EACR Conference on
Cancer Genomics
05 - 07 July 2022, Oxford, UK

Pocket Programme

Scientific Programme Committee
Carlos Caldas (Chair)
Elaine Mardis, James Brenton,
Yardena Samuels

Scan the QR code to access online conference resources, including speaker and poster abstracts
eacr.org/conference/cancergenomics2022
Accelerating the future of cancer genomics

See you at the Thermo Fisher Scientific booth #4

Watch our industry spotlight on Thursday, 7th July 2022 at 8:45 am: Characterisation of breast cancer immune microenvironment - focus on DCIS and cancers during pregnancy.

Learn more about our complete suite of cancer genomics solutions at thermofisher.com/cancergenomics

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Day 1 - Tuesday 05 July

From 12.00

REGISTRATION

12.00 – 13.15

>Welcome LUNCH & EXHIBITION
A chance to meet fellow participants and enjoy a light buffet lunch before the first session.

13.15 – 13.25

CONFERENCE WELCOME
Scientific Programme Committee

SESSION 1: IMMUNO-GENOMICS
Chair: James Brenton

13.25 – 13.45

Yardena Samuels Weizmann Institute of Science, Israel
"Deciphering the highly complex cancer immunopeptidome"

Q&A: 13.45 – 13.55

13.55 – 14.15

Michael Platten DKFZ, Germany
"Immune targeting of driver mutations in glioma"

Q&A: 14.15 – 14.25

14.25 – 14.35

Aviyah Peri Weizmann Institute of Science, Israel
Proffered Paper 1: “Combined presentation and immunogenicity analysis reveals a recurrent RAS.Q61K neoantigen in melanoma”

Q&A: 14.35 – 14.40

14.40 – 14.50

EXHIBITOR INTRODUCTIONS

14.50 – 15.20

Coffee Break & Exhibition

15.20 – 15.40

Johanna Olweus Oslo University, Norway
"Cancer immunotherapy: Targeting shared neoantigens with T-cell receptors"

Q&A: 15.40 – 15.50

15.50 – 16.10

Kornelia Polyak Harvard Medical School, USA
(presenting remotely)
“Mutated epigenetic regulators in breast cancer"

Q&A: 16.10 – 16.20
16.20 – 16.30  **Felix Dietlein** Boston Children's Hospital, USA
Q&A: 16.30 – 16.35
Proffered Paper 2: “Genome-wide identification of somatic mutation events in whole genomes of 19 major cancer types”

16.35 – 16.45  **POSTER SPOTLIGHTS**
*Posters 1, 25 & 53 will be presented in short ‘flash talks’ of 3 minutes each.*

16.45 – 17.15  **MEET THE EXPERT**
**Mireia Crispin-Ortuzar** University of Cambridge, UK
An informal session where Mireia will share her own personal and professional experiences of her path to scientific leadership.

17.15 – 18.15  **WELCOME RECEPTION**
*Drinks reception with buffet served from 17:35.*

18.15 - 19.45  **POSTER DISCUSSION SESSION 1**
*Presenters of odd numbers stand by their posters.*

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**Day 2 - Wednesday 06 July**

08.15 – 08.45  **POSTER VIEWING** with coffee and biscuits

08.45 – 09.00  **INDUSTRY SPOTLIGHT - QIAGEN**
**Abraham Iwakun** QIAGEN, UK
“Introduction to Digital PCR”

**SESSION 2: DNA METHYLATION**
Chair: Elaine Mardis

09.00 – 09.20  **Carlos Caldas** CRUK CI, Cambridge, UK
Q&A: 09.20 – 09.30
“DNA methylation landscapes of breast cancer - What have we learned that is new?”

