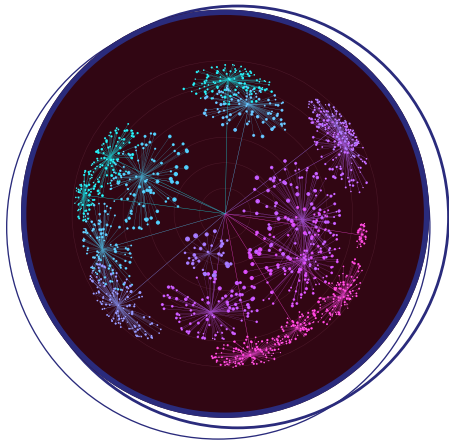




3RD INTERNATIONAL SPATIAL BIOLOGY CONGRESS

THE HAGUE, NETHERLANDS
THE HAGUE CONFERENCE CENTRE

11-12 July 2024



[#spatialbiologycongress](#)

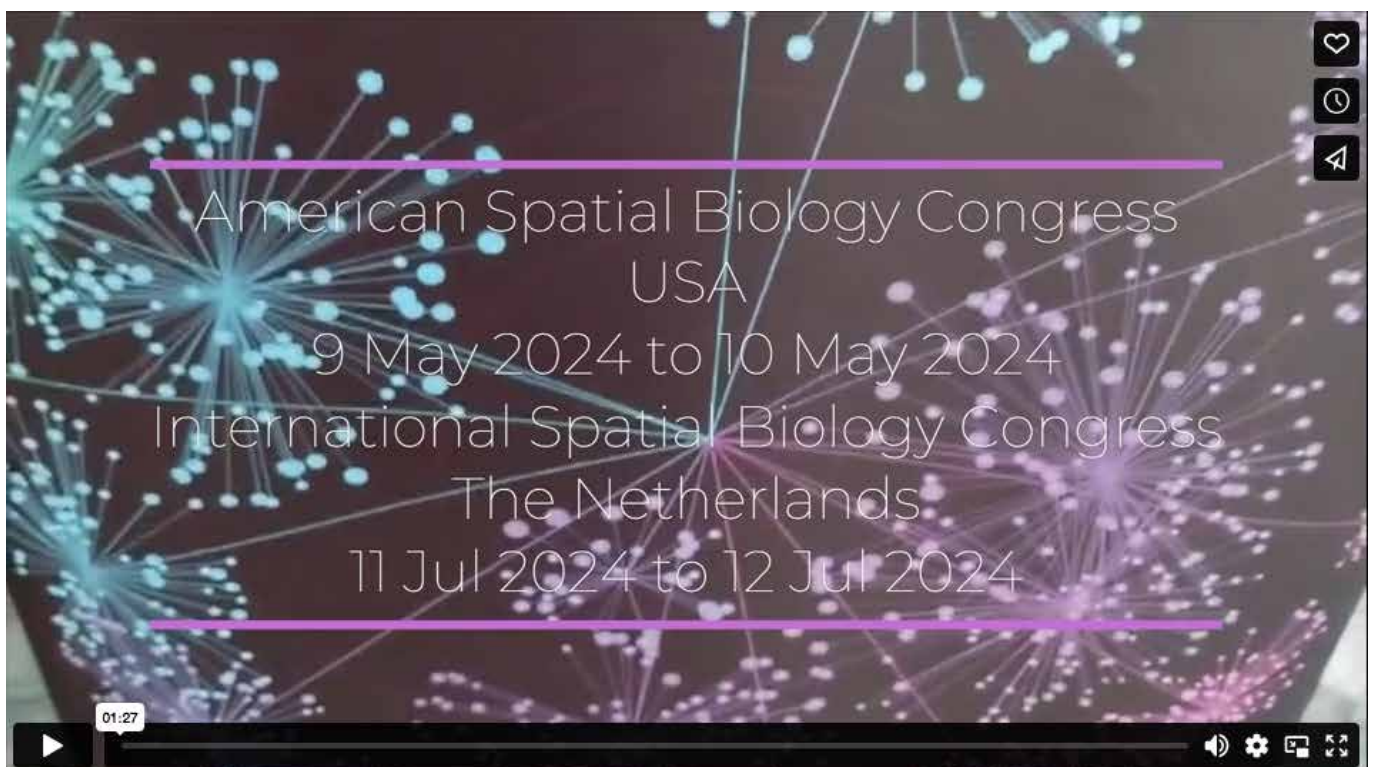
www.global-engage.com



Global Engage is pleased to announce the **3rd International Spatial Biology Congress: Europe**, which is confirmed to be held on 11-12 July 2024 in The Hague, Netherlands.

