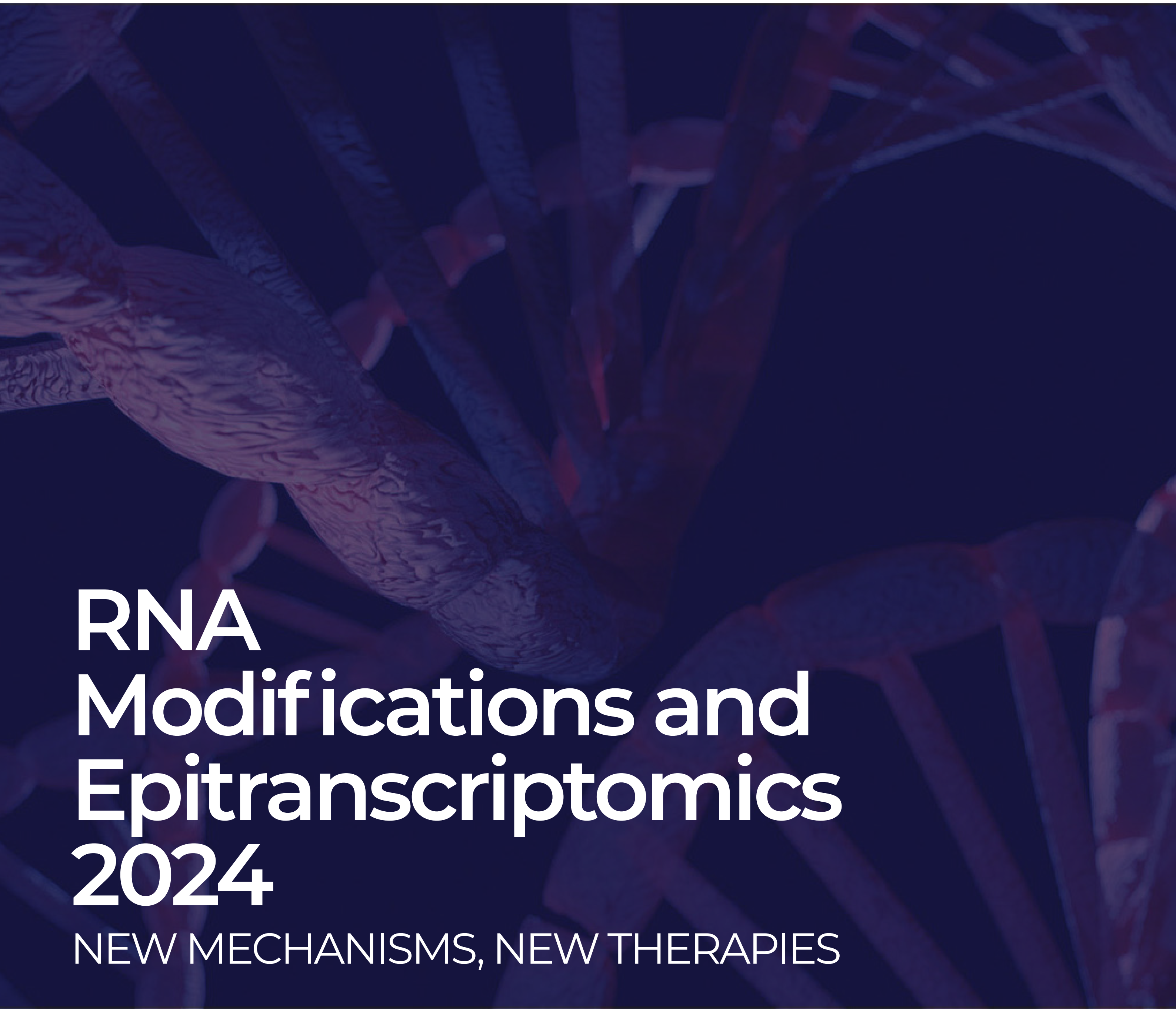
RNA **Modifications & Epitranscriptomics**
New Mechanisms, New Therapies
14th – 15th November 2024, Brussels

In partnership with: ULB CANCER RESEARCH CENTER INSTITUT JULES BORDET



RNA Modifications and Epitranscriptomics 2024

NEW MECHANISMS, NEW THERAPIES

14-15 November 2024 | Brussels

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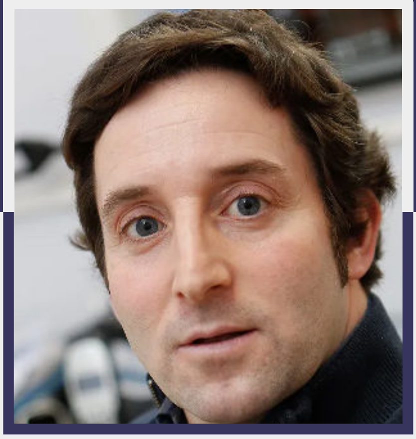

Welcome to Brussels.

