EACR

European Association
for Cancer Research

CONFERENCES

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EACR Conference

Cancer Genomics, Multiomics and Computational Biology

30 April-02 May 2024 | Bergamo, Italy

Scientific Programme Committee

James Brenton
Elaine Mardis
Carlos Caldas
Yardena Samuels
Núria López-Bigas

Scan the QR code to access online conference resources, including speaker and poster abstracts

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eacr.org/conference/cancermultiomics2024

Save the date

eacr.org/conference

EACR
2024

10-13 June 2024
Rotterdam
Netherlands

Join us for the EACR Annual Congress

2024.eacr.org

European Association for Cancer Research
EARLY CAREER RESEARCHERS' CONFERENCE
VIRTUAL EVENT
25 - 26 June 2024

EACR Conference
NEXT GENERATION CANCER THERAPIES
Virtual event
24 - 25 September 2024

EACR Conference
CANCER METABOLISM
Bilbao Spain
08 - 10 October 2024

EACR Conference
LIQUID BIOPSIES
Lyon, France
12 - 14 November 2024

EACR Conference
DEFENCE IS THE BEST ATTACK
Immuno-Oncology Breakthroughs
Barcelona, Spain
13 - 15 May 2025

EACR Conference
CANCER NEUROSCIENCE
Bilbao, Spain
14 - 16 October 2025

Day 1 | Tuesday 30 April

Posters 1-64 can be put up

From 11:30	REGISTRATION
12:00-13:00	WELCOME LUNCH *A chance to meet fellow attendees and enjoy a light buffet lunch*
13:00-13:10	CONFERENCE WELCOME **Scientific Programme Committee**
	SESSION 1: INTERSECTION OF FUNCTIONAL AND IMMUNOGENOMICS FOR THERAPY Chair: Carlos Caldas
13:10-13:40 Q&A: 13:40-13:55	OPENING KEYNOTE LECTURE **Julian Downward** Francis Crick Institute, UK “Investigating the interplay between oncogenic signaling and tumour immune evasion in lung cancer”
13:55-14:15 Q&A: 14:15-14:25	**Elaine Mardis** Institute for Genomic Medicine, USA “Oncolytic Viral Therapy Immunogenomics in adult GBM”
14:25-14:35 Q&A: 14:35-14:40	**Diego Chowell** Icahn School of Medicine at Mount Sinai, USA Proffered Paper 1: “An immunogenetic basis for lung cancer risk”
14:40-14:50	EXHIBITOR INTRODUCTIONS *60-second intro pitches by each company*
14:50-15:20	COFFEE BREAK, EXHIBITION & SOLO MEET-UP *Solo travellers meet-up at the EACR banner near the registration desk to connect with fellow adventurers*
	Chair: James Brenton
15:20-15:40 Q&A: 15:40-15:50	**Elisa Oricchio** EPFL, Switzerland “Modulation of 3D chromatin structures to support tumor evolution”
15:50-16:00 Q&A: 16:00-16:05	**Tancredi Massimo Pentimalli** Max Delbruck Center, Germany Proffered Paper 2: “Single cell-resolved multimodal atlas of a lung tumor in 3D”

16:05-16:15 Q&A: 16:15-16:20	**Clare Puttick** Francis Crick Institute, UK Proffered Paper 3: "HLA disruption through genetic and non-genetic mechanisms is pervasive in lung and breast tumours"
16:20-16:30	MOLECULAR ONCOLOGY: CALL FOR CONTENT
16:30-16:40	POSTER SPOTLIGHTS *Posters 1, 30 and 60 will be presented in short 3-minute 'flash talks'*
16:40-17:10	BIOMODAL SYMPOSIUM **Dr Jacob Househam** The Institute of Cancer Research (ICR), UK "Combined genetic and epigenetic analyses of a Lynch syndrome tumour"
17:10-17:40	NETWORKING QUIZ *Our fun, informal quiz offers conference participants the chance to make new connections on the first evening of the meeting*
17:40-18:20	WELCOME RECEPTION *with drinks and a light buffet*
18:20-19:50	POSTER DISCUSSION SESSION 1 *Presenters of posters 1-64 should stand by their boards*

Day 2 | Wednesday 01 May

08:15-08:45	EARLY POSTER VIEWING WITH COFFEE
	Chair: Núria López-Bigas
08:45-09:00	LUNAPHORE SPOTLIGHT **Clément Chavelier** Lunaphore and **Euplio Visco** ACD, Italy "True spatial multiomics: when RNA meets protein on the same section"
	SESSION 2: SINGLE CELL CANCER DISSECTION
09:00-09:20 Q&A: 09:20-09:30	**Ido Amit** Weizmann Institute of Science, Israel "The power of ONE: Immunology in the age of single cell genomics"
09:30-09:50 Q&A: 09:50-10:00	**Carlos Caldas** Cancer Research UK Cambridge Institute, UK "Dissecting breast cancer ecosystems at single cell level"
10:00-10:20 Q&A: 10:20-10:30	**Efrat Shema** Weizmann Institute of Science, Israel "Single-molecule and single-cell epigenetics: Decoding the epigenome for cancer research and diagnostics"