09.30 – 09.50  **THE EMBO KEYNOTE LECTURE**
**Amos Tanay** Weizmann Institute of Science, Israel
Q&A: 09.50 – 10.00
“From single cells to tissue dynamics in blood ageing and cancer immunity”

10.00 – 10.10  **Andrew Erickson** University of Helsinki, Finland
Q&A: 10.10 – 10.15
Proffered Paper 3: “The spatial landscape of clonal somatic mutations in benign and malignant tissue”
10.15 – 10:45  
☕ COFFEE BREAK & EXHIBITION

SESSION 3: DATA INTEGRATION
Co-Chairs: Elaine Mardis & Carlos Caldas

10.45 – 11.05  
Kevin Litchfield  University College London, UK
Q&A: 11.05 – 11.15
"Non-classical sources of tumour specific antigen in checkpoint inhibitor response"

11.15 – 11.35  
Mireia Crispin-Ortuzar  University of Cambridge, UK
Q&A: 11.35 – 11.45
"More is different: radiogenomic data integration to predict treatment response"

11.45 – 11.55  
POSTER SPOTLIGHTS
Posters 14, 40 and 70 will be presented in short ‘flash talks’ of 3 minutes each.

11.55 – 12.25  
INDUSTRY SYMPOSIUM - STANDARD BIOTOOLS
Stephen Knight  Field Application Specialist
"Setting the new benchmarks in automated and cost-effective qPCR and NGS assays: Meet the Biomark X and Juno"

12.25 – 13.25  
🔍 LUNCH & EXHIBITION

13.25 – 14.55  
POSTER DISCUSSION SESSION 2
Presenters of even numbers stand by their posters.

SESSION 4: CTDNA/GENOMIC INSTABILITY
Chair: Yardena Samuels

14.55 – 15.15  
James Brenton  CRUK CI, Cambridge, UK
Q&A: 15.15 – 15.25
"Predicting response to treatment for women with high grade serous ovarian carcinoma"

15.25 – 15.45  
Dan Landau  WCM/NYGC, New York, USA
Q&A: 15.45 – 15.55
"Machine learning guided signal enrichment for ultrasensitive plasma tumor burden monitoring"

15.55 – 16.05  
James Black  UCL Cancer Institute, UK
Q&A: 16.05 – 16.10
Proffered Paper 4: "Genomic-transcriptomic evolution in TRACERx Lung Cancer and Metastasis"

16.10 – 16.40  
☕ COFFEE BREAK & EXHIBITION
16.40 – 17.00  
**Nitzan Rosenfeld** University of Cambridge, UK  
“Expanding roles of liquid biopsies for cancer diagnostics”

**Q&A: 17.00 – 17.10**

17.10 - 17.20  
**Andrea Degasperi** University of Cambridge, UK  
Proffered Paper 5: “Cancer mutational signatures in the UK population and how to use them”

**Q&A: 17.20 – 17.25**

17.25 – 18.25  
**MEET THE SCIENTIFIC PROGRAMME COMMITTEE**  
Carlos Caldas, James Brenton, Elaine Mardis, Yardena Samuels  
*Our esteemed Scientific Programme Committee will come together to each provide insight into their personal and professional experiences of their routes into scientific leadership.*

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19.30  
**OPTIONAL CONFERENCE DINNER**

at the conference venue’s own restaurant ‘Taylors Yard’  
*For those who have purchased tickets [sold-out].*

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**Day 3 - Thursday 07 July**

08.15 - 08.45  
**POSTER VIEWING** with coffee and biscuits

08.45 - 09.00  
**INDUSTRY SPOTLIGHT - THERMO FISHER SCIENTIFIC**

**Elena Guerini Rocco** IRCCS, Italy  
“Characterization of Breast Cancer Immune Microenvironment: Focus on DCIS and Cancers During Pregnancy”

**SESSION 5: SINGLE CELL/SPATIAL ANALYSIS**

Chair: Carlos Caldas

09.00 – 09.20  
**Leeat Keren** Weizmann Institute of Science, Israel  
“Unraveling the tumor immune microenvironment by multiplexed imaging”

09.30 – 09.50  
**Nicola Aceto** ETH Zurich, Switzerland (recorded talk)  
“Biology and Vulnerabilities of Circulating Tumor Cells”