Scientific Organiser: François Fuks
Laboratory of Cancer Epigenetics & ULB-Cancer Research Centre (U-CRC). ULB Free University of Brussels & Bordet Institute

Welcome to Brussels.

These are exciting times for discovering the biological scope and the mechanisms of action of epitranscriptomics, the study of RNA modifications. Over 170 post-transcriptional modifications of RNA are known to date, and most RNA species harbor various chemical modifications. Epitranscriptomics plays pivotal roles in gene regulation and is essential for diverse biological processes Inappropriate regulation of RNA modifications has been implicated in common human diseases, such as cancer.

This International Meeting on “RNA modifications & Epitranscriptomics: New Mechanisms, New Therapies” gathers some of the most prominent academic speakers in the field, coming from the top universities around the world. They will highlight the most recent findings on the mechanisms and physiopathological roles of RNA modifications. In addition, speakers from companies dedicated to developing RNA modification targets are also here to discuss exciting and promising novel therapeutic drugs in the epitranscriptomic space.

Agenda - Day One

Thursday November 14th

08:00 - 09:00 - CONFERENCE REGISTRATION

09:00 - 09:15
WELCOME
François Fuks

09:15 - 12:15 - SESSION 1
CHAIR: Kostas Tzelepis

09:15 - 09:35
Role of RNA modifications in health and disease
François Fuks, Belgium

09:35 - 09:55
YTHDF proteins as targets in cancer
Alessandro Quattrone, Italy

09:55 - 10:05
Short talk: ADAR1-mediated RNA editing and its role in prostate cancer
Stefania Kalogera, Sweden

10:05 - 10:25
E4F1 coordinates pyruvate metabolism and the activity of the Elongator Complex...
Laurent Le Cam, France

10:25 - 10:55 - COFFEE BREAK

10:55 - 11:15
The era of high-throughput epitranscriptomics
Theodore Maximilian Nelson, USA

11:15 - 11:35
Link between pseudouridine, carbohydrate metabolism and drosophila behavior
Jean-Yves Roignant, Switzerland

11:35 - 11:45
Short talk: mRNAs, tRNAs, and ribosomes are fundamental to protein synthesis in all living cells
Massimiliano Clamer, Italy

11:45 - 12:05
Crosstalk between histones modifications & m6A
Jianjun Chen, USA

12:05 - 12:25
Understanding and targeting transcriptome dysregulation in T-ALL
Panos Ntziachristos, Belgium

12:30 - 14:00 - LUNCH AND POSTER VIEWING

14:00 - 16:50 - SESSION 2
CHAIR: Alessandro Quattrone

14:00 - 14:20
Uncovering Cancer-Associated Epigenetic Events Using Novel Chemical Tools
Anna Knörlein, USA

14:20 - 14:40
RNA methylation as a regulator of inflammatory response
Justin Wong, Australia

14:40 - 15:00
Chromatin modifications and human disease
Yang Shi, UK

15:00 - 15:30 - COFFEE BREAK

15:30 - 15:50
Therapeutic targeting of the epitranscriptome in disease
Kostas Tzelepis, UK

15:50 - 16:00
Short talk: Insights into cellular dormancy: the role of RNA methylation in shaping ESC plasticity
Evelyne Collignon, Belgium

16:00 - 16:20
Tbd
Eric Miska, UK

16:50 - END OF DAY

Agenda - Day Two

Friday November 15th

08:45 - 9:00 - ARRIVAL

09:00 - 11:50 - SESSION 3
CHAIR: Panos Ntziachristos

09:00 - 09:20
Uncovering mRNA methylation and fate
Michael G Kharas, USA

09:20 - 09:30
Short talk: tRNA optimality drives the identity of colorectal cancer-initiating Lgr5+ cells... Francesca Rapino, Belgium

09:30 - 09:50
Short talk: RNA methyltransferase FTSJ1: Roles in gene expression regulation and neural development
Nassim Meziane, France

10:00 - 10:30 - COFFEE BREAK

10:30 - 10:50
Targeting tRNA methyltransferases in cancer
Sandra Blanco, Spain

10:50 - 11:10
Role of m6A in gene expression and translation
Richard Gregory, UK

11:10 - 11:20
Short talk: Nuclear Ythdc1 is the cytoplasmic m6 A reader for maternal mRNA decay...
Douaa Moussalem, France

11:20 - 11:40
Small molecule inhibition of the RNA methyltransferase METTL3 activates anti-tumour immune responses
Alexandra Sapetschnig

11:50 - 13:30 - LUNCH AND POSTER VIEWING

13:30 - 15:00 - SESSION 4
CHAIR: Sandra Blanco

13:30 - 13:50
Functions of uridine modifying enzymes in health and disease
Wendy Gilbert, USA

13:50 - 14:00
Short talk: Non-canonical m6A readers: molecular selectivity and network regulation
Andres Ramos, UK

