Centre for Cancer Biomarkers

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CCBIO Newsletter

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DIRECTOR'S COMMENTS

Dear all,

The *14th CCBIO Annual Symposium* became another successful event. Thank you to all for coming and contributing: the inspiring speakers, industry, and participants from various teams and environments. And we shall never forget the outstanding and most stimulating keynote lecture presented by Dr. William A. Haseltine – one of the founding fathers of modern molecular biology. Without a single slide, he invited us to a journey from 'the old days' to the era of contemporary precision medicine – and so well aligned with our topic for this meeting – *back to the future*.

Preceding the annual symposium was our pre-meeting and the inaugural edition of OC-INSIGHTS: the *1st European Ovarian Cancer Translational Research Symposium (EurOvaCan)*. A special thanks to Line Bjørge for this initiative and for organizing the meeting together with her team and international colleagues.

We are happy to announce that we will repeat this success and organize the two meetings 'back to back' next year – as the *CCBIO Twin Meetings (May 9-12, 2027, at Solstrand, Bergen.)*

Please read our stories below on exciting scientific and educational collaborations with Japan and Vietnam, and the impressive results presented in highlighted papers, on cellular aging, mapping of TCR diversity, and molecular subtyping of ovarian cancer.

Congratulations to several colleagues: to long-time CCBIO international faculty and collaborator Arne Östman for receiving the Karolinska Institute Silver Medal for his longstanding and important work in the field of translational cancer research. Well deserved! Congratulations also to Harsh Dongre (Bielenberg group, VBP, Boston, and Costea group, CCBIO/UIB) for having been awarded the Marion and Lawrence (Larry) Muller Memorial Fund Scholar Award for Excellence in Inflammation Research at the recently concluded Pathobiology 2026 conference, organized by the American Society of Investigative Pathology (ASIP), and to those having defended their thesis work at CCBIO.

Finally, please take down the dates for important courses and meetings, and relevant future events!

Have a nice summer all of you!

Best regards, Lars A. Akslen, Director

Capturing cancer complexity and clinical challenges

Back to the Future in the search for better cancer treatments

The 14th Annual CCBIO Symposium, held May 12–13, 2026 in Bergen, Norway, brought together researchers, clinicians, and collaborators for two days of scientific exchange, inspiration, and forward-looking discussions. This year's thematic framing - "Back to the Future" - emphasized the importance of understanding the history behind today's research fields.

The program opened with an engaging keynote by molecular biology pioneer William A. Haseltine, who traced the field's evolution and reinforced the symposium's "Back to the Future" theme. (See the complete talk by Haseltine on LinkedIn, *requires LinkedIn access.*) The event maintained its hallmark breadth, showcasing a range of topics from cancer neuroscience to cutting-edge omics technologies.

Photos by Thor Brødreskift.

Emerging research highlighted how nerve cells actively contribute to tumor growth and metastasis, marking a rapidly expanding field in cancer science. A strong focus on proteomics revealed how studying proteins, beyond genes, can improve insights into tumor behavior, treatment response, and precision medicine. Speakers also demonstrated how combining advanced molecular profiling approaches can better map the tumor microenvironment and guide targeted therapies. Throughout the symposium, a clear emphasis on translating research into clinical practice and empowering young scientists illustrated CCBIO's commitment to innovation and the next generation of cancer researchers.

Read the full 14th Annual CCBIO Symposium story here.

First EurOvaCan Symposium marks launch of new ovarian cancer research forum and network

On May 10th and 11th 2026, we had the great pleasure of hosting the 1st Annual European Ovarian Cancer Translational Research Symposium (EurOvaCan 2026). Line Bjørge and the INOvA team members Katrin Kleinmanns, Luka Tandaric, and Minh Thu Le took the lead in organizing this meeting, set up as a pre-symposium to the 14th CCBIO Annual Symposium.

The inaugural EurOvaCan 2026 symposium brought together over 100 international researchers and clinicians to strengthen collaboration in ovarian cancer research. Centered on improving outcomes through better integration of tumor biology, immunology, and clinical translation, the meeting highlighted the importance of bridging disciplines.