09.50 – 10.30  
**COFFEE BREAK & EXHIBITION**

10.30 – 10.50  
**Sam Aparicio** BC Cancer Research Institute, Canada  
“Decoding foreground mutational processes and drug resistance at single genome resolution”

11.00 – 11.10  
**Yaara Oren** Tel Aviv University, Israel  
Proffered Paper 6: “Cycling cancer persister cells arise from lineages with distinct programs”
CLOSING KEYNOTE

Elaine Mardis  Institute for Genomic Medicine, USA
“Pediatric CNS Malignancies at Single-Cell and Digital Spatial Profiling Resolution”

SUMMARY & DEPART

EACR-Worldwide Cancer Research Meeting Bursary Awards

More information about EACR bursaries: eacr.org/meeting-bursary

EACR-Worldwide Cancer Research Meeting Bursaries 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 Meeting Bursaries for this conference. Each winner received a full registration free of charge and funds of up to €500 to assist with the cost of travel and accommodation.

- James Black  UK
- Kate Eason  UK
- Ana Regina de Abreu  Belgium
- Berkcan Dogan  Turkey
- Carolina Di Benedetto  USA
- Joe Ibrahim  Belgium
- James Smith  Australia
1. EACR Reception Desk
2. Ground Floor: Exhibition & Posters
   Upper Floor: Lecture Theatre
3. Taylors Yard Restaurant
Exhibition & Poster Area Floorplan

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**Exhibitors**

1. Oxford Nanopore Technologies
2. QIAGEN
3. Purigen Biosystems
4. Thermo Fisher Scientific
5. Stratech
6. Standard BioTools
7. Don Whitley Scientific
8. Active Motif
9. Nonacus
10. COVARIS
11. PerkinElmer
12. Agena Bioscience
13. 2BScientific
14. PCR Biosystems
15. Immudex

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EACR Conference on Cancer Genomics
Oxford, UK | 05 - 07 July 2022
Meet the Exhibitors

**Oxford Nanopore Technologies**  
*Stand: 1*  
*Website:* nanoporetech.com  
*Represented at the conference by:* Danielle Folkard, Rachel Hipkin, Gerald Goh, Anna Dysko

**QIAGEN**  
*Stand: 2*  
*Website:* www.qiagen.com  
*Represented at the conference by:* Abraham Iwakun, Akshay Acharya, Syed Abedi  
*Spotlight:* Wednesday 06 July 2022 | 08.45-09.00  
Abraham Iwakun: “Introduction to Digital PCR”

**Purigen Biosystems**  
*Stand: 3*  
*Website:* www.purigenbio.com  
*Represented at the conference by:* Aziz Mustafa, Alex Stretton

**Thermo Fisher Scientific**  
*Stand: 4*  
*Website:* www.thermofisher.com  
*Represented at the conference by:* Jack Phillips, Naomi Bruckshaw  
*Spotlight:* Thursday 07 July 2022 | 08.45-09.00  
Elena Guerini Rocco: “Characterization of Breast Cancer Immune Microenvironment: Focus on DCIS and Cancers During Pregnancy”

**Statech**  
*Stand: 5*  
*Website:* www.stratech.co.uk  
*Represented at the conference by:* Adam Stanley, Sital Patel

**Standard BioTools** (formally Fluidigm)  
*Stand: 6*  
*Website:* www.fluidigm.com  
*Represented at the conference by:* Priscilla Lo, James Curtis, Stephen Knight, Niki Wason  
*Symposium:* Wednesday 06 July 2022 | 11.55-12.25  
Stephen Knight: “Setting the new benchmarks in automated and cost-effective qPCR and NGS assays: Meet the Biomark X and Juno”
Don Whitley Scientific  Stand: 7
Website:  www.dwscientific.com | Represented at the conference by: Paul Harrison, Stuart Moore

Active Motif  Stand: 8
Website:  www.activemotif.com
Represented at the conference by: Anne-Sophie Berthomieu

