XXIII Cancer Research KI Retreat

28-29 September, 2026

Djurönäset

Welcome to the Cancer Research KI Retreat 2026

On behalf of Cancer Research KI (CRKI), it is our great pleasure to welcome you to this year's retreat. This annual meeting brings together PhD students, postdocs, clinicians, scientists and additional colleagues from Karolinska Institutet, Karolinska University Hospital, and other hospitals across the Stockholm region and beyond for two days. The retreat is dedicated to **strengthening interactions, fostering interdisciplinary contacts**, and **identifying new opportunities for collaboration**. As a hub for all those engaged in cancer research and clinical care in the region, CRKI remains committed to **inclusivity, transparency, and collaboration**, and we invite each of you not only to discuss science, but to help shape the future of cancer research in the Stockholm region.

A Year of Activity and Growth

The past year has been an active and rewarding one for CRKI, and we would like to share a few highlights.

Our **Annual Report**, presented during the **Karolinska Comprehensive Cancer Centre (Karolinska CCC) Days**, summarized the breadth of our activities and achievements. This year, the Karolinska CCC Day became a particularly memorable event, held jointly with the **10th Cancer Core Europe (CCE) Annual Meeting**. Together, these combined meetings brought together **more than 500 participants** from Karolinska Institutet, Karolinska University Hospital, and other CCE centers across Europe for two days of scientific exchange and networking. In February, we also hosted the third edition of the **PI Retreat** at the Sånga Säby Conference Hotel, offering further opportunities to network and explore new avenues for collaboration and funding.

Public engagement remains central to our mission. The latest edition of **"En dag för cancerforskning" (A Day for Cancer Research)**, held in Swedish for the public, attracted **more than 1,000 registered participants** and showcased the impact of cancer research at KI. Last November, for the first time, the webinar was recorded in a professional studio, hosted by Pamela Andersson Alselind with researchers from Karolinska Institutet taking part. This year's event will be led by Sofia Wistam and will focus on **the patient's journey**, from diagnosis through treatment and aftercare. We also continued our **Patient Workshop series** with two online sessions in Swedish — one on quality of life when living with cancer, and the other on cancers in men, building on the success of last year's workshop on common cancers in women. The next edition will focus on **clinical trials**.

Our seminar and workshop programs have continued to grow. We hosted informative webinars on **funding opportunities from Radiumhemmets Forskningsfonder** for patient-centered research, organized together with Radiumhemmets Forskningsfonder, and on **"Navigating the Regulatory Landscape at Ease,"** an interactive session on ethical and legal requirements at Karolinska Institutet; both now being available on **KI Play**. Our **Industry–Academia Collaboration seminar series** was equally successful, with two well-attended sessions on "Academic Collaborations with the Pharma Industry: How to Do It Right!" — one held for the first time at the Flemingsberg campus in collaboration with the Life Science Cluster Flemingsberg. Building on strong participation in previous years, we also organized our fourth **Intellectual Property seminar** with the External Engagement Office at KI and KI Innovations, and, together with KI Innovations, A Working Lab, and KI Science Park, the joint

seminar **“Implementing Healthcare Data: From Access to Impact.”**

CRKI continues to award research grants that support excellent young researchers, clinical research, and innovative and international collaborations. This year, we awarded the **Translational Seed Funding Grant** to support new partnerships between basic and clinical scientists, and we look forward to launching the **Blue Sky Grant** to support innovative pilot projects in cancer research.

Strengthening Our International Presence

CRKI’s international engagement has continued to deepen and expand. KI researchers took part in the **CCE Summer School in Translational Cancer Research** in Portugal, which brings together PhD students, postdocs, and clinician-scientists from around the world.

Through the **ECHoS project** — an EU-funded initiative supporting implementation of the **European Cancer Mission** — CRKI has helped strengthen collaboration, patient involvement, and citizen engagement in cancer research across Europe, including through our co-organization of the **Second Cancer Mission Fair** in Nicosia, Cyprus, which convened patients, healthcare providers, researchers, policymakers, and industry representatives. CRKI is also a partner in **SweCan**, the recently launched **Swedish Cancer Mission Hub**, established to support Sweden’s contribution to the European Cancer Mission and to coordinate national stakeholders in advancing cancer research, prevention, and care. As we move into **ECHoS Stage II**, we look forward to continuing this work through initiatives such as the **National Cancer Mission Hub Summit** and future Cancer Mission Fairs, further amplifying the voices of patients and citizens in the European Cancer Mission.

Through **EUnetCCC**, an EU-funded project working to establish a **European network of Comprehensive Cancer Centres**, we have contributed to the **MTB Summit** on Molecular Tumor Boards across Europe, the **Deescalation Symposium** on the appropriate use of cancer drugs, and the launch of the **Twinning Initiative**, a bottom-up effort to promote collaboration between cancer research institutes. We also continue to support the clinical trials task, organizing expert meetings and developing materials for professionals and patients, and taking part in key discussions such as the upcoming **ESMO roundtable** on making Europe a more attractive destination for clinical trials.

Our collaborations with the **National Institute of Oncology (NIO)** in Budapest, Hungary, continue to grow and several workshops arising from this collaboration have been organized, both in Stockholm and in Budapest. This year we are particularly happy to invite the Scientific Director of NIO, **Prof. Péter Nagy**, as one of our speakers at this year’s CRKI retreat.

Finally, we were proud to celebrate the seventh **Mayo Clinic Comprehensive Cancer Center and Karolinska Institutet Joint Cancer Research Symposium**, which featured presentations from the 2025 Cancer Research Funding Awardees and reaffirmed our transatlantic collaboration. We are also very pleased to have launched a new even more ambitious initiative to further strengthen our partnership with the Mayo Clinic: the **Cancer Research KI–Mayo Clinic CCC Synergy Grants**, established to support major collaborative research projects between our two institutions. The application deadline is **November 6th, 2026**, and more information can be found at the CRKI website.

Looking Ahead, Together at Djurönäset

We now look forward to welcoming you all to **Djurönäset** for two days of engaging scientific discussion—discussions we are confident will spark new ideas and collaborations that further accelerate cancer research at KI.

We are especially honored to welcome our keynote speakers: **Professor Elaine Fuchs**, Head of the Laboratory of Mammalian Cell Biology and Development at The Rockefeller University; **Dr. Joan Massagué**, Director of the Sloan Kettering Institute for Cancer Research; and **Professor Nicholas McGranahan**, Professor of Cancer Evolution and Genomics at University College London.

A special welcome also to all invited speakers, resident physicians, and students – the new generation of cancer researchers and caregivers. We extend our sincere thanks to the organizing committee, chaired by **Dhifaf Sarhan** and **Ninib Baryawno**, for their work in planning this event, and to **QIAGEN** and **Xpress Genomics** for sponsoring the poster prizes.

On behalf of Cancer Research KI, welcome, everyone!

The Directors of Cancer Research KI

Elias Arnér, Marco Gerling, and Anna Nilsson

Share your experience on social media using the hashtag

#CRKIretreat2026

To access the **digital booklet** and **abstracts,** please scan this QR code

About QIAGEN

Our Poster Prize Sponsor

Founded in 1984, **QIAGEN** is a leading global provider of Sample to Insight solutions that enable researchers and healthcare professionals to unlock valuable molecular and biological insights. The company develops and markets a comprehensive portfolio of more than 500 consumables, instruments, automated solutions, and bioinformatics tools spanning the entire molecular biology workflow. QIAGEN is recognized as the global leader in sample preparation technologies, offering innovative solutions for the isolation and purification of DNA, RNA, and proteins, as well as advanced technologies for downstream applications such as PCR, qPCR, and next-generation sequencing (NGS).