10:30-10:40 Q&A: 10:40-10:45	**Fernando Perez** University of Helsinki, Finland Proffered Paper 4: "Machine learning to reveal the specifc cell-level spatial tumor microenvironment features across Ovarian Cancer clinico-molecular subtypes"
10:45-11:15	COFFEE BREAK & EXHIBITION Take down posters 1-64 Posters 65-129 can be put up
11:15-11:35 Q&A: 11:35-11:45	**Yardena Samuels** Weizmann Institute of Science, Israel "Revisiting the Neoantigen Approach for Cancer Immunotherapy"
11:45-11:55 Q&A: 11:55-12:00	**Daria Romanovskaia** Center for Molecular Medicine, Austria Proffered Paper 5: "Plasticity and epigenetic regulation of Ewing sarcoma cell states"
12:00-12:10 Q&A: 12:10-12:15	**Sahil Sahni** National Cancer Institute, USA Proffered Paper 6: "Deactivation of ligand-receptor interactions enhancing lymphocyte infiltration drives melanoma resistance to Immune Checkpoint Blockade"
12:15-12:25	POSTER SPOTLIGHTS *Posters 65, 95 & 120 will be presented in short 3-minute 'flash talks'*
12:25-13:30	LUNCH & EXHIBITION
13:30-15:00	POSTER DISCUSSION SESSION 2 *Presenters of posters 65-129 should stand by their boards*
	SESSION 3: BIOMARKERS FOR PRECISION ONCOLOGY Chair: Elaine Mardis
15:00-15:20 Q&A: 15:20-15:30	**Eytan Ruppin** National Cancer Institute, USA "Next generation precision oncology: From omics to slides"
15:30-15:40 Q&A: 15:40-15:45	**Shira Sagie** Weizmann Institute of Science, Israel Proffered Paper 7: "KRAS G12V neoantigen-specific therapy modalities development and assessment"
15:45-16:05 Q&A: 16:05-16:15	**Francisco Martinez-Jimenez** VHIO, Spain & Hartwig Medical Foundation, Netherlands "Unravelling the immunogenomic determinants of metastasis"
16:15-16:45	COFFEE BREAK & EXHIBITION
16:45-17:05 Q&A: 17:05-17:15	**Trevor Pugh** Princess Margaret Hospital, Canada "Early cancer surveillance through multi-modal analysis of cell-free DNA fragments in blood"

17:15-17:35
Q&A: 17:35-17:45

James Brenton Cancer Research UK Cambridge Institute, UK
"DNA damage response signatures as therapeutic predictors in recurrent drug-resistant ovarian cancer"

17:45-18:15

MEET THE SCIENTIFIC PROGRAMME COMMITTEE

The committee members will reflect on the conference so far before providing insight into their personal and professional experiences

19:30

OPTIONAL CONFERENCE DINNER

The conference dinner will be held at the atmospheric Ristorante Taverna Valtellinese (optional ticketed event)

Day 3 | Thursday 02 May

08:15-08:45

EARLY POSTER VIEWING WITH COFFEE

Chair: Yardena Samuels

08:45-09:00

NONACUS SPOTLIGHT

Tim Gilbert Nonacus
"GALEAS: Precision bioinformatics for precision oncology - MSH2 to 1p19q"

SESSION 4: SINGLE CELL CANCER ANALYTICS

09:00-09:20
Q&A: 09:20-09:30

Bernd Bodenmiller University of Zurich, Switzerland
"Highly multiplexed imaging of in situ tumor ecosystems towards precision medicine"

09:30-09:50
Q&A: 09:50-10:00

Asaf Madi Tel Aviv University, Israel
"Integration of single-cell RNAseq data and protein-protein interaction networks"

10:00-10:10
Q&A: 10:10-10:15

Kevin Tu University of Cambridge, UK
Proffered Paper 8: "Characterizing the breast cancer microenvironment using different data modalities and clinical associations at cell-state granularity"

10:15-10:45

COFFEE BREAK & EXHIBITION

10:45-11:05
Q&A: 11:05-11:15

Hannah Carter UC San Diego, USA
"Interface-guided phenotyping of coding variants in the transcription factor RUNX1"

11:15-11:45
Q&A: 11:45-12:00

THE EMBO KEYNOTE LECTURE

Núria López-Bigas Institute for Research in Biomedicine, Spain
"Clonal selection in normal tissues and its relation to cancer risk"

12:00

SUMMARY, AWARDS AND DEPART

Travel grants

More information about EACR grants: eacr.org/travel-grant

EACR-Worldwide Cancer Research Travel Grants provide funds to help early-career EACR members and researchers based in low- or middle-income economy countries to participate in our conferences.

Congratulations to the recipients of the Travel Grants for this conference. Each recipient received a full registration free of charge and funds to assist with travel and accommodation costs.

- **BERTHA RUEDA** MEXICO
- **KEVIN TU** UK
- **MARCELLUS AUGUSTINE** UK
- **MARCO FANTUZ** ITALY
- **SHIRA SAGIE** ISRAEL
- **YINGCHENG WU** CHINA
- **JUAN LUIS ONIEVA ZAFRA** SPAIN