14:00 - 14:20
tRNA modifications: a new vulnerability driving cancer heterogeneity and tumor immune response
Pierre Close, Belgium

14:20 - 14:40 - CLOSING REMARKS & POSTER AWARDS

15:00 - END OF MEETING

Invited Speakers

Sandra Blanco, Cancer Research Centre, Spain

Dr Sandra Blanco is group leader at the Epitranscriptomics and Cancer Lab, in the Cancer Research Centre (National Council Research and University of Salamanca) (CIC- CSIC – USAL) and associate researcher at the Biomedicine Research Institute of Salamanca (IBSAL) (Spain). The IP's research has focused since her postdoc in deciphering the role of RNA modifications (epitranscriptome) in stem cell biology, homeostasis and disease. Throughout her training at the Stem Cell Institute, Cambridge University, CIC-bioGUNE and CIC, she became expert in stem cell biology, pre-clinical models, epitranscriptomics, cancer, immunology, the development of novel tools to determine RNA modifications genome-wide. In October 2018, she joined the Cancer Research Centre as CSIC Scientist. Her research has demonstrated how the epitranscriptome, in particular methylation of tRNAs, regulate essential functions for stem cell maintenance and differentiation, migration and survival to stress in humans and mice. Her research has also established that mutations or aberrant expression of the writers of tRNAs can lead to neurodevelopment diseases and cancer. Her findings have established that manipulation (inhibition) of the enzymes that regulate tRNA modifications is a potent and promising strategy to eliminate cancer stem cells or to modulate the tumour immune microenvironment.

Jianjun Chen, City of Hope, USA

Jianjun Chen, PhD, is Professor and Chair, Department of Systems Biology at City of Hope. He is also the deputy director of the Center for RNA Biology and Therapeutics. Before that, he had been serving as an Associate Professor of Cancer Biology at University of Cincinnati College of Medicine from January 2015 through October 2017, and as an Assistant Professor of Medicine at University of Chicago from January 2009 through January 2015. Prof. Chen received his PhD degree from Shanghai Institute of Biochemistry, Chinese Academy of Sciences, Shanghai, China, and then conducted postdoc training with Janet D. Rowley, MD, at University of Chicago. Prof. Chen is a scholar of The Leukemia & Lymphoma Society (2017) and Researcher of the Year, Pamela B. Katten Memorial Leukemia Research Foundation Award (2014). He also received The Leukemia & Lymphoma Society Scholar CDP Achievement Award in 2022. Prof. Chen is an internationally renowned pioneer and leading expert in the field of RNA cancer epigenetics (or epitranscriptomics). The discoveries from his group have demonstrated the functional importance of RNA modifications (especially m6A modification) and the associated modulators in cancer initiation, progression, metastasis, and drug resistance, cancer stem cell self-renewal, cancer metabolism and tumor immune evasion.

Pierre Close, University of Liège, Belgium

Pierre Close obtained his PhD in Molecular Cancer Biology at University of Liège in 2006. He then move to London as post-doctoral fellow in the laboratory of Prof. Svejstrup at the London Research Institute (Cancer Research UK; EMBO fellow 2006-2009) where he became interested in studying RNA and gene expression regulation. He established his own lab at GIGA Institute (ULIEGE, Liege, Belgium) in 2013. Over the last 10 years, his lab made seminal discoveries in the fields of mRNA translation, tRNA epitranscriptomics and cancer. His lab uncovered the importance of wobble tRNA modifications in the reprogramming of mRNA translation that supports tumor development and phenotype switching in cancer. His work has strongly contributed to highlighting the reprogramming of mRNA translation as a central mechanism driving the adaptation of tumor cells during cancer progression and response to therapy. Pr. Pierre Close is Senior FNRS & WELBIO investigator, director of the lab of cancer signaling at GIGA-Institute (ULIEGE). Today, Pierre Close's lab studies the importance of tRNA modifications and specific mRNA translation reprogramming as a driver of cancer heterogeneity and interaction with tumor immune microenvironment.

Manel Esteller, Josep Carreras, Spain

Dr. Esteller graduated in Medicine from the Universitat de Barcelona, where he also obtained his Ph.D. in molecular genetics. Dr. Esteller was a Postdoctoral Fellow and a Research Associate at Johns Hopkins where he studied DNA methylation and human cancer. His work was decisive in establishing promoter hypermethylation of tumor suppressor genes as a common hallmark of cancer. From October 2001 to September 2008 Manel Esteller was the Leader of the CNIO Cancer Epigenetics Laboratory. Since October 2008 until May 2019, Dr Esteller was the Director of the Cancer Epigenetics and Biology Program (PEBC) in Barcelona. He is currently the Director of the Josep Carreras Leukaemia Research Institute (IJC), Chairman of Genetics in the School of Medicine of the University of Barcelona, and an ICREA Research Professor. His current research is devoted to the establishment of the epigenome maps in health and disease, and the development of new epigenetic drugs. Author of numerous and highly cited peer-reviewed manuscripts in biomedical sciences, he has received prestigious recognitions for his scientific achievements among them the World Health Summit Award, the Swiss Bridge Cancer Award and the EACR Cancer Researcher Award Lecture.