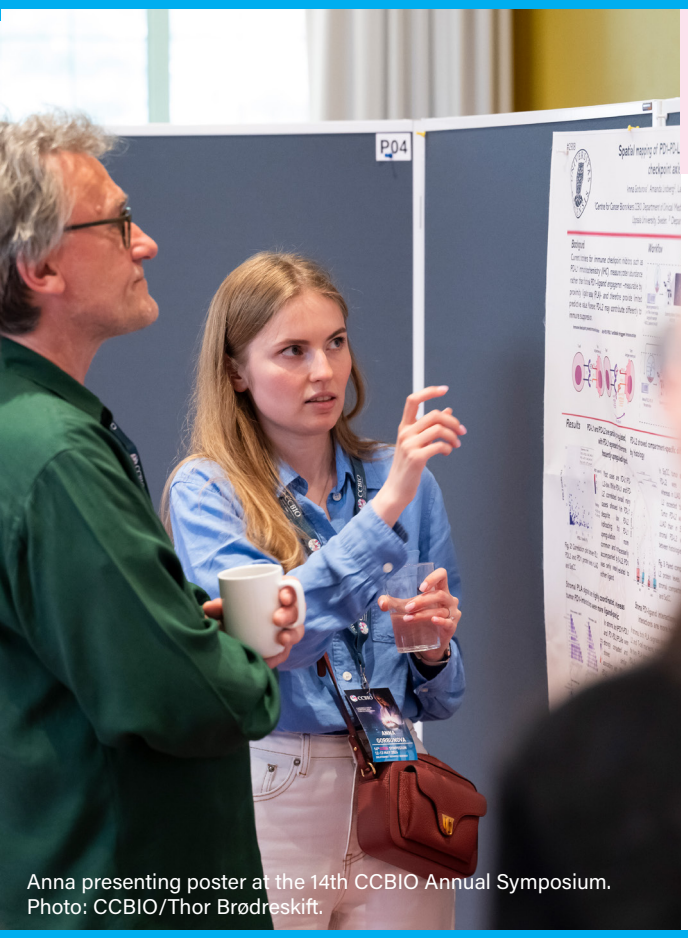
Key sessions emphasized a growing shift toward early detection, with new insights into tumor initiation and advanced screening approaches. Speakers also explored the complexity of ovarian cancer, including rare subtypes, treatment resistance, and the promise of precision medicine. Emerging research on tumor ecosystems showcased how innovative models and spatial biology are advancing understanding of disease mechanisms and therapeutic responses.

Photos by Cecilie Fredvik Torkildsen.

Together, the symposium marked a strong and inspiring start for a new scientific forum aimed at accelerating progress in ovarian cancer care.

Read the full EurOvaCan Symposium story here.

Anna Gorbunova awarded funding and Japan stay for lung cancer research project



Anna presenting poster at the 14th CCBIO Annual Symposium. Photo: CCBIO/Thor Brødreskift.

CCBIO Postdoc Anna Gorbunova has received a fellowship from The Scandinavia-Japan Sasakawa Foundation for a research stay at Kobe University, Japan, alongside new project funding from no less than two Norwegian foundations.

Anna Gorbunova, a member of Carina Strell's research group, has been awarded a fellowship from The Scandinavia-Japan Sasakawa Foundation to spend one month at Kobe University in Japan. Hosted by collaborator Prof. Masafumi Horie, she will work with lung cancer model systems to study neuroendocrine features in non-small cell lung cancer (NSCLC).

Gorbunova wants to test whether neuroendocrine-like tumor states can stimulate neurotransmitter production and secretion, with GABA-related signaling as the main focus. This will include analysis of secreted metabolites from conditioned media after experimental modulation of neuroendocrine features. The stay will also strengthen the group's collaboration with Kobe University and bring complementary model-system expertise to the group's current tissue-based spatial analyses.

In parallel, Gorbunova has secured additional funding for the project itself, including NOK 40,000 from the Family Blix Foundation (awarded November 2025) and NOK 150,000 from the Lilly Constance and Karl Ingolf Larsson Foundation.

Congratulations to Anna with these three grants!

Exploring global partnerships in oral cancer research

From lecture halls in Ho Chi Minh City to historic sites in Hue, a recent visit to Vietnam by CCBIO PI Professor Daniela Elena Costea combined teaching, new learning experiences, and the first steps toward future collaboration in oral cancer research and education.

In March 2026, Prof. Dana Costea travelled to Vietnam as part of an academic mission organized by Global Dental Ambassadors (USA), an organization she has been involved with since her sabbatical at the University of California San Diego (UCSD) in 2018.

The visit, more than a year in the planning, brought together an international team of oral and maxillofacial surgeons, dentists, oral pathologists, oral medicine specialists, and pain experts. Activities took place at Ho Chi Minh City University of Medicine and Pharmacy and Hue University of Medicine and Pharmacy, with a shared focus on strengthening education and exploring opportunities for research collaboration. Alongside teaching, the visit marked the start of discussions between CCBIO and Vietnamese partners on potential collaboration in oral cancer research, pathology education, digital diagnostics, and capacity building.

Prof. Costea delivered lectures on oral cancer biology and modern diagnostic approaches, while meetings with faculty and university leadership focused on possible next steps, including joint research initiatives, student exchanges, and the integration of digital pathology into teaching and clinical practice.

Read the full Vietnam visit story here.

Award to Harsh Dongre at Pathobiology conference

Photo by Diane Bielenberg.