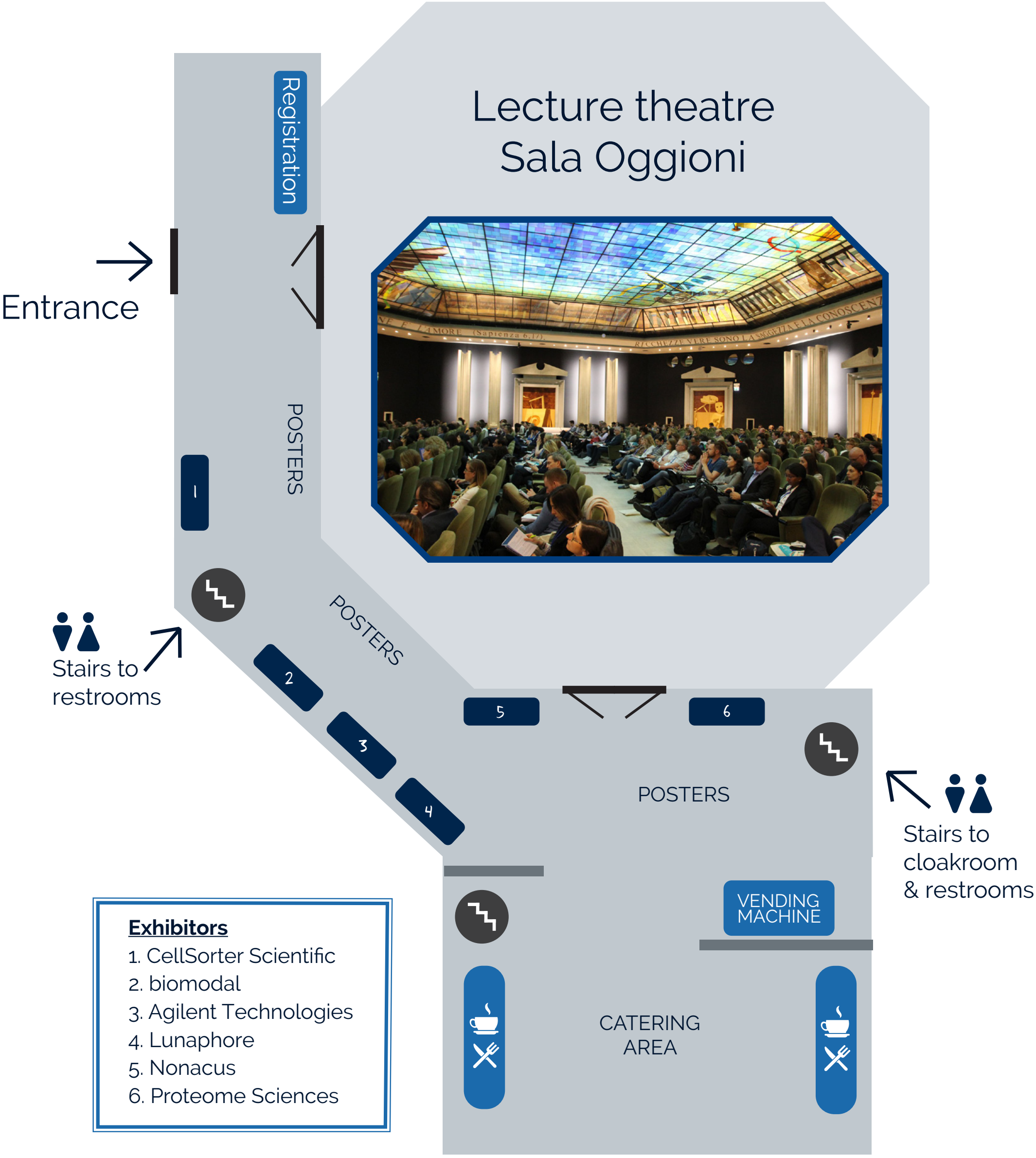
Supporters

We would like to thank the following grant providers:

This activity has been supported by a grant from F. Hoffman-La Roche Ltd, which has had no control over the educational content of this activity.

Our thanks also to the following partners for supporting us in promoting this conference:

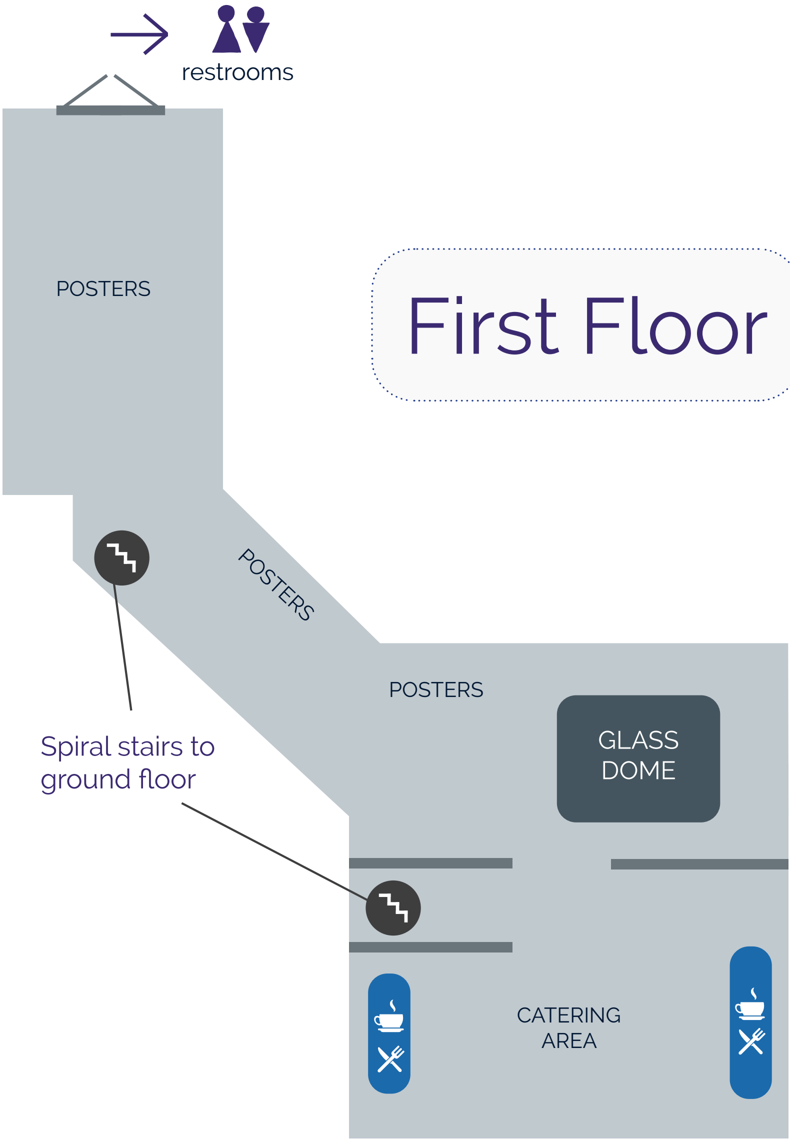
Venue floor plan



Exhibitors

1. CellSorter Scientific
2. biomodal
3. Agilent Technologies
4. Lunaphore
5. Nonacus
6. Proteome Sciences

First Floor


restrooms
POSTERS
POSTERS
POSTERS
GLASS DOME
Spiral stairs to ground floor
CATERING AREA