Wendy Gilbert, Yale University, USA

Wendy Gilbert is a Professor of Molecular Biophysics and Biochemistry. Her work focuses on regulatory elements in messenger RNA that control the cellular expression of the information stored in the genetic code. She earned her PhD at UCSF with Christine Guthrie, studying mRNA export and being fascinated by the exquisite mechanisms that couple export-competence to completion of RNA processing. As a postdoc in Jennifer Doudna’s lab at UC Berkeley, she uncovered a non-canonical mechanism of translation initiation. Her lab’s current work ranges widely across RNA biology with the unifying theme of elucidating the molecular mechanisms of RNA regulatory elements controlling mRNA biogenesis, translation and decay. Most recently, this has been in the area of RNA base modification. Notable awards include the RNA Society’s Early Career Award (2017) for her “paradigm-altering contributions to the field of post-transcriptional gene regulation” and the RNA Society Award for Excellence in Inclusive Leadership (2023) for her efforts to promote the training and professional development of underrepresented scientists. internationally by the Pershing Square Sohn Cancer Alliance (PSSCA) (2019), American Chemical Society “Future of biochemistry” (2019), the Parker Institute for Cancer Immunotherapy and the NIGMS MIRA among others.

Richard Gregory, Harvard Medical School, USA

Richard I. Gregory. Ph.D. is Professor and Stem Cell Biology Chair, in the Departments of Pediatrics, and Biological Chemistry and Molecular Pharmacology at Harvard Medical School. He is Principal Investigator in The Stem Cell Program in the Division of Hematology/Oncology at Boston Children’s Hospital. He is co-Director and executive committee member of the Harvard Initiative for RNA Medicine, and Principal faculty member of The Harvard Stem Cell Institute. Research in the Gregory laboratory is focused on understanding the molecular and cellular mechanisms of RNA regulation and the relevance of these pathways in stem cell biology, development, and human diseases including cancer. He is a recipient of an Outstanding Investigator Award from the National Cancer Institute. He is committed to exploiting fundamental discoveries for the development of new and effective therapies and is a co-founder and scientific advisory board member of Twentyeight-Seven Therapeutics, a biotechnology company that is developing cancer drugs that target RNA pathways.

Michael Kharas, Sloan Kettering Institute, USA

Dr. Michael G. Kharas is a Member of the Molecular Pharmacology Program at the Memorial Sloan-Kettering Cancer Center (New York, NY, USA) and associated with Centers for Hematological Malignancies, Stem Cell Biology, Cellular Engineering, Experimental Therapeutics and Tow Developmental Oncology. Dr. Kharas finished his postdoctoral training at Brigham and Women's Hospital in Boston and studied how signaling pathways alters stem cell regulation with Drs. Gary Gilliland and George Daley. In 2011 he started his laboratory at MSK and focused on the controllers of cellular fate in the blood. His laboratory has uncovered new RNA regulators and how they modulate self-renewal, cell-fate decisions, and differentiation in both normal blood development and in myeloid leukemia. Dr. Kharas has received recognition including the Leukemia Lymphoma Society Scholar Award and American Society of Hematology Scholar Award. His laboratory is developing inhibitors that block the function of RNA regulators as a new therapeutic strategy in leukemia.

Anna Knörlein, Sloan Kettering Institute, USA

Dr. Anna Knörlein earned a Bachelor's degree in Chemistry from the University of Jena, Germany, and a Master's degree in Chemistry from the University of Marburg, Germany. She completed her Master's thesis at the University of Cambridge, UK, where she researched cucurbituril macrocycles in supramolecular catalysis.
Anna earned her PhD from ETH Zurich, Switzerland investigating RNA-protein interactions and the structural basis of UV cross-linking in RNA-protein complexes. She specialized in solid-phase oligonucleotide synthesis, RNA chemistry, and the biophysical characterization of RNA-protein interactions.
Currently, Anna is a postdoctoral researcher at Memorial Sloan Kettering Cancer Center in New York City, working with Prof. Yael David. Her research focuses on non-enzymatic RNA-histone glycation and its implications for RNA structure and function.

Kamil Kranc, The Institute of Cancer Research, UK

Professor Kamil R. Kranc is the Chair of Haemato-Oncology and Director of the Centre for In Vivo Modelling at The Institute of Cancer Research (ICR) in London. Kamil graduated in medicine from the Medical University of Silesia (Poland) in 2000 and obtained a DPhil (PhD) in Biochemistry from the University of Oxford in 2003. He established his first lab as a Beit Memorial Fellow at Oxford, followed by group leader positions in Glasgow, Edinburgh, and London. His central aim is to discover the key processes governing cancer stem cells in acute myeloid leukaemia (AML), with the goal of selectively targeting these treatment-resistant cells, thus pioneering curative, non-toxic therapies. Specifically, the Kranc lab focuses on the therapeutic targeting of diverse RNA modifications and metabolic pathways in AML. The Kranc lab is supported by the CRUK Programme Grant, Barts Charity Research Grant, and the ICR.

