

Annual Conference 2026

“Decoding the Dark Side of Cancer”

Book of Abstracts

5 & 6 November 2026

Koninklijk Instituut voor de Tropen, Amsterdam

Organizing committee:

Reuven Agami, Miao-Ping Chien, Sebastiaan van Heesch

Day 1
November 5
2026

Decoding the Dark Side of Cancer

Scientific Committee: Reuven Agami, Miao-Ping Chien, Sebastiaan van Heesch

Time Program

08.30 Walk in, registration and coffee
09.30 Welcome by Scientific Committee

Session I

09.40 Maria Abad - Altos Labs, Cambridge Institute, United Kingdom
When the non-coding codes: Mining the hidden microproteome for new therapeutic targets

10.15 Ataman Sandoel - University of Zurich, Switzerland
Single-cell approaches for dissecting tissue-wide microprotein function

10.50 Break

11.35 Oded Rechavi - Tel Aviv University, Israel
What is the role of transgenerational small RNA inheritance?

12.10 Marvin Tanenbaum - Hubrecht Institute and Oncode Institute, The Netherlands
Beyond the Kozak sequence: mechanism of translation start codon selection

12.45 Lunch, network and Meet the speakers

Session II

14.00 Alberto Bardelli - University of Torino, Italy
Inhibition of DNA mismatch repair for therapeutic purposes

14.35 Karen Adelman - Harvard Medical School, USA
RNA quality control in disease

15.10 Break and Meet the speakers

15.55 Jennifer Dionne - Stanford University, USA and CEO of PumpkinSeed Bio
Decoding the Tumor Immune Microenvironment: Metasurface-Enhanced Raman Spectroscopy for Peptide Sequencing and Single-Cell Phenotyping

16.30 César de la Fuente - University of Pennsylvania, USA
Can machines discover function in the code of life?

17.05 Scientific Committee
Closing

17.10 - 18:10 Networking drinks & bites

Day 2
November 6
2026

Decoding the Dark Side of Cancer

Scientific Committee: Reuven Agami, Miao-Ping Chien, Sebastiaan van Heesch

Time Program

08.30	Walk in, registration and coffee
09.30	Welcome by Scientific Committee

Session III - part 2

09.40	Michal Bassani-Sternberg - Ludwig Cancer Research, Switzerland HLA-I-presented microproteins and non-canonical peptides linked to transposable element activation
10.15	Paul Bastard - Institut Imagine, France Do autoantibodies shape cancer immunosurveillance?
10.50	Break
11.35	Natalie Scholes - Netherlands Cancer Institute, the Netherlands Inhibitors supercharge protein turnover through native proteolytic circuits
12.10	Sandra Blanco - Centro de Investigación del Cáncer, Spain Targeting RNA methylases in Cancer Therapy: A Novel Approach to Revolutionize Treatment
12.45	Lunch, network and Meet the speakers

Session IV

14.00	Žiga Avsec - DeepMind, United Kingdom Advancing regulatory variant effect prediction with AlphaGenome
14.35	Andrea Ventura - Memorial Sloan Kettering Cancer Center, USA Understanding ecDNA-Driven Cancer Evolution
15.10	Break and Meet the speakers
15.55	Yasuhiro Murakawa - RIKEN, Japan A full-length transcriptome atlas reveals hidden coding elements and functional peptides in human cancers
16.30	Shira Weingarten-Gabbay - Harvard Medical School, USA Illuminating the viral dark proteome to advance our understanding on antiviral immunity
17.05	Scientific Committee Closing
17.10 - 18.10	Networking drinks & bites

Abstracts oral presentations

When the non-coding codes: Mining the hidden microproteome for new therapeutic targets

Maria Abad

Altos Labs, Cambridge Institute, United Kingdom

Thursday November 5, 09:40 – 10:15

Recent advances in ribosome profiling and peptidomics have revolutionized our understanding of the "non-coding" genome. We now know that many genomic regions previously assumed to be non-coding encode small, functional proteins termed microproteins. Though an emerging field, the microproteome is estimated to be double the size of the canonical proteome, representing a vast, hidden layer of the molecular landscape with significant therapeutic potential.

