protein levels, and enhanced mitochondrial respiratory capacity. NTHL1-deficient cells also displayed enlarged mitochondria together with increased expression of the mitochondrial biogenesis regulator PGC1α and the membrane fusion protein OPA1, indicating an adaptive remodeling of the mitochondrial network. Consistent with this, NTHL1-knockout cells show increased resistance to MPP+ -induced mitochondrial stress and elevated phosphorylation of eIF2α, suggesting activation of the integrated stress response. These findings indicate that loss of NTHL1 promotes mitochondrial adaptation and resilience to oxidative stress through mitohormetic and stress-adaptive pathways.

More recently, we have generated NTHL1-deficient iPSCs derived from a patient with Parkinson's disease and are differentiating them into 2D and 3D neuronal models. These systems provide a physiologically relevant framework to further investigate the neuroprotective effects of NTHL1 loss in an aging context. Using these models, we aim to further understand the impact of NTHL1 deficiency on mitochondrial DNA stability and function, transcriptomic remodeling, and activation of cellular stress response pathways.

P14

The role of autotransporter adhesins in Enterobacter cloacae infections

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To combat bacterial infections a variety of antibiotics are currently applied in the clinical context. However, antibiotic mechanisms of action often do not distinguish between highly virulent pathogens and low-virulent commensals/ colonizing strains, applying selection pressure for the development of antimicrobial resistance and consequently its proliferation. In this regard, bacterial pathogens belonging to the ESKAPE group have demonstrated increasing levels of antimicrobial resistance, while the selection of new appropriate antimicrobial targets for the elimination of pathogens or containment of the infection has become more challenging.

A well-known, but often not initially targeted part of the infection and immune evasion chain is the first step: attachment of the pathogen to host cells or associated surfaces through adhesins present on the bacterial cell surface. Previous work in Yersinia enterocolitica, Acinetobacter baumannii and Bartonella henselae has identified trimeric autotransporters (TAA) as key mediators of bacterial attachment and characterized the corresponding TAAs. To expand on this comparative collection, this project investigates the much more complex TAAs of Enterobacter cloacae and Enterobacter cloacae complex (ECC) strains. The TAA binding characteristics to host proteins are characterized in vitro by enzyme-linked immunosorbent assay (ELISA) and surface plasmon resonance (SPR) on a molecular level and through plate-based whole-cell assays. To complement the data, an in vivo infection model using Caenorhabditis elegans is being established.

Obtained results for ECC strains allow for the comparison of adhesion characteristics across Gram-negative pathogens and provide the base for further testing and refinement of novel adhesion inhibitor candidates currently under development.

P15

Transcriptional Perturbation of DNA Replication Timing Following CDK12/13 Inhibition in Pancreatic Cancer Cells

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Transcription and DNA replication are tightly coordinated processes that operate on a shared genomic template, and disruption of this coordination is a major source of genomic instability in cancer. Many cancer cells exhibit transcriptional addiction, rendering them particularly vulnerable to perturbations in transcriptional regulation. The transcriptional cyclin-dependent kinases CDK12 and CDK13 play key roles in RNA polymerase II phosphorylation and transcriptional elongation, and their inhibition has been shown to induce widespread transcriptional repression accompanied by impaired DNA synthesis. The aim of this Master's project is to investigate how transcriptional inhibition mediated by CDK12/13 affects DNA replication in cancer cells, using the pancreatic ductal adenocarcinoma cell line PANC-1. Replication timing is employed as a genome-wide readout of replication dynamics, as it reflects the temporal order of DNA synthesis across the genome and is highly sensitive to changes in transcriptional activity and chromatin organization. Analysis of replication timing therefore provides complementary insight into how transcriptional perturbations reshape replication control. PANC-1 cells are treated with CDK12/13 inhibitors followed by EdU incorporation, flow-cytometric separation into distinct S-phase fractions, and sequencing of nascent DNA. This approach enables identification of genomic regions that shift between early and late replication upon transcriptional inhibition. Together, this work aims to clarify the mechanistic coupling between transcription and DNA replication in cancer cells and to assess replication timing alterations as potential vulnerabilities associated with transcription-targeted therapies.