CCBIO researcher Harsh Nitin Dongre in Costea's group was awarded the Marion and Lawrence (Larry) Muller Memorial Fund Scholar Award for Excellence in Inflammation Research at the recently concluded Pathobiology 2026 conference, organized by the American Society of Investigative Pathology (ASIP).

Dongre resented his research titled "Neuropilin-2 (NRP2) Driven T-Cell Suppression: Implications for Tumor Development," highlighting a novel role of NRP2 as a key modulator of the tumor immune microenvironment. His findings suggest that disrupting NRP2-mediated interactions may alleviate T-cell suppression, enhance endogenous antitumor immunosurveillance, and improve cancer immunotherapy outcomes. This recognition underscores the impact of his work in advancing the understanding of inflammation and tumor biology. The project is funded by the Norwegian Research Council under its FRIPRO International Mobility program.

Congratulations to Harsh!

Karolinska's Silver Medal to Arne Östman

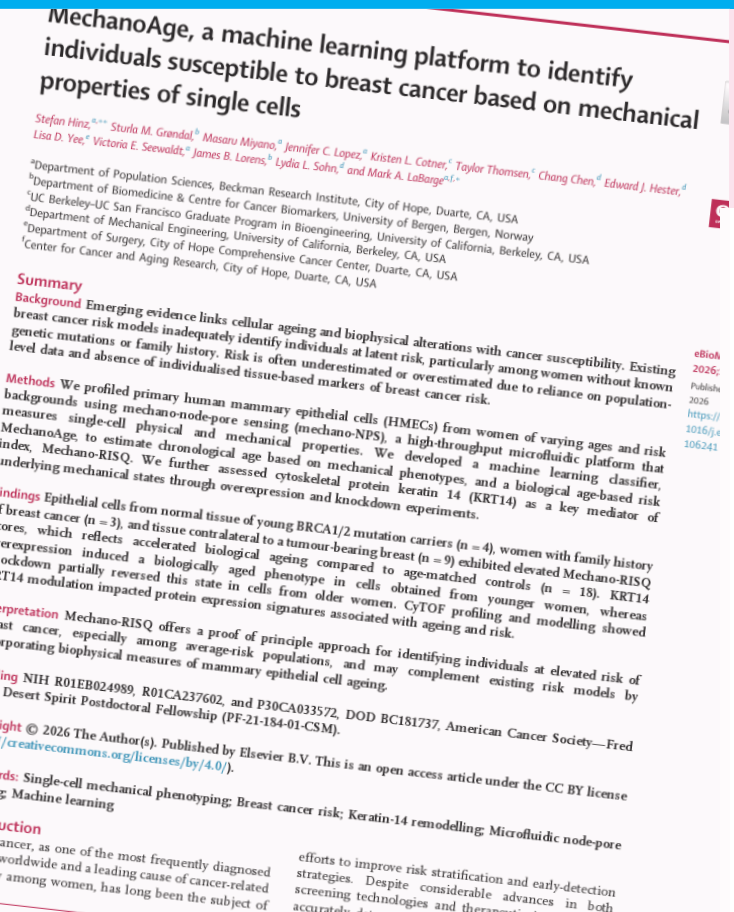

Photo by Ingvild F. Melien.

Long-time CCBIO collaborator Arne Östman recently received the Karolinska Institute Silver Medal for his longstanding and important work in the field of translational cancer research.

In their announcement, they state that Östman's research on the tumor microenvironment and stroma biology has led to a deeper understanding of cancer development and the therapeutic response, and that he has also built an internationally leading research environment and held several positions of strategic leadership at KI. See the announcement here.

Congratulations to Arne!

New tool uses cell aging to predict breast cancer


MechanoAge, a machine learning platform to identify individuals susceptible to breast cancer based on mechanical properties of single cells

Stefan Hinz,[a,*,**] Sturla M. Grøndal,[b] Masaru Miyano,[a] Jennifer C. Lopez,[a] Kristen L. Cotner,[c] Taylor Thomsen,[c] Chang Chen,[d] Edward J. Hester,[d] Lisa D. Yee,[e] Victoria E. Seewaldt,[e] James B. Lorens,[b] Lydia L. Sohn,[d] and Mark A. LaBarge[a,f,*]

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Summary

Background Emerging evidence links cellular ageing and biophysical alterations with cancer susceptibility. Existing breast cancer risk models inadequately identify individuals at latent risk, particularly among women without known genetic mutations or family history. Risk is often underestimated or overestimated due to reliance on population-level data and absence of individualised tissue-based markers of breast cancer risk.

