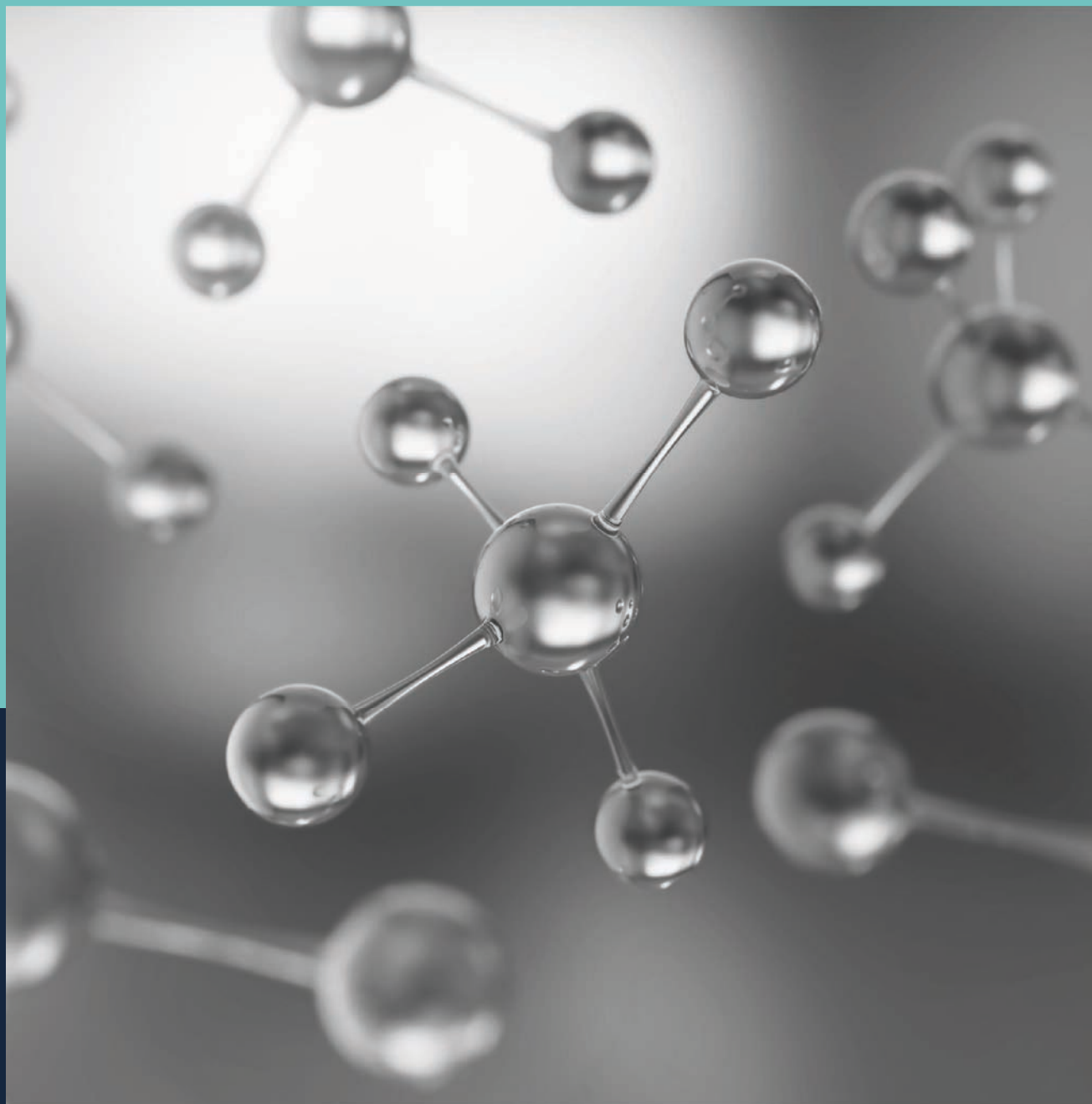
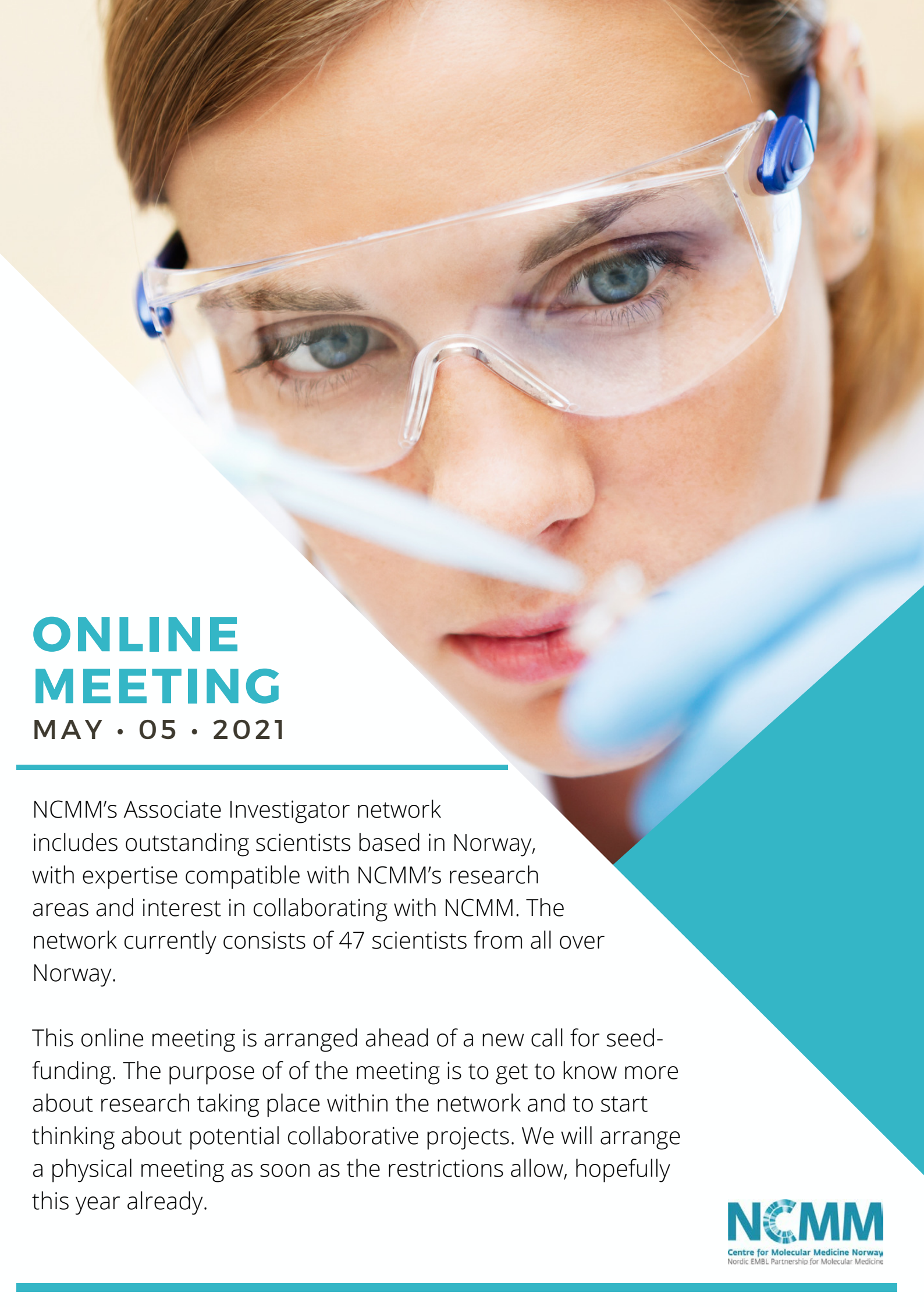




NCMM ASSOCIATE INVESTIGATORS' NETWORK MEETING 2021



ONLINE MEETING

MAY • 05 • 2021

NCMM's Associate Investigator network includes outstanding scientists based in Norway, with expertise compatible with NCMM's research areas and interest in collaborating with NCMM. The network currently consists of 47 scientists from all over Norway.

This online meeting is arranged ahead of a new call for seed-funding. The purpose of the meeting is to get to know more about research taking place within the network and to start thinking about potential collaborative projects. We will arrange a physical meeting as soon as the restrictions allow, hopefully this year already.

PROGRAMME

10:00 - 10:15

WELCOME AND OVERVIEW OF
SEED FUNDING OPPORTUNITIES BY
DIRECTOR OF NCMM, JANNA SAARELA

10:15 - 11:15

PITCHES FROM NCMM GROUP LEADERS

11:15- 11:35

BREAK

11:35- 12:45

SHORT PRESENTATIONS BY ASSOCIATE
INVESTIGATORS. 3 PARALLEL SESSIONS

12:45 - 13:30

LUNCH BREAK

13:30 - 14:40

SHORT PRESENTATIONS BY ASSOCIATE
INVESTIGATORS. 3 PARALLEL SESSIONS

14:40 - 15:00

BREAK

15:00 -15:25

ONGOING COLLABORATIONS:
PRESENTATIONS BY CAMILA ESGUERRA
AND LYNN BUTLER

15:25 - 15:30

CLOSING REMARKS BY JANNA SAARELA

15:30 - 16:00

OPPORTUNITY FOR ONE-TO-ONE
DISCUSSION IN THE BREAKOUT ROOMS

**A SLACK CHANNEL IS AVAILABLE FOR
INTERACTION AND DISCUSSION**

[HTTP://BIT.LY/NCMMNETWORK2021](http://bit.ly/ncmmnetwork2021)



NCMM GROUP LEADERS

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Research keywords

Zebrafish,
disease modelling
and mechanisms,
drug discovery,
toxicology,
precision medicine,
neurological disorders

Collaboration Interests

Neurodevelopment,
neurological disorders,
rodent disease models,
brain imaging,
glial biology,
bioinformatics (signaling
networks, biomarkers),
'omics' methods,
drug discovery of body text



Research summary

The overarching aim of the Chemical Neuroscience Group research program is to determine how genetic mutations induce a cascade of events that lead to a disequilibrium in brain development and homeostasis. We seek to elucidate the underlying mechanisms involved in the etiology of pharmacoresistant epilepsies and neuropsychiatric disorders, by probing the function of novel disease-associated gene variants. We use genetically engineered zebrafish and pharmacological models for performing phenotypic analysis and chemical modifier screens to identify novel disease-relevant pathways, pharmacological tools and drug leads. These models and neuroactive small molecules will serve as valuable tools towards understanding the development, function, and diseases of the brain.