P16

Metabolic Aging Signature of the mitochondrial OXPHOS

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One of the protein complexes that powers the act of reading this sentence by generating ATP is the oxidative phosphorylation (OXPHOS) system located in mitochondria. Intriguingly, recent metabolic labeling experiments suggest that OXPHOS proteins are among the longest-lived proteins in the mammalian brain. At the same time, OXPHOS activity inevitably produces reactive oxygen species (ROS), which can induce mitochondrial dysfunction, particularly in tissues with high energy demand such as the brain, skeletal muscle, and heart. Consistent with this vulnerability, defects in OXPHOS are associated with some of the most socially impactful diseases, such as cardiomyopathy, Alzheimer's disease, and Parkinson's disease. These observations underscore the critical need for cells to maintain OXPHOS in a functional state over extended periods of time.

This raises several fundamental questions: why do proteins within such a central energy-producing system exhibit remarkable longevity, and how does OXPHOS preserve its functionality under continuous environmental stress, such as ROS exposure? My project aims to establish an experimental framework to evaluate the metabolic age of OXPHOS proteins and to investigate how metabolic age influences OXPHOS function. To achieve this, old and new OXPHOS proteins will be metabolically labeled in cell cultures using stable isotopes, OXPHOS complexes will be isolated at defined time points, and quantitative mass spectrometry will be employed to identify and quantitatively examine differences between young and old OXPHOS proteins. Furthermore, mathematical modeling will be integrated to construct a model of the temporal dynamics of the OXPHOS lifecycle. Together, these strategies will provide an in-depth understanding of how protein aging affects OXPHOS function, ultimately advancing our knowledge of mitochondrial homeostasis.

P17

Effects of simulated diving on inhibitory cyclic nucleotide signaling in human platelets

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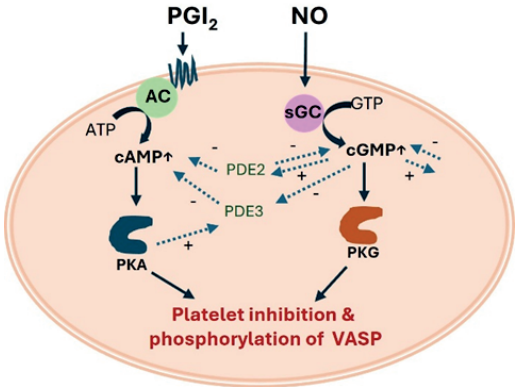
Decompression sickness (DCS) is a potentially serious condition from diving. The pathogenesis of DCS is not completely understood, however, animal experiments point to the involvement of platelets. Thus, anti-platelet therapies reduce severe DCS and death in rats. Gas bubbles entering the circulation may damage the endothelial cell lining and are recognized as foreign surfaces, eliciting an activation response from plasma proteins and platelets. This is reflected in the reduction in platelet count after diving. Platelets exist in a constant ready-to-go state but are kept in quiescence through constant inhibitory signaling from cAMP and cGMP signaling pathways. The aim of this project is to investigate the impact of simulated diving on the inhibitory signaling pathways of platelets. To address this, we used ex vivo human blood models from volunteering donors. Platelets were isolated by multiple centrifugation steps and their purity was confirmed. The activity of cyclic nucleotide signaling pathways was assessed using the well-established PKA and PKG target vasodilator-stimulated phospho-protein (VASP) by phospho-site specific antibodies against Ser157 and Ser239. Functional signaling was confirmed for EDTA, ACD and sodium citrate tubes, however, sodium citrate was chosen for compatibility with platelet functional assays. Isolated platelets were exposed to simulated diving in hyperbaric chambers for 2 hours (heliox), after which the activity of the inhibitory signaling pathway was assessed by western blotting. A synergistic relationship between cGMP and cAMP signaling pathways was found for phospho-Ser157-VASP, using a NO donor (sodium nitroprusside) and a prostacyclin analogue (iloprost). This synergy was amplified after pressure exposure (2.5MPa He), whereas hyperoxia (pO2 = 0.06 MPa) decreased NO- and increased iloprost-mediated VASP phosphorylation. These results suggest an adaptive behavior of platelet inhibitory signaling in diving, possibly protective of DCS.