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About Xpress Genomics

Our Poster Prize Sponsor

Xpress Genomics is an end-to-end NGS service provider, supporting research and industry across genomics, single-cell RNA sequencing, transcriptomics, proteomics, and beyond. We handle the full workflow, from sample to data output so our clients can focus on the science, not the logistics. Our mission is to accelerate discovery through fast, cost-effective, and high-quality sequencing services. For more information, visit https://xpress-genomics.com.

Take the opportunity to meet our sponsors during the poster session!

Their representatives will be available to discuss the technologies and services they provide to support biomedical and cancer research.

PRACTICAL INFORMATION

TRANSPORTATION (STOCKHOLM – DJURÖNÄSET – STOCKHOLM)

Buses will depart from **Cityterminalen** (Klarabergsviadukten 72) on **Monday, September 28 at 08:30** sharp.

Please check the monitors for the gate number for our buses labeled **"KI till Djurönäset."** The journey takes approximately one hour. Return buses will depart from Djurönäset on **Tuesday afternoon, September 29**, arriving at Cityterminalen around 17:00, depending on traffic conditions.

REGISTRATION

Upon arrival at Djurönäset, you will receive a **name badge** and a printed copy of the **program**. Please wear your badge visibly at all times during the conference.

Coffee/tea and sandwiches will be served before the conference begins at **10:05**. Luggage will be stored temporarily until check-in.

ACCOMMODATION

Room keys will be distributed during the afternoon coffee break at **15:15**. **Check-out** is scheduled for **Tuesday, September 29 at 09:00**, before the morning session begins.

Note: Students will be accommodated in shared rooms.

MEALS

Lunches will be served buffet-style in the restaurant located in the main building. If you have informed us of any dietary requirements, please speak directly with the restaurant staff as they have been notified.

Dinner on **Monday, September 28** will be served at **18:00**, and **breakfast** on **Tuesday, September 29** will be available from **07:30 to 09:00**.

POSTERS

The **poster session** will take place on **Monday evening at 20:00** in the main hall. Posters should be mounted between 17:30 and 18:00.

Please refer to the **digital abstract book** to find your poster number, as the poster frames will be numbered accordingly.

INTERNET

WiFi is available free of charge throughout the Djurönäset complex. Network name: **djuronaset-guest**. Each room also includes a wired internet connection.

LEISURE FACILITIES

The conference center features a 25-meter swimming pool, gym, and sauna, open on **Monday, September 28 from 15:30 to 23:00** (bar service available). The seaside **wooden sauna** will be open from **22:00 to 00:00** (pre-order your drinks in the main building until 21:00).

On **Tuesday, September 29**, the spa will be open from **06:00 to 08:00**.

PROGRAM

To access the digital booklet and abstract booklet, please scan the QR code.

1-7 Konferenslokaler och hotellrum / Conference and Hotel rooms
8 Seregården
9 Reception, Restaurang Matsalen, Barer / Reception, Restaurant & Bars
10 Skärgårdsspa / Spa
11 Spapaviljongen / Spa treatments
12 Skärgårdskrogen Sjöboden / Restaurant Sjöboden
13 Vedeldad bastu och badtunnor / Wood burning sauna and hot tubs
14 Svit och Längan / Suite and Hotel rooms

A Varm infinitypool / Hot outdoor infinity pool
B Cyklar / Bicycles
C Naturstig / Nature trail
D Badstrand / Beach
E Äventyrscenter / Adventure Center
F Helikopterplatta / Helipad
G Motionsslinga / Running trail
H Utegymstationer / Outdoor gym stations
I Busshållplats / Bus stop
J Tennisbana / Tennis court
K Folkparken / Outdoor event area
L Gästhamn / Guest harbour
M Mötesplats / Meeting spot
P1 Parkering / Parking
P2 Parkering Seregården och Folkparken / Parking for Seregården and Folkparken

XXIII Cancer Research KI Retreat

September 28-29, 2026

GENERAL PROGRAM OUTLINE

Monday, September 28:

Bus departure from Stockholm: **08:30**

Arrival, coffee, and registration: **09:30**

Morning session: **10:05**

Group photo: **12:30**

Lunch: **12:45**

Afternoon session: **13:45**

Coffee break and collection of keys: **15:15**

Breakout sessions: **16:00**

Mingle and welcoming drink: **17:30**

Dinner: **18:00**

Poster session: **20:00**

Tuesday, September 29:

Breakfast and check out: **07:30**

Morning session: **09:15**

Coffee break: **10:35**

Panel disucssion: **11:45**

Lunch: **13:00**

Afternoon session: **14:00**

Coffee break: **15:30**

Bus departure: **16:00**

Arrival to Stockholm: **17:00**

Keynote Speakers:

Prof. Elaine Fuchs, Howard Hughes Medical Institute, The Rockefeller University

Dr. Joan Massagué, Sloan Kettering Institute, Memorial Sloan Kettering Cancer Center

Prof. Nicholas McGranahan, University College London, Cancer Institute

Monday, September 28

08:30 Buses depart from Stockholm Cititerminalen

09:30 - 10:00 Arrival at Djurönäset (estimated time), Coffee & Registration

Morning session

10:05 - 10:15 **Opening and Welcome Remarks**

Chairs: **Jonas Muhr** and **Hala Habash**

10:15 - 11:00 **Keynote Lecture: Elaine Fuchs**, Howard Hughes Medical Institute, The Rockefeller University, New York, USA
"Tissue Stem Cells: Coping with Stress"

11:00 - 11:20 **Ioannis Zerdes**, Dep. of Oncology-Pathology, Karolinska Institutet; Theme Cancer, Karolinska University Hospital
"Deciphering tumor-immune microenvironment determinants of treatment response and resistance in breast cancer"

11:20 - 11:35 **Celine Hafkesbrink**, Dep. of Women's and Children's Health, Karolinska Institutet
"Chemotherapy rewires neuroblastoma into a targetable NCAM1–FGFR1 state"

11:35 - 11:50 **Rodrigo Morales Castro**, Dep. of Laboratory Medicine, Karolinska Institutet
"Novel histone deacetylase inhibitors limit tumor expansion in a zebrafish KRAS-driven intestinal tumor model"

11:50 - 12:05 **Heshuang Qu**, Dep. of Oncology-Pathology, Karolinska Institutet
A Transcriptomics- and AI-Guided 3D NSCLC Spheroid Platform for "Modeling EMT and Phenotypic Drug Screening"

12:05 - 12:20 **Yujie Xiang**, Dep. of Medical Epidemiology and Biostatistics, Karolinska Institutet
"AI-based multi-modal prognostic modelling of histopathology images, mRNA expression, and clinical information in a Swedish study including 3,000 patients"

12:30 - 12:40 **Group Picture**

12:45 - 13:45 **Lunch**

Afternoon session

Chairs: **Kasper Karlsson** and **Sara Abu Ajamieh**

13:45 - 14:30 **Keynote Lecture: Nicholas McGranahan**, University College London, Cancer Institute, London, United Kingdom
"Cancer Evolution Beyond the Genome"

14:30 - 14:50 **Erik Benson**, Dep. of Microbiology, Tumor and Cell Biology, Karolinska Institutet
"Discovery of cell targeting DNA structures by evolutionary selection"

14:50 - 15:10 **Poster pitches**
Moderated by **Pablo Martí Andrés**

15:15 - 16:00 **Coffee break and collection of keys**

16:00 - 17:30 **Breakout sessions** (see detailed program on the next page)

17:30 - 18:00 **Mingle and mounting of posters**

18:00 - 20:00 **Dinner**

20:00 - 22:00 **Poster session**

Breakout Sessions

Monday, September 28 (16:00 - 17:30)

Please note:

- **Pre-registration is required for all sessions.** If you haven't registered yet, please contact the organizers to check if there are any available spots.
- Abstracts and additional information about the speakers can be found in the **extended abstract booklet available online**.