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Research keywords

Biomembranes,
Bionanotechnology,
Microfluidics

Collaboration Interests

Biosensing,
Bio/cell mechanics,
Single-Cell Pharmacology

Research summary

My research programs aim to understand the biophysical and materials science aspects of complex biological problems which involve lipid membranes. I bring together biomembranes with solid interfaces as well as with micro and nanotechnology, to mimic the behavior of living cells and observe the unique membrane interactions with high resolution microscopy.

Emma Haapaniemi

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Research keywords

CRISPR,
gene editing,
primary immunodeficiency,
T cells

Collaboration Interests

Basic immunology,
T cells, human hematopoietic
stem cells, mouse infection
models, human xenograft
mice models

Research summary

Our group focuses on developing targeted therapies for rare immunological conditions, such as primary immunodeficiency diseases and immunological conditions of unknown origin. We aim to optimize the CRISPR-Cas gene editing technology as a gene therapy in these diseases, and stratify the existing therapies – such as biologic drugs and small molecule inhibitors – to better target the underlying molecular pathways that malfunction in individual patients. We utilize custom genomics methods and high-throughput screening to understand immune diseases and optimize CRISPR-Cas9 genome editing towards safe and efficient use in patients. We work with cell models and patient material, and strive to create teams with diverse expertise in molecular and computational biology and clinical medicine.

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Research keywords

Network science,
computational biology,
network medicine,
cancer genomics,
gene regulation

Collaboration Interests

We'd be happy to collaborate on projects that require computational tools, large-scale data analyses, statistics analysis, or network approaches to analyze data.

Research summary

My group develops computational tools that integrate different omics data types to model large-scale, genome-wide gene regulatory networks for individual samples. We also have a focus on developing new approaches to analyze these large-scale networks and network rewiring between different biological conditions, using techniques from network science. We have a main interest in applying our computational tools to better understand what drives cancer and cancer heterogeneity. We have a pan-cancer focus, but also work on specific applications in sarcomas and breast cancer. In addition to modeling network rewiring in cancer, we are interested in tissue-specific gene regulation in general, and in modeling the disruption of gene regulation in other complex diseases.

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Research keywords

Phosphatases/PP2A/TOR
signaling/Mitosis/Differentiation/
Quiescence-Proliferation

Collaboration Interests

Cell division/Mechanisms of
differentiation/Control of gene
expression/Chromatin
regulation/Cell fate decisions

Research summary

The work in my laboratory is focused on understanding the role of regulated phosphatase activity during cell cycle progression, differentiation and quiescence, using the fission yeast *Schizosaccharomyces pombe* as model organism. We are particularly interested in phosphatases belonging to the PP2A family, which in the last years have been shown to play instrumental roles in counteracting the activity of cyclin dependent kinases (CDKs). Moreover, work from our group and others has shown that PP2A is central to TOR signalling and hence a key element in the responses to nutritional stress. Therefore, we aim at identifying relevant targets of the different PP2A subcomplexes that contribute to their cell cycle functions and that link environmental cues (such as nutrient availability) to the proliferation/quiescence decision.

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Research keywords

Strutural Biology,
Membrane protein structure,
Structure-based drug discovery,
Cryo-EM,
Electron microscopy



Research summary

The Luecke Group aims to better understand the structure and function of integral membrane proteins. We also aim to identify and develop drugs that inhibit or re-activate our targets.

Anthony Mathelier

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Research keywords

Our computational biology research programme focuses on gene expression regulation and the mechanisms by which it can be disrupted in human diseases such as cancers.

Collaboration Interests

Gene expression regulation,
microRNAs,
cancer somatic alteration and
gene expression alteration,
CRISPR screening of cis-regulatory
regions,
Cap Analysis of Gene Expression



Our group's research program aims to improve our understanding of the non-coding portion of genomes by deciphering the cis-regulatory code controlling gene expression. The derived knowledge benefits our capacity to study the mechanisms by which gene expression can be disrupted in cancers. To achieve this goal, our group develops and uses computational approaches and resources to analyze in-house and public multi-omics data.

Specifically, our focus lies within the following main lines of research: (i) develop computational tools and resources to model and map genome-wide transcription factor (TF)-DNA interactions; (ii) characterize somatic cis-regulatory alterations that alter gene regulatory networks in cancer cells; (iii) decipher patient-specific cis-regulatory activity to provide cis-regulatory signatures and onco-enhancers in cancer subtypes.

The ultimate goal is to conduct basic research that will fuse experimental approaches with the parallel development of computational methods to patient samples. This approach has the potential to shed light on the molecular mechanisms underlying transcriptional dysregulation in cancers and deliver new knowledge in cancer research that will benefit cancer patients in the future.

Janna Saarela

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Research keywords

Rare diseases, primary immunodeficiency, autoimmunity, immune dysregulation, lymphoproliferation, hematological malignancy, multifactorial diseases, disease risk, genomics, population cohorts, health data,

Collaboration Interests

Primary immune deficiencies, disease models, immune cell biology, multifactorial diseases, disease modeling



Research summary

Our long-term research goal is to identify and understand mechanisms causing autoimmunity and immune dysregulation. We aim to improve understanding of biological pathways and pathogenic mechanisms behind common and rare immune diseases, specifically multiple sclerosis (MS), primary immune deficiencies (PIDs) and rare hematological diseases. We aim to identify novel gene defects causing rare diseases to trigger functional studies of the consequences of these genetic variants to shed light on pathogenic mechanisms of the disease and normal functions of the immune system. This may also allow repurposing of existing immune modifying treatments, or identification of novel treatment targets. We further aim to develop methods for safe sharing of sensitive health data, and utilize multi-omics, clinical and environmental information to improve the diagnostics and classification of immune diseases and develop risk models for early detection and potentially prevention of immune and age-related diseases.

Nikolina Sekulic

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Research keywords

The Sekulic Group is interested in understanding the molecular mechanisms that assure genomic stability during cell division.

Collaboration Interests

Chromatin, epigenetics,
centromere,
kinetochore,
cancer,
protein kinase,
structural biology,
cryoEM,
protein dynamics,
hydrogen-deuterium exchange
coupled to mass-spectrometry

Research summary

Our research focuses on centromeres. We want to understand:

- 1) What are the structural determinants of centromere formation and maintenance?
- 2) How does the centromere recruit major effector proteins in mitosis?
- 3) What is the molecular basis for the activation of central mitotic kinase, Aurora B?

Our Lab is equipped with state-of-the-art instrumentation for structural biology and mass spectroscopy. We also collaborate closely with experts in yeast genetics and cell cycle regulation.

Judith Staerk

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Research keywords

Stem cells, pluripotency, cell fate, mitochondria, epigenetics

Collaboration Interests

Metabolism,
gene regulation,
organelles,
epigenetics,
signaling

Research summary

In developmental biology a major interest is to identify the molecular mechanisms that direct cell fate decisions and define how stem cells renew and differentiate into more specialized cell types. Pluripotent stem cells can renew indefinitely, while retaining the ability to differentiate into any cell type found in the body. Pluripotency and differentiation are tightly regulated through transcription factors as well as epigenetic mechanisms and metabolism. My group uses human pluripotent stem cells to understand the interplay between mitochondria, the cells' metabolism and gene regulation during pluripotent stem cell renewal as well as early blood and neuronal cell specification.

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Research keywords

Computational Oncology, Clinical
Cancer Genomics, Pediatric Brain
Tumors, Diffuse Intrinsic Pontine
Glioma, Diffuse Midline Glioma,
Rare Disease Genetics

Collaboration Interests

Gut-brain axis and genetic
tumor syndromes, pre-cancer
atlas, laser capture
microdissection

Research summary

The Computational Oncology research group is dedicated to studying the development of pediatric brain tumours and identifying personalised treatment strategies. We develop computational methods for precision diagnostics, analysis and interpretation of clinical cancer genomes, and molecular and clonal evolution of brain tumour (epi)genomes. Our lab works closely with translational teams and clinical trial networks to improve outcomes for children with diffuse midline glioma and high-grade glioma.



NCMM ASSOCIATE INVESTIGATORS

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Research keywords

Computational Systems Medicine
in Cancer

Collaboration Interests

Precision oncology, AI, machine
learning, drug sensitivity testing,
CRISPR-Cas9



Research summary

Our group has expertise in integrating multi-omics profiling and clinical information from cancer patients using mathematical and statistical approaches such as machine learning and network modeling. The medical aim is to optimize treatment outcomes for individual patients using maximally predictive models and minimal biomarker signatures that enable real-time and cost-effective routine diagnostics and prognosis. We believe that combining functional, molecular and genomic profiling information is critical for next-generation precision medicine applications, where integrative modeling and clever use of big data will pinpoint effective and selective targets for personalized therapies.