Methods We profiled primary human mammary epithelial cells (HMECs) from women of varying ages and risk backgrounds using mechano-node-pore sensing (mechano-NPS), a high-throughput microfluidic platform that measures single-cell physical and mechanical properties. We developed a machine learning classifier, MechanoAge, to estimate chronological age based on mechanical phenotypes, and a biological age-based risk index, Mechano-RISQ. We further assessed cytoskeletal protein keratin 14 (KRT14) as a key mediator of underlying mechanical states through overexpression and knockdown experiments.

indings Epithelial cells from normal tissue of young BRCA1/2 mutation carriers (n = 4), women with family history f breast cancer (n = 3), and tissue contralateral to a tumour-bearing breast (n = 9) exhibited elevated Mechano-RISQ cores, which reflects accelerated biological ageing compared to age-matched controls (n = 18). KRT14 erexpression induced a biologically aged phenotype in cells obtained from younger women, whereas ockdown partially reversed this state in cells from older women. CyTOF profiling and modelling showed T14 modulation impacted protein expression signatures associated with ageing and risk.

erpretation Mechano-RISQ offers a proof of principle approach for identifying individuals at elevated risk of ast cancer, especially among average-risk populations, and may complement existing risk models by rporating biophysical measures of mammary epithelial cell ageing.

ing NIH R01EB024989, R01CA237602, and P30CA033572, DOD BC181737, American Cancer Society—Fred Desert Spirit Postdoctoral Fellowship (PF-21-184-01-CSM).

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rds: Single-cell mechanical phenotyping; Breast cancer risk; Keratin-14 remodelling; Microfluidic node-pore ; Machine learning

uction

ancer, as one of the most frequently diagnosed worldwide and a leading cause of cancer-related among women, has long been the subject of efforts to improve risk stratification and early-detection strategies. Despite considerable advances in both screening technologies and therapeutic

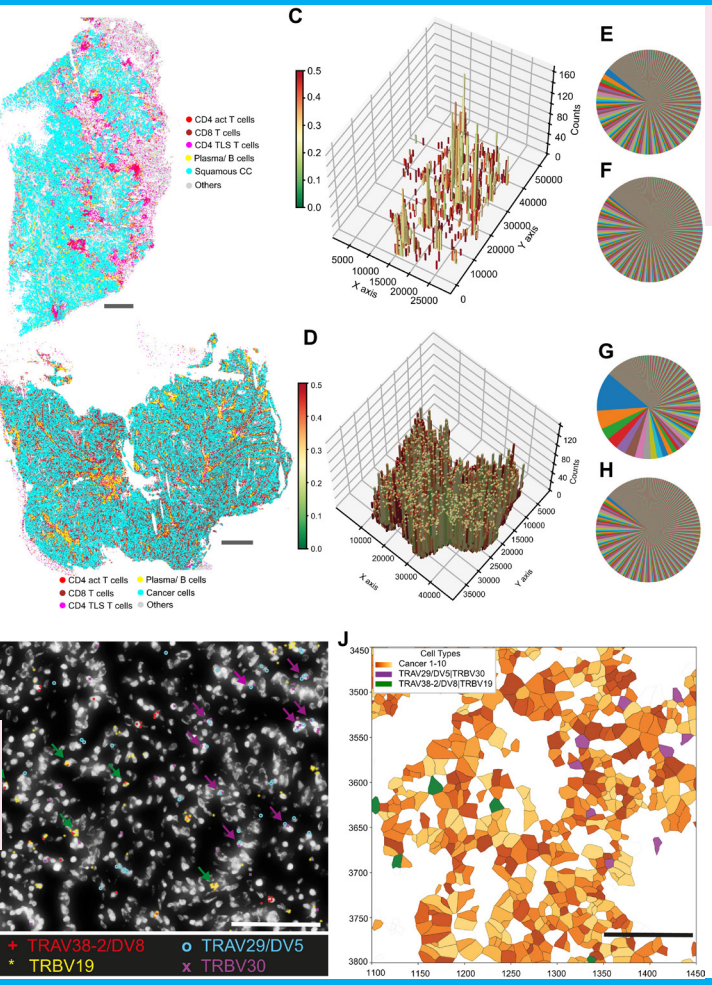
In this collaboration study published in in eBioMedicine, Hinz et al. present a new approach to identifying breast cancer risk by measuring the physical properties of cells. Working with collaborators from City of Hope, and the University of California, Berkeley, Sturla Grøndal and Jim Lorens from CCBIO explored how cellular aging and mechanics relate to cancer susceptibility.

Current breast cancer risk models often miss individuals at elevated risk, particularly women without known genetic mutations or family history. To address this, the team analysed primary human mammary epithelial cells (HMECs) using a high-throughput microfluidic platform (mechano-NPS) that captures single-cell mechanical properties. They developed a machine learning model, MechanoAge, to estimate biological age, and a corresponding risk score, Mechano-RISQ.

Their findings show that cells from young BRCA1/2 mutation carriers, women with family history of breast cancer, and tissue adjacent to tumours exhibit higher Mechano-RISQ scores, indicating accelerated biological ageing versus controls. The study highlights the role of the cytoskeletal protein keratin 14 (KRT14): increasing its expression induced ageing-like traits in younger cells, while reducing it reversed these traits in older cells. Together, this suggest Mechano-RISQ could provide a personalised way to assess breast cancer risk, complementing existing models by incorporating biophysical measurements of cell ageing.