P18

The cytosolic enzyme NAT16 acetylates histidine potentially impacting kidney physiology

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Histidine is an essential amino acid that is found acetylated in human blood plasma. This modification involves the transfer of an acetyl group from Acetyl-CoA to the α-amino group of histidine, a reaction catalyzed by an unknown histidine acetyltransferase (HisAT). NAT16 has previously been proposed as a candidate HisAT, but its role has remained unclear. Here, we identify NAT16 as the human HisAT responsible for histidine acetylation. Using cell fractionation assays, we show that NAT16 localizes to the cytosol in vivo. We also investigated a common NAT16 F63S missense variant (present in >5% of the population) that has previously been associated with reduced acetylhistidine levels in the blood and increased risk of kidney disease. We performed in vitro assays comparing purified NAT16 wild-type (WT) and the F63S variant, which revealed that the variant has reduced histidine affinity, providing an explanation for lower plasma acetylhistidine. In summary, NAT16 is a cytosolic histidine acetyltransferase, and the F63S variant decreases acetylhistidine production, with possible consequences for kidney function.

P19

Structures, activity and heme binding capacity of heme degrading proteins HmoA and HmoB

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Bacteria need free iron to be able to grow and multiply. As most iron in the human body is protein-bound, bacteria have developed several mechanisms to extract iron from the host. One such mechanism is the acquisition of heme and the subsequent degradation to release free iron. The proteins responsible for heme degradation are heme oxygenases (HOs), and Bacillus cereus has three potential HOs: IsdG, HmoA and HmoB. The structure of IsdG has already been solved, therefore this project focuses on solving the structures of HmoA and HmoB with and without its substrate (heme) bound. In addition, their affinity for heme is to be investigated using Microscale Thermophoresis (MST) and their activities assessed using Iron-uptake oxidoreductase (IruO) as a reduction partner. So far, a protocol for purification of the two proteins has been developed and the structure of HmoA without heme bound has been solved which showed the structure to be very similar to the one of IsdG. Binding studies have been carried out for both HmoA and HmoB, resulting in the determination of binding constants in the micromolar range for both proteins. Together with our ongoing activity studies, we aim to elucidate the effectiveness of HmoA and HmoB in heme degradation and to explain their differences by comparing their structures and heme-binding capabilities.

P20

Mapping the initial effects of carcinogen-induced oncogenic transformation in the mouse bladder

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Bladder cancer (BC) is the most prevalent malignancy of the urinary tract and one of the most common cancers worldwide. Although around 80% of BC cases are non-muscle invasive at diagnosis, many patients relapse with more severe muscle invasive bladder cancer. Identifying predictive BC signatures is required to anticipate recurrence and provide more efficient therapy.

To investigate the molecular mechanisms of tumour induction, we used N-butyl-N-(4-hydroxybutyl) nitrosamine (BBN), a bladder-specific carcinogen, to treat mice for a short period (12 days) and collected bladders at several time points together with age-matched controls. We combined genetic cell tracing, global proteomics and immunofluorescence techniques to dynamically map the initial oncogenic effects of BBN. Proteomic changes over time were steadfast and intensified or diversified. We observed a swift and cumulative proteomic dysregulation dominated by altered energy metabolism, immune signatures and proliferation. The immediate effect of BBN involved lipid metabolism, with increased lipid transport and fatty acid metabolism, followed by immune infiltration. A distinct increase in cell-cycle pathways and proliferation was observed, with proliferative cells mainly in the basal layer, resulting in layer thickening. Moreover, energy balance shifted towards increased glucose metabolism and reduced fatty-acid β-oxidation. Notably, these molecular signatures resemble predictive signatures previously identified in bladder cancer patients with rapid relapse.

To analyse the impact of a competent immune system in tumorigenesis, we performed long-term BBN treatment (20 weeks) in immunodeficient NSG mice and compared them with immunocompetent B6 mice. Muscle invasive bladder cancer developed in B6 mice but not in NSG mice. Further analyses will provide important insights into immune cell contributions to cancer initiation and progression.