Meet the exhibitors

CellSorter Scientific Stand: 1

Website: www.cellsorter-scientific.com

Represented at the conference by:
Balint Szabo, Heléna Domokos

biomodal Stand: 2

Website: www.biomodal.com

Symposium: Tuesday 30 April | 16:40-17:10

Dr Jacob Househam ICR, UK
"Combined genetic and epigenetic analyses of a Lynch syndrome tumour"

Represented at the conference by:
Aziz Mustafa, Roel Sprengers, Jane Hayward, Tom Charlesworth

Agilent Technologies Stand: 3

Website: www.agilent.com

Represented at the conference by:
Claudia Scaccabarozzi, Emma Nora Di Capua

Lunaphore Stand: 4

Website: www.lunaphore.com

Spotlight: Wednesday 01 May | 08:45-09:00

Clément Chevalier Lunaphore, Switzerland and Euplio Visco, ACD, Italy
"True spatial multiomics: when RNA meets protein on the same action"

Represented at the conference by:
Clément Chevalier, Raphaël Sandoz

Nonacus Stand: 5

Website: www.nonacus.com

Spotlight: Thursday 02 May | 08:45-09:00

Tim Gilbert Nonacus
"GALEAS: Precision bioinformatics for precision oncology - MSH2 to 1p19q"

Represented at the conference by: Katie Shepherd, Tim Gilbert

Proteome Sciences Stand: 6

Website: www.proteomics.com

Represented at the conference by: Illip Burmester

Poster index

View abstracts when logged-in at www.eacr.org/conference/cancermultiomics2024

1 **[POSTER SPOTLIGHT]** Dissecting the evolutionary progression of small intestine neuroendocrine tumors using whole genome sequencing Presented by Alice Schiller, University of Gothenburg, SWEDEN

2 The impact of treatment-free intervals on T-cell exhaustion and clonotypic diversity in multiple myeloma patients treated with BCMA bispecific antibodies Presented by Nazia Afrin, University Hospital Würzburg, GERMANY

3 Deep Learning for Detecting and Segmenting Perineural Invasion in Colon, Prostate, and Pancreatic Cancers Presented by Ahmad Alkhan, University of Limerick, IRELAND

4 Identifying new immunotherapy targets using machine learning and ex vivo validation Presented by Marcellus Augustine, UCL Cancer Institute and The Francis Crick Institute, London, UK

5 Tumour ecosystem and molecular dynamics in clinical triple-negative breast cancer depend on the chemotherapy regimen Presented by Marco Barreca, University of Milano-Bicocca and Fondazione Michelangelo, Milan, ITALY

6 Network analysis of ER-positive breast cancer patients identify co-regulation of TRM45, ESR1, and MYC that is associated with patient survival. Presented by Anne Berge, The Arctic University of Norway, Tromsø, NORWAY

7 Deciphering transcription factor driven metabolic rewiring in lung cancer Presented by Sebastian Bors, University Basel, SWITZERLAND

8 Identification of leukemia stem cell subsets with distinct transcriptional, epigenetic and functional properties Presented by Helena Boutzen, UHN, Toronto, CANADA

9 Acidic tumour microenvironment promotes S1P-mediated histone acetylation to increase osteosarcoma aggressiveness Presented by Nicolò Bozzini, University of Bologna (UNIBO), ITALY

10 Application of machine-learning methods to multi-omic datasets to develop prognostic models in prostate cancer Presented by Timothy Brendler-Spaeth, University of East Anglia, Norwich, UK

11 Whole genome duplication shapes evolution and confounds clinical biomarker assessment in high grade serous ovarian cancer Presented by Nikki Burdett, Peter MacCallum Cancer Centre and University of Melbourne, AUSTRALIA

12 Unsupervised transcriptomic analysis of post-neoadjuvant treatment triple-negative breast cancer reveals its heterogeneity and therapeutic vulnerabilities Presented by Maurizio Callari, Fondazione Michelangelo, Milan, ITALY

13 Integrated analysis of multi-omics data reveals new functional signatures to predict intestinal Cancer Stem Cells Presented by Coralie Capron, University of Liège, BELGIUM

14 Building a Platform for Integrative Discovery and Diagnostics in Cancer Presented by Ferran Cardoso Rodriguez, The Institute of Cancer Research & The Royal Marsden Hospital, London, UK

15 Unveiling the spatial dynamics of the tumor microenvironment: integrated RNA and protein profiling on the same section through automated spatial multiomics analysis Presented by Clément Chevalier, Lunaphore, Lausanne, SWITZERLAND

16 Protein structural context of cancer mutations reveals molecular mechanisms and identifies putative driver genes Presented by Diego Chillón Pino, MRC Human Genetics Unit and The University of Edinburgh, UK

17 NOTCH 1 and NOTCH 3 expressions for early stage of non-small cell lung cancer Presented by Eun Kyung Cho, Gachon University Gil Medical Center, Incheon, SOUTH KOREA

18 MHC class II genotypes are independent predictors of anti-PD1 immunotherapy response in melanoma Presented by Arne Claeys, Ghent University, BELGIUM

19 Molecular mechanisms and prognostic implications of an epigenetic regulation related gene in colorectal cancer Presented by Hsiang Dai, Chang Gung University, Taoyuan, TAIWAN

20 Immune-Related Gene Expression Signatures Identify a Patient's Subset Achieving Durable Complete Response to Brentuximab Vedotin in Relapsed/Refractory Hodgkin Lymphoma Presented by Alessandro Davini, IEO European Institute of Oncology IRCCS, Milan, ITALY