See the publication here: *MechanoAge, a machine learning platform to identify individuals susceptible to breast cancer based on mechanical properties of single cells*

Mapping TCR diversity in tumors



In a new collaboration publication in eBioMedicine, Magoulopoulou et al. present a novel approach for spatially resolved mapping of T cell receptor (TCR) diversity in tissue sections. Carina Strell is co-corresponding author in this work led by the Mats Nilsson team from the SciLifeLab and Stockholm University, with more colleagues from Sweden and Germany.

Characterising the T cell receptor (TCR) repertoire is of great biomedical interest but it has been challenging due to its high structural diversity. In situ sequencing (ISS) enables spatial cell typing by linking gene expression to histopathological features in tissue sections. Here, ISS was applied on the Xenium platform with a custom panel targeting TCR genes selected from the IMGT database. An analysis pipeline was developed to assign putative clonotypes at single-cell level based on paired TCRVβ/Vα chain expression.

This approach captured specific immune cell distributions in relation to the individual sample clonality, as well as regional dominance of certain TCRVβ/Vα pairs in surgical non-small cell lung cancer (NSCLC) specimens and matching lymph node samples. Furthermore, the team was able to study the spatiotemporal evolution of TCR repertoire on longitudinal FFPE biopsies from patients with breast cancer, during neoadjuvant treatment.

This study highlights the implementation of target-based spatially resolved transcriptomics for the spatial characterisation of TCRVβ/Vα pairs at the single-cell level, without the need for prior sequencing. The approach allows for spatial immune characterisation of diagnostic tissue samples with emphasis on T cell biology and accompanying T cell diversity.

See the publication here: *Spatially resolved T cell receptor diversity mapping uncovers variability of the cancer immune microenvironment*

Study examining transcriptomic subtypes in ovarian cancer

Exploring survival-associated transcript… using RNAseq from FFPE tissues in a clinical trial cohort

Maj K Kjeldsen [a,b,c], Frederik Otzen Bagger [b], Henrik Roed [a,c], Gitte-Bettina Nyvang [c,d], Charlotte Aaquist Haslund [c,e], Anja Oer Knudsen [c,d], Anne Krejbjerg Motavaf [c,e], Susanne Malander [c,f], Maarit Anttila [c,g], Gabriel Lindahl [c,h,i], Johanna Mäenpää [c,j], Maria Dimoula [c,k], Theresa Werner [l], Trine Zeeberg Iversen [c,m], Sakari Hietanen [c,n], Lars Fokdal [c,o], Hanna Dahlstrand [c,p], Line Bjørge [c,q,r], Michael Birrer [s,t], Mansoor Raza Mirza [a,c,1], Maria Rossing [b,1,*]

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PMCID: PMC13018888 PMID: 41861658

Highlights

- Transcriptomic subtyping was applied to RNAseq data from advanced EOC patients using established algorithms.
- FFPE tumor tissues yielded high-quality RNAseq data, demonstrating feasibility for transcriptomic analyses.
- Subtype classification showed significant agreement across algorithms but lacked OS differences in this patient cohort.
- Distinct immunoreactive clusters were identified, suggesting utility in stratifying patients for immunotherapy trials.
- DEGs between long- and short-term survivors highlight prognostic markers and potential therapeutic targets inEOC.

Keywords: Epithelial Ovarian Cancer (EOC), RNA sequencing (RNAseq), Overall Survival (OS), Transcriptomic subtypes, Differentially Expressed Genes (DEGs)

Abstract

Objective

Transcriptomic subtyping is not yet standardized for prognostic use in epithelial ovarian cancer (EOC). This study aims to validate RNA sequencing (RNAseq) from formalin-fixed, paraffin-embedded (FFPE) tissues and to evaluate survival-associated transcriptomic subtypes and differentially expressed genes (DEGs) in a clinical trial cohort.

Methods

In this collaboration study published in Translational Oncology, Kjeldsen et al. investigate how gene expression patterns can improve understanding of prognosis in ovarian cancer. The work brings together colleagues from Denmark, Sweden, Finland, the United States, and Norway, including CCBIO PI and Co-Director Line Bjørge.

Accurately predicting outcomes in epithelial ovarian cancer remains challenging, and transcriptomic subtyping has not yet been standardised for clinical use. In this study, the team explored whether RNA sequencing (RNAseq) from routinely collected FFPE tissue samples could be used to identify clinically meaningful subtypes and survival-associated gene signatures.

Using samples from patients enrolled in a Nordic clinical trial, the researchers analysed gene expression profiles and applied established subtype classifications. While subtype assignment showed moderate consistency, links between subtypes and patient outcomes proved limited.