Nonacus  Stand: 9
Website:  nonacus.com
Represented at the conference by: Karen Cook, Anthony Faulkes, Chris Sale

COVARI S  Stand: 10
Website:  www.covaris.com | Represented at the conference by: Richard Willis

PerkinElmer  Stand: 11
Website:  www.perkinelmer.com
Represented at the conference by: Anona Bamford

Agena Bioscience  Stand: 12
Website:  www.agenabio.com
Represented at the conference by: Carlo Bottari

2BScientific  Stand: 13
Website:  www.2bscientific.com
Represented at the conference by: Rasikh Raza

PCR Biosystems  Stand: 14
Website:  pcrbio.com | Represented at the conference by: Rachael Roberts, Sophie Osborn

Immudex  Stand: 15
Website:  www.immudex.com
Represented at the conference by: José Guerra, Henrik Pfundheller

Media Partner:  Molecular Oncology

Keynote Lecture Sponsor:  EMBO
1 [POSTER SPOTLIGHT] Tumour clonal dynamics measured in 1093 plasma samples from lung TRACERx predicts metastatic competency of subclones before surgery Presented by Alexander Frankell, Francis Crick Institute, London, UK | University College London, London, UK

2 Analysis of the Effect of MBL2 Alterations on the Microbiota of Uterine Corpus Endometrial Carcinoma: An In silico study Presented by Bayan Abu Alragheb, School of Medicine, The University of Jordan, Amman, JORDAN

3 Annihilation of micrometastases by vascular targeted photodynamic therapy with immunomodulation Presented by Lilach Agemy, Weizmann Institute of Science, Rehovot, ISRAEL

4 Using RAD51 foci, in circulating cancer cells to determine relapse / remission in ovarian cancer (OC) patients on treatment Presented by Zena Alizzi, Brunel University, Uxbridge, UK | Mount Vernon Cancer Centre, Northwood, UK

5 Identification of disease specific dependence and tumour suppressor genes through comparative analysis of B-Cell derived malignancies using a novel bioinformatic approach Presented by Hande Atasoy, Newcastle University Bioscience Institute, Newcastle Upon Tyne, UK

6 Finding tumour microenvironment drivers of gene expression using spatial transcriptomics integrated in a microfluidics workflow Presented by Jamie Auxillos, The Bioinformatics Centre, Department of Biology and Biotech Research and Innovation Center (BRIC), University of Copenhagen, DENMARK

7 Development and validation of a Breast Cancer Purity Signature (BCPS) to improve bulk transcriptomics data interpretation and prognostic performance Presented by Marco Barreca, Michelangelo Foundation, Milan, ITALY

8 9p arm loss is an important predictor of immune evasion in several human cancers Presented by Joy Bianchi, NYU Langone Hospital, New York, USA

9 Activation of the branching morphogenesis programme marks aggressive lung adenocarcinomas Presented by Kamila Bienkowska, School of Cancer Sciences, University of Southampton, Southampton, UK

10 Global profiling of extrachromosomal circular DNA in pancreatic ductal adenocarcinomas Presented by Julie Boertmann Noer, Department of Biology, University of Copenhagen, Copenhagen, DENMARK

11 Longitudinal transcriptomics in ER+/HER2+ breast cancer patients enrolled in the NA-PHER2 neoadjuvant trial: study of treatment induced dynamics and prediction of response Presented by Maurizio Callari, Michelangelo Foundation, Milan, ITALY

12 Impact of Sex-Related Differences on Susceptibility, Prognosis and Therapy of Head and Neck Squamous Cell Carcinoma Presented by Cristina Conde-Lopez, Radiooncology/Radiobiology, German Cancer Research Center (DKFZ), Heidelberg, GERMANY
13 Genomic tumour evolution in neoadjuvant treated HER2-positive breast cancer
Presented by Nicola Cosgrove, Genomic Oncology Research Group, Department of Physiology and Medical Physics, RCSI University of Medicine and Health Sciences, Dublin, IRELAND