P21

Pathogenic NAA10 variants cause rare congenital disease in humans

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N-terminal (Nt) acetylation is one of the most prevalent protein modifications in human cells. The major Nt-acetyltransferase (NAT) complex NatA comprises the catalytic subunit NAA10 and the ribosome-anchoring subunit NAA15. The NatA complex co-translationally Nt-acetylates around 40% of the human proteome and is essential for normal cell function. In addition to NAA10's evolutionary conserved role in the NatA complex, there is a cellular population of monomeric NAA10 that can catalyse lysine acetylation and regulate proteins in a non-catalytic manner. Moreover, monomeric NAA10 has a NAT substrate specificity that differs from the NatA complex in vitro.

NAA10-related syndrome is a rare congenital disease in humans caused by pathogenic variants in the X-linked NAA10 gene. Affected individuals show phenotypic heterogeneity with regards to severity and type of clinical manifestations, but commonly present with developmental delay, intellectual disability, ophthalmic conditions and cardiac anomalies. The specific disease mechanisms associated with NAA10 deficiency are currently poorly understood. Different NAA10 variants can likely have distinct impacts on the multifaceted functions of NAA10, which may in part explain the phenotypic spectrum of NAA10-related syndrome. Here, we have investigated the biochemical profiles of the four novel NAA10 missense variants A6P, R79C, Q129P, and E157K.

P22

Targeting Transcriptional Vulnerabilities in Pancreatic Cancer by Integrated SLAM-seq and ATAC-seq

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Transcription by RNA polymerase II is tightly regulated and essential for maintaining gene expression programs. The cyclin-dependent kinases CDK12 and CDK13 promote productive elongation through Ser2 phosphorylation of the polymerase C-terminal domain and their inhibition arrests cell proliferation, RNAPII elongation and mRNA synthesis. However, the immediate transcriptional and chromatin-level consequences of their inhibition remain incompletely understood.

Here, we used a time-resolved integration of SLAM-seq and ATAC-seq to quantify nascent transcription and chromatin accessibility following CDK12/13 inhibition in a pancreatic cancer cell line. SLAM-seq revealed rapid repression of newly synthesized mRNA, with pronounced effects on elongation-dependent gene programs, including cell-cycle and DNA damage response genes. Concurrent ATAC-seq profiling identified coordinated changes in chromatin accessibility accompanying transcriptional repression. Notably, similar transcriptional responses to CDK12/13 inhibition were observed in glioblastoma cells from previous work. Together, these findings capture early, mechanistically informative consequences of transcriptional elongation perturbation and establish a general framework for studying transcriptional regulation beyond steady-state expression analyses.

P23

Exploring the 14:3:3 gamma and tyrosine hydroxylase (TH) interaction: a biochemical and therapeutical approach

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Tyrosine hydroxylase (TH) is the rate-limiting enzyme in dopamine biosynthesis. Impaired regulation of TH contributes to dopamine deficiency and is a central feature of parkinsonism. TH activity and stability are in part regulated by phosphorylation-dependent interactions with 14-3-3 proteins, which act as molecular scaffolds and chaperones. Among these, the 14-3-3 gamma (γ) isoform has been implicated in supporting TH function through direct binding.

Recent identification of a Parkinsonism-associated mutation in 14-3-3γ (R132C) highlights the potential pathological relevance of this interaction. However, the impact of this mutation on TH binding, regulation, and enzymatic activity remains poorly understood.

This work aims to explore the interaction between TH and 14-3-3γ through enzimatic assays and differential scanning fluorimetry (DSF). In this study we found that 14:3:3γ may release the dopamine inhibition from the Ser19 tyrosine hydroxylase. Additionally, we found that the 14:3:3 disease causing variant R132C is more strongly destabilized by Ebselen derivatives than its wild-type counterpart. This represents a great opportunity to explore this group of molecules. Also, through a high troughput screening we found a possible hit that showed a 0.8 degree stabilization between 14:3:3 gamma R132C and tyrosine hydroxylase. Elucidating how disease-associated alterations in 14-3-3γ influence TH regulation may provide new insights into molecular mechanisms underlying parkinsonism and identify novel targets for therapeutic intervention.