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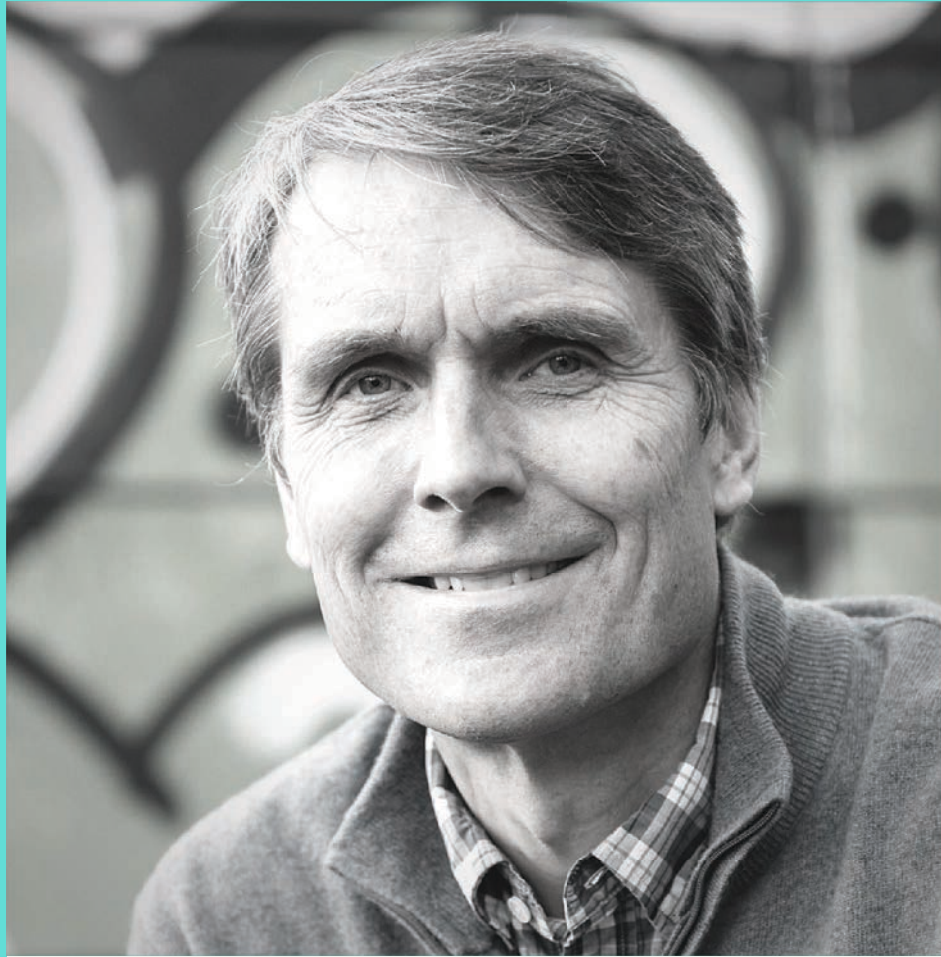
[https://www.med.uio.no/norment/
english/](https://www.med.uio.no/norment/english/)

Research keywords

Neuroscience
Genetics,
Psychiatry

Collaboration Interests

Psychiatry and brain-related disorders, genomics, brain imaging, precision medicine research, statistical genetics, big data prediction/stratification



Research summary

At the Centre of Excellence NORMENT I combine my basic neuroscience, genetics and clinical expertise to reveal mechanisms of psychiatric disorders. Due to the large sample sizes needed for progress in psychiatric genetics, I co-founded several international consortia, and contributed to important breakthroughs in psychiatric genetics and imaging. I have also developed biostatistical methods to integrate different dimensions of big data, including clinical characteristics, brain MRI, cognitive function, and DNA variation. These tools are leveraged in the large Nordic biobank/registry network infrastructures I have developed partly supported by recent EU grants, and led to discoveries of genetic factors and pleiotropic variants for a range of brain-related disorders and traits.

Thomas Arnesen

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Research keywords

Cancer, Endocrine tumors,
Congenital disorders, Proteins,
Protein modifications

Collaboration Interests

Functional protein studies,
Protein modifications, Model
systems, yeast, zebrafish, C.
elegans,

Research summary

The focus of my lab is the biochemistry and molecular biology of proteins and protein modifications, in particular N-terminal acetyltransferases (NATs) and N-terminal acetylation. We are using eukaryotic model systems combined with in vitro approaches to elucidate the basic mechanisms and the clinical importance of these protein modifications. So far we and our collaborators have i) elucidated the presumed complete human NAT-machinery including functionally defining several uncharacterized genes/proteins, ii) quantitatively analysed the N-terminal acetylomes of yeast and human cells, iii) developed novel assays for NAT-profiling, iv) gained mechanistic insights of the cellular effects following NAT-knockdown, v) contributed to the understanding of the physiological and clinical importance of NATs by revealing the importance of NatA for cancer cell survival, the link between NatA and cancer cell drug sensitisation, and by identifying genetic disorders caused by NAT-variants including their functional characterization, vi) solved the first structures of the NATs, and vii) developed the first potent NAT-inhibitors.

The NAT enzymes are of great interest in relation to cancer, neurodegenerative diseases, congenital disorders and hormone regulation

Magnus Aronsen

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Research keywords

Experimental cardiology, aiming to develop new treatments for cardiac disease by identification of molecular mechanisms that control ion transporters or gene networks in the heart

Collaboration Interests

Molecular biology techniques such as protein-protein interaction assays, RNA-seq, ChIP-seq and corresponding bioinformatics analyses.

Our main competence: Cellular electrophysiology and *in vivo* preclinical models and phenotyping.

Research summary

The laboratory for experimental cardiology aims to identify molecular mechanisms that regulates short term and long term cardiac function. The group focus on compartmentalized cAMP-PKA regulation of ion transporters in cardiomyocytes, with special focus on phosphodiesterases and its role in cardiac arrhythmias. The group has an expertise in preclinical and *in vivo* phenotyping of rodent models of heart disease, and gene program regulation by histone methylations is another focus in the group. The NAT enzymes are of great interest in relation to cancer, neurodegenerative diseases, congenital disorders and hormone regulation.

Lorena Arranz

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Research keywords

Use of stem cells and their niche
as therapeutic targets in
hematological malignancies

Collaboration Interests

Epigenetics, single-cell omics,
hematopoietic stem cells,
microenvironment, CRISPR-
Cas9, acute myeloid leukemia,
myeloproliferative neoplasms,
clinical trial, inflammation



Research summary

Long life expectancy is resulting in aged societies and a remarkable increase in age-related diseases, including cancer. Stem cells self-renew and provide the source for replenishing mature cells in the organism throughout its life. These fascinating abilities ensure tissue regeneration, but must be fine-tuned regulated as their imbalance may contribute to both, aging and cancer. Stem cell behavior relies on integration of cell-autonomous and extracellular signals received from their surrounding stem cell niche. My research interest focusses on the processes that control stem cell behavior. Taking the hematopoietic system as the primary model, my group aims at understanding the mechanisms of stem cell malignant transformation using an integrative perspective that considers cell-autonomous alterations in the stem cell and remodelling of the stem cell niche. My goal is the identification of novel and efficient therapeutic targets of clinical interest that will improve survival rates and quality of life in patients of hematological malignancies

Charlotte Boccara

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Research keywords

System neurosciences, Sleep,
Cognitive development,
Electrophysiology, Neural coding,
Hippocampus, Spatial cognition,
neurodevelopmental disorders

Collaboration Interests

Neurodevelopmental disorders and
sleep to test functional hypotheses
and elicit translational projects.

Zebra fish models of
neurodevelopmental disorders
(autism, schizophrenia) to make light
of the molecular pathways and
network mechanisms that may link
early sleep disturbance and E/I
imbalance (Esguerra).

Investigate the interplay between
poor sleep and MS flares (Saarela).

Bioinformatics; developing
computational tools to study sleep.

Develop transgenic and
optogenetics tools to manipulate
sleep.



Research summary

Sleep is essential for healthy cognitive development. The last decade has seen a dramatic increase in chronic sleep deprivation among children that amounts to what is now a public health epidemic. Despite the substantial societal impact of sleep deprivation on cognitive neurodevelopmental disorders, we still know very little about the neural mechanisms that promote cognitive development during sleep.

The Boccara lab mission is to address this crucial gap in our knowledge with innovative research projects at the junction of developmental neurobiology, system neuroscience and sleep research. We propose to combine miniaturised electrophysiological in vivo recording devices with advance viral and molecular tools to monitor and manipulate sleep in developing rodents.

In addition, we use computational methods to analyse how representations are encoded and updated both in the adult and the developing brain.

Lynn M. Butler

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Research keywords

We are interested in human endothelial cells, with a specific focus on endothelial specifically expressed genes and their role in cell function

Collaboration Interests

Endothelial cells, in vitro model vessels, primary cell culture, plasma proteomics, RNAseq, cell profiling, thrombosis, cardiovascular risk fact

Research summary

We use bioinformatic based analysis of RNAseq data to identify genes that are specifically expressed in endothelial cells in different human organs. We study the expression of these candidates in population based or clinical cohorts, using both plasma proteomics and genetics, to identify candidates that are associated with endothelial dysfunction or cardiovascular disease development. We investigate the function of such candidate genes in endothelial cells, using model vessels generated using human cells in culture, studying processes such as leukocyte recruitment and thrombosis development from whole blood. We also have an interest in the temporal response of endothelial cells to inflammatory mediators, particularly in the less well studied later phases, including response resolution.

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Research keywords

Epigenetic mechanisms in obesity
and fat distribution

Collaboration Interests

We are looking for collaboration within (epi) genetics of complex diseases with a special interest in integrating “omics” data in networks describing sample-specific interactions. Integration of cell type-specific and sample-specific methylation and RNA seq data will enable us to touch upon different dimensions of cell-state activities. An overlap of genetic data with epi-transcriptomic data, gene expression and open chromatin regions by bioinformatics tools will open an avenue to describe patient-specific biological networks in individuals presenting different co-morbidities (e.g. T2D, insulin-resistance etc.).



Research summary

We are working on “Functional Genetics of Obesity” with main research interests in genetic and epigenetic mechanisms in obesity, fat distribution and relevant co-morbidities such as type 2 diabetes (T2D). Individual fat distribution can predict co-morbidities better than overall fat mass and patients with high visceral fat mass are more prone to T2D and metabolic syndrome. In our research program, we generate adipose tissue depot-specific (epi) genetic/transcriptomic data in human adipose tissue, that shall, in the long-run, help to identify patient-specific patterns to pave the road towards precision medicine in obesity research.