21 DNA methylation biomarker panel can distinguish Pleural Mesothelioma from healthy pleura and blood Presented by Nele De Meulenaere, University of Antwerp, BELGIUM

22 Kinetic analysis reveals involvement of premature termination of transcription in gene expression regulation Presented by Arjun Devadas Vasanthakumari, Max Planck Institute for Multidisciplinary Sciences, Goettingen, GERMANY

23 Single-cell genomics to accelerate the development of precision RNA therapeutics in lung cancer Presented by Bhavya Dhaka, University College Dublin and CRT Genomics Datascience, Dublin, IRELAND

24 The co-accessibility network enables the identification of Accessible Regions involved in Multiple Myeloma Bortezomib resistance Presented by Stefano Di Giovenale, IRCCS National Cancer Institute and University of Rome, ITALY

25 High-level Biomedical Data Integration in a Semantic Knowledge Graph with OncodashKB for finding Personalized Actionable Drugs in Ovarian Cancer Presented by Johann Dreo, Université Paris Cité, FRANCE

26 Copy number aberrations that drive metastasis in genomic subtypes of breast cancer Presented by Kate Eason, Cancer Research UK Cambridge Institute, UK

27 Mechanistic basis of atypical TERT promoter mutations Presented by Kerryn Elliott, University of Gothenburg, SWEDEN

28 Different somatic gene mutations in HPV-induced and HPV-independent penile carcinogenesis Presented by Mikhail Ermakov, Medical University of Graz, AUSTRIA

29 Divergent trajectories to structural diversity impact patient survival in high grade serous ovarian cancer Presented by Ailith Ewing, MRC Human Genetics Unit and Cancer Research UK Scotland Centre, Edinburgh, UK

30 **[POSTER SPOTLIGHT]** Single-nuclei RNA sequencing resolves osteosarcoma cell diversity and maturation Presented by Felipe Luz, Wellcome Sanger Institute, Cambridge, UK and Boldrini Children's Hospital, Campinas, BRAZIL

31 Mapping the Phenotypic Diversity of Healthy Fallopian Tubes Identifies Genomically Unstable Secretory Epithelial Cells Presented by Yaniv Eyal-Lubling, Cancer Research UK Cambridge Institute, UK

32 Single-nuclei multiomic approach reveals permanent reprogramming of exocrine cells after pancreatitis Presented by Marco Fantuz, Veneto Institute of Molecular Medicine (VIMM) and University of Padua, ITALY

33 Design of a surface-accessible epitope panel using Brewpitopes to empower early lung cancer detection Presented by Roc Farriol Duran, Barcelona Supercomputing Center, SPAIN and University College London Cancer Institute, UK

34 Primary prostate cancer subtypes identified by chromatin compartments profiling at time of diagnosis. Presented by Francesco Ferrari, National Research Council, Pavia and the AIRC Institute of Molecular Oncology, Milan, ITALY

35 Tissue differences in predicting platinum-free interval in high-grade serous ovarian cancer Presented by Océane Fourquet, Institut Pasteur and LIP6, Paris, FRANCE

36 A novel signature-based classification of the immune context in limited small cell lung cancer (SCLC) Presented by Jose Gracia-Rodriguez, Research Institute (i+12) Hospital 12 de Octubre and Spanish National Cancer Research Center (CNIO), Madrid, SPAIN

37 Resolving clone copy number and the evolution of metastasis in lung cancer with ALPACA Presented by Kristiana Grigoriadis, University College London Cancer Institute, UK

38 Understanding functional clonality in breast cancer patient-derived tumour xenografts: the impact of cellular dosing on heterogeneity and growth dynamics Presented by Daniel Guerrero-Romero, Cancer Research UK Cambridge Institute, UK

39 Demystifying HEVs in humans under inflammation conditions Presented by Swati Gupta, VIB KU Leuven Center for Cancer Biology, BELGIUM

40 Spatial profiling and single-cell analysis unveil the presence of fibroblast niches within draining lymph nodes of triple-negative breast cancer. Presented by Moutaz Helal, University Hospital Würzburg, GERMANY

41 Leveraging Synthetic Data Generation and Vision Transformers in a high throughput screening platform for cancer immunotherapy. Presented by Miguel Hernandez Roca, Instituto de Investigaciones Biomedicas Sols-Morreale (IIBM), CSIC-UAM, Madrid, SPAIN

42 Molecular characterization of the Basal-like intrinsic molecular subtype in ER-positive/HER2-negative primary breast cancer Presented by Lennart Hohmann, Lund University, SWEDEN

43 Tracking Adaptation and Response to Targeted Therapies in EGFR-driven Non-small Cell Lung Cancer: One Cell at A Time Presented by Regina Hoo, National Cancer Centre Singapore and Genome Institute of Singapore, SINGAPORE

44 The potential of whole-body donors in studying mutant clones in normal tissues Presented by Sofie Hoogstoel, Ghent University, BELGIUM

45 Platelets contain extracellular cell-free DNA displaying tumour-derived signal Presented by Jeanne Inchauspe, University of Oxford, UK

46 Sonic hedgehog medulloblastoma cell states in vitro mirror in vivo malignant states upon co-culture with cerebellar organoids Presented by John Jacob, University of Oxford, UK

47 Hidden tumor microenvironment RNA profiles accurately revealed by malignant cell fraction-informed deconvolution Presented by Jurriaan Janssen, Amsterdam UMC, NETHERLANDS

48 RNA allelic frequencies of somatic mutations encode substantial functional information in cancers Presented by Thomas Jones, University College London Cancer Institute, UK

49 Advancing Non-Invasive Cancer Detection: Platelet RNA Expression and Machine Learning Presented by Maksym Jopek, Medical University of Gdansk, POLAND