P24

The influence of ERK2 autophosphorylation at threonine 188 on the embryonic development of Danio rerio

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Extracellular signal-regulated kinases (ERK) are effector kinases of the MAPK pathway and are essential cellular signalling molecules for vertebrate embryonic development. In addition to their physiological properties, they are also known to mediate maladaptive processes. In particular, the pathological effects are associated with the dimerization of ERK and the subsequent phosphorylation of ERK at threonine 188, which leads to nuclear localisation of the ERK dimer. To selectively influence maladaptive processes, the inhibition of ERK dimerization and thus phosphorylation at threonine 188 (pERKT188) appears to be a form of therapy with fewer side effects compared to the kinase inhibitors used in clinical practice, as adaptive processes in the cytosol are not affected. My doctoral research project aimed to clarify whether pERKT188 is important for survival and the course of physiological embryogenesis in zebrafish embryos. Therefore, the influence of ERK on embryonic development, on the phenotype in terms of the formation of the body axis and the morphogenesis of the heart, as well as the heart function of zebrafish embryos, was investigated. ERK knockdown and rescue experiments demonstrated that pERKT188 is important for tail and heart morphogenesis as well as heart function. Inhibition of phosphorylation led to a shortened, curved body axis as well as underdeveloped, tubular hearts that didn't undergo looping. In addition, there was significantly poorer heart function in the sense of significantly impaired contraction during systole and a reduced heart rate. Stimulation of phosphorylation at pERKT188, on the other hand, normalised heart function and morphogenesis of the zebrafish tail and zebrafish heart. The experiments conducted thus enable conclusions to be drawn about the physiological functions of pERKT188 for the first time and point to contraindications that would need to be considered in the potential clinical use of dimerization inhibition in patients.

P25

FlickerPrint for Monitoring Intracellular Droplet Organelles

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Liquid-like biomolecular condensates have long been suggested as the origin of the pathological aggregates observed in several age-related neurodegenerative disorders, yet the mechanisms underpinning liquid to solid-like transition remain unclear. Proximity labelling studies have elucidated critical compositional changes occurring within condensates in different cellular contexts, but understanding how this relates to changes in their material properties remains an open question. Here we have implemented a novel application of flicker spectroscopy to capture subtle changes in the material properties of condensates, including surface tension and bending rigidity, demonstrating that these properties are highly dependent on condensate composition and cellular fitness. These properties have the potential to dictate the biological functions of condensates by controlling their ability to fuse, grow, exchange components, and form hierarchical structures.

By applying this methodology across in vitro condensate and cellular models of neurodegenerative disease and ageing, we aim to assess how pathological mutations in protein/RNA manifest as a change in condensate material state, understand the biophysical limitations to condensate size, and the influence of non-equilibrium processes such as those driven by ATP. Together, the project addresses the significant need for systematic quantitative studies of condensate material properties, and how these material states are linked to biological process, cellular fitness, and human health.

P26

Tunable AMPA receptor function via recurrent evolution of hetero-tetramers

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Rapid signalling between neurons is mediated by oligomeric membrane proteins with extracellular ligand-binding domains and a central membrane-spanning ion channel. At most synapses in the mammalian brain, these are AMPA-type ionotropic glutamate receptors (AMPARs) that bind glutamate and conduct sodium and /or calcium ions into postsynaptic cells. Mammalian AMPARs can assemble as homo-tetramers and often assemble as hetero-tetramers of two or three subunits. Here, we have investigated AMPARs in all animal lineages using phylogenetics, heterologous expression of receptors, and electrophysiological experiments. This revealed that AMPARs emerged in the earliest bilaterians and they radiated independently in each bilaterian lineage. These novel AMPAR subunits in diverse bilaterians have come to rely on each other for functional expression, resulting in obligate hetero-tetrameric AMPARs. Various subunits contribute differently to channel activation and ion permeation. This also revealed a remarkable example of convergent evolution, in which a complement of calcium-permeable and -impermeable AMPARs exists in mammals and worms, achieved via biophysically similar but genetically drastically different mechanisms.