Using a computational pipeline for phylogenetic analysis, we have identified several novel, evolutionarily conserved microproteins that are dysregulated during cancer progression and cellular differentiation. We experimentally validated their translation and characterized their molecular functions in vitro and in vivo. Our results demonstrate that these microproteins are pivotal regulators of cell identity, influencing the epigenetic landscape to induce differentiation, inhibit Epithelial-Mesenchymal Transition (EMT), and modulate mitochondrial metabolism—collectively acting as potent tumor suppressors.

Our data provides pioneering evidence that the microproteome is a critical, underexplored component of the regulatory circuitry governing cell plasticity. These findings expand the definition of the functional genome and highlight microproteins as key players in the control of cell identity

Single-cell approaches for dissecting tissue-wide microprotein function

Ataman Sendoel

University of Zurich, Switzerland

Thursday November 5, 10:15 – 10:50

The dark proteome comprises a rapidly expanding catalog of microproteins with largely unknown functions. Here, we exploit an in vivo single-cell CRISPR screening strategy in the mouse epidermis to systematically investigate the tissue-wide function of microproteins in an oncogenic context. We document the global and cell-type-specific roles of microproteins during epidermal development and homeostasis at single-cell transcriptomic resolution and identify a cohort of functional ribosomal protein-like microproteins. Focusing on select candidates, we characterize a novel microprotein on Gm10076, identical to the ribosomal intersubunit bridge protein RPL41, whose perturbation strongly impairs proliferation and protein synthesis. Single-particle cryo-electron microscopy reveals that, unlike canonical RPL41, Gm10076-encoded RPL41 is not incorporated into the ribosomal intersubunit bridge. Instead, Gm10076-encoded RPL41 localizes exclusively to the nucleolus. By contrasting the translational landscapes of Gm10076 and Rpl41 knockouts, we document that Gm10076 loss profoundly remodels translational programs, altering the translational efficiency of ribosome biogenesis factors and disrupting the balance between 40S and 60S maturation programs. Together, our study comprehensively charts the tissue-wide functional landscape of the dark proteome in the epidermis, implicates transcript context-dependent diversification of identical microproteins in shaping tissue-wide translational landscapes and establishes a basis for exploring the impact of microproteins on cancer.

What is the role of transgenerational small RNA inheritance?

Oded Rechavi

Tel Aviv University, Israel

Thursday November 5, 11:35 – 12:10

In *C. elegans* nematodes, dedicated machinery enables transmission of small RNAs which regulate gene expression across multiple generations, independently of changes to the DNA sequence. Different environmental challenges, for example starvation or high temperatures, generate heritable small RNA responses, that change the descendants' physiology. In addition, neuronal processes and even neuronal activity can produce small RNA-mediated heritable responses. However, the function of these processes is unclear. In my talk I will discuss the underlying mechanisms, and present one of the biggest questions in the field: "Can epigenetic inheritance affect evolution?"

Beyond the Kozak sequence: mechanism of translation start codon selection

Marvin Tanenbaum

Hubrecht Institute and Oncode Institute, The Netherlands

Thursday November 5, 12:10 – 12:45

Human genes act together in complex networks to perform a myriad of functions. Whereas details maps exist for most biochemical pathways, the wiring of genetic networks in human cells is poorly understood. Using genetics in haploid human cells we have assigned genes to more than a hundred quantitative cellular phenotypes. This approach enables us to identify missing enzymes in cell biology and alternative factors involved in metabolism, cell death and gene regulation.