Laurent Le Cam, Institute for Cancer Research, France

Laurent Le Cam is the head of the « Molecular Oncogenesis » laboratory and deputy director of the Institute for Cancer Research in Montpellier (France). He graduated from Montpellier University in 1999 and then moved to Pr P. Sicinski's laboratory at the Dana Faber Cancer Institute (Harvard Medical School, Boston, USA) where he developed genetically engineered mouse models to study the in vivo functions of several cell cycle regulators and checkpoint proteins. He started his own laboratory at Montpellier Cancer Center in 2008 where he started to study the role of the p53 pathway in metabolism. His team develops multidisciplinary research projects standing at the frontier of different fields including cancer development, inborn metabolic disorders and normal physiological responses to nutrient challenges. Recently, his laboratory uncovered unexpected roles of different key components of the p53 tumor suppressor pathway and metabolism, and showed how deregulation of these metabolic networks impinges on the epigenome and the epitanscriptome.

Eric Miska, University of Cambridge, UK

Eric Miska is Head of Department and Senior Group Leader at the Department of Biochemistry, a Herschel Smith Professor of Molecular Genetics at the Genetics Department, and affiliated Senior Group Leader at the Gurdon Institute, at the University of Cambridge, UK. He is an associated faculty member of The Wellcome Trust Sanger Institute, and coordinator of the Cambridge RNA Club. He is a molecular geneticist most known for his pioneering work furthering our understanding of the biology of non-coding RNA.

Theodore Maximilian Nelson, Weill Cornell Medicine, USA

Theodore Nelson is an Associate Lecturer at Weill Cornell Medicine. He completed a B.A. in Computer Science at Columbia University (2024) and is currently a Churchill Scholar completing an MPhil in Medical Science at Cambridge University. He additionally serves as a bioinformatics specialist in Christopher E. Mason's Lab, known for its contribution to the development of the MeRIP-seq technique and the application of the synthetic curlcake strands to epitranscriptomics validation. He leads the informatics and analysis of all current epitranscriptomic projects in the lab. He manages the lab's collaborations for the Colossus Biosciences iPSC characterization project, the Columbia Mailman School of Public Health Environmental Epitranscriptomics project, and the National Institute of Technology Standards Genome in a Bottle project. His first author publications in Nature Communications and the International Journal of Molecular Sciences further the application of long-read sequencing, also known as third-generation sequencing, to astronaut health and cancer biology. He has served a reviewer for Nature Genetics. He founded a high school biology lab program at Columbia University called Glass Half Full or Empty: Illuminating the Human Transcriptome, which gives underserved high school students the opportunity to perform wet-lab long-read sequencing research. He teaches a course at Weill Cornell Medicine, entitled Single-Molecule Sequencing: Methods, Training, and Applications, as a part of the Physiology, Biophysics & Systems Biology graduate program. His bioinformatics YouTube Channel (MakeTheBrainHappy) – Scientific Exploration), has over 600 subscribers, 80,000 views, and 6,000 watch hours.

Panos Ntziachristos, Ghent University, Belgium

Dr. Panos Ntziachristos is a molecular and cancer biologist trained in University of Athens, Greece, and New York University, US. He is a Professor at the Department of Biomolecular Medicine, Faculty of Medicine and Health Sciences, Ghent University, Belgium. His research focuses on uncovering how post-transcriptional and epigenetic mechanisms influence leukemia progression and drug resistance. Key areas of investigation include how large biochemical complexes such as RNA biology players are regulated, how their dysregulation occurs, and how this affects cancer progression. Dr. Ntziachristos has authored several high-impact peer-reviewed publications in journals including Nature, Nature Medicine and Cancer Discovery. He serves in intramural committees at Ghent University and has guided the careers of several early-career scientists. He also serves on the Research Committee of the European Hematology Association (EHA) and is a coorganizer of major scientific events, e.g. the 2025 Research Conference of the EHA. His research has been supported by the National Cancer Institute, USA, the Research Foundation Flanders, Belgium, and numerous Foundations, including the American Society of Hematology.

Alessandro, Quattrone, University Of Trento, Italy

Alessandro Quattrone is a faculty member at the University of Trento, Italy, where he teaches Molecular Pathology. From 2007 to 2021, he served as the founding director of the Department for Cellular, Computational, and Integrative Biology at the same university. Prior to that, he was a visiting scientist at the US National Institutes of Health and held associate professorships at Johns Hopkins University and West Virginia University. Early in his scientific career, he pioneered the development of antisense oligonucleotide technology and discovered one of the first long noncoding RNAs implicated in cancer. His current research focuses on the preclinical development of therapeutic solutions for rare neural tumors and rare neurodegenerative diseases. He targets models of these conditions by modulating translational control and epitranscriptomic signaling with small molecules and gene editors. In addition to his academic pursuits, he is a science communicator for newspapers and the founder of biotech startups, through which he translates laboratory innovations into entrepreneurial ventures.