14 [POSTER SPOTLIGHT] Intercellular extrachromosomal DNA copy number heterogeneity drives phenotypic diversity in cancer cells
Presented by Maja-Celine Cwikla, Berlin Institute for Medical Systems Biology at the Max Delbrück Center for Molecular Medicine in the Helmholtz Association, Berlin, GERMANY | Charité - Universitätsmedizin Berlin, Berlin, GERMANY

15 Multi-omic characterization of T-cell populations at the single-cell level utilizing sensitive dCODE Dextramer® reagents on the BD Rhapsody™ Single-Cell Analysis System
Presented by José Costa Guerra, Immudex, Copenhagen, DENMARK

16 Evaluation of whole-genome DNA (hydroxy)methylation sequencing methods as a biomarker discovery tool in cancer
Presented by Ana Regina de Abreu, Center of Medical Genetics, University of Antwerp and Antwerp University Hospital, Edegem, BELGIUM

17 A Novel Super-Enhancer-Regulated Gene Is Linked To Poor Prognosis And Therapy Resistance In Breast Cancer
Presented by Carolina Di Benedetto, University of California San Francisco, San Francisco, CA, USA

18 In Silico Investigation of Cancer Biomarkers Induced by Smoking-Associated Salivary Microbiome Alterations
Presented by Berkcan Dogan, Bursa Uludag University, Bursa, TURKEY

19 Distinct p53 hotspot mutations differentially regulate immune composition and immunotherapy response in breast cancer
Presented by Danique E.M. Duits, Oncode Institute, Utrecht, NETHERLANDS | Netherlands Cancer Institute, Amsterdam, NETHERLANDS

20 A cellular model for extrachromosomal circular DNA (eccDNA) in cancer genomes
Presented by Weijia Feng, University of Copenhagen, Copenhagen, DENMARK

21 Application of circulating cell free DNA (cfDNA) as a prognostic biomarker for ovarian cancer.
Presented by Alice Filipe, College of Health, Medicine and Life Sciences, Brunel University London, , Uxbridge, UK

22 Dissecting regulatory mechanism of TCF3-PBX1 positive pediatric acute lymphocytic leukemia with multi-omics data
Presented by Wanwan Ge, MPI-MG, Berlin, GERMANY

23 Identifying epigenetic drivers of breast cancer stem cells and their associated phenotypes
Presented by Mariana Gomes da Silva Araujo, International Agency for Research on Cancer, Lyon, FRANCE

24 A comprehensive comparison framework of known prostate cancer molecular subtypes
Presented by Valeriia Haberland, University of East Anglia, Norwich, UK
25 **[POSTER SPOTLIGHT]** Breast cancer subtype dynamics in reconstructed temporally-resolved copy number profiles Presented by Katherine Eason, Department of Oncology, Cancer Research UK Cambridge Institute and Cancer Centre, Cambridge, UK

26 Cell cycle G1/S transition gene variation and prostate cancer risk
Presented by Márk Híveš, Department of Medical Biochemistry, Jessenius Faculty of Medicine in Martin, Comenius University in Bratislava, Slovakia, Martin, SLOVAK REPUBLIC

27 Simultaneous analysis of DNA variation and mRNA expression of oxysterol-related genes and the miRNome in early-stage luminal breast cancer Presented by Petr Holý, Third Faculty of Medicine, Charles University, Prague, CZECH REPUBLIC | Toxicogenomics Unit, National Institute of Public Health, Prague, CZECH REPUBLIC

28 FGFR3-TACC3 fusion protein drives cell migration, lower differentiation state and enhanced calcium signaling response in glioblastoma Presented by Laura Huhtala, Faculty of Medicine and Health Technology, Tampere University, Tampere, FINLAND | TAYS Cancer Center, Tampere University Hospital, Tampere, FINLAND

29 Genome-wide DNA methylation profiling and identification of potential pan-cancer and tumor-specific biomarkers Presented by Joe Ibrahim, Center of Medical Genetics & Center for Oncological Research, University of Antwerp and Antwerp University Hospital, Edegem, BELGIUM