50 AP1 Transcription Factors drive multidrug tolerance in Triple Negative Breast Cancer Presented by Grégoire Jouault, Institut Curie, Paris, FRANCE

51 A deep-learning framework for quantitative spatial analysis of the tumor microenvironment Presented by Ziqi Kang, University of Helsinki, FINLAND

52 Evaluation of anti-hepatocellular carcinoma activity of pan-inhibitor of cyclin-dependent kinases AT7519 Presented by Kaja Karaś, Polish Academy of Sciences, Lodz, POLAND

53 Genetic Concordance in Melanoma: Insights from Early stage Primary Tumors and their matched Distant Metastases. Presented by Thamila Kerkour, Erasmus MC, Rotterdam, NETHERLANDS

54 Roridin E has anti-cancer effects on MDA-MB-231 cells through S6K signaling with minimal transcriptional alterations of cardiomyocytes. Presented by Kyungtae Kim, Sungkyunkwan University, Gyeonggi-do, SOUTH KOREA

55 Recurrent mechanisms of biallelic epigenetic inactivation reveals new putative tumour suppressor genes in prostate cancer. Presented by Daria Kiriy, Rigshospitalet and University of Copenhagen, DENMARK

56 Learning from CRISPR loss-of-function screens for robust and interpretable drug response prediction Presented by Dom Kirkham, MRC Biostatistics Unit, Cambridge, UK

57 Multi-Feature Fragment-Level Classifier for In Silico Enrichment of Circulating Tumor DNA Presented by Bianca Kirsh, University of Toronto and Princess Margaret Cancer Centre, CANADA

58 Germline predisposition across hematological disorders Presented by Jessica Koski, University of Helsinki, FINLAND

59 *(discussion session 2)* Spatial distribution of IL1B+ TAMs in human pancreatic cancer Presented by Federica La Terza, San Raffaele Telethon Institute for Gene Therapy (SR-Tiget), Milan, and University of Turin, ITALY

60 **[POSTER SPOTLIGHT]** Unveiling Homologous Recombination Deficiency Signatures through Single-Cell Analysis Presented by Shadi Shafighi, Cancer Research UK Cambridge Institute, UK

61 Implementation of an online platform for the quantification of genomic instability scores in microarrays and exome samples. Presented by Ariadna Lara Gutierrez, Medical University of Graz, AUSTRIA

62 Prediction by machine learning of the occurrence of late skin side effects after radiotherapy using blood biomarkers Presented by Carine Laurent, Université de Caen-Normandie and SAPHYN-ARCHADE (Advanced Resource Center for HADrontherapy in Europe), Caen, FRANCE

63 In silico prediction of the impact of tRNA modifications on mRNA translation Presented by Marine Leclercq, Université de Liège, BELGIUM

64 Multimodal analysis of phenotypic and spatial ecological heterogeneity in breast cancer patient-derived tumour xenografts Presented by Giulia Lerda, Cancer Research UK Cambridge Institute, UK

65 **[POSTER SPOTLIGHT]** Evolutionary Trajectories of Small Cell Lung Cancer under Therapy Presented by Maria Cartolano, University Hospital Cologne and Centre for Molecular Medicine, Cologne, GERMANY

66 Alternative splicing in non-small cell lung cancer evolution Presented by Michelle Leung, University College London Cancer Institute, London, UK

67 Transcriptomic profiling of small intestine neuroendocrine tumors Presented by Markus Lindberg, University of Gothenburg, SWEDEN

68 Quest for Novel Biomarkers: Multi-omics Analysis of Vulvar Squamous Cell Carcinoma Presented by Flavio Lombardo, University Hospital Basel, SWITZERLAND

69 Investigating heterogeneity of homologous recombination deficiency status and underlying mutational status in High Grade Serous Ovarian Cancer Presented by Marc Lorentzen, Imperial College London, UK

70 Differential dependency analysis of genome-wide viability CRISPR screens: A comparison between MAGeCK, drugZ, and Chronos Presented by Allan Lui, Cancer Research UK Cambridge Institute, UK

71 Predicting TP53 mutations from spatial transcriptomics data using a Graph Neural Network Presented by Tom Luijts, Ghent University and Cancer Research Institute Ghent, BELGIUM

72 demuxSNP: supervised demultiplexing of scRNAseq data using cell hashing and SNPs Presented by Michael Lynch, University of Limerick, IRELAND

73 Epigenetic Fingerprints Link Early-Onset Colorectal Cancer to Lifestyle and Environmental Exposures Presented by Silvana Maas, Vall d'Hebron Institute of Oncology, Barcelona, SPAIN

74 Computational Discovery of Polygenic Synthetic Lethal Vulnerabilities Presented by Santiago Madera, The Institute of Cancer Research, London, UK

75 nf-BLISS: A Nextflow pipeline for genome wide double-strand breaks mapping Presented by Alexandra Mancheno Ferris, The AIRC Institute of Molecular Oncology, Milano, ITALY

76 Molecular characterisation of RNA variants in breast cancer Presented by Raquel Manzano, Cancer Research UK Cambridge Institute, UK

77 Hypoxic stress favours somatic mutation in normal kidneys Presented by Jean Piero Margaria, IRCCS Ospedale San Raffaele/ Università Vita-Salute San Raffaele, Milan, ITALY

78 Transcriptome-wide gene expression outlier analysis pinpoints therapeutic vulnerabilities in colorectal cancer Presented by Elisa Mariella, University of Torino and the AIRC Institute of Molecular Oncology, Milano, ITALY

79 Epigenetic and TCR Repertoire as Predictive Biomarkers of Immunotherapy Response in Advanced NSCLC Patients Presented by Mónica Martínez Fernández, IIS Galicia Sur, Vigo, SPAIN