Oliver Rausch, STORM Therapeutics, UK

Oliver has overall responsibility for STORM's biology platform and for the delivery of small molecule drugs from STORM's drug discovery pipeline. Oliver worked closely with scientific founders Professors Tony Kouzarides and Eric Miska to secure the initial series A investment that launched STORM, and subsequently joined the company full time in October 2016. Prior to STORM, Oliver was Programme Director at the National Institute for Health Research (NIHR), where he led the Translational Research Partnerships (TRPs) initiative and other industry-focused programmes in experimental medicine and early drug development. He served as Vice President Biology at Cellzome until the company's acquisition by GSK in 2012, and as Director of Biology at UCB Pharma until 2008. Oliver has over 25 years' drug discovery experience in inflammation, neurology and oncology. He holds a degree in Biochemistry from the Free University Berlin and a PhD in Biochemistry and Cell Biology from the Institute of Cancer Research in London.

Yang Shi, University of Oxford, UK

Yang Shi received his PhD from NYU Medical Center and postdoctoral training with Dr. Tom Shenk at Princeton University where he discovered the transcription factor YY1. He began his independent research career at Harvard Medical School as a tenure track assistant professor in 1991 and received tenure and full professorship in the Department of Pathology at Harvard Medical School in 2004. In 2009 he joined Boston Children's Hospital where he held a Merton Bernfield Professorship in the Department of Medicine and was also professor of Cell Biology of Harvard Medical School, where he was honored with the inaugural C. H. Waddington Professorship of Pediatrics in 2018. He joined Oxford University in 2020 and is currently Professor of Epigenetics of Oxford University and member of the Ludwig Cancer Research. His honors include election to the American Association for the Advancement of Science (2011), The Ellison Medical Foundation Senior Scholar in Aging (2012), American Cancer Society Research Professor (2012), election to the American Academy of Arts and Sciences (2016), election to EMBO (2022), to AACR Academy (2022), the National Academy of Medicine (2022) and UK Academy of Medical Sciences (2023).

Konstantinos Tzelepis, University of Cambridge, UK

Konstantinos Tzelepis is a Wellcome Principal Investigator at the Cambridge Stem Cell Institute and the University of Cambridge (UK). Prior to this, he was a Wellcome Trust Sir Henry Wellcome Fellow at Harvard University (USA) and the University of Cambridge (UK). He obtained his Ph.D. in Molecular Genetics from the Wellcome Sanger Institute and the University of Cambridge, in 2017, where he developed one of the first genome-wide CRISPR screening platforms for the identification and therapeutic translation of novel cancer vulnerabilities. His lab is focusing on the mechanistic understanding and therapeutic targeting of RNA and its modifications in cancer and ageing. Recently, his group co-developed and characterised first-in-class pre-clinical and clinical RNA methyltransferase inhibitors.

Justin Wong, University of Sydney, Australia

Dr Justin Wong is the Head of the Epigenetics and RNA Biology Laboratory at the School of Medical Sciences, Faculty of Medicine, the University of Sydney. Dr Wong completed his PhD training in cancer epigenetics at the University of New South Wales, Australia and postdoctoral training in RNA processing at the Centenary Institute, Sydney, Australia. He established his independent research Program in 2018 and has since led studies into the roles of RNA splicing and modifications (e.g. m6A and 5hmC) in normal physiology and disease. His laboratory is now focusing on understanding the interplay between RNA modifications and splicing in the context of inflammatory response and cancer. Dr Wong has been awarded with fundings from the Australian Federal and State Governments (ARC, NHMRC, NSW Health). In 2019, he received the Ruth Stephens Gani Medal from the Australian Academy of Science in recognition of his contribution to the field of human molecular genetics.

Jean-Yves Roignant, University of Lausanne, Switzerland

Jean-Yves Roignant carried out his thesis in the laboratory of Dr. Jean-Antoine Lepesant at the Jacques Monod Institute and received his Ph.D. in 2003 from the University of Paris Diderot. He became postdoctoral fellow and research associate in the group of Dr. Jessica Treisman at New York University Langone Medical Center. He then started his independent group in 2012 at the Institute of Molecular Biology in Mainz and joined the Center for Integrative Genomics at the University of Lausanne in August 2019 where he was appointed Associate Professor. His research is focusing on post-transcriptional gene regulation, in particular the role of RNA modifications in the nervous system, using drosophila and human cells as experimental models. His group has pioneered the characterization of the m6A mRNA modification pathway in Drosophila melanogaster and demonstrated its involvement in the function of the nervous system.