30 An indel-based Naïve Bayesian methodology for classifying homologous recombination deficiency in exome sequenced breast cancers Presented by Daniel Jacobson, UCL Genetics Institute & Cancer Institute, London, UK

31 Mesotheliomas harbour early clonal fusions involving both tumor suppressor drivers and novel oncogenic alterations Presented by Maymun Jama, University of Leicester, Leicester, UK

32 Identification of differently expressed genes in estrogen metabolism and signaling pathway associated with the risk of prostate cancer Presented by Jana Jurečeková, Comenius University in Bratislava, Jessenius Faculty of Medicine in Martin, Department of Medical Biochemistry, Martin, SLOVAK REPUBLIC

33 Genome-wide copy number analysis identifies AKT as new therapeutic target for malignant pleural mesothelioma Presented by Claudia Kalla, Dr. Margarete Fischer-Bosch Institute of Clinical Pharmacology, Stuttgart, GERMANY | Eberhard Karls University, Tuebingen, GERMANY

34 BRAF V600E Levels in Blood Cells, Plasma, and Urine as a Marker of Disease Burden in Langerhans Cell Histiocytosis. A Patient-Specific ctDNA Analysis. Presented by Robert Khashan, Sahlgrenska Center for Cancer Research, University of Gothenburg, Gothenburg, SWEDEN | Wallenberg Centre for Molecular and Translational Medicine, Gothenburg, SWEDEN
35 Association between variations in cell cycle genes (CDK2, CCNE1 and p27KIP1) and prostate cancer risk. Presented by Monika Kmetová Sivoňová, Jessenius Faculty of Medicine in Martin, Comenius University in Bratislava, Department of Medical Biochemistry, Martin, SLOVAK REPUBLIC

36 Copy-number load and heterogeneity for predicting tumor progression and patient outcome in early-stage colorectal cancer. Presented by Sara Lahoz, Institut D’Investigacions Biomèdiques August Pi i Sunyer (IDIBAPS), Barcelona, SPAIN | Hospital Clinic de Barcelona, Barcelona, SPAIN

37 Copy number-aware deconvolution of tumor-normal DNA methylation profiles unlocks unique insights into non-small cell lung cancer. Presented by Elizabeth Larose Cadieux, The Francis Crick Institute, London, UK | University College London Cancer Institute, London, UK

38 ASCAT v3: towards a robust and platform-independent CNA caller. Presented by Tom Lesluyes, The Francis Crick Institute, London, UK

39 EGFR T790M in treatment naive lung cancer samples of patients who developed T790M positive relapse. Presented by Weiting Li, Department of Pathology and Medical Biology & Department of Genetics, University of Groningen, University Medical Centre Groningen, Groningen, NETHERLANDS

40 [POSTER SPOTLIGHT] Refining the liquid biopsy: generating more data from cell-free DNA for early cancer diagnostics and research. Presented by Jane Hayward, Cambridge Epigenetix, Cambridge, UK

41 Establishment of a robust pan-cancer classifier analysis pipeline based on DNA methylation. Presented by Daniel Lipka, Division of Translational Medical Oncology & Section Translational Cancer Epigenomics, German Cancer Research Center (DKFZ) & National Center for Tumor Diseases (NCT), Heidelberg, GERMANY

42 Circadian rhythms of cortisol, -amylose and cytokines of osteosarcoma pediatric patients undergoing chemotherapy in relation to healthy controls. Presented by Luis Carlos Lopes-Júnior, Universidade Federal do Espírito Santo, Vitoria, ES, BRAZIL

43 The use of Multinational Association for Supportive Care in Cancer (MASCC) risk index score and its impact on the length of inpatient stay. Presented by Geetin Majhail, Milton Keynes University Hospital, Milton Keynes, UK

44 Landscape of pharmacogenomic associations in breast cancer Patient-Derived Tumour Xenografts. Presented by Riccardo Masina, Cancer Research UK Cambridge Institute and Department of Oncology, Cambridge, UK