Simona Chera

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Research keywords

Omics,
molecular networks,
cell fate,
cell conversion,
transdifferentiation,
disease modeling

Collaboration Interests

Omics (proteomics,
transcriptomics, scRNA),
molecular networks and
pathway analyses,
cell differentiation,
regeneration

My research is directed at mapping and exploiting the master regulators controlling the regeneration brakes. These are molecular switches acting as cell-plasticity brakes in higher vertebrates. They block the onset of regeneration, by actively maintaining the cell fate, thereby ensuring the strict regulation of cell identity and/or numbers. For studying these aspects, we employ in my laboratory two strategies based on distinct types of homeostasis disruption. First, we induce minor, yet progressive, changes in homeostasis, by exploiting single gene mutations known to promote the natural gradual decay of a specific cell compartment and assess its impact on cell identity of the neighbouring cell populations. We targeted the developmental regulator Hnf1a (involved in kidney, gut, liver and pancreas development). Genetic cell tracing, timed conditional gene expression and diverse dynamic omics assays (proteomics, single cells and bulk RNAseq) revealed a critical role of Hnf1 α in cell identity reinforcement. We also use differentiating human induced pluripotent stem cells (hiPSC) for demultiplexing the role of key regulators in the cell fate acquisition and confinement following homeostasis disruption. We recently characterized the positive impact of mechanical forces on cell identity acquisition via an integrin-based mechanism (Legøy*, Vethe* et al.[Chera], Sci. Reports, 2020). This line of research is continued through a NCMM-financed interdisciplinary collaboration with Dr. Irep Gozen. Moreover, we pinpointed an essential role of the Hnf factors (HNF1A and HNF4A) in restricting and maintaining islet cell identity in vivo (Legøy et al.[Chera], Front. Cell Dev. Biol, 2020), a beneficial effect reversed by mild homeostatic disruption such as in vivo hyperglycemia-induced oxidative stress resulting in the accumulation of cells with mixed identity (Legøy et al.[Chera], Acta Physiol., 2020).

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Research keywords

Posttranscriptional gene regulation; RNA; RBP; hypothermia; hibernation; suspended animation

Collaboration Interests

Structural basis of RNA/protein interactions, gene regulatory networks, neuroprotection & drug screens

Research summary

I am chiefly interested in gene regulation, particularly posttranscriptional. Among other findings, my laboratory showed that, in addition to widely publicized transcription factors and chromatin modifiers, certain conserved RNA-binding proteins function as cytoplasmic “roadblocks” to reprogramming into pluripotency during animal development. In the future, following this line of research, we will continue studying novel mechanisms of RNA regulation. Additionally, we became interested in cellular responses to cold. Thus, the second line of future research focuses on molecular mechanisms facilitating cold survival, with exciting biomedical implications.

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Research keywords

Glia-neuron interaction,
neuroscience, sleep, epilepsy,
migraine

Collaboration Interests

Two-photon microscopy,
electrophysiology, genetically
encoded sensors and
actuators, sleep, migraine,
epilepsy

Research summary

My research is mainly focused on astrocyte physiology in the healthy and dysfunctional brain. By in vivo optical imaging I study in the interaction between glial cells, neurons, blood vessels and the extracellular fluids of the brain. I study the sleeping brain and mouse disease models for epilepsy, migraine and Alzheimer's disease, and my research goal is to elucidate the physiological functions of the glial cells, with the potential of identifying targets for future treatment of brain disorders.

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Research keywords

Glia-Multidisciplinary approach to investigate mechanisms of learning and memory.

Key words; animal models, systems neuroscience, in vivo imaging, electrophysiology, learning and memory, behavior interaction, neuroscience, sleep, epilepsy, migraine

Collaboration Interests

Translational medicine, AI research, molecular biology, neuroscience,

Technology we use: in vivo multiphoton laser scanning microscopy and electrophysiology, confocal microscopy, animal behavior, genetic perturbations, viral vectors, optogenetics, anatomical tracing and histology



The brain shows an outstanding ability to adapt, learn from experience and use this knowledge to quickly learn new domains. In my research, we take an interdisciplinary approach to understand mechanisms of brain plasticity and memory processing. We have recently focused on the interplay between specialized extracellular matrix, called perineuronal nets (PNNs) and neuron network function. We have shown how PNNs are critical for establishing new representations and for recall of remote memories. This strongly indicates that PNNs stabilizes neural networks both at short and long time scales. We are currently tapping into the endogenous regulation of the PNNs to directly assess their role for neural network and cognitive function. We are also interested to use our animal model approaches to dissect mechanisms of mental disorders. For this, we combine targeted genetic perturbations with in vivo measurements of neural activity and behavior. Finally, for deep insight into the processes we investigate, we integrate computational approaches in close collaborations with experts in computational physics. Lately, we have established an activity integrating AI research with experimental neuroscience for insight into brain function and improve performance of AI systems.

Joel C. Glover

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Research keywords

The Laboratory of Neural Development and Optical Recording is dedicated to the study of the functional development of brain and spinal cord networks with special focus on motor and premotor circuitry, and the use of human stem cell-derived neurons and glia to model neurological diseases *in vitro*.

Collaboration Interests

Technical expertise and competence,
Electrophysiology (extracellular,
sharp electrode, whole cell and
patch clamp), Optical recording (non-
genetic calcium, genetic calcium,
non-genetic voltage sensitive dye),
Advanced neuronal tract tracing and
virus-mediated trans-synaptic
tracing, Optogenetic stimulation and
inhibition,
Immunohistochemistry, *in situ*
hybridization, qPCR, RNAseq, Small
animal models, *Ex vivo* preparations
of brain and spinal cord



Our research focuses on several areas related to the development and regeneration of motor circuits in the brain and spinal cord, and on the *in vitro* modeling of human neurological diseases affecting the motor system. We have a major focus on mammalian and avian reticulospinal, vestibulospinal and vestibulo-ocular circuits, encompassing the developmental patterning and molecular characterization of motoneuron and projection neuron subpopulations, anatomical studies of synaptic connectivity, and functional studies of synaptic activation patterns using optical and electrophysiological recording.

We are heavily involved in characterizing the molecular mechanisms underlying regenerative regeneration in the embryonic spinal cord, wherein spinal cord tissue is replaced by compensatory proliferation and differentiation, and of spontaneous functional regeneration in the neonatal spinal cord, wherein compensatory synaptic reorganization leads to functional recovery not seen in the adult spinal cord. We have a translational research program where we generate neurons, glia, and other cell types from human patient-derived induced pluripotent stem cells (iPS cells) and use these in advanced compartmentalized microfluidic platforms to model neurological diseases such as ALS, spinocerebellar ataxias and dystonias. Lastly, we have a keen interest in brain evolution channeled through comparative studies of vertebrate brainstem patterning and molecular and cellular characterization of urochordate (tunicate) nervous systems.

Victor Greiff

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Research keywords

Systems immunology,
antibody,
T cell,
machine learning

Collaboration Interests

Network analysis,
machine learning,
high-throughput screening,
structural biology

Research summary

Dr. Greiff's group develops machine learning, computational and experimental tools for analyzing antibody and T-cell repertoires to develop immune-repertoire-based immunodiagnostics and immunotherapeutics.

Gunnveig Grødeland

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Research keywords

Immunology and novel vaccine
development

Collaboration Interests

Immunology, vaccine
development, antibody
functionality, mouse models,
human clinical evaluation, T
cell subsets, obesity,
immunological history,
immunome, and genetic
background.



A main objective for my group is to study immunological mechanisms behind protective immunity, and use the generated knowledge for development of improved vaccine formats against variable pathogens. Current vaccines are still mostly being developed by the principle established by Edward Jenner in the late 18th century: A less pathogenic version of a virus is injected to protect against the threatening version. While this principle has proven highly successful in the past, it falls short when aiming for broad protection against highly mutagenic pathogens, or pathogens that have developed mechanisms to thwart the immune system. The SARS-CoV-2 pandemic represents the breakthrough for subunit vaccines, which enable steering of immune responses towards the most relevant antigens for protective immunity. However, their efficacy is dependent on identification of an effective correlate of protection, which may differ between different groups of the population and between individuals. The aim for my group is thus to identify the immunological responses to an antigen at the group and individual levels, with the aim of identifying new strategies that can tailor vaccine development more specifically to formation of relevant immune responses under different circumstances

John-Bjarne Hansen

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Research keywords

Identify novel risk factors and unravel molecular mechanisms for venous thromboembolism in order to improve risk stratification and disclose targets for prevention.

Collaboration Interests

Genomics, proteomics,
metabolomics,
immunothrombosis

Research summary

Identify novel risk factors and unravel molecular mechanisms for venous thromboembolism in order to improve risk stratification and disclose targets for prevention. To achieve this I have a translational approach including clinical epidemiological studies along with experimental in vitro and in vivo (animal) studies.

Nils Halberg

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Research keywords

Obesity,
Cancer (breast and pancreas),
Metabolism,
Epigenetics,
Systems Biology

Collaboration Interests

- i) Developments of new technologies;
- ii) Tumor evolution/adaptation mechanisms;
- iii) computational pipelines

Research summary

My lab is applying systems-based approaches to investigate how the physiological state of the host affects tumor initiation and progression. Currently, our main focus is on how obesity links to tumor initiation through epigenetic remodeling. To this end, we combine obese animal model with transplant tumor systems. Systems approaches comprising single cell profiling of the tumor ecosystem by mass cytometry (cell suspension and imaging-based), loss-of-function screens in the in vivo functional tumor microenvironment and single cell epigenetic/transcriptional regulation of obesity-induced reprogramming events are used to identify key molecular mechanisms.