80 Whole genome and transcriptome sequencing of pre- and post-treatment biopsies in a rectal cancer patient using long-read and short-read technologies Presented by Lauren McAuley, Royal College of Surgeons in Ireland, Dublin, IRELAND

81 Single-cell RNA-seq analysis of human lung adenocarcinoma unveil mechanisms of epithelial cell plasticity which drive tumor progression. Presented by Valentina Melocchi, Fondazione IRCCS Casa Sollievo della Sofferenza, San Giovanni Rotondo, ITALY

82 Metastatic hormone-naïve prostate cancer: a distinct biological entity Presented by Isabel Mendizabal, CIC bioGUNE, Derio, and Basque Foundation for Science, Bilbao, SPAIN

83 A spatial transcriptomic exploration of the neuroblastoma tumour microenvironment in response to ATR inhibition Presented by Peter Merseburger, Ghent University and Cancer Research Institute Ghent, BELGIUM

84 Identification of diagnostic and prognostic biomarkers in oligodendroglioma Presented by Hajar Mikaeili, UCL, London, UK

85 Probing the role of hypoxia and tumour microenvironment in prostate cancer disease trajectories Presented by Migle Mikutenaite, University of Copenhagen and Rigshospitalet, Copenhagen, DENMARK

86 Intercellular communication and CD8+ T cell trajectory analysis in ovarian cancer tissues Presented by Ankita Murmu, Semmelweis University and HUN-REN Research Centre for Natural Sciences, Budapest, HUNGARY

87 Multiomics assessment of lung adenocarcinoma subtypes defined through tumor purity-adjusted DNA methylation Presented by Deborah Nacer, Lund University, SWEDEN

88 Integration of highly-multiplexed imaging and spatial transcriptomics reveal contact-dependent differences in key immune-related molecular pathways and cell states in ovarian cancer Presented by Iga Niemiec, University of Helsinki, FINLAND

89 Systematic CRISPR-enhanced assessment of variants of unknown significance in cancer cells nominates new therapeutic targets and drug repositioning opportunities Presented by Athanasios Oikonomou, Human Technopole, Milano, ITALY

90 Multi-Omics Profiling in Immune Checkpoint Inhibition Response: Revealing Longitudinal Regulatory Biomarkers via Liquid Biopsy Analysis Presented by Juan Luis Onieva Zafra, Regional and Virgen de la Victoria University Hospitals and Universidad de Málaga, SPAIN

91 Comparing blood-platelet RNA-profiles of glioblastoma and brain metastasis patients against healthy controls reveals potential disease mechanisms Presented by Krzysztof Pastuszak, Gdansk University of Technology and Medical University of Gdańsk, POLAND

92 PHF19 gene transcripts as potential biomarkers of early colorectal cancer Presented by Dunja Pavlovic, Institute of Molecular Genetics and Genetic Engineering, Belgrade, SERBIA

93 Liquid biopsy derived multi-omic characterisation of head and neck squamous cell carcinoma: capturing genomic and methylomic intra-tumoural heterogeneity Presented by Karl Payne, University of Birmingham, UK

94 Genomic landscape and single base substitution mutational signatures in Juvenile Myelomonocytic Leukemia: a new JMML portrait Presented by Alberto Peloso, Padua University and Hospital and Pediatric Research Institute "Città della Speranza", Padua, ITALY

95 **[POSTER SPOTLIGHT]** Drug Response in High-Throughput Screening is Predicted by the Integrated Multiomic Profile of Breast Cancer Xenografts. Presented by Riccardo Masina, Cancer Research UK Cambridge Institute, UK

96 An integrated platform for the discovery of non-canonical antigens in pediatric and adult cancers Presented by Marina Reixachs Solé, Prinses Máxima Center for Pediatric Oncology and Oncode Institute, Utrecht, NETHERLANDS

97 Prioritisation of Targets for Precision RNA Therapeutics via Cancer Genomics Data Integration. Presented by Jack Roban, Centre for Research Training in Genomics Data Science , Galway, and University College Dublin, IRELAND

98 A multiomic approach to elucidate the role of GCN2 in translation regulation in cancer Presented by Monica Roman-Trufero, Lausanne University Hospital (CHUV), SWITZERLAND and Imperial College London, UK

99 FIERCE: Reconstructing Dynamic Trajectories from the Differentiation Potency of Single Cells Presented by Oriana Romano, University of Padova, ITALY

100 Single Sample Prediction of Immune Response in Triple Negative Breast Cancer based on Gene Expression Presented by Suze Julia Roostee, Lund University, SWEDEN

101 The impact of IDH1 mutation on immune cells in experimental gliomas as revealed by single-cell transcriptomics Presented by Patrycja Rosa, Nencki Institute of Experimental Biology and University of Warsaw, POLAND

102 Addressing challenges from limited cohort studies: Detecting biased positive selection mutational patterns in Mexican patients with lung adenocarcinoma Presented by Bertha Rueda, Instituto Nacional de Medicina Genómica and Universidad Nacional Autónoma de México, Ciudad de México, MEXICO

103 Harnessing EMT Signature for Deciphering Intratumoral Heterogeneity in Breast Cancer: A Single-Cell Transcriptomic Approach Presented by Saikat Das Sajib, The Arctic University of Norway, Tromsø, NORWAY

104 Supervised Non-Negative Matrix Factorisation for the Identification of Resistance-Related Gene Expression Programs in Clinical Single-Cell RNA-sequencing Data Presented by Mara Santarelli, Institut Pasteur and Sorbonne Université, Paris, FRANCE

105 Tumor purity estimated from bulk DNA methylation can be used for adjusting beta values of individual samples to better reflect tumor biology Presented by Iñaki Sasiain Casado, Lund University, SWEDEN