Instead, the analysis identified 18 genes that differed between short- and long-term survivors, with genes such as DPEP3 and SLC14A1 notably elevated in patients with better outcomes.

Overall, the study demonstrates that RNAseq from FFPE samples is feasible, while highlighting the need for improved molecular tools to refine prognostic classification and guide future treatment strategies.

See the publication here: *Exploring survival-associated transcriptomic subtypes in ovarian cancer using RNAseq from FFPE tissues in a clinical trial cohort*

Coming CCBIO Seminar, June 11

Join us for the next CCBIO seminar, June 11 with Ricardo Coletta from Universidade Estadual de Campinas (UNICAMP), Brazil

When: June 11, 2026, at 14:30-15:30
Where: The auditorium in Armauer Hansens Hus
Speaker: Professor Ricardo Coletta, Universidade Estadual de Campinas (UNICAMP), Brazil.
Title: *Biomarkers in Oral Cancer: From Discovery to Clinical Impact*
Abstract: Is available on this page.
Chair: Professor Dana Costea

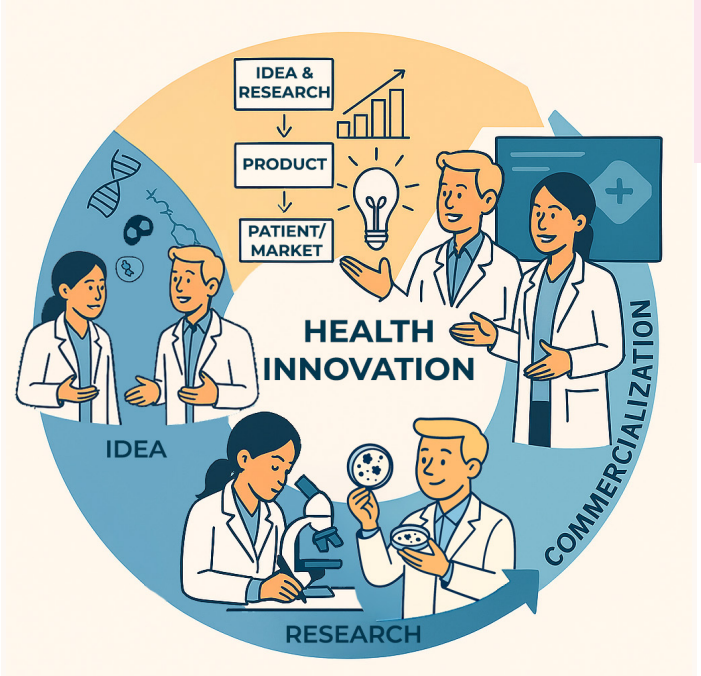
CCBIO905 - Methods in Cancer Biomarker Research

This course focuses on the full panel of standard and advanced methods with relevance for cancer biomarker research. The intention is to provide an understanding of the various methodologies and their application in basic and translational cancer research. The course further covers relevant topics like optimal sample collection and biobanking.

The course will focus on methods to study biomarkers in tissue samples, blood samples, circulating tumor cells and DNA, and other biologic materials. Methodologies like PCR techniques, microarray, next-generation sequencing, bioinformatics and artificial intelligence, immunohistochemistry, in situ hybridization, protein ligation assays, Western blot and ELISA, tissue microdissection and proteomics, flow cytometry, flow and imaging mass cytometry, and biobanking will be presented. Changes in nucleic acids and proteins in different settings will be discussed, as will the clinical applications.

Time: September 22-24, 2026
Place: Auditorium at campus Haukeland University Hospital, Bergen.
ECTS: 5 ECTS for UiB students
Registration: UiB students register via Studentweb, deadline *September 1*. Also open to non-ECTS participation via this link.
Webpage: See more information here.

CCBIONEUR912 - Health Innovation



Explore how cutting-edge research can be transformed into real-world impact. This course in Health Innovation introduces key concepts in entrepreneurship, intellectual property, and commercialization, and provides hands-on experience with developing and pitching innovation ideas.

The course is designed to inspire participants to explore and realize the innovation potential of their own research. Through lectures, case-based learning, and practical group work, participants will gain insight into how scientific discoveries can be translated into products, services, or solutions with value for healthcare and society. The program includes contributions from experienced medical entrepreneurs and international partners.

Participants will gain a solid understanding of innovation, entrepreneurship, and intellectual property in a research context. They will learn how to identify and develop ideas with innovation potential, assess their feasibility, and apply practical methods such as design thinking.

Time: October 12–13 and November 9–10, 2026.
Place: Auditorium at campus Haukeland University Hospital, Bergen.
ECTS: 4 ECTS for UiB students
Registration: Through Studentweb, deadline September 1.
Webpage: See more information here.