Inhibition of DNA mismatch repair for therapeutic purposes

Alberto Bardelli

University of Torino, Italy

Thursday November 5, 14:00 – 14:35

TO BE ADDED

RNA quality control in disease

Karen Adelman

UHarvard Medical School, USA

Thursday November 5, 14:35 – 15:10

Gene expression in metazoans centers on the regulated maturation of RNA polymerase II (RNAPII) into a productive elongation complex. This maturation is critical for transcription across long human genes, as RNAPII must transcribe processively to the gene end to form a mature mRNA, a distance that can exceed 100 kb. In the absence of proper maturation, RNAPII can terminate prematurely within through gene bodies, creating aberrant, partial transcripts. These incomplete pre-mRNAs often retain intronic sequences containing repetitive retroelements such as Alu elements. When present as inverted repeats, these retroelements form double-stranded RNA (dsRNA) that, if exported to the cytoplasm, instigate antiviral signaling. Retained introns can also be aberrantly translated, creating neoantigens. Thus, defects in productive elongation caused by mutations in elongation factors are associated with diseases including cancer, neurological and immune disorders. Here, we discuss how RNAPII maturation safeguards transcriptome integrity and how its failure links transcriptional dysregulation to innate immune activation and disease.

Decoding the Tumor Immune Microenvironment: Metasurface-Enhanced Raman Spectroscopy for Peptide Sequencing and Single-Cell Phenotyping

Jennifer Dionne

Stanford University, USA and CEO of PumpkinSeed Bio

Thursday November 5, 15:55 – 16:30

Cancer is written in a molecular language of mutated, modified, and misfolded proteins, yet most of this information goes unread by conventional methods. Raman spectroscopy captures each letter of this language but has historically been confined to bespoke, unscalable measurements due to low sensitivity. We present high-Q silicon metasurfaces that resolve this limitation, delivering SERS-level enhancement while remaining reproducible and wafer-scale manufacturable. We demonstrate these metasurfaces for two cancer biology applications: peptide sequencing and spatial, single-cell phenotyping.

First, we combine dynamic Raman with computational metadynamics for de novo peptide and glycoconjugate sequencing, tethering peptides from major histocompatibility complex molecules to Si resonators. Using a single vibrational reagent, we identify each of the 20 canonical amino acids with 96% class-mean accuracy, as well as post-translational modifications relevant to disease state and neoantigen presentation. Second, we use these same metasurfaces to enable spatial characterization of individual cells in the tumor immune microenvironment (TIME), predicting drug resistance and characterizing immune cell state. Because each resonator enhances Raman by >5 orders of magnitude, spatial Raman profiling that would take ~ 100 days can now be completed in under an hour. We show how these spatial Raman profiles can predict immunotherapy resistance, where conventional methods struggle. Collectively, we anticipate these nanophotonic platforms will open new windows into tumor biology at the molecular and cellular scale, from decoding modifications invisible to mass spectrometry to mapping tumor heterogeneity for clinically actionable information.

Can machines discover function in the code of life?

César de la Fuente

University of Pennsylvania, USA

Thursday November 5, 16:30 – 17:05

For centuries, machines have extended human understanding. Telescopes illuminated the cosmos; microscopes revealed the invisible. Today, artificial intelligence is emerging as a scientific instrument for searching life's molecular sequences and uncovering principles that connect sequence to function.

Evolution explored biological sequence space over billions of years, preserving molecular solutions that perform useful tasks. AI offers a way to learn from and compress that search, turning patterns shaped across deep time into experimentally testable hypotheses.

In this talk, I will describe our efforts to build AI systems that discover functional matter and translate it into therapeutics and tools for emerging pathogens. Peptides are central because they are diverse, synthesizable, and scalable to test, providing a tractable bridge between computation and experiment. By integrating deep learning, large-scale mining, standardized datasets, molecular design, and laboratory validation, we have discovered antimicrobial peptides across the tree of life, from human microbiomes and extinct organisms to archaea and venoms. Our standardized dataset hypothesis holds that consistent, high-quality measurements enable models to learn generalizable relationships between sequence and function. We are also developing systems that predict activity and safety and design new peptides. Coupling computation with experiment may allow us to read, test, and rewrite life's information.