Scan the QR code to access more information about the breakout sessions

Breakout session 1: Patient Perspectives

In these sessions, you will join one of our oncologists and one of their patients for an honest conversation about their real-life journey. You will meet patients and their relatives who will share their own experiences and perspectives, so please be prepared for an intimate and personal session.

Pancreatic Cancer
Marco Gerling, House 4 (Room 4A)

Childhood Cancer
Anna Nilsson, House 5 (Room 5A)

Breakout session 2: Scientific Presentations

In this session, participants will have the opportunity to attend several scientific presentations selected by the Scientific Committee from submitted abstracts. A detailed program and information about each presentation can be found in the digital booklet, accessible by scanning the QR code above.

Chairs: **Ewa Kurzejamska** and **Sara Abu Ajamieh**

House 7 (Conference Room 7A)

Breakout session 3: The AI Landscape at KI

In this session, **Robert Svebeck** will present how AI is being applied across Karolinska Institutet, highlighting available resources, ongoing initiatives, and opportunities for future development. The session will be chaired by **Mattias Rantalainen**.

House 3 (Room 3A)

Breakout session 4: Meet the Scientist

In these sessions, participants will have the opportunity to engage in conversation with our keynote speakers in a more relaxed and informal setting. This format allows for questions that might otherwise be difficult to ask due to time constraints or their personal nature.

Prof. Elaine Fuchs, House 1 (Coffee Lounge)

Dr. Joan Massagué, House 2 (Coffee Lounge)

Prof. Nicholas McGranahan, House 3 (Coffee Lounge)

Tuesday, September 29

07:30 - 09:00 **Breakfast and check-out**

Morning session

Chairs: **Marie Arsenian Henriksson** and **Sammy Se Whee Park**

09:15 - 10:00 **Keynote Lecture: Joan Massagué**, Sloan Kettering Institute, Memorial Sloan Kettering Cancer Center, New York, USA
"A TGF-β dormant metastasis program"

10:00 - 10:20 **Aline Pfefferle**, Dep. of Medical Cell Biology, Uppsala University, Sweden
"Pan-cancer profiling of tumor-infiltrating natural killer cells"

10:20 - 10:35 **Thuy Tran**, Dep. of Oncology-Pathology, Karolinska Institutet; Theranostics Trial Center, Karolinska University Hospital
"Development of a Novel TROP2-targeted Monoclonal Antibody for Radiotheranostics of Solid Tumors - A New Modality in Precision Oncology"

10:35 - 11:05 **Coffee break**

Chairs: **Eva Jolly** and **Mindaugas Raitelaitis**

11:05 - 11:25 **Péter Nagy**, National Institute of Oncology, Budapest, Hungary
"Cysteine metabolism in cancer"

11:25 - 11:45 **Highlights from Karolinska Comprehensive Cancer Center**

- **Patrik Rossi:** *Updates from Karolinska CCC: Coordination Group and Regional CCC Network*
- **Fredrik Döberl:** *Patient Involvement in Karolinska CCC and the Role of the Patient Network*
- **Yvonne Wengström:** *Nursing Perspective in Karolinska CCC: Connecting Practice, Strategy and Research*
- **Marco Gerling:** *Educational Strategy Group: Highlighting the New Strategic Collaboration*

11:45 - 13:00 **Panel discussion:** *"New challenges in cancer treatment: What are we doing wrong?"*
Moderated by **Ingemar Ernberg** and **Andri Papakonstantinou**
With *Elaine Fuchs*, *Joan Massagué*, *Nicholas McGranahan*, *Signe Friesland*, *Patrik Rossi*, and *Nils Wilking*

13:00 - 14:00 **Lunch**

Afternoon session

Chairs: **Hong Qian** and **Mingzhi Liu**

14:00 - 14:15 **Flora Mikaeloff**, Dep. of Oncology-Pathology, Karolinska Institutet
"Multi-omics integrative clustering revealed three independent molecular subtypes of poor prognosis and drug resistance in acute myeloid leukemia"

14:15 - 14:30 **Isabel Barragán**, Dep. of Oncology-Pathology, Karolinska Institutet
"Immune phenotyping of molecular subtypes derived from early multiomic blood profiling for prognostic stratification in NSCLC"

14:30 - 14:50 **Amanda Rolf**, Dep. of Medical Biochemistry and Biophysics, Karolinska Institutet
"Long-term in vitro expansion of a human tripotent fetal pancreas stem cell"

14:50 - 15:10 **Filipe Pereira**, Division of Molecular Medicine and Gene Therapy, Lund University, Sweden
"Building the Dendritic Cells that Build TLS"

15:15 - 15:30 **Conclusion & Poster Prizes**

15:30 - 16:00 **Coffee break** (takeaway available)

16:00 **Buses depart for Stockholm**

17:00 **Arrival at Stockholm Cityterminalen** (estimated)

Highlights from Karolinska CCC

Tuesday, September 29, 11:25

Karolinska Comprehensive Cancer Center (Karolinska CCC) is a strategic partnership between Karolinska University Hospital and Karolinska Institutet, bringing together world-leading expertise in cancer research, diagnostics, treatment, education, and innovation. As a regional hub for cancer care and research, Karolinska CCC works to accelerate the translation of scientific discoveries into improved outcomes for patients through precision medicine, multidisciplinary collaboration, and person-centered care.

During this session, you will hear updates from the following speakers:

Patrik Rossi, Managing Director, Cancer Theme Karolinska University Hospital; Chair, Board of Directors Karolinska CCC
Updates from Karolinska CCC: Coordination Group and Regional CCC Network

Fredrik Döberl, Vice chair, Karolinska CCC PNN
Patient Involvement in Karolinska CCC and the Role of the Patient Network

Yvonne Wengström, Professor
Nursing Perspective in Karolinska CCC: Connecting Practice, Strategy and Research

Marco Gerling, Oncologist, Co-director of Cancer Research KI
Educational Strategy Group: Highlighting the New Strategic Collaboration

More information about Karolinska Comprehensive Cancer Center

In 2025, Karolinska CCC became the first Comprehensive Cancer Centre in Sweden to receive renewed accreditation from the Organization of European Cancer Institutes (OECI), securing its status as an internationally recognized center of excellence until 2030. The renewed accreditation reflects the center's commitment to the highest standards in cancer research and care, while reinforcing the close collaboration between Karolinska Institutet and Karolinska University Hospital. A major recent development is the inclusion of childhood cancer within the center, creating new opportunities for research, innovation, and seamless care throughout a patient's life.

By combining clinical expertise with cutting-edge academic research, Karolinska CCC continues to drive advances that shape the future of cancer prevention, diagnosis, treatment, and survivorship, both in Sweden and internationally.

Scan the QR code to access more information about Karolinska Comprehensive Cancer Center

Panel Discussion

Tuesday, September 29, 11:45

New challenges in cancer treatment: What are we doing wrong?

This year's panel builds on the discussion opened by Prof. Robert Weinberg at our previous Cancer Research KI Retreat. It takes up one of the questions the cancer community keeps returning to: given how much we have learned about cancer biology, and how far the technology has come, why is it still so hard to turn that progress into better outcomes for patients?

The panel will consider where progress stalls in prevention, diagnosis, treatment, and the move from discovery to clinical practice. Panelists will be asked to reflect on whether research priorities, funding structures, healthcare systems, regulatory frameworks, and innovation strategies are well matched to what patients and society actually need. The session will also address challenges that have emerged more recently: cancer care is becoming more complex, access to treatment remains unequal, and fast-moving technologies such as artificial intelligence and precision medicine still have to be fitted into everyday practice.