In this rapidly developing field, spatial biology provides significant potential for creating novel clinical insights. Recent technological advancements in spatial biology have provided insights into new strategies to prevent and treat disease, particularly the interactions between the tumour and the tumour microenvironment in cancers to target patients to more specific treatments. New spatial research has focused more on the analysis of the transcriptome, epigenome, and metabolomics as well as gene and protein expression to discover how these influence cellular and molecular distributions and interactions.

With a single track over two days, featuring more than 30 presentations, you will discover the latest developments in spatial omics and techniques, bioinformatics, and spatial biology data analysis, as well as the application of spatial biology to disease and drug development. There will also be a dynamic exhibition room filled with providers showcasing their spatial technologies with ample networking opportunities, an inclusive panel discussion, roundtables, and a poster competition.



Spatial multiomics techniques and approaches

- Spatial genomics and proteomics
- Spatial transcriptomics, metabolomics and epigenomics
- Single cell analysis
- Combining omics data and technologies
- Transitioning from a 2D to a 3D perspective

Analysis and interpretation of spatial data, bioinformatics, and computational tools

- Data standardization
- Computational platforms
- Bioinformatics
- Tissue imaging and analysis using AI

Application of Spatial Biology in translational and clinical medicine

- Oncology
- Tumour microenvironment
- Personalised medicine
- Biomarker identification and diagnostics

Panel Discussion

- Spatial Biology Data Analysis, Standardisation and Storage
- Applying Spatial Biology to drug development

Roundtables

- Challenges with spatial biology data standardisation and analysis
- Spatial Biology beyond cancer- how spatial biology is applied to other disease areas
- Role of AI in Spatial Biology

	Track 1
Day 1	Spatial multiomics techniques and approaches Analysis and interpretation of spatial data, bioinformatics, and computational tools
Day 2	Application of spatial biology in translational and clinical medicine



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CONFIRMED & RESERVED SPEAKERS



FRANCESCA CICCARELLI
Professor of Cancer Genomics,
Principal Group Leader, King's College
London, The Francis Crick Institute



NIGEL JAMIESON
Professor of Surgery and Consultant
HPB Surgeon, Group Leader of Jamieson
Spatial Laboratory, Cancer Research
UK Clinician Scientist, School of Cancer
Sciences, University of Glasgow



PHILIP MAINI
Statutory Professor of Mathematical
Biology, University of Oxford



CHRIS HANLEY
Lecturer in Quantitative Cell Biology,
University of Southampton



DANA MUSTAFA
Assistant Professor and Leader of the
Spatial Biology Laboratory, Erasmus
University Medical Center



ELEANOR O'ROBERTS
Researcher, SciLifeLab



FANI MEMI
Senior Staff Scientist, Wellcome
Sanger Institute



KONSTANTIN MAK SIN
Locum Consultant Cellular Pathologist,
Royal Berkshire NHS Foundation Trust



MENGXIAO HE
Doctoral Researcher, KTH Royal
Institute of Technology



MIAO-PING CHIEN
Associate Professor and Principal
Investigator, Erasmus University
Medical Centre, Oncode Institute



STEPHANIE CRAIG
Lecturer in Precision Medicine,
Queen's University Belfast



THIERRY VOET
Professor and Director, KU Leuven
Institute of Single Cell Omics



VICTOR PEREZ
Postdoctoral Researcher at Schapiro
Laboratory, Heidelberg University
Hospital



VOLKER BRUNS
Group Manager Medical Image
Processing, Fraunhofer IIS



ANDERS ERIKSSON
Lead Field Application Scientist,
Canopy Biosciences



BRIAN REICHHOLF
Principal Scientist, Boehringer
Ingelheim



DEBAYAN MUKHERJEE
Investigator- Spatial Imaging, Oncology
Translational Research, GSK