Recent doctoral defenses

Camilla Tvedt Ekanger defended June 9, 2026 her doctoral work at the University of Bergen with the thesis "Development and Characterization of Human Organoid Models to Study Respiratory Virus Infections and Pulmonary Pathologies". Supervisors have been Researcher Agnete Engelsen (main supervisor), Professor Karl Albert Brokstad, and Professor Sushma Nagaraja Grellscheid (co-supervisors).

Camilla Tvedt Ekanger. Photo by Ghazal Lessan Toussi.

Lung diseases remain a major global health burden, driving significant morbidity and mortality. Improved mechanistic insight is critical for advancing prevention and therapeutic strategies.

In this PhD work, Ekanger established and characterized preclinical human lung organoid models to study viral infections and lung pathology. These three-dimensional, self-organizing systems recapitulate key features of human lung tissue, including cellular heterogeneity and functional responses.

The organoids are permissive to infection with influenza virus and SARS-CoV-2 and exhibit tissue responses that closely resemble actual lung biology, supporting their utility for investigating viral tropism, host responses, and transmission dynamics.

Importantly, patient-derived lung cancer organoids were also developed, retaining key histological and molecular characteristics of the primary tumors. These models provide a platform for studying tumor heterogeneity, disease progression, and for informing precision oncology approaches. Beyond oncology, the models offer insight into disrupted lung development and disease in vulnerable populations, such as preterm infants.

Overall, this work highlights organoid systems as robust and scalable platforms for modeling both infectious and non-infectious lung disease, with clear translational potential in oncology and precision medicine.

See the press release.

Marta Espevold Hjelmeland defended March 26, 2026 her doctoral work at the University of Bergen with the thesis "Towards improved treatment for women with endometrial cancer; vimentin as a robust biomarker and the search for mechanisms to overcome chemotherapy resistance". Supervisors have been Professor Camilla Krakstad (main supervisor) and Professor Jone Trovik (co-supervisor).

Marta Hjelmeland. Photo by Thor Brødreskift.

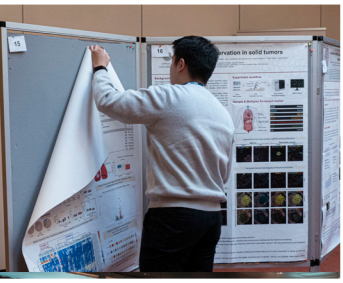
Endometrial cancer is the most common gynecologic cancer in women in Western countries, and its incidence is increasing. While many patients are cured by standard treatment, a subset develops aggressive disease with metastasis and poorer outcomes. Hjelmeland's doctoral work focuses on improving risk stratification and understanding why standard chemotherapy is less effective in some patients.

A key finding of the thesis centers on the protein vimentin, a cyto-skeletal marker often associated with increased invasiveness in cancer. Interestingly, Hjelmeland's research shows the opposite pattern in endometrial cancer: tumors with loss of vimentin expression are more aggressive, with higher metastatic potential and poorer survival. By combining analyses of patient samples with advanced cell models, the work demonstrates that loss of vimentin increases tumor cell migration and alters the activity of genes linked to cell movement and aggressive disease behavior.

The thesis also investigates mechanisms of chemotherapy resistance. Using CRISPR-based gene editing, Hjelmeland identified genes and molecular pathways that enable cancer cells to better withstand chemotherapy. These insights could, over time, support the development of more targeted and effective treatment strategies.

See the press release.

Coming CCBIO events



Make sure to save the dates in your calendar, and register when applicable. You can see all planned CCBIO events in the CCBIO web calendar.

- June 11, 2026, CCBIO Seminar, speaker Ricardo Coletta. Time: 14:30–15:30
- August 27, CCBIO Seminar, speaker tba. Time: 14:30–15:30
- September 22-24, the course CCBIO905 – Methods in Cancer Biomarker Research, Bergen
- September 24, CCBIO Seminar, speaker tba. Time: 14:30–15:30
- October 12–13 and November 9–10, the course CCBIONEUR912 – Health Innovation, Bergen
- October 29, CCBIO Seminar, speaker tba. Time: 14:30–15:30
- November 26, CCBIO Seminar, speaker tba. Time: 14:30–15:30
- December 10, CCBIO Seminar, speaker tba. Time: 14:30–15:30
- January 26–27, 2027, the 3rd Nordic Breast Pathology Symposium, Solstrand, Bergen

Other relevant coming events

Illustration: colourbox.com

Events from collaboration partners and other relevant events.