Because these challenges are at once scientific, clinical, organizational, and economic, the panel brings together experts from cancer research, clinical care, healthcare leadership, and health economics. They will discuss how the different parts of the cancer ecosystem interact, where the gaps lie, and what would have to change for scientific advances to reach patients as real benefit.

Ingemar Ernberg and **Andri Papakonstantinou** will moderate.

Panelists:

Elaine Fuchs, Professor
Howard Hughes Medical Institute, The Rockefeller University, New York, USA

Joan Massagué, Director
Sloan Kettering Institute, Memorial Sloan Kettering Cancer Center, New York, USA

Nicholas McGranahan, Professor
University College London, Cancer Institute, London, United Kingdom

Patrik Rossi, Managing Director
Cancer Theme, Karolinska University Hospital
Chair
Board of Directors Karolinska CCC

Signe Friesland, Associate Professor
Department of Oncology-Pathology, Karolinska Institutet
Patient Area Manager & Head of Department
Cancer Theme, Karolinska University Hospital

Nils Wilking, Associate Professor
Department of Oncology-Pathology, Karolinska Institutet

KEYNOTE SPEAKERS

Elaine Fuchs

Rebecca C Lancefield Professor

Howard Hughes Medical Institute, The Rockefeller University, New York, USA

Time: Monday 28, 10:15

Tissue Stem Cells: Coping with Stress

To survive harsh environments and continually generate and rejuvenate their tissues, epithelia must maintain reservoirs of self-renewing stem cells that can produce tissue long-term. When the barrier has been breached, for example by wounding, the stem cells must not only repair the damaged tissue but also call to the immune system to help guard against pathogen entry. All the while the stem cells must protect themselves from a variety of assaults, including not only injury but also mechanical stress, ultraviolet radiation and allergens that stimulate an inflammatory response. My laboratory focuses on how epithelial stem cells equip themselves to respond to these different stresses. We discovered that these cells keep epigenetic memories of their stressful encounters within their chromatin and unleash them upon subsequent encounters. The underlying mechanisms have tantalizing similarities to the memories we store in our brain. Our discoveries also have broad implications across many tissue stem cells, and while evolutionarily advantageous in healing wounds and encountering subsequent pathogens, these epigenetic memories can be maladaptive. Our focus is on dissecting the complex interactions that take place between the stem cells and their environment that are optimized for tissue fitness but which become aberrant in times of stress and in disease states, including chronic inflammation and cancer.

About Prof. Elaine Fuchs

Elaine Fuchs is renowned for her research in skin biology, its stem cells and associated disorders, including cancers and inflammation, and has published >380 manuscripts. She received her Ph.D. from Princeton, postdoctorate at MIT, and has been faculty at University of Chicago and now Rockefeller University, where she is an Investigator of the Howard Hughes Medical Institute. Her awards include the National Medal of Science, L'Oreal-UNESCO Award, International Society for Stem Cell Research Innovation Award, the Gairdner International Award and most recently the Franklin Medal. Fuchs holds membership in the National Academy of Sciences, National Academy of Medicine, American Philosophical Society, Pontifical Academy of Sciences, and the Royal Society.

Joan Massagué

Director

Sloan Kettering Institute, Memorial Sloan Kettering Cancer Center, New York, USA

Time: Tuesday 29, 09:15

A TGF-β dormant metastasis program

Cancer cells that disseminate from a primary tumor can enter a dormant state that persists for months to decades before giving rise to clinically detectable metastases. Eliminating dormant metastatic cells to prevent relapse remains a major goal in cancer research. We have developed models of dormant metastasis from human and murine early-stage lung adenocarcinomas (LUAD). These tumors contain a rare population of SOX2-expressing metastasis-initiating cells with features of malignant regenerative progenitors. Unlike their more differentiated progeny, $SOX2^{+}$ LUAD cells respond to TGF-β with a series of activities that collectively support long-term dormancy and survival. Following dissemination, these cells localize to perivascular niches with ready access to oxygen and nutrients and activate a TGF-β–dependent dormancy program which includes cell-cycle arrest, suppression of MHC-I and STING immunoreactive pathways, an atypical epithelial-to-mesenchymal transition (EMT), and extensive metabolic reprogramming. These adaptations enable dormant cells to evade immune surveillance while remaining metabolically active, whereas their reentry into the cell cycle increases susceptibility to immune-mediated elimination. Dormant metastatic cells can progress to overt metastasis by resuming proliferation under conditions of decreased immune surveillance. Together, these findings identify mechanisms that sustain metastatic dormancy and immune evasion and suggest vulnerabilities and therapeutic strategies for the elimination of dormant metastatic cells to prevent relapse.

About Dr. Joan Massagué

Joan Massagué (Barcelona, 1953), received a PhD degree in Pharmacy and Biochemistry from the University of Barcelona in 1978, postdoctoral training at Brown University (1979-1981), and a faculty appointment at the University of Massachusetts Medical School (1982-1989). He joined Memorial Sloan Kettering Cancer Center in 1989 as Chair, Cell Biology Program (1989–2003), Chair, Cancer Biology and Genetics Program (2003–2013), and Director, Sloan Kettering Institute (2014–), where he holds the Marie-Josée and Henry R. Kravis Chair. He was a HHMI Investigator from 1990 until he became HHMI Scientific Advisor in 2014. He was Adjunct Director (2004-2013) and Advisory Board Chair (2014–) of the Institute for Research in Biomedicine Barcelona.

Joan Massagué's scientific contributions have advanced our understanding of signaling pathways and transcriptional programs that maintain tissue integrity or promote cancer metastasis. He elucidated the TGF-β signal transduction pathway from membrane receptors to nuclear target genes. With his team, Massagué defined mechanisms by which TGF-β regulates cell proliferation, differentiation, immune reactivity, phenotypic plasticity, and survival. He explained how TGF-β turns from tumor suppressor to pro-metastatic signal during cancer progression. He went on to discover central principles and molecular mechanisms driving cancer cell dissemination, dormancy, immune evasion, and organ-specific metastasis. His work has opened new avenues for the prevention and treatment of cancer relapse.

Massagué is a member of the US National Academy of Sciences, National Academy of Medicine, American Academy of Arts and Sciences, European Molecular Biology Organization, and the Spanish Royal Academies of Medicine and of Pharmacy. He received the Prince of Asturias Prize, BBVA Frontiers Prize, Vilcek Prize, Pezcoller-AACR International Award, and Brupbacher Prize, among many other honors.

Nicholas McGranahan

Professor of Cancer Evolution

University College London, Cancer Institute, London, United Kingdom

Time: Monday 28, 13:45

Cancer Evolution Beyond the Genome

Lung cancer remains the leading cause of cancer-related mortality worldwide. Understanding the evolutionary principles governing tumour development, metastasis, and treatment resistance is critical to improving patient outcomes. Drawing on data from the TRACERx and PEACE studies — longitudinal multi-region sequencing cohorts tracking non-small cell lung cancer from diagnosis through recurrence and death — I will present an integrated view of cancer evolution across genetic, non-genetic, and environmental axes.

I will discuss how tumour phylogenetic reconstruction can illuminate the metastatic process, revealing unexpected complexity in how cancers spread and the genomic features that underpin metastatic capacity. I will then turn to the role of phenotypic plasticity in cancer evolution, presenting new approaches that link tumour genotype to phenotype at single-cell resolution, and discussing how plasticity — beyond genetics alone — shapes clinical outcomes.

Together, these findings advance a framework for understanding lung cancer evolution that may ultimately inform strategies for earlier intervention and more durable treatment responses.