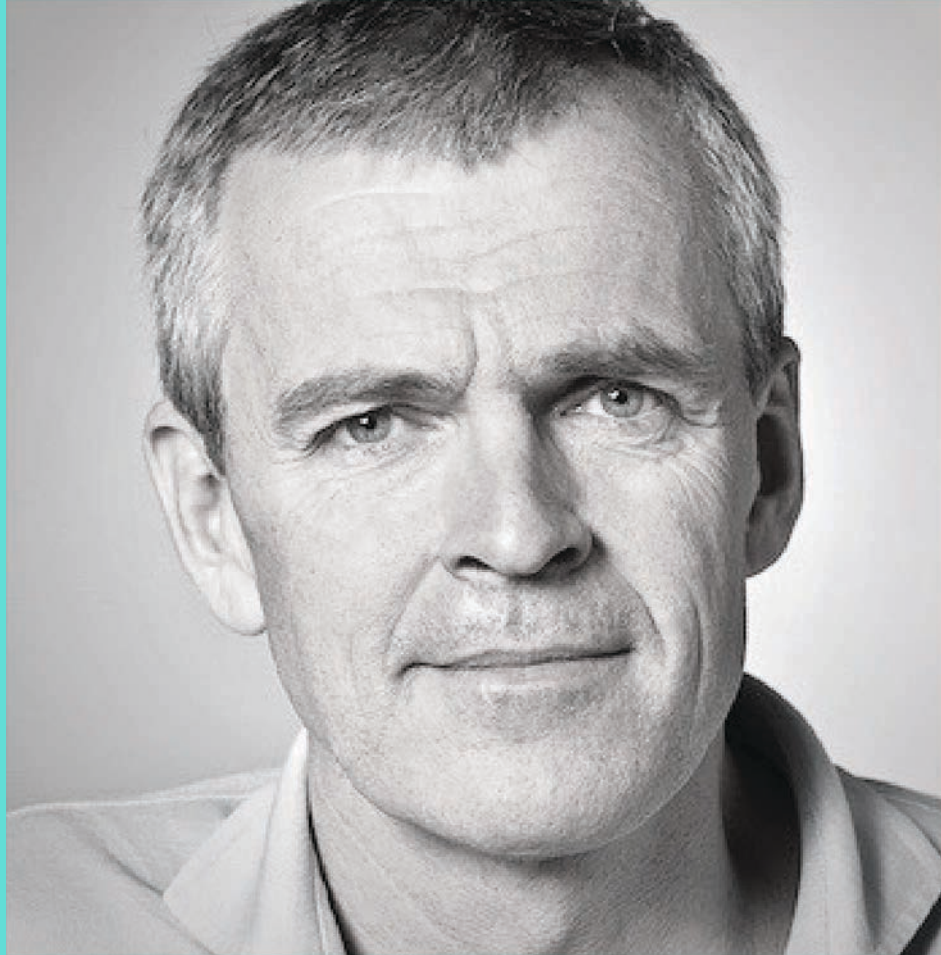
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Research keywords

Inflammation,
drug profiling and
therapeutic resistance

Collaboration Interests

Single cell multi-omics, drug
targeting, recombinant human
antibodies (we have a phage
display platform and an industrial
collaboration on synthetic libraries)

Research summary

We have productive experience in chemokine biology and in recent years the cloning and characterization of interleukin-33, a proinflammatory cytokine that appears to act as an alarmin. The mouse has a tissue expression of IL-33 that is very different from that seen in other mammals – including man – and we are therefore currently characterizing IL-33-deficient rats. We are also developing one of the Notch receptors as a drug target, based on efficacy in rodent arthritis and lack of side effects, moving to assessment of Notch receptor inhibition in mixed cell cultures from rheumatoid arthritis-derived synovial cultures. We know the identity of cells that that have active receptor signalling and are pursuing single cell transcription data to assess the modulation of Notch signalling at the molecular level in a therapeutic context.

Helene Knævelsrud

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Research keywords

Regulation of autophagy *in vivo* and
mechanisms of leukemia and
kidney cancer development using
Drosophila, cell culture and patient
samples.

Collaboration Interests

Autophagy, hematopoiesis,
leukemia, kidney cancer.

Technology/methods: *Drosophila*
stem/progenitor cells,
computational analysis of screen
results, fly models of (rare) disease.



My project group "Mapping and disrupting cancer circuits" is focused on two main goals: 1) Unraveling the mechanisms of leukemia development and 2) Understanding how autophagy is switched off *in vivo*. My team uses *Drosophila melanogaster* as a model organism, to take advantage of the unique tools and ability for rapid unbiased *in vivo* screening that this organism offers. In addition, we are following up on results generated with our fly models in mammalian cell culture and patient samples, especially related to kidney cancer. I have generated a fruit fly model of leukemia based on expression of the human leukemic oncogene MLL-AF4. Using this model system I have discovered that MLL-AF4 expression in the hematopoietic system of *Drosophila* leads to development of leukemia-like disease, whereas expression of the very same oncogene in a non-hematopoietic tissue results in growth restriction. We use this experimental system to tease apart mechanisms of leukemia development and tumor defense in a living organism. Upon starvation, cells and tissues activate the lysosomal degradation pathway autophagy, which provides energy and building blocks to sustain essential cellular functions. Importantly, cells must also turn off autophagy when nutrient supplies are replenished, because unrestricted autophagy is harmful to cellular fitness. Surprisingly little is known about how autophagy is terminated, especially in the context of a multicellular organism. My team works on uncovering novel mechanisms of autophagy termination. In a follow-up project with clinical collaborators, my team is investigating the role of autophagy in a rare inherited form of kidney cancer. We are also developing one of the Notch receptors as a drug target, based on efficacy in rodent arthritis and lack of side effects, moving to assessment of Notch receptor inhibition in mixed cell cultures from rheumatoid arthritis-derived synovial cultures. We know the identity of cells that have active receptor signalling and are pursuing single cell transcription data to assess the modulation of Notch signalling at the molecular level in a therapeutic context.

Arne Klungland

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Research keywords

Epitranscriptomic regulation,
epigenetics, DNA repair and
genome stability, embryology,
meiosis

Collaboration Interests

We collaborate with excellent
national groups, and also research
groups in China, Holland, UK and
USA. Our main interests for
collaboration include the
contribution of novel mice models
for understanding epigenetic and
epitranscriptomic reprogramming.
We would also like to contribute
expertise in mechanistic studies on
genome regulation and stability for
cancer, stem cell biology and the
evolution and adaptation of
organisms.



Research summary

While the core building blocks of our DNA, RNA and proteins were characterized decades ago, recent research has unraveled a remarkable diversity of chemical modifications that modify the coding properties of bases in DNA and RNA and the amino acids of a protein. Such chemical groups are often dynamic, e.g. bases can be methylated and demethylated, providing a reversible gene-regulation mechanism.

Our aim is to identify writers, readers and erasers of such marks and to gain understanding of their biological relevance. We are particularly interested in the reprogramming of the human genome in meiosis and in the preimplantation embryo. Moreover, key mechanisms for gene-regulation in these early stages of a new life might also be critical for understanding cancer development.

Our current studies also include several novel models for post-translational modifications in RNA. The reversible nature of some chemical modifications of RNA is a very recent discovery. Most of our studies rely on novel mutants in various model organisms.

Dirk Linke

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Research keywords

Bacterial adhesion, bacterial
virulence factors, membrane
transport processes in bacteria

Collaboration Interests

Structural biology (NMR, x-ray,
electron microscopy), Cell biology
(infection assays, binding assays to
eukaryotic cells), animal models
(zebrafish, galleria)

Research summary

My research group focusses on the structure and function of the bacterial cell surface.

Our work is typically comparative – we do not work on a single pathogenic “pet” organism, but instead compare related surface proteins from different species, studying their similarities and subtle differences. Our work is also interdisciplinary – we use methods from bioinformatics, structural biology and biophysics on top of classical methods from microbiology, molecular biology and biochemistry.

Vessela Kristensen

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Research keywords

As a cancer researcher Kristensen has developed and applied existing methods to study how genetic variation affects occurrence of somatic alterations, gene expression patterns and genome wide copy number alterations in human breast and ovarian tumors.

Collaboration Interests

Genomic instability and next generation sequencing. Integrated pathway analysis in breast cancer. The epigenetic landscape of cancer: application for prognostic and predictive biomarkers
Functional studies in the post-omics era. Integrated molecular analysis of miRNAs in breast cancer with clinical outcome. Genetic and epigenetic mechanisms of gene regulation.
Germline biomarkers for clinical management of sporadic and familial tumors
The immune system in breast carcinogenesis and treatment response
NorMa: Normal mammary tissue and cancer development.
Sequencing the non-canonical genomes.



Research summary

The tumor initiation, progression and clinical presentation are directly dependent on its genetic and biochemical environment – the entire body. Our group is working on different projects related to how genetic variation affects occurrence of somatic alterations, gene expression patterns and genome wide copy number alterations in human breast and ovarian tumors. Understanding inherited genetic variability and how it affects crucial biological pathways will lead to new successful prevention and treatment strategies.

Karl-Johan Malmberg

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Research keywords

Three main projects:

- 1) INSIDE-NK: Role of inter-organelle communication for effector function
- 2) DIVERSIFY-NK: Functional diversification of human NK cell repertoires
- 3) SYNTHETIC KILLER: Genetic engineering of iPSC-derived NK cells for off-the-shelf cell therapy

Collaboration Interests

Innate immunity, NK cells, Inter-organelle communication (lysosomes, mitochondria), iPSC editing and differentiation. Cell therapy.



Research summary

Research in the Malmberg Lab aims at understanding the cellular and molecular mechanism underlying the formation and diversification of human NK cell repertoires. A central aspect of these studies is to examine the dynamic tuning of NK cell function by killer cell immunoglobulin-like receptors (KIR) during NK cell differentiation and education. We develop and use a wide range of single cell technologies, advanced imaging and computational tools to study the regulatory gene circuits involved in shaping the interior of the NK cell with a primary focus on lysosomal signaling. In more translational efforts, we seek to implement new insights into NK cell biology in clinical trials for patients with advanced cancer.

Hans-Peter Marti

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Research keywords

Chronic kidney diseases, hypertensive nephropathy, and kidney cancer: i) RNA-sequencing and proteomics of archival human kidney tissues to detect novel prognostic markers and drug targets, and ii) evaluation of novel therapies in experimental animal models based on mice and zebrafish.