HENRIK FAILMEZGER
Associate Director, Spatial Data
Science, AstraZeneca



LORENZ ROGNONI
Director of Image Data Science, Ultivue



MARC CLAESEN
Chief Executive Officer, Aspect
Analytics NV



ROBERTO SPADA
Director of Marketing, Standard BioTools



TIANKUI PENG
Senior Application Scientist,
SeekGene Biosciences



SENIOR REPRESENTATIVE
Lunaphore



SENIOR REPRESENTATIVE
(Reserved)
Sanofi



CHRISTOPH KUPPE
Professor, RWTH Aachen University



FRANCESCA TRAPANI
Molecular Pathology Laboratory Head,
Boehringer Ingelheim

8:50-9:00

Global Engage Welcome Address

**KEYNOTE ADDRESS:
NIGEL JAMIESON**

Professor of Surgery and Consultant HPB Surgeon, Group Leader of Jamieson Spatial Laboratory, Cancer Research UK Clinician Scientist, School of Cancer Sciences, University of Glasgow

Insights from molecular mapping of gastrointestinal cancer across space and time

Studying clinical cohorts using spatial transcriptomics technologies offers the potential to impact our understanding of patient's tumours. Our central hypothesis is single-cell spatial characterisation will reveal therapeutic vulnerabilities not apparent when studying immune cell populations without spatial context. We aim to unravel the spatial interplay between cancer cells, and microenvironment as determinants of tumour progression across a variety of GI cancers including pancreatic and colorectal cancers. We have characterised large cohorts of human GI cancers using regional and single-cell transcriptomics strategies in the primary and metastatic setting in effort to better understand the impact of treatment and disease progression.

9:00-9:30

**KEYNOTE ADDRESS:
FRANCESCA CICCARELLI**

Professor of Cancer Genomics, Principal Group Leader, King's College London, The Francis Crick Institute

Topic TBC

9:30-9:55

**LORENZ ROGNONI**

Director of Image Data Science, Ultivue

Advancing Precision Oncology through AI-Enhanced Spatial Image Analysis and Multiplex Assays

The tumour microenvironment (TME) is a complex and dynamic mix of cancer and immune cells, significantly influencing tumour progression, metastasis, and therapeutic response. Comprehensive understanding of TME is crucial for developing effective precision oncology therapies.

Innovations in computational pathology and artificial intelligence (AI), combined with advanced multiplex biomarker assays, are pivotal in this endeavour. In this presentation, we will discuss how Ultivue's InSituPlex[®] assays and AI-enabled spatial image analysis platform STARVUETM deliver scalable and accurate insights. We will highlight the application of deep learning to transform multiplex immunofluorescence (mIF) data into actionable insights, showcasing Ultivue's 12-plex assay and its capacity to provide a detailed view of TME. This integration of AI and mIF gives scientists a look into the tumour microenvironment by better characterizing the unique cancer cell populations, spatial relationships, and differences in immune responses.



9:55-10:25

10:25-11:35

Morning Refreshments / One-to-One Meetings / Poster Presentations

SPATIAL MULTI-OMICS TECHNIQUES & APPROACHES

**THIERRY VOET**

Professor and Director, KU Leuven Institute of Single Cell Omics

Methods and applications for spatial multi-omics

- Methods for spatial transcriptomics and other modalities
- Integration of Multiple Spatial Omics Modalities
- Spatial biology in health and disease

11:35-11:55

**MIAO-PING CHIEN**

Associate Professor and Principal Investigator, Erasmus University Medical Centre, Onco Institute

Microscopy-based functional & spatial single cell sequencing

Our lab has developed microscopy-based functional single-cell sequencing (FUNseq) and analysis technologies, which can be applied to subtype heterogeneous populations of cells and link tumorigenic phenotypes to causative genotypes. FUNseq can be combined with single-cell genome, transcriptome and proteome profiling, providing a comprehensive understanding of cellular dynamics. In this talk, I will delve into the application of FUNseq technology in profiling subpopulations of cancer cells displaying different dynamic phenotypes of interest, particularly aberrant cell mitosis associated with chromosomal instability. We have also expanded the technology to enable spatial profiling of tumor cells with deep scRNAseq and single cell resolution. I will elaborate on how we applied this method to profile cells situated in different spatial locations in cell monolayers as well as tissue slices.