About Prof. Nicholas McGranahan

Professor Nicholas McGranahan is a leading researcher in cancer evolutionary biology, applying evolutionary principles to understand how cancers develop, spread, and evade the immune system. Based at the UCL Cancer Institute, where he leads a research group focused on cancer evolution and genome instability and holds a position within the CRUK Lung Cancer Centre of Excellence, his work addresses a central question: if cancers evolve, can understanding the rules of that evolution help us predict - and ultimately better treat - them?

His research spans the natural history of lung cancer, from the genomic events that shape primary tumours to the evolutionary processes underlying metastasis and treatment resistance. He is a computational lead on the TRACERx study, one of the world's largest prospective longitudinal studies of tumour evolution, and co-leads analysis of the PEACE post-mortem study. Through this work, he has contributed important insights into intratumour heterogeneity, clonal neoantigens, genomic instability, and the evolving relationship between cancer and the immune system.

Professor McGranahan also develops computational approaches for reconstructing tumour evolution , allowing researchers to infer how individual cancers have changed over time and across metastatic sites and in response to the immune system. His work has been published in Nature, Science, and Cell and has contributed to the growing understanding of cancer evolution as both a fundamental biological process and a potential framework for improving cancer treatment.

INVITED SPEAKERS

Erik Benson

Assistant professor

Department of Microbiology, Tumor and Cell Biology, Karolinska Institutet; SciLifeLab

Time: Monday 28, 14:30

Discovery of cell targeting DNA structures by evolutionary selection

Synthetic DNA nanostructures can be precisely designed and have a strong potential for targeted drug delivery, yet different types of structures have different interactions with cells and current discovery approaches rely on testing individual designs one by one. In our group we work to develop the tools to turn DNA structure discovery into an evolutionary process where the best candidates are selected from millions of possible variants. We do this by creating new types of DNA structures as diverse libraries where each structure folds from a long single stranded ‘structure genome’ that can be copied by PCR and read by sequencing. In order to understand what structures are taken up by what cells we use cellular internalization as the selection pressure: libraries are incubated with mammalian cells, internalized structures are recovered from lysates, and the process is iterated across multiple rounds in cancer and non-cancer cells as well as mouse models. The sequencing data allows us to both understand the trends in cellular uptake preferences as well as identify individual structures with strong positive selection that we can validate individually.

Péter Nagy

Professor, Scientific Director

Dep. of Molecular Immunology and Toxicology, National Tumor Biology Laboratory, NIO, Budapest, Hungary

Time: Tuesday 29, 11:05

Title

Cysteine is a non-essential amino acid, because human cells can produce it via the transsulfuration pathways. Despite this intrinsic biosynthetic capacity, many tumors exhibit a marked dependence on exogenous cysteine supply. Emerging evidence, including findings from our group and others, demonstrates that rewired transsulfuration metabolism in tumor cells is exploited to promote proliferation, metastatic dissemination, and therapeutic resistance.

In this presentation, I will discuss the mechanistic basis by which cystine/cysteine utilization, mediated through distinct transsulfuration enzyme activities, drives tumor progression across multiple cancer types. At the end of my presentation I will spend a couple of slides presenting the activities and future plans along the KI-NIO Memorandum of Understanding.

Key references:

- Péter Nagy et. al.: *Multifaceted Roles for Persulfide Species in Redox Chemical Biology* **Nature Chemical Biology** (2026) 22, 540–555
- Edward E. Schmidt et. al.: *Cystine C-S bond cleavage fuels cysteine production under disulfide reductase deficiency* **Nature Chemical Biology** (2026) Online ahead of print
- Klaudia Borbényi-Galambos et. al. *Realigned Transsulfuration Drives BRAF V600E-Targeted Therapy Resistance in Melanoma* **Cell Metabolism** (2025)
- Klaudia Borbényi-Galambos et. al. *Versatile roles of cysteine persulfides in tumor biology* **Current Opinion in Chemical Biology** (2024) 79, 102440
- Ágnes Czikora et. al. *Cystathionine B-Synthase Overexpression Drives Metastatic Dissemination in Pancreatic Ductal Adenocarcinoma Via Inducing Epithelial-to-Mesenchymal Transformation of Cancer Cells* **Redox Biology** (2022) 57:102505.
- Katalin Erdélyi et. al. *Reprogrammed transsulfuration promotes basal-like breast tumor progression via realigning cellular cysteine persulfidation* **PNAS (**2021) 118, e2100050118
- Éva Dóka et. al. *Control of protein function through oxidation and reduction of persulfidated states* **Science Advances** (2020) 6(1):eaax8358.

Filipe Pereira

Professor

Division of Molecular Medicine and Gene Therapy, Lund University, Sweden

Time: Tuesday 29, 14:50

Building the Dendritic Cells that Build TLS

Tertiary lymphoid structures (TLS) in tumors are associated with improved responses to immunotherapy, but their controlled induction remains elusive. Here, we used reprogramming of tumor cells into type-1 conventional dendritic cell (cDC1)–like cells to remodel the tumor microenvironment and induce immunogenic TLS (imgTLS) across melanoma, colon, bladder, breast and pancreatic cancer models with distinct genetic backgrounds. cDC1-like cells activated lymphotoxin, TNF, and interferon programs, and engaged early with T cells through MHC-I and CD40 signaling to induce imgTLS containing $BCL6^+$ germinal centers, independently of endogenous cDC1s. Spatial transcriptomics identified $DC\text{-}LAMP^+$ $CCR7^+$ migratory cDC1s nucleating niches enriched in $CD4^+$, $CD8^+$ T cells, and B cells in mouse and human tumors. ImgTLS sustained B cell and T cell responses, and promoted systemic immunity through expansion of shared clonotypes in distant, untreated tumors. Together, our findings establish cellular reprogramming as a strategy to engineer intratumoral lymphoid niches and overcome resistance to immunotherapy.

Aline Pfefferle

SciLifeLab Fellow; Associate Senior Lecturer

Department of Medical Cell Biology, Uppsala University, Sweden

Time: Tuesday 29, 10:00

Pan-cancer profiling of tumor-infiltrating natural killer cells

Natural killer (NK) cells have tremendous potential in the fight against cancer, yet clinical trials so far have come up short. This is partly due to the functional regulation of NK cells, which is intricate, poorly understood, and highly dynamic. Differentiation, homeostatic receptor-ligand interactions and adaptive-like responses to viral infections shape the functional diversity of NK cell repertoires. Yet the regulatory gene-circuits that define the manifold of cell states at steady state in blood and tissues, and how they are perturbed within the solid tumor microenvironment (TME) remained unclear.

To address this knowledge gap, we first generated a single-cell transcriptional reference map of healthy human blood and tissue-derived NK cells, with temporal resolution and fate-specific expression of gene regulatory networks defining NK cell differentiation. Transfer learning facilitated incorporation of tumor-infiltrating NK cell transcriptomes (39 datasets, 7 solid tumors, 427 patients) into the reference map to analyze TME-induced perturbations. We identified six functionally distinct NK cell states, a dysfunctional stressed $CD56^{bright}$ state susceptible to TME-induced immunosuppression and a cytotoxic TME-resistant effector $CD56^{dim}$ state which were commonly enriched across tumor types. The ratio of these two states was also predictive of patient outcome in malignant melanoma and osteosarcoma.

This resource may inform the design of novel NK cell therapies and can be endlessly extended through transfer learning to interrogate new datasets from experimental perturbations or disease conditions.