P27

Mechanisms and Consequences of Bacterial Persistence Within Breast Cancer Cells

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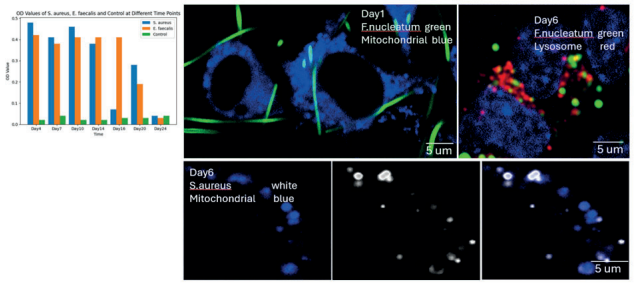
Increasing evidence suggests that tumor-associated bacteria can reside within cancer cells and influence tumor behavior, yet the mechanisms governing bacterial entry, intracellular persistence, and functional consequences remain poorly understood. In this study, we investigated the ability of different bacterial species to survive intracellularly in the triple-negative breast cancer cell line HCC1806. Screening multiple bacterial species revealed that Staphylococcus aureus and Enterococcus faecalis exhibit prolonged intracellular survival, persisting for up to approximately 20 days, whereas other tested bacteria were rapidly eliminated.
Using quantitative assays and imaging approaches, we observed that intracellular bacteria display heterogeneous subcellular localization. A fraction of bacteria localizes within lysosomal compartments, while others escape lysosomal confinement and associate with mitochondria or additional, yet-unidentified intracellular niches. These observations suggest that cancer cells provide multiple permissive environments that support long-term bacterial persistence.
Our central questions focus on how bacteria enter breast cancer cells, which host molecules facilitate bacterial uptake, and how intracellular bacteria evade clearance and maintain long-term survival. To address these questions, we performed CRISPR-based genetic screening and RNA sequencing, identifying candidate host genes potentially involved in bacterial entry and intracellular persistence. Ongoing functional validation experiments aim to determine whether these target genes regulate bacterial internalization and long-term survival within cancer cells. In parallel, advanced imaging approaches are being employed to further characterize bacterial behavior, intracellular trafficking, and spatial interactions with host organelles.



P28

Tankyrase inhibition demonstrates anti-fibrotic effects in preclinical pulmonary fibrosis models

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Iidiopathic pulmonary fibrosis (IPF) is a progressive and fatal lung disease with limited therapeutic options. Although transforming growth factor beta 1 (TGFB1, TGFβ) is a central driver of fibrosis, additional pathways, including Wingless/INT-1 (WNT)/β-catenin and yes-associated protein 1 (YAP), contribute to IPF pathogenesis, and inhibition of TGFβ alone has shown limited efficacy. Tankyrase (TNKS) 1 and 2, post-translational regulators of WNT/β-catenin and YAP signaling, therefore represent promising antifibrotic targets. OM-153, a potent and selective TNKS inhibitor, was evaluated across primary human lung fibroblasts, Scar-in-a-Jar assays, lung-on-a-chip models, and precision-cut lung slices (PCLS) stimulated with an IPF-relevant cytokine cocktail or TGFβ, as well as in bleomycin-challenged mice and PCLS from end-stage pulmonary fibrosis donors. OM-153 stabilized the TNKS substrates axin 1 (AXIN1) and angiomotin-like 1 (AMOTL1), suppressed WNT/β-catenin and YAP signaling, and reduced profibrotic extracellular matrix synthesis and deposition in vitro, in vivo, and ex vivo. These findings support selective TNKS inhibition as a mechanistically distinct antifibrotic strategy with translational potential for IPF.

P29

Tankyrase Inhibition Reprograms Melanoma Metastases to Overcome Resistance to PD-1 Blockade

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Immune checkpoint inhibitors targeting programmed cell death protein 1 (PD-1) have transformed melanoma treatment, but many tumors remain non-responsive, in part due to immune exclusion driven by canonical WNT/β-catenin signaling. To overcome this resistance, we evaluated the tankyrase 1/2 inhibitor OM-153, which suppresses WNT/β-catenin and Yes-associated protein (YAP) signaling, in combination with anti-PD-1 in immunocompetent melanoma models. Melanoma lung metastases were established in a syngeneic in vivo model using the B16-F10 cell line and treated with anti-PD-1, OM-153 or combination therapy. An efficacy study using bioluminescence imaging showed a significant reduction in tumor burden only in the combination group compared to control. Showing drug combination effects.