11:55-12:15

**MARC CLAESEN**

Chief Executive Officer, Aspect Analytics NV

Dedicated Software to Support High Throughput Spatial Multi Omics Applications

Spatial omics technologies enable detailed molecular analyses from tissue sections. In parallel, multi-omics approaches combining different omics levels to obtain a holistic view are increasingly in demand. However, spatial multi-omics studies can generate hundreds of gigabytes of complex data, creating a daunting bioinformatics task. Dedicated software for the management, integration, and QC of spatial multi-omics is required. Aspect Analytics provides software enabling spatial multi-omics research across a range of techniques and user bases. Our platform supports a variety of spatial applications, e.g. different spatial transcriptomics platforms, multiplexed antibody detection, and classical histopathology. Our software can extract maximal knowledge from data, scale up for high-throughput applications, provide integrated data management, reporting capabilities and more, bridging the gap between bioinformatics research and development, and enterprise-grade platforms.



12:15-12:30

**ANDERS ERIKSSON**

Lead Field Application Scientist, Canopy Biosciences

Precise spatial multiplexing with ChipCytometry: An open-source solution to high-throughput spatial biology

- Spatial biology is an interdisciplinary field examining the spatial organization of biological entities in ecosystems, merging genomics, imaging, and computational biology.
- Recent advancements in spatial biology leverage innovative technologies, enabling precise visualization and analysis of biological processes.
- ChipCytometry, a novel highly multiplexed technology, preserves both spatial context and multiplexing, allowing deep profiling of immune cell diversity at single-cell resolution, aiding in understanding the immune system's role in cancer progression.



12:30-12:45

**BRIAN REICHHOLF**

Principal Scientist, Boehringer Ingelheim

The role of multimodal spatial data in translational research

In addition to classical approaches such as immunohistochemistry and in situ hybridisation, recent advances such providing multiplexed stainings and tissue-based transcriptomics provide many different angles of analysing the same physical tissue sample. At Boehringer Ingelheim we are increasingly using multiple modalities and intersecting these to add value to our projects and inform our clinical trial strategies. Here, we will provide an overview of our approaches and how we see different spatial approaches providing novel insights into our translational research strategy.

12:45-13:05





13:05-14:05

Lunch


POSTER COMPETITION WINNER TALK:

If interested in submitting a poster and/or applying to present a poster on the programme, please [CLICK HERE](#) and apply before the deadline 21st June 2024.


14:05-14:20



14:20-14:40	 <p>ELEANOR O'ROBERTS Researcher, SciLifeLab Unlocking Cellular Complexity Through Multiplexed Immunofluorescence - the Spatial Proteomics Unit at SciLifeLab Spatially resolved omics technologies have emerged in recent years and have undoubtedly changed the way we understand the spatial organization of complex multicellular biological systems. The aim of the Spatial Proteomics unit is to do full-service multiplexed immunofluorescence projects covering discovery, translational and diagnostic research questions. In the unit we offer two main technologies: the Phenocycler-Fusion from Akoya Biosciences uses conjugated antibodies detected in cycles by addition of fluorescent reporters; and the COMET from Lunaphore uses off-the-shelf antibodies in sequential rounds of immunofluorescence. Both these methodologies allow us to run targeted spatial proteomics analysis of up to 40 markers at single cell level in tissue sections. Furthermore, the unit also works on method development and implementation of new services such as isPLA and multiomics analysis.</p>	
14:40-14:55	 <p>ROBERTO SPADA Director of Marketing, Standard BioTools High-plex whole slide spatial biology assays powered by the Hyperion XTi Introducing Hyperion XTi, a revolutionary Imaging Mass Cytometry System. 5x faster detection, unparalleled sensitivity for dim markers, walk-away flow cytometry, and new imaging modes. Ultra-fast whole slide imaging and intelligent ROI selection redefine high-throughput cytometry.</p>	
14:55-15:10	 <p>SENIOR REPRESENTATIVE Lunaphore</p>	


ANALYSIS AND INTERPRETATION OF SPATIAL DATA, BIOINFORMATICS, AND COMPUTATIONAL TOOLS


15:10-15:30	 <p>VOLKER BRUNS Head of Medical Image Analysis group, Fraunhofer IIS Do it yourself - Programming-free Spatial Proteomics Image Analysis for Biologists The analysis of multiplexed immunofluorescence scans does not have to be difficult and does not have to involve programming. In his talk, Volker will walk through a typical cell typing and spatial analysis of a proteomics scan step by step and explain challenges as well as different options. A focus will lie on the MIKAlA software, developed by the Medical Image Analysis (MIA) research group of Fraunhofer IIS. This cross-vendor analysis solution seeks to enable biologists to carry out these quantitative analyses themselves, without having to rely on a bioinformatician.</p>	
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15:30-16:20 Afternoon Refreshments / One-to-One Meetings / Poster Presentations