HLA-I-presented microproteins and non-canonical peptides linked to transposable element activation

Michal Bassani-Sternberg

Ludwig Cancer Research, Switzerland

Friday November 6, 09:40 – 10:15

Ovarian cancer is characterized by a low tumor mutational burden, resulting in a limited repertoire of conventional neoantigens and poor responses to immune checkpoint blockade. This has driven the search for alternative sources of tumor-specific antigens. Transposable elements (TEs) represent a promising but largely unexplored reservoir of immunogenic targets. We analyzed tumors from 67 patients with ovarian cancer, predominantly high-grade serous ovarian carcinoma, using integrated short- and long-read RNA sequencing, ribosome profiling, and large-scale immunopeptidomics to identify HLA class I-presented peptides derived from tumor-restricted TE chimeric gene transcripts (TcGTs). TcGTs were widespread and generated numerous HLA-presented peptides, several of which were shared across patients in an HLA-restricted manner while being absent from healthy tissues. These findings establish TcGTs as a rich source of shared, tumor-specific antigens and highlight their potential as targets for next-generation immunotherapies in ovarian cancer.

Do autoantibodies shape cancer immunosurveillance?

Paul Bastard

Institut Imagine, France

Friday November 6, 10:15 – 10:50

The ATLAS team is taking on the cancer avoidance challenge through the lens of immune-modulating autoantibodies, which may change the course of tumour biology. Our team is exploring their role in cancer resistance by studying remarkable groups of people including: centenarians, people who have remained cancer-free despite high-risk exposures, and twins where one has had cancer and the other hasn't. We hope to uncover novel immunological pathways underlying cancer resistance and cancer occurrence.

Inhibitors supercharge protein turnover through native proteolytic circuits

Natalie Scholes

Netherlands Cancer Institute, The Netherlands

Friday November 6, 11:35 – 12:10

Sporadic reports have highlighted that inhibitors can induce target degradation, which often governs their superior drug action. However, we lack an understanding of frequency, generalizability, and mechanistic underpinnings. To close this gap, we established dynamic abundance profiles of 98 kinases after cellular perturbations with 1570 kinase inhibitors. Kinases prone to destabilisation are frequently annotated as HSP90 clients, thus affirming chaperone deprivation as one important degradation route. However, detailed investigation of the three kinases LYN, BLK and RIPK2 revealed a differentiated, yet common mechanistic logic. The inhibitors elicit degradation by inducing a kinase state that is efficiently cleared by the native degradation routes. Mechanistically, these effects manifest by changes in activity, localisation, or multimerisation, and can be prompted by direct target engagement or network effects. We further extended our observations to the non-kinase IDO1. We similarly uncovered that a suite of inhibitors and degraders enables supercharging of native turnover, in this scenario, however, by inducing a structural state that is more permissive to endogenous E3 engagement. In sum, our data indicates that inhibitor-induced degradation is a frequent event and positions supercharging of endogenous degradation circuits as an alternative to classical proximity-inducing degraders.

Targeting RNA methylases in Cancer Therapy: A Novel Approach to Revolutionize Treatment

Sandra Blanco

Centro de Investigación del Cáncer, Spain

Friday November 6, 12:10 – 12:45

Variations in ribosomal RNA (rRNA) modifications have been observed in both healthy and diseased tissues, raising questions about their role in translation regulation and potential contributions to disease. However, the dynamic regulation of these modifications and their impact on translation remain unresolved.

Here, we identify differential cytosine-5-methylation (m5C) of rRNA as a significant source of ribosome heterogeneity in human cells. Using nascent proteomics, RNA bisulfite and ONT RNA direct sequencing, and molecular dynamics simulations, we demonstrate that rRNA m5C, mediated by the NSUN5 methyltransferase, undergoes dynamic changes during the cell cycle. High-resolution cryo-EM analysis reveals that the loss of m5C induces structural rearrangements at the subunit interface, altering codon usage to preferentially translate mRNAs enriched in optimal codons. This shift enhances the expression of early mitotic regulators and impacts the efficiency and accuracy of mRNA decoding during mitosis.

Through biochemical, genetic, and functional analyses, we establish that rRNA m5C methylation dynamics are essential for cell cycle progression and tumor growth in vivo. Our findings demonstrate that differential rRNA m5C methylation generates specialized ribosomes with unique functional roles, providing a mechanism for fine-tuning translation, regulating codon usage, and modulating genome decoding during cell cycle progression.