In parallel, to define OM-153-specific effects, B16-F10 cells were treated in vitro with OM-153 and analyzed by bulk RNA sequencing and quantitative proteomics. OM-153 induced broad transcriptional and proteomic remodeling of pathways associated with WNT/β-catenin, Hippo, PI3K, and Notch signaling. Notably, OM-153 enhanced signaling driven by the key melanoma transcription factor MITF, and complementary experiments demonstrated increased nuclear MITF localization following treatment. MITF stabilization has previously been linked to altered antigen presentation, PD-L1 expression, cytokine release, immune cell infiltration, enhanced CD8+ T cell cytotoxicity, and increased sensitivity to immune checkpoint inhibition. To test whether OM-153 increases melanoma cell susceptibility to T-cell cytotoxicity and promotes dendritic cell recruitment, we set up in vitro cytotoxicity and migration assays. OM-153 pretreatment of B16-F10 cells increased the tendency for T cell-mediated killing, and in a transwell assay, OM-153 treated B16-F10 cells attracted certain dendritic cell subsets, suggesting altered susceptibility to cytotoxic killing and chemokine release. Together, these findings suggests that tankyrase inhibition can reprogram melanoma cells and the tumor microenvironment to overcome checkpoint inhibitor resistance. Identifying MITF as a potential key regulator of OM-153-induced programs and position OM-153 as a mechanistically targeted partner for PD-1 blockade.

P30

Exploring the different conformations of hepatic transporters

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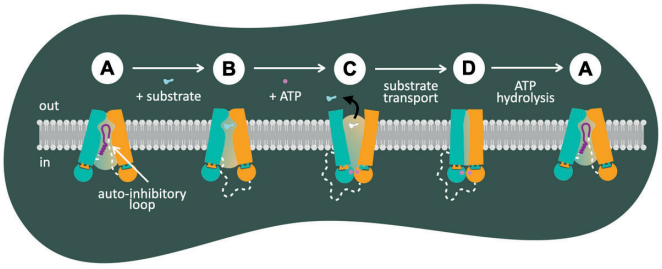
Bile salts play a crucial role in the digestion and absorption of dietary fats in the small intestine, particularly in the duodenum. The human bile salt exporter ABCB11, is an ATP-binding cassette (ABC) transporter essential for the enterohepatic circulation of bile salts. Located in the apical membrane of hepatocytes, BSEP actively transports bile salts into bile canaliculi against a steep concentration gradient, a process driven by ATP hydrolysis. Maintaining low intracellular concentrations of bile salts is vital, as their accumulation can disrupt cellular membranes and promote the formation of reactive oxygen species, leading to hepatocyte injury. Mutations in the BSEP gene (ABCB11) impair bile salt export, contributing to liver diseases such as cholestasis, characterized by bile salt accumulation, inflammation, and hepatocyte necrosis or apoptosis. Structurally, ABCB11 consists of two transmembrane domains (TMDs), each comprising six α-helices, and two nucleotide-binding domains (NBDs) with conserved motifs involved in ATP binding and hydrolysis. During its transport cycle, ABCB11 alternates between multiple conformational states: an inward-facing (IF) conformation for substrate binding, and an outward-facing (OF) conformation, induced by ATP binding, for substrate release into the bile canaliculus. Hydrolysis of ATP resets the transporter to the IF state, completing the cycle. In this study, we employed cryo-electron microscopy (cryo-EM) and single-particle analysis to investigate the structure of ABCB11 reconstituted in nanodiscs in the presence of ATP and chenodeoxycholic acid (CDCA), a major bile salt. Our analysis revealed two distinct inward-facing conformations: IFwide, featuring an autoinhibitory loop that blocks substrate entry, and IFnarrow, characterized by tightly associated NBDs with bound ATP but lacking substrate, likely representing a post-translocation state. These findings provide new insights into the dynamic mechanism of ABCB11 and its critical role in bile salt transport.



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