16:20-16:40	 <p>EARLY CAREER RESEARCH PRESENTATION: MENGXIAO HE Doctoral Researcher, KTH Royal Institute of Technology Early Career Researcher Presentation: Single-tissue section transcriptomics profiling</p> <ul style="list-style-type: none"> An approach combining spatially resolved transcriptomics and single nuclei RNA sequencing from a single tissue section, enhancing molecular insights into tissue architecture. Demonstrated effectiveness using mouse brain tissue sections and application on human breast cancer specimens, showcasing the method's versatility and potential in medical research. Comprehensive analysis of archival FFPE tissue sections, addressing current challenges in spatial transcriptomics, cell type identification, and constraints posed by rare or limited tissue availability. 	
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16:40-17:10	 <p>CHRISTOPH KUPPE Professor, RWTH Aachen University Decoding spatially regulated disease drivers in human heart and kidney disease This presentation focuses on decoding spatially regulated disease drivers within human heart and kidney diseases using MERFISH. Utilizing a multimodal data approach, the interplay of molecular mechanisms governing disease progression is explored. Cutting-edge methodologies such as spatial transcriptomics and single-cell sequencing are discussed and how they can be used to unravel the spatial heterogeneity underlying pathology. Through novel data analysis and integration approaches, key spatially defined biomarkers and regulatory networks can be identified and validated using high-throughput in-vitro screening approaches. Insights gained pave the way for a deeper understanding of disease etiology and progression, offering promising targets for cardiac and renal disorders.</p>	
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17:10-17:30	 <p>EARLY CAREER RESEARCH PRESENTATION: VICTOR PEREZ Postdoctoral Researcher at Schapiro Laboratory, Heidelberg University Hospital Building an analysis pipeline for antibody-based multiplexed images</p> <ul style="list-style-type: none"> Reproducibility and scalability in analysis pipelines. Orchestrating the variety of algorithms applied in multiplexed images. Integration of new modules/algorithms into pipelines with nf-core 	
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17:30-17:50	 <p>STEPHANIE CRAIG Lecturer in Precision Medicine, Queen's University Belfast Help, my image is haunted: how to reduce image artefacts in your multiplex immunofluorescent research</p> <ul style="list-style-type: none"> How to validate your MIF protocol to avoid unwanted guests Good housekeeping - the importance of continued QA/QC following assay validation Minimise Impact - Computational methods to overcome inherent MIF-dependent image bias 	
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17:50-18:10	 <p>HENRIK FAILMEZGER Associate Director, Spatial Data Science Spatial heterogeneity of cancer associated protein expression in immunohistochemically stained images as an improved prognostic biomarker In oncology it is crucial to determine the expression of biomarkers that can help to stratify patients into potential responders vs. non-responders. The status of these biomarkers is typically scored visually by a pathologist, mostly without considering the spatial heterogeneity of the protein's expression in the tissue. We present two novel image analysis-based approaches for quantitative scoring of spatial marker expression heterogeneity. The first approach is based on a co-occurrence analysis of the marker expression in neighboring cells. The second approach accounts for the local variability of the protein's expression by tiling the tissue and assigning local heterogeneity phenotypes per tile. We apply our scores to quantify the spatial expression of HER2, CMET, CD44, and EGFR in immunohistochemically stained tissue sections of colorectal cancer.</p>	
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18:10 End of Day / Networking Drinks Reception

8:50-9:00

Global Engage Welcome Address

9:00-9:30

**KEYNOTE ADDRESS:****PHILIP MAINI**

Statutory Professor of Mathematical Biology, University of Oxford

Mathematical Modelling of Solid Tumours

We use mathematical modelling to understand how cancerous tumours grow and invade their surrounding tissue, with a view to elucidating the underlying mechanisms that give rise to various collective cell behaviours. Here, I will present some modelling we have done using the hypothesis that phenotypic switching and co-operation may enhance tumour invasion. I will also present modelling work on how adaptive therapy may enhance treatment of certain cancers.