Amanda Rolf

Assistant professor

Department of Medical Biochemistry and Biophysics, Karolinska Institutet

Time: Tuesday 29, 14:30

Long-term in vitro expansion of a human tripotent fetal pancreas stem cell

The mammalian pancreas consists of three epithelial compartments: the acini and ducts of the exocrine pancreas and the endocrine islets of Langerhans. Murine studies indicate that these three compartments derive from a transient, common pancreatic progenitor. Here, we report derivation of 18 human fetal pancreas organoid (hfPO) lines from gestational weeks 8-17 (8-17 GWs) fetal pancreas samples. Four of these lines, derived from 15 to 16 GWs samples, generate acinar-, ductal-, and endocrine-lineage cells while expanding exponentially for >2 years under optimized culture conditions. Single-cell RNA sequencing identifies rare $LGR5^{+}$ cells in fetal pancreas and in hfPOs as the root of the developmental hierarchy. These $LGR5^{+}$ cells share multiple markers with adult gastrointestinal tract stem cells. Organoids derived from single $LGR5^{+}$ organoid-derived cells recapitulate this tripotency in vitro. We describe a human fetal tripotent stem/progenitor cell capable of long-term expansion in vitro and of generating all three pancreatic cell lineages.

Ioannis Zerdes

Associate Professor; Clinical Fellow in Medical Oncology

Dep. of Oncology-Pathology, Karolinska Institutet; Theme Cancer, Karolinska University Hospital

Time: Monday 28, 11:00

Deciphering tumor-immune microenvironment determinants of treatment response and resistance in breast cancer

The tumor-immune microenvironment plays a central role in breast cancer progression and treatment response. Beyond immunotherapy, accumulating evidence indicates that chemotherapy and targeted therapies can profoundly modulate anti-tumor immunity, highlighting the importance of understanding treatment-induced changes in both local and systemic responses.

Our translational research program investigates the immunological and molecular determinants of treatment response and resistance across breast cancer subtypes and therapeutic modalities. Using patient material from randomized clinical trials and large national and international real-world cohorts, we integrate digital pathology and machine learning with spatial transcriptomics, proteomics, genomic and transcriptomic profiling, and circulating biomarkers. Through longitudinal analyses of pre-treatment and on-treatment samples, we aim to characterize the abundance, spatial organization, and dynamic evolution of the tumor immune microenvironment, together with systemic immune changes induced by immunotherapy, chemotherapy, HER2-targeted therapies, and emerging treatments such as antibody-drug conjugates.

By integrating multidimensional and multiomics profiling with experimental models, we aim to identify clinically relevant biomarkers, elucidate mechanisms of treatment sensitivity and resistance, and uncover novel therapeutic vulnerabilities. Ultimately, our work seeks to translate insights into tumor-immune interactions into improved patient stratification and rational biomarker-driven therapeutic strategies and new-generation clinical trials in patients with breast cancer.

SELECTED FROM ABSTRACTS

Isabel Barragán

Principal Investigator

Department of Oncology-Pathology, Karolinska Institutet

Time: Tuesday 29, 14:15

Immune phenotyping of molecular subtypes derived from early multiomic blood profiling for prognostic stratification in NSCLC

Background: Immune checkpoint inhibitors (ICIs) have transformed the treatment landscape for non–small-cell lung cancer (NSCLC). However, primary resistance occurs in approximately 70% of patients, representing a critical clinical challenge. Consequently, there is an urgent need for predictive, minimally invasive biomarkers that not only accurately anticipate clinical outcomes but also elucidate the systemic biological mechanisms driving the anti-tumour immune response.

Methods: Using blood samples collected at the second cycle of ICI therapy, we integrated circulating cell-free DNA (cfDNA) methylation and extracellular vesicleassociated microRNA (EV-miRNA) signatures via MOFA2 to define post-treatment molecular subtypes (MDCs; MOFA2-derived clusters). This approach identified three distinct molecular clusters (MDC1, MDC2, and MDC3). To characterise the immunological context associated with these MDCs, we analysed matched flow cytometry data and evaluated bulk RNA-seq profiles from peripheral blood mononuclear cells (PBMCs) representative of the three clusters. Transcriptomic profiles were deconvoluted using CIBERSORT to estimate immune cell composition, and these findings were subsequently correlated with both MDC assignments and the flow cytometry data.

Results: The MDCs robustly stratified patients into clinically distinct risk categories. MDC1 and MDC2 formed a low-survival state associated with poor outcomes, demonstrating median progression-free survival (PFS) of 4.66 and 7.71 months, and median overall survival (OS) of 7.78 and 9.90 months, respectively. Conversely, MDC3 patients exhibited a highly favourable profile with markedly prolonged survival (median PFS: 28.89 months; median OS: 40.79 months), achieving statistical separation between risk groups (log-rank $p < 0.001$). Furthermore, integration with circulating immune cell subsets highlighted key immunological correlates: MDC1 and MDC2 were associated with immunosuppressive or dysfunctional profiles, whereas MDC3 strongly correlated with signatures of active anti-tumour immunity. The correlation among MDC assignments, CIBERSORT-derived cellular composition, and flow cytometry confirmed that these molecular subtypes capture systemic immune differences at an early on-treatment time point.

Conclusion: This integrative multiomic analysis of cfDNA methylation and EVmiRNAs establishes MDCs as clinically relevant, minimally invasive biomarkers of early treatment adaptation. The correlation of MDCs with CIBERSORT and flow cytometry data supports the utility of integrated liquid biopsy approaches to refine NSCLC patient stratification and to uncover the systemic mechanisms mediating immunotherapy efficacy.

Celine Hafkesbrink

PhD Student

Department of Women's and Children's Health, Karolinska Institutet

Time: Monday 28, 11:20

Chemotherapy rewires neuroblastoma into a targetable NCAM1–FGFR1 state

Neuroblastoma (NB) is the most common extracranial solid tumour in infants and is characterised by substantial heterogeneity in tumour biology, treatment response and clinical outcome. Despite intensive multimodal therapy, approximately half of the patients with high-risk disease relapse due to therapy resistance and face poor survival, underscoring the need for new targeted treatment strategies. Longitudinal patient-derived xenograft (PDX) models were used to recapitulate clinical treatment trajectories and relapse-associated disease states, enabling dissection of chemotherapy-induced remodelling of neoplastic and microenvironmental cell states and their spatial organisation.

Single-cell transcriptomic profiling of NB patient samples and a chemoresistant PDX NB tumour model revealed chemotherapy-driven remodelling of neoplastic and microenvironmental cell states and identified NCAM1 and FGFR1 as candidate therapeutic targets linked to an acquired relapse-associated state driven by the tumor niche. Ligand–receptor inference analysis highlighted NCAM1–FGFR1 as a prominent autocrine and paracrine signalling axis, and spatial analyses demonstrated that NCAM1–FGFR1-positive cells assemble into treatment-induced microniches in tumours following chemotherapy. Furthermore, elevated NCAM1/FGFR1 co-expression in patient cohorts correlated with adverse clinical features and poor overall survival

Therapeutic targeting of the axis was assessed using the CD56 (NCAM1)-directed antibody–drug conjugate Adcitmer® and the FGFR1 inhibitor erdafitinib in NB cell lines and multicellular tumour spheroids. Pharmacological inhibition impaired tumour cell viability. Moreover, FGFR1 blockade affected multiple downstream pathways, including RAS-MAPK, PI3K-AKT, PLCγ and STAT signalling. Together, these findings identify the NCAM1-FGFR1 axis as a spatially organised, therapeutically actionable target in relapsed NB and provide a rationale for further preclinical and clinical evaluation of Adcitmer® and erdafitinib.

Flora Mikaeloff

Postdoctoral Researcher

Department of Oncology-Pathology, Karolinska Institutet

Time: Tuesday 29, 14:00

Multi-omics integrative clustering revealed three independent molecular subtypes of poor prognosis and drug resistance in acute myeloid leukemia

Background: Acute myeloid leukemia (AML) is a rapidly progressing bone marrow and blood cancer defined by the abnormal proliferation of myeloid cells. Despite the improvement of classification and therapeutic strategies based on genomic abnormalities, AML is still prognostically unfavorable due to its heterogeneity, significant relapse rate and drug resistance.