Collaboration Interests

Human and animal kidney and hypertension research; mRNA/miRNA sequencing, proteomics and epigenetic analyses from archival tissues and serum samples; zebrafish technology; organ (kidney)-on-chip technology; registry research; statistical machine learning methods; (semi-)automated image analyses.



Hans-Peter Marti represents the leader of the Renal Research Group (RRG) belonging to the Department of Clinical Medicine at UiB and to the Department of Medicine at Haukeland University Hospital. Our group has combined animal studies of disease mechanisms with epidemiological and translational studies of chronic kidney diseases and in the recent years also of human and experimental renal cell carcinoma. Six senior scientists belong to the group, including Prof. Hans-Peter Marti. Prof. Einar Svarstad and Camilla Tøndel, PhD, are intensely engaged in all clinical and histological Fabry nephropathy studies. Prof. Bjørn E. Vikse at UiB and Haugesund Hospital has a particular focus on epidemiology (low birthweight and kidney diseases) and on proteomics and together with Thomas Knoop, PhD, on IgA nephropathy. Assoc. Prof. Sabine Leh, Pathology, participates as renal pathologist of the Norwegian Kidney Biopsy Registry (NKBR). The core group of the RRG led by Hans-Peter Marti currently consists of one postdoc, four PhD students, four technicians (two former postdoc fellows), and three forskerlinje students. This group currently focuses on hypertensive nephropathy and kidney cancer in humans and in animal models in addition to Fabry nephropathy (Zebrafish model).

Hilde Loge Nilsen

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Research keywords

Genome stability, RNA quality control, mutations, ageing,

Collaboration Interests

Interplay between DNA repair and chromatin dynamics
Genetic and epigenetic basis of common, age related diseases
RNA processing/RNA quality control in age related neurodegenerative diseases

DNA repair is the main interest in the group. The term DNA repair covers many different mechanisms that remove damaged or inappropriate bases from DNA. Historically, studies of DNA repair has been motivated by the need for these mechanisms in order to prevent mutations - changes in the genetic code. Studies of DNA repair is therefore important in order to understand how cancer develops and how cancer can be treated. In recent years it has become clear that DNA repair enzymes have many important functions in cells other than to prevent mutations; such as in maturation of the immune system and to ensure healthy ageing. We have also recently demonstrated that DNA repair proteins contribute to RNA quality control. Our research focuses on the base excision repair pathway (BER): We study how BER affects tumour development using mouse models. We use *C. elegans* to study the impact of BER on healthy ageing (focusing on neurodegeneration), and mammalian cells to study BER biochemistry/cell biology.

Ragnhild A. Lothe

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Research summary

Our main research program involves translational studies of primary and metastatic colorectal cancers (CRC), using genomics, drug screening, digital pathology and functional analyses. We are also the core lab of a European multicenter research study on MPNST (malignant peripheral nerve sheath tumor), an orphan disease. To gain knowledge of the complex dynamics of cancer development we combine large-scale and detailed biology research using in vitro models and patient samples. The main goal is to translate biological discoveries into improved patient stratification and treatment.

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Research keywords

cancer, prostate cancer,
extracellular vesicles, liquid
biopsies, cancer molecular
biomarkers, intercellular
transport

Collaboration Interests

Omics technologies, biobanking,
advanced microscopy,
bioinformatics

Extracellular vesicles (EVs), such as exosomes and microvesicles, shed from tumor cells into biofluids have recently emerged as a new type of liquid biopsy. Two aspects have boosted the interest of using EVs as liquid biopsies: their diverse molecular composition (proteins, nucleic acids, lipid and metabolites) and their ubiquitous presence in human biofluids (blood, urine, milk, semen, cerebrospinal fluid, etc). Numerous studies have recently demonstrated the potential of EV as a source of cancer biomarkers. My group is particularly interested in the potential use of EVs in urine as liquid biopsies for prostate cancer. During the last years we have developed the methodology required to isolate EVs from urine and established analytical tools to profile the molecular composition of EVs using omics methods. We have extensively characterized the protein and lipid profile of urinary EVs by mass spectrometry and the miRNA profile by next-generation sequencing. Our goal is to find molecular biomarkers that can help us to identify prostate cancer patients that can safely be included in active surveillance programs.

Reidar Lund

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Research keywords

Soft matter, polymer science,
drug delivery, lipid membrane
interactions

Collaboration Interests

Drug delivery applications,
biomaterials based on polymers
and hybrid materials, studies of
lipid membrane systems in viruses
and bacteria, membrane
solubilization processes. May also
offer expertise in synchrotron and
neutron scattering techniques.

Research summary

We focus on understanding of self-assembled systems and the physical chemistry of soft matter systems based on polymers, surfactants proteins. We currently work on drug delivery of therapeutic peptides and low molecular weight drugs, antibiotics and their interactions with lipid membranes and general applications of polymer materials. The group uses a wide range of experimental techniques and computational tools, but has a particular expertise in scattering methods based on light, neutrons and X-rays.

Espen Melum

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Research keywords

Translational research on bile
duct inflammation

Collaboration Interests

Immunology,
organ-on-a-chip,
translational studies,
liver diseases,
tissue transcriptomics,
organoids



Research summary

My research focuses on understanding the immunological processes regulating inflammation in the bile ducts. Specifically we are focusing on unconventional T-cells. Two of the main subsets of unconventional T-cells are natural killer T (NKT)-cells and mucosal associated invariant T (MAIT)-cells. By using knock-out and conditional knock-out murine models we investigate the role of NKT and MAIT-cells in the bile ducts in surgically induced and spontaneous bile duct inflammation. My group is also focusing on using novel technologies like tissue transcriptomics to understand the interaction between immune cells and the liver tissue in the human liver disease primary sclerosing cholangitis (PSC). Recently, we have adapted some of the scientific questions we are investigating to a organ-on-a-chip platform aiming to generate a bile duct on a chip using organoids and microfluidics that we will use for immune focused studies.

Emmet Mc Cormack

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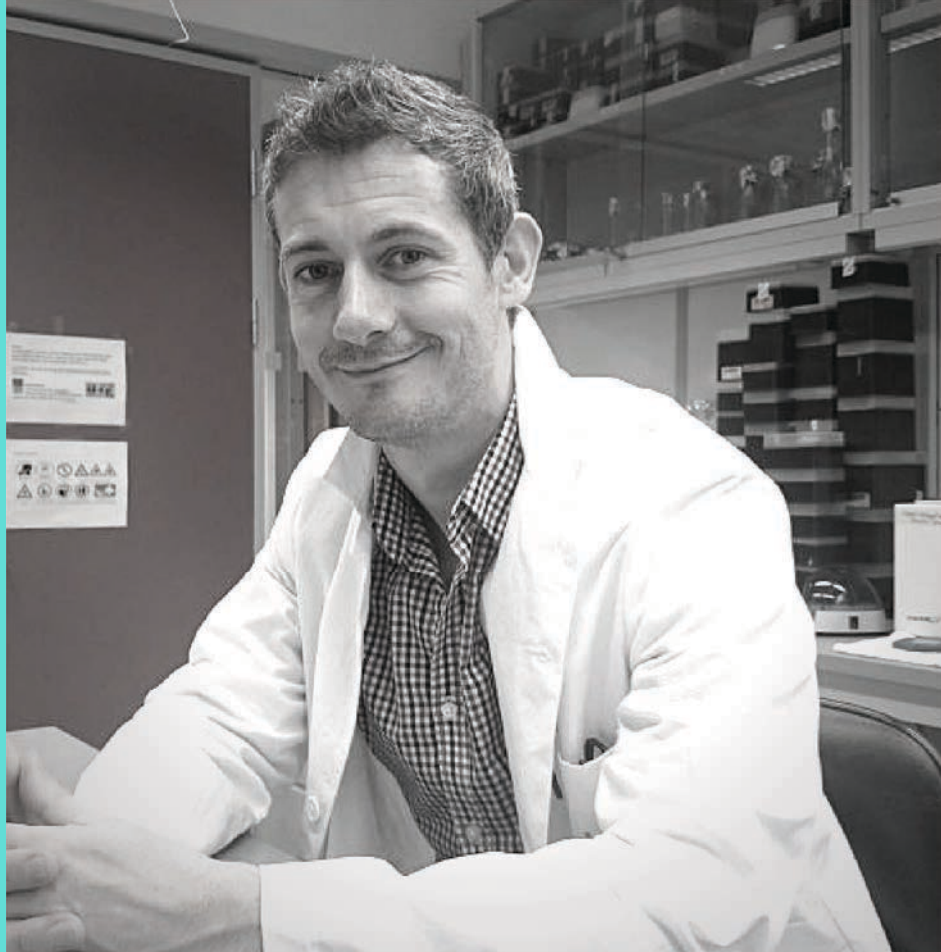
<https://www.uib.no/en/ccbio/107680/emmet-mccormack>

Research keywords

Preclinical model development,
Molecular imaging strategies,
Preclinical drug development,
Immunotherapy

Collaboration Interests

Assessment of novel molecular
imaging probes - particularly
optical approaches, Assessment of
novel therapeutics in oncology,
Assessment of novel
immunotherapeutics in oncology,
CAR T expertise.



Research summary

It is the group's belief that the current dogma of rushing novel pharmaceuticals through inappropriate preclinical models is one of the major reasons for their limited clinical penetration. This can be solved through multidisciplinary development of preclinical surrogates, models and diagnostic tools that more accurately mimic clinical conditions. Subsequently, the group has led the development of patient derived xenograft models and multimodal imaging for use in the evaluation of novel therapies. Also, lab-on-a-chip scaffolds for greater in vitro understanding of the bone marrow microenvironments have been established.

June Helen Myklebust

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Research keywords

Understanding B-cell lymphoma
biology to identify new
therapeutic targets and treatment
strategies

Collaboration Interests

Bioinformatics: Integrative
analysis of multi-omics data
(whole exome sequencing,
copy number changes, RNA
sequencing, imaging data), and
single-cell data.