106 A human metabolic map of pharmacological perturbations unlocks new modes of action for conventional drugs Presented by Laurentz Schuhknecht, University of Basel and ETH Zürich, SWITZERLAND

107 Machine learning in analysis of scRNA-seq profiles of Circulating Tumour Cells Presented by Michał Sieczczyński, Medical University of Gdańsk, POLAND

108 Pathogenic mtDNA mutations associated with shorter overall survival in high-grade serous ovarian cancer Presented by Ryan Silk, MRC Human Genetics Unit, Edinburgh, UK

109 Expression of HPV viral genes influences molecular and immune traits of cervical cancers. Presented by Anurag Kumar Singh, National Centre for Biological Sciences, Bangalore, INDIA

110 Cancer cell plasticity explained through context specific network models. Presented by Divyanshu Srivastava, University of Lausanne and Swiss Institute for Experimental Cancer Research, EPFL, Lausanne, SWITZERLAND

111 Single base pair substitution patterns and genomic contexts in clinical and molecular subgroups of primary breast cancer Presented by Johan Staaf, Lund University, SWEDEN

112 Malignant cell fraction-informed RNA deconvolution to address the heterogeneity within tumor intrinsic molecular subtypes of Pancreatic Ductal AdenoCarcinoma in large cohorts Presented by Mischa Steketee, Amsterdam UMC, NETHERLANDS

113 Advancing Pediatric Oncology: Integrating Gene Dependency for Targeted Therapy and Biomarker Discovery in Paediatric-focused Multi-Omics Cancer AI models Presented by Claire Sun, Hudson Institute of Medical Research and Monash University, Clayton, AUSTRALIA

114 Enhancing Ovarian Cancer Detection via Platelet RNA Profiling: Investigating Clinical Factors' Influence on Classification Accuracy Presented by Anna Supernat, Medical University of Gdansk, POLAND

115 Identifying Patients Similar Tumour Molecular Profiles but Different Cancer Types Diagnosis Using DeepClustering Presented by Oznur Tastan, Sabanci University, Istanbul, TURKEY

116 Learning single-cell high-content phenotypes and their genetic determinants in healthy blood donors Presented by Veera Timonen, University of Helsinki, FINLAND

117 Multi-omic analysis implicates ER-related mechanism of KMT2C/D mutations in breast tumorigenesis Presented by Emily Tinsley, RCSI University of Medicine and Health Sciences, Dublin, IRELAND

118 NanoCMSer: A Clinically Applicable Stratification Tool for Stratification of Colorectal Cancer Samples Presented by Arezo Torang, Amsterdam University Medical Centers and Oncode Institute, Amsterdam, NETHERLANDS

119 Mutant p53 sustains serine-glycine synthesis and essential amino acids intake promoting breast cancer growth Presented by Luca Triboli, University of Trieste and International Centre for Genetic Engineering and Biotechnology (ICGEB), Trieste, ITALY

120 **[POSTER SPOTLIGHT]** Heterogeneity and evolution of DNA mutation rates in microsatellite-stable colorectal cancer Presented by Elena Grassi, University of Torino and Candiolo Cancer Institute, ITALY

121 Transcriptomic profiling identifies pathways associated with auranofin response in high grade serous ovarian cancer Presented by An Truong, Cancer Research UK Cambridge Institute, UK

122 The role of PRC2 in gene regulation and chromatin architecture in acute myeloid leukaemia Presented by Cosmin Tudose, Systems Biology Ireland, UCD, Dublin, and The SFI Centre for Research Training in Genomics Data Science, Galway, IRELAND

123 Kataegis in clinical and molecular subgroups of primary breast cancer Presented by Srinivas Veerla, Lund University, SWEDEN

124 Arrest the metastasis: Arrestin protein emerges as a novel tumor suppressor gene in CTC studies Presented by Aakanksha Verma, Weizmann institute of Science, Rehovot, ISRAEL

125 The effects of ALDH1A3 on gene expression and DNA methylation changes are connected to a fibroblast-rich and immunosuppressive breast tumour microenvironment Presented by Olivia Walker, Dalhousie University, Halifax, Nova Scotia, CANADA

126 SpottedPy quantifies relationships between spatial transcriptomic hotspots and uncovers new environmental cues of epithelial-mesenchymal plasticity in cancer Presented by Eloise Withnell, University College London, UK

127 Pan-cancer neutrophil encyclopedia illuminates anti-tumor antigen-presenting potency Presented by Yingcheng Wu, Fudan University, Shanghai, CHINA

128 Developing a novel prediction algorithm for SLC substrates leveraging cancer multi-omics Presented by Yimo Zhang, University of Oxford, UK

129 Molecular determinants of response to neoadjuvant chemotherapy in esophageal adenocarcinoma at single-cell spatial resolution Presented by Giulia Lopatriello, San Raffaele Hospital, ITALY

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EACR on-site team

Chris Iliffe
Conference Officer

Kathryn Wass
Programmes Manager

Rachel Warden
Communications and Marketing Manager

Alexandra Boitor
Scientific Officer

Conference dinner

Optional ticketed event: Wednesday 01 May, 19:30

The conference dinner will take place on the final night of the meeting at the atmospheric Ristorante Taverna Valtellinese, a short walk from the conference venue. It will be an excellent opportunity for participants and speakers to get to know each other in a relaxed and informal environment.

A four-course meal will be served with wine and coffee included in the ticket price.

Venue
Taverna Valtellinese
Via G. Tiraboschi 57
24122 Bergamo
www.tavernavaltellinese.it

Directions from the conference venue
It takes less than 10 minutes to walk from the conference venue to the dinner venue. Head north-west on Viale Papa Giovanni XXIII and turn left onto Largo Porta Nuova, which becomes Via G. Tiraboschi. The entrance to the Taverna is just down the side street called Passeggiata Zeduri.

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