Aims: To improve AML risk prediction and identify new potential treatments, we aim to determine omics-based clusters in AML, understand their underlying mechanisms and validate them in independent datasets.

Methods: AML patients (n =110) with complete RNA-seq, MS-proteomics, DNA methylation and mutational screening profiles were integrated and clustered using robust consensus clustering. Identified clusters were characterized by comparing survival, clinical parameters, drug sensitivity from functional ex vivo drug testing data, and finding specific biomarkers, pathways and AML cell types proportions from cell typing. Clusters were validated in four external transcriptomics datasets using cluster genes markers.

Results: Four cancer subtypes (C1-C4) were identified based on muti-omics clustering. C4 showed the best prognosis, younger age, larger % of remission and a favorable ELN compared to the other clusters. On the other hand, C1 and C2 had a bad prognosis which was partially explained by their mutation pattern : high-frequency mutation of NPM1 (84%) and FLT3_ITD (76%) in C1 and NPM1 (57%), FLT3_ITD (43%) and DNMT3A (39%) in C2. C1 was sensitive to venetoclax but resistant to FLT3 inhibitors due to the large proportion of immature cells and up-regulation of stemness markers and pathways. C2 had the opposite drug profile and showed a much larger proportion of differentiated cells, including monocytes and dendritic cells, as well as activation of immune processes. C3 had the worst prognosis, including patients with secondary AML (30%) and myeloproliferative neoplasm (MPN/MPD) diagnosis (20%), and had a large proportion of adverse ELN2017 (77%). Up-regulation of calcium pathways were identified in C2 and C3 linked to venetoclax resistance, but driven by independent sets of genes. Clusters were validated in four independent datasets in terms of survival, mutation profile and drug screening profile. Relapse samples showed an enrichment of c3 compared to diagnosis indicating the rewiring of cells into a pathogenic drug resistant subtype. Potential drug combinations and predicted drugs were computed to suggest cluster-specific personalized treatment.

Discussion/conclusion: We have shown that the molecular heterogeneity among patients should be considered as AML patients displayed different profiles despite sharing the same mutations. Identified omics subtypes can be applied for prognosis in other cohorts and new targeted therapies can be developed to improve multi-omics based precision medicine in the future.

Rodrigo Morales Castro

Assistant Professor

Department of Laboratory Medicine, Karolinska Institutet

Time: Monday 28, 11:35

Novel histone deacetylase inhibitors limit tumor expansion in a zebrafish KRAS-driven intestinal tumor model

Colorectal cancer (CRC) is one of the deadliest cancers worldwide. This is attributed to the presence of oncogenic mutations in the *KRAS* gene, which are found in approximately 40% of CRC patients. These mutations drive aggressive tumor growth and confer resistance to therapy, leaving patients with limited treatment options. Despite the recent development of oncogenic KRAS-specific inhibitors and their promising results in experimental models (e.g., mice), efficacy in CRC trials has been modest, with low response rates, rapid development of resistance, and adverse side effects. These challenges underscore the need to identify alternative strategies to target KRAS-driven CRC, and to implement experimental models amenable to large-scale therapeutic and off-target evaluation of novel anti-tumorigenic candidates. Histone deacetylase inhibitors (HDACi), particularly those targeting class I histone deacetylases (HDAC), have emerged as promising drugs for CRC treatment, as these enzymes are commonly overexpressed in CRC tumors. While the selective class I HDACi Entinostat has shown anti-tumor potential in experimental models, its clinical application remains limited due to suboptimal efficacy and toxicity. Therefore, we aimed to evaluate the anti-tumor activity and toxicological profiles of novel class I HDACi using a zebrafish genetic tumor model, in which a human oncogenic variant of KRAS ($KRAS^{G12D}$) is expressed in the zebrafish intestine. Briefly, zebrafish larvae were exposed to test compounds from 3 to 5 days post-fertilization (dpf), and toxicological endpoints were assessed. EGFP-labeled $KRAS^{G12D}$ intestinal tumor cells were quantified through whole-larvae flow cytometry, enabling measurement of both the frequency and absolute number of EGFP-$KRAS^{+}$ tumor cells per larva. Additionally, gene expression of intestinal epithelial functional markers was analyzed by qRT-PCR to evaluate potential adverse effects on non-tumor intestinal epithelial cells (IECs). A dose-dependent analysis of AKT-011, a novel HDACi, exhibited antitumor activity, although this was accompanied by moderate toxicity. Gene expression analysis showed that AKT-011 did not adversely affect the expression of intestinal epithelial functional markers, suggesting no toxicity or adverse effects on non-tumor IECs. Building on these findings, we evaluated newly designed entinostat derivates. Among these, one compound showed comparable tumor inhibition respect to AKT-011 but with increased toxicity, whereas a second compound exhibited moderate anti-tumor efficacy without observed toxicity, emerging as a potentially safer therapeutic candidate. Overall, the tested HDACi demonstrated promising anti-tumor activity with distinct toxicity profiles, supporting their potential as therapeutic candidates for CRC.

Heshuang Qu

Postdoctoral Researcher

Department of Oncology-Pathology, Karolinska Institutet

Time: Monday 28, 11:50

A Transcriptomics- and AI-Guided 3D NSCLC Spheroid Platform for Modeling EMT and Phenotypic Drug Screening

Background: Three-dimensional (3D) cell-based models have become valuable platforms for drug screening. In non-small-cell lung cancer (NSCLC), metastasis is driven by epithelial–mesenchymal transition (EMT), a process associated with treatment resistance. Advances in morphological profiling provide opportunities to uncover novel drug mechanisms and disease phenotypes using EMT-focused 3D models.

Methods: We established NSCLC spheroid models using A549 cells under three culture formats and conditions. Spheroid viability, volume, sphericity, and compaction were characterized by high-content imaging, while transcriptomic analyses identified distinct phenotypic states. The spheroid models were further characterized by bulk RNA sequencing and immunostaining of the EMT markers. To support high-throughput screening, we developed an AI/ML-based image analysis workflow that extracted morphological features from brightfield and Cell Painting fluorescence images and classified spheroids according to their invasive potential.

Results: The resulting spheroid models captured distinct EMT-associated phenotypes, including both invasive and non-invasive growth patterns. Transcriptomic profiling and immunostaining confirmed substantial molecular differences between the models. The AI/ML workflow successfully identified image-derived features associated with invasiveness and enabled the classification of spheroids with different EMT states. These models provide a platform for screening compounds that reverse EMT-related phenotypes in NSCLC.

Conclusions: We present a robust 3D spheroid platform that combines phenotypic characterization, transcriptomic profiling, and AI-driven image analysis to identify compounds capable of reversing EMT-associated invasiveness. This approach offers a promising tool for NSCLC drug discovery and mechanism-of-action studies.

Thuy Tran

Associate Professor; Group leader; Principal Researcher

Department of Oncology-Pathology, Karolinska Institutet;
Theranostics Trial Center, Karolinska University Hospital

Time: Tuesday 29, 10:20

Development of a Novel TROP2-targeted Monoclonal Antibody for Radiotheranostics of Solid Tumors - A New Modality in Precision Oncology

Introduction and aim: Trophoblast cell-surface antigen 2 (TROP2) is a clinically validated therapeutic target in multiple solid tumors, yet current antibody-drug conjugates (ADCs) have a suboptimal benefit-risk ratio with variable response rates and risk for toxicities. Radiotheranostics combining both positron emission tomography (PET) diagnostics and radionuclide therapy offers a complementary strategy by enabling non-invasive target assessment and targeted radiation delivery.