Short Talk Speakers

Massimiliano Clamer, IImmagina Biotechnology, Italy

Massimiliano Clamer, a biomolecular scientist with a strong pharmaceutical background from the University of Padua (Italy) and the University of Bonn (Germany), is driven by a passion for translating cutting-edge research into practical solutions. His PhD, a unique collaboration between the University of Trento (Italy) and the University of Oxford (UK), delved into the fascinating realm of host-pathogen interactions and single-molecule RNA sensing. While at Oxford, he also expanded his knowledge by taking courses at the Saïd Business School. Upon returning to Italy, Dr. Clamer worked across three research institutions—the Institute of Biophysics (CNR), the University of Trento, and the Bruno Kessler Foundation—where he validated promising business concepts. This diverse academic and research experience culminated in the founding of Immagina Biotechnology s.r.l. in 2014, a company dedicated to advancing RNA drug development and RNA processing technologies. Today, he leads the company as CEO. In 2023, Immagina Biotechnology joined the Technicon Spa holding, further solidifying its presence in the biotech industry. A strong advocate for collaboration, Dr. Clamer maintains close working relationships with his team, advisors, and investors, seamlessly bridging the gap between academia and the commercial sector.

Evelyne Collignon, ULB, Belgium

Evelyne Collignon is a postdoctoral researcher studying epigenetic and epitranscriptomic mechanisms at the Université Libre de Bruxelles (ULB), Faculty of Medicine, in Belgium. Her work centers on how gene regulation impacts cancer and early embryonic development, with a particular focus on the crosstalk between different layers of regulation. She completed her Ph.D. at ULB, focusing on the role of DNA and RNA modifications in breast cancer. Following this, she undertook postdoctoral research at the University of California, San Francisco (UCSF), USA, and the University of Toronto, Canada, in Dr. Ramalho-Santos's lab, where she investigated gene regulation in embryonic diapause and cancer dormancy. Now back in Brussels, she continues to explore the role of epitranscriptomic modifications, with the goal of advancing our understanding of gene regulation in both health and disease.

Stefania Kalogera, Lund University, Sweden

I completed my bachelor's degree in biology at the University of Patras in Greece, followed by an MSc in Human Genetics at the University of Thessaly. After my Master's, I spent a year collaborating with a genetics lab in Athens, gaining hands-on experience with molecular biology techniques. In October 2019, I started my PhD at the University of Copenhagen, in collaboration with the biotechnology company Nordic Bioscience. My PhD project, "Towards a Biomarker-Driven Characterization of Osteoarthritis Pain," was part of the Marie Curie-funded European network, BonePain II. My research focused on developing robust biomarker assays for structural changes and pain in osteoarthritis which were validated with clinical cohort studies. Following my PhD defense in March 2023, I joined Lund University as a postdoctoral researcher in April 2024. My current work explores epitranscriptomics, specifically RNA editing, in prostate cancer.

Nassim Meziane, Institut de Biologie Paris-Seine, France

Nassim Meziane, PhD student
Institut de Biologie Paris-Seine (IBPS)
Sorbonne Université

Douaa Moussalem, Institute of Human Genetics, France

Douaa Moussalem is a post-doctoral researcher in the institute of Human Genetics (IGH) of Montpellier France, in the group of mRNA Regulation and Development. She is working on the role of m6A methylation during Drosophila early embryogenesis. After finishing her master degreein Lebanon, she obtained her PhD at 2020 in France from the university of Toulouse where she addressed the role of factors of GATA family during fly development, work published at 2022, in Front Cell Dev Bio.
She participated in several meetings related to RNA biology or Development, as speaker, poster presenter or session chair. She won the best poster award during her last attendance to the national meeting, 34th French Drosophila meeting. She takes part in public activities to share sciences with the public, in particular young people. Recently she was elected as representative of PhD students and post-docs at the Institute council.

Francesca Rapino, GIGA-R Uliege, Belgium

Dr. Francesca Rapino is a Research Professor at GIGA-R, University of Liège, Belgium, and the Chief Operating Officer and co-founder of THERAtRAME SA. With a Ph.D. in Molecular Biology, Dr. Rapino specializes in tRNA biology, focusing on how tRNA modifications impact cancer transformation, particularly in cancer stem cells. Her research delves into the role of translational control mechanisms mediated by tRNA dynamics in driving cancer stem cell renewal and therapy resistance, providing new insights into cancer progression. Supported by an ERC Starting Grant and other prestigious awards, Dr. Rapino’s work is advancing RNA-based cancer therapies. Her findings, published in high-impact journals, are paving the way for innovative therapeutic strategies targeting the vulnerabilities of cancer stem cells.