Advancing regulatory variant effect prediction with AlphaGenome

Žiga Avsec

DeepMind, United Kingdom

Friday November 6, 14:00 – 14:35

Deep learning models that predict functional genomic measurements from DNA sequences are powerful tools for deciphering the genetic regulatory code. Existing methods involve a trade-off between input sequence length and prediction resolution, thereby limiting their modality scope and performance. We present AlphaGenome, a unified DNA sequence model, which takes as input 1 Mb of DNA sequence and predicts thousands of functional genomic tracks up to single-base-pair resolution across diverse modalities. The modalities include gene expression, transcription initiation, chromatin accessibility, histone modifications, transcription factor binding, chromatin contact maps, splice site usage and splice junction coordinates and strength. Trained on human and mouse genomes, AlphaGenome matches or exceeds the strongest available external models in 25 of 26 evaluations of variant effect prediction. The ability of AlphaGenome to simultaneously score variant effects across all modalities accurately recapitulates the mechanisms of clinically relevant variants near the *TAL1* oncogene. To facilitate broader use, we provide tools for making genome track and variant effect predictions from sequence.

Understanding ecDNA-Driven Cancer Evolution

Andrea Ventura

Memorial Sloan Kettering Cancer Center, USA

Friday November 6, 14:35 – 15:10

Focal oncogene amplifications mediated by extrachromosomal DNA (ecDNA) are common in human cancers, where they play key roles in tumor evolution, cellular plasticity, and therapeutic response. Despite their importance, this class of cancer-associated mutations has been difficult to recapitulate in cellular or in vivo models. Surrogate approaches, such as transgene overexpression, fail to capture the complex regulation, copy-number variability, and rapid evolution that characterize ecDNA-mediated focal amplifications. Here, I will present a general approach we developed to generate large (>1 Mb), multigenic focal amplifications mediated by ecDNA in a temporally controlled and tissue-specific manner, both in cells and in genetically engineered mouse models. I will describe how we are leveraging this technology to generate the first autochthonous mouse models of some of the most aggressive human cancers driven by ecDNA, and how these models are enabling us to interrogate the most pressing questions about ecDNA biology and its role in cancer progression.

A full-length transcriptome atlas reveals hidden coding elements and functional peptides in human cancers

Yasuhiro Murakawa

RIKEN, Japan

Friday November 6, 15:55 – 16:30

Gene expression is regulated through complex transcriptional and post-transcriptional mechanisms that are fundamental to human development and tumorigenesis. Recent studies have revealed that numerous previously unrecognized small open reading frames (sORFs) encode functional peptides, highlighting the importance of accurately defining complete transcript structures. However, conventional RNA sequencing often fails to reconstruct RNA molecules from transcription start sites to transcription termination sites, limiting the accurate identification of their coding potential. Here, we developed an improved “full-length” cDNA sequencing approach and applied it to hundreds of human samples spanning diverse cell types, normal tissues, and multiple cancer types. Accurate reconstruction of complete transcript structures enabled the gene annotation-independent identification of coding and non-coding transcripts, novel genes, and previously unrecognized sORFs. This comprehensive atlas substantially expands the current human transcriptome and establishes a new framework for systematically exploring hidden coding elements and functional peptides in human biology and cancer.

Illuminating the viral dark proteome to advance our understanding on antiviral immunity

Shira Weingarten-Gabbay

Harvard Medical School, USA

Friday November 7, 16:30 – 17:00

Viruses are among the most fascinating biological entities on Earth. With genomes 10,000 times smaller than ours, they nonetheless hijack host cells and execute remarkably complex life cycles. This paradox raises a fundamental question: how well do we truly understand the coding capacity of viral genomes?

In my talk, I will present Massively Parallel Ribosome Profiling, a technology that combines synthetic biology with ribosome profiling to map viral translation across thousands of viral sequences in parallel. Using this approach, we unveiled more than 4,000 previously unknown microproteins across nearly 700 viruses. Among them are unexpected targets for T cells and regulatory elements that fine-tune viral gene expression.

Shedding light on the viral dark proteome could reshape our understanding of the viral life cycle and antiviral immunity.