- Open ended, Nordic Masterclass on HER2 Testing in upper GI cancer, webinar video by Onkologisk tidsskrift
- Open ended, SOTA HER2 Low/Ultralow High-Risk Breast Cancer – Diagnostics, Treatment and Clinical Implementation, webinar video by Onkologisk tidsskrift
- BBB Seminars spring 2026, keep an eye on this webpage
- August 10–14, Arendalsuka, Arendal
- Sept. 3–4, 2026, 2026 SITC EU Immuno-Oncology Drug Development Summit, Lausanne, Switzerland
- September 7–10, the 51st Annual Meeting of the Scandinavian Society for Immunology, Grieghallen, Bergen
- September 8–9, Nordic Life Science Days 2026, Stockholm
- September 9, Symposium: "Breaking the T cell - cancer recognition code," Oslo
- September 10–11, the Molecular Analysis for Precision Oncology Congress 2026, London
- September 14–15, 3rd European Cancer and Oncology Congress, London
- September 21–23, Cancer R&D World Conference 2026, Miami
- September 24–26, World Cancer Congress 2026, Hong Kong
- October 14, Oslo Cell Therapy Innovation Symposium and Ecosystem Event; Oslo
- October 23–27, the ESMO Congress, Madrid
- November 2–3, the 10th ScanPath Meeting, Finland

Publications

You can find the CCBIO publications on this pubmed link. See the most recent below.

- **Hinz S, Grøndal SM, Miyano M, Lopez JC, Cotner KL, Thomsen T, Chen C, Hester EJ, Yee LD, Seewaldt VE, Lorens JB, Sohn LL, LaBarge MA.** MechanoAge, a machine learning platform to identify individuals susceptible to breast cancer based on mechanical properties of single cells. *EBioMedicine*. 2026 May;127:106241. doi: 10.1016/j.ebiom.2026.106241. Epub 2026 Apr 23. PMID: 42031621. Free PMC article.

- **Magoulopoulou A, Chatzinikolaou M, Metousis A, Hu T, Yu H, Zerdes I, Wang K, Foukakis T, Long M, Leandersson K, Micke P, Strell C, Nilsson M.** Spatially resolved T cell receptor diversity mapping uncovers variability of the cancer immune microenvironment. *EBioMedicine*. 2026 May;127:106264. doi: 10.1016/j.ebiom.2026.106264. Epub 2026 Apr 24. PMID: 42034048. Free PMC article.

- **Gullovsen VL, Pavlicenco D, E Hjelmeland M, Woie K, S Haldorsen I, Trovik J, F Berg H, Krakstad C.** High expression of the ADC target Claudin-6 associates with aggressive endometrial cancer and remains high in metastatic lesions. *BJC Rep*. 2026 Apr 15;4(1):17. doi: 10.1038/s44276-026-00225-x. PMID: 41986616.

- **Wang Z, Ingebriktsen LM, Bekkhus T, Ma L, Queiro-Palou A, Shi W, Bazioti A, Panagias MA, Vigorelli M, Lehrstrand JH, Ring S, Dimberg A, Wik E, Hoivik EA, Fuxe J, Ulvmar MH.** Podoplanin-defined tumour plasticity and CCR7-mediated lymphatic metastasis in triple-negative breast cancer. *Br J Cancer*. 2026 Apr 9. doi: 10.1038/s41416-026-03402-4. Online ahead of print. PMID: 41957138

- **Finne K, Kjølle S, Romero MR, Birkeland E, Vethe H, Aziz S, Knutsvik G, Wik E, Lindström LS, Akslen LA.** Stromal-based proteome data improve stratification of hormone receptor-positive breast cancer. *NPJ Breast Cancer*. 2026 Apr 9. doi: 10.1038/s41523-026-00943-y. Online ahead of print. PMID: 41957022.

- **Kotsos D et al. incl. Gjertsen BT.** Treatment of therapy-related acute myeloid leukemia and acute myeloid leukemia with myelodysplasia-related changes: a comparative analysis of higher-dose intensive 7+3 induction chemotherapy versus liposomal cytarabine and daunorubicin. *Haematologica*. 2026 Mar 26. doi: 10.3324/haematol.2025.300065. Online ahead of p. PMID: 41885025.

- **Kjeldsen MK et al. incl. Bjørge L.** Exploring survival-associated transcriptomic subtypes in ovarian cancer using RNAseq from FFPE tissues in a clinical trial cohort. *Transl Oncol*. 2026 May;67:102740. doi: 10.1016/j.tranon.2026.102740. Epub 2026 Mar 19. PMID: 41861658.

Recent CCBIO in the media

Recent media appearances by CCBIO PIs and group members. Date, medium, headline, and CCBIO person interviewed or referred to. For all media hits, see CCBIO's web pages.

- 01.06.26, MSD Oncocast: "Kreftsykepleierens rolle i kreftomsorgen." Minh Thu Le.
- 01.06.26, Helse Vest: "Forskning som bidrar til bedre pasientbehandling." Bjørn Tore Gjertsen.
- 28.05.26, Tidsskriftet: "Hvordan kan norske kreftpasienter få økt tilgang til kliniske studier?" Line Bjørge.
- 27.05.26, Haugesunds Avis: "Carine (41) trodde hun manglet vitaminer. Så kom den livsendrende telefonen." Bjørn Tore Gjertsen.
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