We developed TT331, a novel fully human anti-TROP2 monoclonal antibody, and evaluated its potential as a theranostic agent for TROP2-targeted PET imaging using zirconium-89 (^{89}Zr) and radioimmunotherapy using terbium-161 (^{161}Tb).

Materials and Methods: TT331 was identified through phage display screening of in-house antibody libraries and subsequently radiolabeled with ^{89}Zr or ^{161}Tb. Cellular uptake and internalization were evaluated in multiple TROP2-expressing cancer cell lines and compared with the approved ADCs sacituzumab govitecan (SG) and datopotamab deruxtecan (Dato-DXd). Tumor targeting was assessed by PET/CT imaging and biodistribution studies in mice bearing human tumor xenografts with varying TROP2 expression. Therapeutic efficacy of ^{161}Tb-TT331 was compared with saline controls and ADC-treated cohorts.

Results: TT331 demonstrated significantly higher internalization than both approved TROP2-targeted ADCs across all evaluated cell lines ($p<0.0001$). Live-cell imaging confirmed efficient trafficking to lysosomal compartments, supporting its suitability for intracellular radionuclide delivery. PET/CT imaging with ^{89}Zr-TT331 showed high, specific, and sustained tumor uptake that correlated with TROP2 expression and exceeded that of SG. *Ex vivo* biodistribution confirmed these findings.

Therapy with ^{161}Tb-TT331 produced marked antitumor effects. A single administration achieved durable complete responses in 9 of 10 mice in both BxPC3 and MDA-MB-468 tumor models, with responses maintained for at least 91 days. In contrast, ADC-treated cohorts demonstrated substantially lower cure rates. Although complete responses were not observed in the lower TROP2-expressing SKOV3 model, ^{161}Tb-TT331 significantly prolonged survival compared with both controls and ADC benchmarks.

Conclusion: TT331 outperformed clinically approved TROP2-targeted ADCs in both cellular internalization and preclinical therapeutic efficacy, supporting its development as a next-generation TROP2 radiotheranostic for patient selection and targeted radionuclide therapy.

This work was supported by grants from the Swedish Research Council, the Swedish Cancer Society, the Erling-Persson Foundation, the Radiumhemmet Research Funds, the Karolinska Institutet KID Grant, the Knut and Alice Wallenberg Foundation, and the Novo Nordisk Foundation Proof-of-Concept Program.

Yujie Xiang

PhD Student

Department of Medical Epidemiology and Biostatistics, Karolinska Institutet

Time: Monday 28, 12:05

AI-based multi-modal prognostic modelling of histopathology images, mRNA expression, and clinical information in a Swedish study including 3,000 patients

Prognostic stratification of breast cancer patients has a central role in guiding adjuvant chemotherapy treatment decisions in the $ER^+/Her2^-$ subgroup of patients. Current routine diagnostics are utilising either clinicopathological (including routine biomarkers assessed by IHC) factors alone, or together with gene-expression based assays. Recently, AI-based analyses of routine H&E stained histopathology images has emerged as another approach to provide prognostic risk-stratification of breast cancer patients. In this study, we are evaluating the relative prognostic performance in each data modality, and we are also evaluating if multi-modal models, which combine the different data types, can improve prognostic patient-stratification.

This study includes over 3000 early-stage breast cancer patients diagnosed at three different sites in Sweden that were part of the prospective SCAN-B study. For each patient, clinicopathological information is available from the Swedish National Quality Register for breast cancer (NKBC), together with a H&E stained whole slide image, and a RNA-seq gene-expression profile. We optimised time-to-event (time to recurrence) models for each individual data modality, and we also evaluated multiple modelling strategies that combined information across different data modalities. Tabular data were modelled using a Elastic-Net regularised Cox proportional hazards model, WSI image data was modelled using features from the UNI foundation model together with a CLAM model optimised with a Cox PH loss. Prognostic performance was evaluated by C-index. Analyses were performed in the full breast cancer population, and in the subset of $ER^+/HER2^-$ subgroup of patients separately. Preliminary results suggest relatively similar performance across the different data modalities, indicating that histopathological image data offer similar prognostic performance as gene expression profiles.

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Our Mission:

To support the generation of new scientific discoveries that can be rapidly translated into clinical practice for the benefit of patients and society.

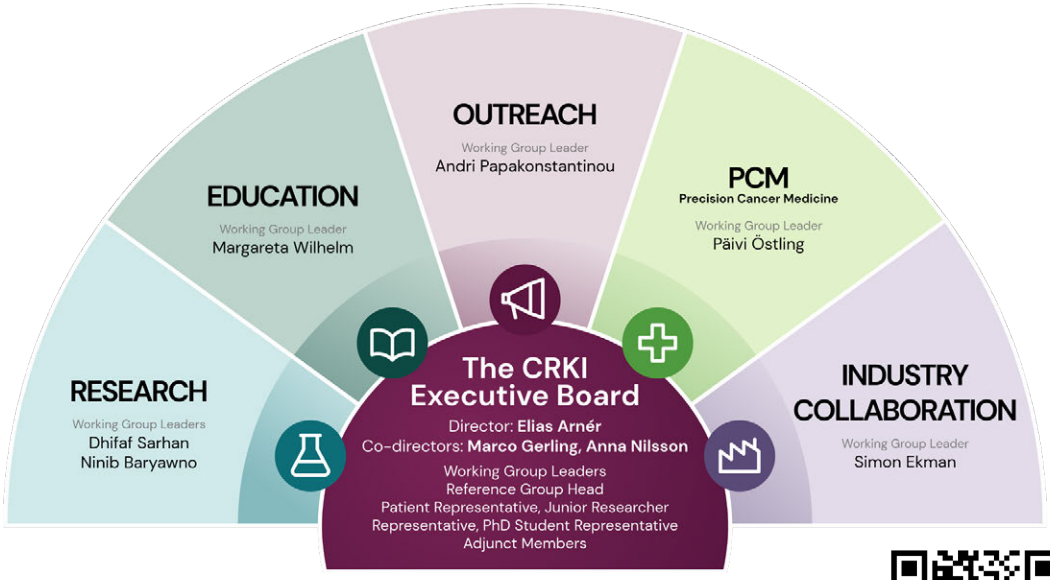
An umbrella organization for cancer research at Karolinska Institutet

A Strategic Research Program in Cancer since 2009 (formerly StratCan)

An initiative that provides various types of support for all cancer researchers at KI

A hub for communicating cancer research at KI to the general public

Over 400 PIs in cancer research representing 21 departments



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News from Cancer Research KI

Advancing the Future of Oncology Through AI

Part of the Industry-Academia Collaborations Seminar Series

Join Cancer Research KI for the next seminar in our Industry-Academia Collaborations Seminar Series, bringing together researchers from Karolinska Institutet and experts from industry to explore the opportunities and challenges of AI in oncology.

The seminar will highlight how AI is being used to improve cancer detection and diagnosis, support screening, and accelerate cancer research. Speakers from academia and industry will share their perspectives and experiences, highlighting how collaboration across sectors can help translate AI-driven innovation into practice.

Stay after the seminar for a networking mingle, where you can meet fellow attendees, exchange ideas, and continue the conversation with our speakers. Places are limited, so **register now** to avoid missing out!

October 21, 2026, 14:30
Eva & Georg Klein lecture hall, Biomedicum

Register now!

Cancer Research KI Interview Series

Meet our Researchers!

Get to know researchers from KI and Karolinska CCC and hear about their research, advice, challenges, and hopes for the future of cancer research.

Meet Elias Arnér, Hildur Helgadottir, Marco Gerling, Margareta Wilhelm, Mattias Carlsten, Nick Tobin, Simon Ekman, and Yvonne Wengström.

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