45 Multi-omics analysis in matched primary, recurrent and metastatic osteosarcoma to find novel therapeutic targets. Presented by Debora Meijer, Leiden University Medical Center, Leiden, NETHERLANDS | Leiden Center for Computational Oncology, LUMC, Leiden, NETHERLANDS
46 Genetic inactivation of transcriptional repressor ATF7IP: functional analysis in lung cancer Present by Juan Morillas Viñuales, Josep Carreras Leukaemia Research Institute (IJC), Badalona. Barcelona, SPAIN

47 Methylation differences between colorectal normal tissue, adenoma and carcinoma have great potential to become important new biomarkers in the clinic Present by Isabelle Neefs, Centre of Medical Genetics Antwerp, Edegem, BELGIUM | University of Antwerp, Wilrijk, BELGIUM

48 Potential of mRNA Variables in Prediction of Poor Prognosis Prostate Cancer Present by Autumn O’Donnell, University College Cork, Cork, IRELAND

49 Evaluating potential genomic biomarkers for immunotherapy response in lung and bladder tumors Present by Ana Oitabén, Translational Molecular Oncology Unit. IIS Galicia Sur. SERGAS-UVIGO. Álvaro Cunqueiro Hospital, Vigo, SPAIN | Genomes & Disease Lab. CiMUS (USC), Santiago de Compostela, SPAIN

50 HBV-mediated genomic rearrangements and their impact on the origins of hepatocellular carcinoma Present by Paula Otero Sanchez, Center for Research in Molecular Medicine and Chronic Diseases (CiMUS) & Department of Zoology, Genetics and Physical Anthropology, Universidade de Santiago de Compostela, Santiago de Compostela, SPAIN

51 [Abstract withdrawn]

52 Comprehensive genomic analysis of ALK-rearranged non-small cell lung cancer Present by Hansol Park, Graduate School of Medical Science and Engineering, Korea Advanced Institute of Science and Technology, Daejeon, SOUTH KOREA

53 [POSTER SPOTLIGHT] Reconstructing the evolutionary timeline of immunoediting from early to late stage lung cancer Present by Sonya Hessey, University College London Cancer Institute, London, UK | CRUK Lung Cancer Centre of Excellence, London, UK

54 The contribution of cancer-associated fibroblasts in immune evasion of homologous recombination deficient cancers Present by Su Myat Phy, University of Oxford, Oxford, UK

55 Individualised circulating tumour DNA analysis as a biomarker of treatment response in paediatric acute lymphoblastic leukaemia Present by Fani Pujol-Calderon, Sahlgrenska Center for Cancer Research, Department of Paediatrics, Institute of Clinical Sciences, Sahlgrenska Academy & Wallenberg Centre for Molecular and Translational Medicine, University of Gothenburg, Gothenburg, SWEDEN

56 Involvement of specific clusters of immune cells in tissues adjacent to hepatocellular carcinoma revealed by single-cell transcriptomics Present by Pauline Robbe, RIKEN Center for Integrative Medical Sciences, Yokohama, JAPAN
57 Chemotherapy curability in leukaemia, lymphoma, germ cell tumours, gestational malignancies and the rare childhood cancers reflects the unique physiology and epigenetics of their cells of origin. Presented by Philip Savage, Brighton and Sussex University Hospitals, Brighton, UK.

58 Establishing the clinical and pathogenic significance of Sin3B spliced variant in Oral Squamous Cell Carcinoma. Presented by Sakshi Sharma, Dr. B. R. Ambedkar Center for Biomedical Research, Delhi, INDIA.

59 Comprehensive omics analysis of intrahepatic and extrahepatic cholangiocarcinoma identifies distinct biological subclasses. Presented by Marco Silvestri, Department of Applied Research and Technological Development, Fondazione IRCCS Istituto Nazionale dei Tumori di Milano, Milano, ITALY.

60 Non-canonical NFαB signalling and ETS1 cooperativity is required for TWEAK driven invasion in Glioblastoma. Presented by Nicholas Sim, Nanyang Technological University, School of Biological Sciences, Singapore, SINGAPORE.