Andres Ramos, University College London, UK

Andres Ramos is Chair of RNA Biology at University College London and a group leader in the Institute of Structural and Molecular Biology. He has a long-term interest in the molecular aspects of RNA regulation and his current work focuses on how the metabolism and translation of mRNAs are controlled during neuronal development and in disease. Andres earned his doctoral degree at the Laboratory of Molecular Biology in Cambridge. During his PhD and postdoc, he developed new methodologies to study dynamic protein-RNA complexes and applied them to study how the neuronal regulators Staufen and FMRP recognise the RNA targets.
As a group leader, first at the Mill Hill National Institute for Medical Research and then at UCL, his work has provided mechanistic models to understand the processes driving RNA target selection and regulation in miRNA biogenesis and transport, and in the regulation of neuronal mRNA translation. It has also provided pointed tools to directly probe this understanding in the cell, which are currently being used in his work on the m6A-mediated regulation of neuronal development.

Poster Information

1) Role of m6A methylation of RNA in salivary gland epithelial cells: a new pathogenic pathway in Sjögren's disease?
Alejandro Arco-Hierves

2) Targeting ALKBH5 and METTL3 proteins modulates HIV-1 latency reversal: implications for novel therapeutic approaches.
Ali Haider

3) Unraveling RNA modifications dynamics in prostate cancer progression and spatial tumor-immune interactions at single-cell resolution
Ana M. Añazco-Guenkova

4) Deciphering the role of the putative RNA-Binding Protein TFIP11 in regulating tissue-specific alternative splicing
Anna Maria Obeid

5) tRNA modification levels mediate ATII stem cells malignant transformation in lung cancer
Sharon Brembati

6) Dysregulation of N6Methyladenosine (m6A) mRNA Pathway in Microglia Mediated Neuroinflammation in Parkinson's Disease Models
Cameron J Miller

7) Integrated analysis of multi-omics data reveals new functional signature to predict intestinal Cancer Stem Cells
Coralie Capron

8) KEOPS complex links tRNA modification to T cell activation in melanoma
Cléa Dziagwa

9) Development Of Small Molecule Inhibitors To Curb Antibiotic Resistance
Damini Sahu

10) Understanding the role of tRNA modifications in lung cancer resistance to therapy
Debora Ehlardo

Poster Information

11) mRNA sequence parameters and formulation optimization increase mRNA therapeutics performance
Elena Khazina

12) High-Resolution Study of Translational Dynamics in human Epithelial Stem Cells
Elisabetta Dangelo

13) EAccurate Identification of Differentially Regulated RNA Modifications in Diseases
Frank Morales Shnaider

14) Understanding the epitranscriptomic landscape regulated by the p53 pathway
Javier Florido Ruiz

15) Ribosomal RNA methyla0on controls the cell cycle through protein synthesis
Judith López Luis

16) Deciphering the molecular mechanisms related to proteasome inhibitors resistance in the pathology of multiple myeloma
Léa Pautet

17) The reprogramming of mRNA translation plays a crucial role in cancer development
Marine Leclercq

18) Circadian dynamics in the liver epi-transcriptome
Khushi Mamgain

19) Decoding m6A RNA modification in ovarian cancer: Clinical and functional evaluation of FTO m6A demethylase
Margaritis Avgeris

20) Integrative genomic profiling of m6A RNA machinery in bladder cancer
Margaritis Avgeris

Poster Information

21) tRNA epitranscriptome reprogramming restores proteostasis impairments in Alzheimer’s disease models

Marisa Pereira

22) The role of the ribosomal RNA methyltransferase Nsun5 in aging and physiology of mice

Markus Schosserer

23) tRNA optimality shapes colorectal cancer-initiating Lgr5+ identity through the regulation of mRNA translation

Lorena Martin-Morales

24) Evaluation of the N6-methyladenosine (m6A) RNA modification pathway as a driver of tumor proliferation via high-throughput CRISPR screening

Martina Scichilone

25) Decoding the Escherichia coli epitranscriptome

Sebastian Riquelme Barrios

26) tRNA fragments as possible indicators of different stages of cell differentiation

Ugo Maria Iannacchero

27) The role of m6A mRNA modification during Endothelial-to-Mesenchymal transition (EndMT)

Benedetta Zuliani

ULB Guest WiFi Procedure

Wifi Connection Option 1

EDUROAM
(present in universities of >100 countries)

- https://eduroam.org/where
- Use your own existing login and password

Wifi Connection Option 2

Wifi Connection (2)

Guestroam form

https://www.guestroam.be/

-> You will automatically receive your personnal userid / pwd per e-mail and / or per SMS

! Procedure can take ~5 min. !

https://www.guestroam.be

Welcome to Belnet guestroam interface

Fill out the form below to request temporary WI-FI access in institution you wish to visit.

Name :
Firstname :
E-mail :
Mobile Number : 0470 12 34 56
Institution you wish to visit : Université Libre de I
Department / Event you wish to visit : ALL
Contact person in the institution : Pauline Chatelet
Visit from : 2024-11-14 to : 2024-11-15
I have read and accepted the policy ☑

Université Libre de Bruxelles

ALL

Pauline Chatelet

2024-11-15

2024-11-14

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