CRISPR/Cas9 editing



We perform translational studies in B-cell lymphoma to define tumor clonal evolution and early cancer driver genes, and to identify immunosuppressive mechanisms in the tumor microenvironment. A key question is how we can increase response rates to therapy, including immunotherapy. We have used whole exome sequencing of tumor samples from unique cohorts of B-cell lymphoma patients, to identify mutations in cancer driver genes associated with poor outcome. By analyzing longitudinal tumor samples, we have identified early genetic changes in lymphomagenesis. To gain further insight into lymphoma biology and to explore the heterogeneity in the tumor microenvironment even within existing diagnostic types, we are expanding with additional datasets. We have implemented imaging mass cytometry, a technology facilitating imaging analysis of tissues with subcellular resolution of more than 30 different markers simultaneously. This allows for new insight into the tumor microenvironment architecture and cellular interaction patterns. The goal is to link tumor genetic subtypes to distinct patterns of tumor microenvironment architecture. The tumor microenvironment in lymphoma is characterized by immunosuppression, including higher numbers of regulatory T cells that suppress the activity of effector T cells. To unveil the complexity in intratumor immune cells, we are using single-cell RNA sequencing and functional in vitro assays. Collectively, we hope that our effort should provide a better understanding of lymphomagenesis, identify genetic alterations associated with high-risk disease, and reveal new targets for immunomodulation to overcome immunosuppression.

Pål Rasmus Njølstad

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Research keywords

Genetics of diabetes, monogenic
and polygenic forms of diabetes,
clinical trials, cellular and animal
models

Collaboration Interests

pGWAS consortia, clinical trials,
functional studies of transcription
factors



During my entire career, my driving focus has been to bridge clinical medicine and experimental research to discover and implement precision diagnostics and precision treatment for patients with diabetes. Over the past decades I have established an internationally acclaimed research group and together with my team and in collaboration with national and international experts we have made several ground-breaking findings. We have identified and characterized several novel subtypes of diabetes (GCK neonatal diabetes, *N Engl J Med* 2001; CEL MODY, *Nat Genet* 2006; PIK3R1 lipodystrophy, *Am J Hum Genet* 2013) and made a life-altering discovery that a precise diagnosis can alter treatment from insulin to oral tablets (KCNJ11 neonatal diabetes, *Diabetes* 2004; *N Engl J Med* 2006; *Lancet* DE2018). Furthermore, we have revealed the mechanisms of disease for several diabetes subtypes (CEL MODY, *J Biol Chem* 2011; GCK MODY, *J Biol Chem* 2013; PIK3R1 lipodystrophy, *J Clin Invest* 2013 and *FASEB J* 2020). I am also interested in genetics of early growth and we have discovered signals (LEPR and LEP) that confer a transient effect on normal growth in children (*Nat Commun* 2019). I have extensive experience with organizing and running large projects and centers leading an ERC Advanced Grant, a Center for Diabetes Research (70 empl), and the Department of Clinical Science at UiB (350 empl).

Jacob Odeberg

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Research keywords

We are interested in human endothelial cells, with a specific focus on endothelial specifically expressed genes and their role in cell function

Collaboration Interests

Endothelial cells, in vitro model vessels, primary cell culture, plasma proteomics, RNAseq, cell profiling, thrombosis, cardiovascular risk fact

My current research involves identification, characterisation and clinical translation of plasma biomarkers for vascular disease. We use high throughput proteomic approaches to identify novel protein plasma biomarkers of cardiovascular disease (CVD), with a focus on venous thromboembolism (VTE) and unstable plaque disease, e.g acute coronary syndrome. This work is based on our access to resources generated within the Human Protein Atlas (HPA) (www.proteinatlas.org), which have enabled us to perform both targeted and agnostic (untargeted) discovery screens, followed by characterisation and validation of identified targets. More recently, with the COVID-19 pandemic, we refocused our work towards identification of biomarkers predictive of progression to severe or critical disease in patients initially presenting with moderate symptoms. Our aim here is to develop and validate biomarker-based prediction models for short- and long-term prognosis that can be used as clinical tools to predict the likely course of disease progression and risk of complications, to enable patient stratification with respect to treatment and management decisions. My research group include basic scientists and active clinicians, and we collaborate closely with the group of NCMM associated investigator Dr. Lynn Butler, (IKM/UiT), through this collaboration forming a translational constellation with a focus on vascular biology from both a clinical and biological perspective. We would welcome opportunities to expand this collaboration to involve groups and scientists in NCMM who have complementary research profiles and interests.

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Research keywords

Cancer
Immunotherapy

Research summary

Our group aims to develop new T-cell based concepts for cancer immunotherapy that overcome the major challenge of self-tolerance in cancer. To this end, one of our main strategies involves studies of how the immune system from healthy donors can target patient cancer cells. We have a strong focus on the development of new technologies that allow high-throughput identification of therapeutic targets that can evoke immune responses, as lack of immunogenic targets represents a major limitation in therapeutic efficacy. The group furthermore has a strong translational focus and performs penetrating mechanistic analyses in clinical trials together with our clinical partners.

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Research keywords

Membrane trafficking, organelle dynamics, cytoskeleton, cell migration

Collaboration Interests

Immunology, cancer biology, biophysics, bionanotechnology, bioinformatics, protein biochemistry.

Research summary

Defects in the intracellular transport machineries are often associated with different human diseases, including cancer and neurodegenerative disorders. Our research aims to understand how membrane traffic and organelle dynamics are regulated in eukaryotic cells, and their contributions to disease pathology. We are particularly interested in elucidating the molecular mechanisms coordinating membrane traffic and cytoskeleton dynamics, as well as cell motility in cancer and immune cells. To study these processes, we employ a combination of various imaging approaches, such as live cell confocal microscopy, FRAP and high-content RNAi screenings, in addition to a broad range of molecular biology, biochemistry and cell biology techniques.

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[Universitetssykehuset Nord-Norge \(unn.no\).](https://universitetssykehuset.nord-norge.unn.no)



Research keywords

Basic virology, clinical virology, BK polyomavirus (BKPyV), JC polyomavirus (JCPyV), Hepatitis E-virus (HEV), Severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2), cytomegalovirus (CMV), culturing of primary human cells in monolayers and polarized form, viral replication, viral transformation, functional characterisation, antivirals, extracellular vesicles, sequencing, immunofluorescence, confocal and electron microscopy, humoral immune responses.

Collaboration Interests

In vitro studies of potential direct-acting antiviral drugs against SARS-CoV-2. Cryo electron microscopy studies of the BKPyV replication cycle, including viral membrane proteins, and generation of extracellular vesicles. BKPyV large T antigen (LTag) is essential for driving viral replication and inducing cellular transformation. Binding of LTag to p53 is abrogating the ability of p53 to stimulate gene expression. Compounds that restore mutant p53 activity could be tested for antiviral activity against BKPyV.

My research is focusing on clinically relevant virus infections in humans. Regarding BKPyV, we have sequenced viral genomes in samples from kidney transplant patients suffering from BKPyV-nephropathy and studied replication of these viruses in primary renal proximal tubule epithelial cells (RPTECs), the target cells of BKPyV. Moreover, we have studied their antibody response and identified compounds inhibiting BKPyV replication in RPTECs and human urothelial cells, some of which are actively studied/applied to treat patients. However, a highly potent and selective antiviral to treat BKPyV and JCPyV is still an unmet clinical need. A detailed understanding of the replication cycle is urgently needed. Recently, we found the late agnoprotein to target mitochondria, thereby evading immune sensing, possibly explaining the lifelong persistent infection of the human renourinary tract. JCPyV is causing the fatal disease progressive multifocal leukoencephalopathy (PML) in immunocompromised patients or patients undergoing immunotherapy. We have performed in vitro antiviral studies and been involved in compassionate use of recombinant human interleukin-7 in patients with CD4+ T-cell lymphocytopenia. Our work is well received and led to invitations to develop European guidelines on human polyomaviruses in hematopoietic stem cell transplant recipients (ECIL, 2018) and in solid organ recipients (ESCMID, 2014), an invited lecture at ESCMID, and to be editor of a special issue in APMIS. Regarding HEV, a neglected cause of acute and chronic viral hepatitis, we performed the first seroprevalence study of a normal adult Norwegian population. Regarding SARS-CoV-2, we have studied replication in vitro and the antibody response in COVID-19 patients.

Hege G. Russnes

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Research keywords

Pathologist trained in molecular cancer diagnostics. Combines MD/senior consultant and research group leader. Molecular classification of cancer for improved prognostication and prediction of therapy response. Experimental diagnostics for clinical cancer trials.

Collaboration Interests

Inter-tumor heterogeneity, tumor evolution, metastatic process, multi-level integrative molecular analyses, molecular diagnostics, clinical trials. Translational research; bulk- and single-cell analyses (identification/sorting/procurement /selection), sequencing, bioinformatics, liquid biopsies (CTC; DTC, ctDNA), in-situ tissue analyses.



My research group aims at defining, refining and implementing molecular classification and biomarker analyses to improve stratification of cancer patients into treatment relevant groups. We are addressing the impact of inter- and intra-tumor heterogeneity as well as host response on disease progression, response to therapy and patient outcome. The group has a special focus on breast cancer but is also exploring molecular features across tumor types. We have built a diversity within the group to have both a major focus on 1) developing excellent laboratory protocols suited for clinical tumor material (fresh frozen, small biopsies, FFPE tissue, ctDNA, single cells etc.) and 2) develop tailored computational methods based on mathematics and bioinformatics.

As co-PI/partners in several clinic trials we perform “state of the art” analyses of patient material, both on bulk tumors, single cells and liquid biopsies, at various stages of the disease. As senior consultant at Dept. of Pathology, OUS, I am head of “Section for experimental pathology and research support”, a lab developing and performing molecular diagnostics for clinical trials and coordinating “Infrastructure for Precision Diagnostics” (InPreD, cancer).