61 Single-cell RNA sequencing identifies common components of the dormant tumour cell niche across metastatic tissues. Presented by James T. Smith, Bone Biology Laboratory, Garvan Institute of Medical Research, Sydney, NSW, AUSTRALIA | Faculty of Medicine, St Vincent’s Clinical School, Sydney, NSW, AUSTRALIA.


63 Epigenetic mechanisms at the origins of childhood Central Nervous System tumors: from birth to diagnosis. Presented by Natalia Spitz, Epigenomics and Mechanisms Branch, International Agency for Research on Cancer, Lyon, FRANCE.

64 Analysis of ccfDNA and ccfRNA markers of prostate cancer progression and therapy failure in liquid biopsy samples. Presented by Eva Szczyrbová, Department of Clinical and Molecular Pathology, Palacký University Olomouc, Olomouc, CZECH REPUBLIC.

65 The compartment-specific spatial transcriptomic landscape of 3D cultured Gleason 7 prostate cancer. Presented by Vithurran Thavarajah, UCL Division of Surgery & Interventional Science, University College London, London, UK.

66 Gatekeeper inactivation is driving tumor progression to secondary glioblastoma. Presented by Aliisa M. Tiihonen, Prostate Cancer Research Center, Faculty of Medicine and Health Technology, Tampere University and Tays Cancer Center, Tampere University Hospital, Tampere, FINLAND.
67 The interrelation of polyploidy, circadian clock deregulation and embryonal stemness in the development of treatment-resistant malignant tumours Presented by Ninel Miriam Vainshelbaum, Latvian Biomedical Research and Study Centre, Riga, LATVIA

68 The role of structural variation: both 1q gain and CTNNB1/WT1-mutated Wilms tumors show Wnt pathway activation Presented by Ianthe A.E.M. van Belzen, Princess Maxima center for Pediatric Oncology, Utrecht, NETHERLANDS

69 Elucidating immune regulatory mechanisms of PI3K alterations in breast cancer Presented by Antoinette van Weverwijk, Netherlands Cancer Institute, Amsterdam, NETHERLANDS | Oncode Institute, Utrecht, NETHERLANDS

70 [POSTER SPOTLIGHT] Intra-prostatic tumour evolution and steps in metastatic spread revealed by integration of multi-region whole genome sequencing with histopathological features Presented by Srinivasa Rao, Nuffield Dept. of Surgical Sciences, University of Oxford, Oxford, UK

71 Genomic hallmarks of cancer cell quiescence and therapeutic implications Presented by Anna Julia Wiecek, University College London, London, UK

72 Overlapping miRNA cargo profiles of extracellular vesicles released by different colorectal cancer cell subpopulations Presented by Zoltán Wiener, Semmelweis University, Department of Genetics, Cell and Immunobiology, Molecular Cancer Biology Research Group, Budapest, HUNGARY

73 Inhibition of phosphodiesterase 4D as a mechanism to suppress GNAS mutated colorectal cancers Presented by Sadia Zafar, Applied Tumor Genomics Research Program, Research Programs Unit, University of Helsinki, Helsinki, FINLAND
EACR on-site team

Chris Iliffe
Conference Officer

Kathryn Wass
Programmes Manager

Andrew Binns
Membership Manager

Ola Olotu
Membership Coordinator

Conference Dinner

Optional Ticketed Event, Wednesday 06 July, 19:30 CEST - SOLD OUT

The Conference Dinner will take place on the final night of the meeting at the conference venue’s own restaurant - Taylors Yard. It will be an excellent opportunity for participants and speakers to get to know each other in a relaxed and informal environment. A three course meal will be served, with wine (or alternative) and coffee included in the ticket price.

See the campus map on page 8 for directions
EACR Industry Partners

The European Association for Cancer Research gratefully acknowledges our Industry Partners, who offer ongoing support to the EACR and provide the means for the Association to develop important initiatives.