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Research keywords

Translational research in cancer immunotherapy. Expertise in genomics, immunology, computational biology, multiple myeloma and other B-cell malignancies

Collaboration Interests

Infrastructure for storage and analysis of patient-derived omics data

Regulation/perturbation of intracellular peptide processing and antigen presentation

Translation-heavy clinical trials with immunological interventions



Research summary

Current on-going projects are within two main domains:

1. Deep biological characterization of patient materials from immunotherapy trials (e.g.. tumor whole exome/genome sequencing, bulk/single cell RNA sequencing of tumor/immune compartments, functional immune profiling)
2. Target discovery for T-cell receptor-based therapies. Identifying mutant or constitutional peptides uniquely expressed in the tissue or tumor of interest based on large-scale transcriptomic and proteomic data analysis and in vitro experiments

Axel Sandvig

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Research keywords

Neuroplasticity; CNS damage and
repair; regeneration;
neurodegenerative disease; in
vitro, in vivo and computational
models

Collaboration Interests

Cellular and molecular
techniques; in vivo
electrophysiology; clinical
neuroimaging



Research summary

The main research interest of my group is the study and elucidation of neuroplasticity mechanisms in the context of CNS damage and repair. Specifically, we model and investigate dynamic structure-function relationships in neuronal assemblies in healthy and perturbed conditions with the goal of identifying and engaging key aspects of complex neural network behaviour that determine adaptive or maladaptive neuroplasticity in the lesioned CNS, including injury and neurodegenerative disease. The overarching aim of my research activities is to promote translational neuroscience research based on (i) developing beyond-the-state-of-the-art preclinical disease models (ii) correlating findings from preclinical modelling to those of clinical studies and vice versa; (iii) elucidating key mechanisms of neuroplasticity relevant for improved functional outcome after CNS lesion, and (ii) accelerating translation of basic research findings into the clinic by promoting patient-specific diagnostic and therapeutic tools and fostering genuine interdisciplinary research collaborations between academia and the clinic.

Anne Simonsen

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Research keywords

Molecular mechanisms of
autophagy

Collaboration Interests

Machine learning, mathematic
modeling, protein structure
analysis.



Research summary

The main focus of the “Simonsen Lab” is to characterize of the molecular mechanisms involved in cargo sequestration and autophagosome biogenesis during non-selective and selective types of autophagy with a long-term goal to identify novel targets for diagnosis or treatment of human disease. Current work in my laboratory is focused on identification of novel lipid-binding proteins involved in autophagy. We use high-content imaging-based siRNA screens in combination with different autophagy reporters to identify lipid-binding proteins important for different types of autophagy, such as mitophagy and aggrephagy. To further characterization the mechanisms underlying their function in autophagy and links to disease we employ various state-of-the-art imaging, genomic and computational approaches, as well as disease-related cellular and in vivo model systems.

Rolf Skotheim

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Research keywords

Transcriptomics – the expressed genome mistakes and a source for clinical biomarkers

Collaboration Interests

Research collaboration with NCMM researchers is of highly interest, either with complementary expertise and/or with common research goals



Research summary

Our research group currently investigates cancer genomes by integrated computational and laboratory-based approaches. Our aim is to identify and characterise critical genes involved in the cancer development. Such genes may serve as diagnostic or prognostic biomarkers and as targets for molecularly tailored therapy. We focus our research on prostate cancer, but are also involved in research on colorectal, ovarian and testicular cancers. Across these diseases, we go deeply into cancer-specific RNA variation as a source of cancer biomarkers. These appear both from aberrant pre-mRNA splicing and from fusion genes, with or without association with genomic rearrangements. On prostate cancer, we study in particular how the interfocal heterogeneity of primary cancers affects the disease course. By whole-exome and RNA-sequencing, we have recently uncovered that separate tumour foci of localized prostate cancers, within the same prostate, have entirely distinct genetic changes. We believe these results will impact how genome-based personalized cancer medicine can be implemented for this disease.

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Research keywords

Genetics
Newborn screening
Primary immunodeficiency
diseases (PID)

Kjetil Taskén

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and Tasken Group at

<https://www.ous-research.no/home/kt/home>

<https://www.med.uio.no/klinmed/english/people/aca/ktasken/index.html>

Research keywords

Immune regulation and cancer immunology, cancer precision medicine, cancer biology, cell signaling in health and disease, drug development, translational medicine and innovation.

Collaboration Interests

Cell signalling analysis by phosphoflow cytometry, CyTOF and Hyperion analyses, protein-protein interaction studies, chemical biology, functional precision medicine approaches and systems pharmacology.



The Taskén group aims to understand tumor immune evasion mechanisms, and how we can interfere to boost anti-tumor immunity. We want to define future precision immune oncology strategies. We proceed with cancer drug sensitivity screening (CDSS) to explore individual drug responsiveness and resistance patterns in patient cancer cells. We aim to develop models to assist individualised clinical decisions in precision cancer medicine (PCM) in oncology and haematology. We aim to understand intracellular signalling networks, the anchoring and localization of signaling complexes through scaffold proteins, how these signalling networks mediate physiological and pathophysiological processes and can be perturbed using drug-like small molecules.

Projects:

- Tumor immune evasion mechanisms, T cell function in cancer and immune-related diseases
 - Identification of regulatory T cell targets that can be perturbed to reverse tumor immune suppression
 - CDSS in chronic lymphocytic leukemia (CLL) and multiple myeloma, understanding drug synergies and predicting effective drug combinations in individual patients
 - Functional PCM approaches in solid tumors, hereunder CDSS on pancreatic cancer, breast cancer and ovarian cancer
 - IMPRESS-Norway national PCM clinical implementation trial (trial management)
- Acetyl salicylic acid clinical intervention study in metastatic colorectal cancer (ASAC)

Alfonso Urbanucci

PhD

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Research keywords

Molecular signatures,
radiobiology,
prostate cancer,
melanoma,
RNA biology,
chromatin structure,
bromodomain-containing
proteins, gene regulation,
androgen receptor,
MITF, single cell

Collaboration Interests

Precision oncology,
spatial transcriptomics,
cancer progenitor cells,
neurobiology,
bioinformatics,
statistical genomics,
crystallography,
mathematical models,
machine learning,
single nuclei sequencing

My research interests revolve around:

- 1) chromatin structure and transcriptional-mediated mechanisms of tumor initiation and progression.
- 2) understanding how to enhance the effect of radiotherapy and DNA repair inhibitors for cancer patients by combining those with epigenetic treatments;
- 3) implement patients' stratification methods based on RNA sequencing;
- 4) implement sequencing strategies with routine pathology work;

I use mainly prostate cancer as a model disease.

Eivind Valen

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Research keywords

RNA biology,
translational regulation, nanopore
sequencing,
CRISPR

Collaboration Interests

Our group can offer three
interfaces that could form the
basis of a collaboration with the
members of NCMM: First, we have
extensive CRISPR expertise, also
with uses beyond genome editing.

Second, we have worked on
sequencing-based NGS assays for
over a decade including many
non-standard assays. Third, we
are a leading group on nanopore
sequencing-based
transcriptomics.



Research summary

Our research spans the fields of computational and molecular biology with a focus on method development for RNA biology and genome editing. Among other things our group has developed CHOPCHOP, one of the most popular tools for CRISPR genome editing in the world, as well as several novel methods for high-throughput monitoring of translation initiation, RNA features and RNA structures. Our current major focus is on harnessing the potential of direct RNA nanopore sequencing to study the features and regulation of RNAs..

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Research keywords

Data science for precision
medicine against pediatric
metabolic disorders

Collaboration Interests

Genomics,
proteomics,
biological networks,
obesity,
diabetes.



Pediatric metabolic disorders result from a combination of genetic and environmental factors, setting children on health trajectories that are poorly understood, and resulting too often in inadequate or lack of health care for those who need it the most. My research tackles this injustice through the establishment of precision medicine strategies combining modern biobank-scale data and innovative data science. The aim is to refine our understanding of pediatric metabolic disorders, identify families at risk, and improve therapeutic strategies.

Can diabetic children avoid insulin shots? We combine genomics and proteomics to identify patients who can be transitioned to oral antidiabetic drugs. What influences the growth of babies? We use population registries and pregnancy-based cohorts to identify the genetic, metabolic, and environmental factors associated with health trajectories. In addition to yielding fundamental knowledge, we aim at providing researchers, medical teams, and families with a better understanding of complex biomedical data, as well as the methods and tools to analyze them.

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Research keywords

Neuroscience, imaging,
microscopy, physiology, sensory
systems, epilepsy, zebrafish,
neural circuits, behavior

Collaboration Interests

High-throughput chemical
screening, spatial transcriptomics,
neurological diseases, second
messenger systems Ca, cAMP,
astroglia



Our primary goal is to understand how sensory world (smell, vision and taste) is represented in animal brain and how these computations regulate different behavioral programs (e.g. fear, arousal, feeding). Moreover, we are interested in understanding how these representations are modulated by behavioral states of animals (e.g. stress, reproduction and hunger). We achieve this by focusing on those brain areas that integrate information from multiple sensory modalities and closely relate to behavior (e.g. telencephalon, habenula, brainstem). Small and accessible brain of zebrafish provides an exceptional framework for studying the neural circuit computations both locally and across multiple brain regions simultaneously.

Moreover, a small core in our laboratory is interested in applying systems neuroscience tools to zebrafish models of neurological diseases (e.g. epilepsy). Our aim is to understand the alterations in neural circuit computations and connectivity in zebrafish models of neurological diseases.

Can diabetic children avoid insulin shots? We combine genomics and proteomics to identify patients who can be transitioned to oral antidiabetic drugs. What influences the growth of babies? We use population registries and pregnancy-based cohorts to identify the genetic, metabolic, and environmental factors associated with health trajectories. In addition to yielding fundamental knowledge, we aim at providing researchers, medical teams, and families with a better understanding of complex biomedical data, as well as the methods and tools to analyze them.