9:30-9:55

**DEBAYAN MUKHERJEE**

Investigator- Spatial Imaging, Oncology Translational Research, GSK

Application of Spatial Multiplex Imaging in Oncology and Biomarker research

- Application of Spatial Imaging in Pre-clinical and Translational Oncology Research
- Multi-modal approach in Oncology research
- Improving Robustness and Reproducibility for Multiplex Imaging and Spatial analysis

9:55-10:25

**TIANKUI PENG**

Senior Application Scientist, SeekGene Biosciences

Commercialized Spatial Transcriptomics at Physical Single-Cell Level: Mapping Expression to Location

SeekSpace, a spatial single-cell technology developed by SeekGene Biosciences, offers a novel approach to spatial transcriptomics. By utilizing spatial labels and position probes, single cells are accurately marked and dissociated into individual states before being processed through the SeekOne® DD system for cell labeling. This process results in the creation of separate single-cell transcriptome libraries and spatial libraries, facilitating the integration of single-cell transcriptomes with spatial positional information. SeekSpace achieves physical single-cell resolution, providing precise characterization of cell types and states while mitigating RNA cross-contamination. Moreover, it enables simultaneous detection of gene expression and spatial positioning on the same tissue slice. Notably, SeekSpace streamlines experimental procedures by eliminating the need for determining tissue permeabilization conditions, offering a user-friendly approach to spatial omics research.



10:25-11:35

Morning Refreshments / One-to-One Meetings / Poster Presentations

11:35-12:25

PANEL DISCUSSION:**Applying Spatial Biology to drug development****DANA MUSTAFA** (Moderator)

Assistant Professor and Leader of the Spatial Biology Laboratory, Erasmus University Medical Center

**DEBAYAN MUKHERJEE**

Investigator- Spatial Imaging, Oncology Translational Research, GSK

11:35-12:25

ROUNDTABLE DISCUSSION:**ROUNDTABLE 1****FRANCESCA TRAPANI**

Molecular Pathology Laboratory Head, Boehringer Ingelheim

12:25-12:55

30-Minute Solution Provider Presentation
For sponsorship opportunities contact Gavin Hambrook
gavin@globalengage.co.uk

12:55-13:55

Lunch

APPLICATION OF SPATIAL BIOLOGY IN TRANSLATIONAL AND CLINICAL MEDICINE

13:55-14:10

POSTER COMPETITION WINNER TALK:

if interested in submitting a poster and/or applying to present a poster on the programme, please [CLICK HERE](#) and apply before the deadline 21st June 2024.

14:10-14:30

**CHRIS HANLEY**

Lecturer in Quantitative Cell Biology, University of Southampton

Fibroblast heterogeneity drives disease progression and therapy resistance in multiple solid cancers

- This presentation will cover recent work in lung and oral cancers integrating single-cell, spatial and bulk tissue transcriptomics
- Spatial co-localisation was found between distinct fibroblast subpopulations and different states of epithelial differentiation in lung cancer.
- Novel fibroblast subpopulations were identified in oral cancers associated with discrete immunological niches from immune hot and cold tumours

14:30-14:50

**FANI MEMI**

Senior Staff Scientist, Wellcome Sanger Institute

Mapping the rules of glioblastoma using single cell and spatial genomics

14:50-15:10

**KONSTANTIN MAK SIN**

Locum Consultant Cellular Pathologist, Royal Berkshire NHS Foundation Trust

Endothelial S100 protein as a novel assessment tool of doubtful cases "dysplasia vs invasive cancer" in cervical pathology

Anti-S100 antibody is not currently applicable in routine histopathology practice as an immunohistochemistry (IHC) marker of tumour vascularity. However, there is evidence of its high potential as a helpful tool in tumour growth evaluation and differentiation between in-situ and invasive lesions with S100-protein positive endothelial cells identification. Two types of malignant lesions, squamous cell carcinoma (SCC) and adenocarcinoma (AC), of the cervix were stained by anti-S100 antibody. The morphological appearance of SCC was covered up by intensive inflammatory processes, on the other hand, the AC morphological appearance was difficult to differentiate between adenocarcinoma in-situ and early invasive stage. The expression of S100 protein in the endothelial cells of tumour vessels revealed significant differences in non-neoplastic, in-situ and invasive forms. The highest expression of S100 protein was observed in the invasive forms which allowed to distinguish it from in-situ changes and to define the direction of tumour spreading. Anti-S100 antibody has high potential in tumour vascularity and invasiveness evaluation, particularly in doubtful cases. However, this IHC method requires clarification due to overlapping with other S100-positive cells, probably through the co-staining with using additional endothelial markers, such as CD31 or CD34.

15:10-15:30

SENIOR REPRESENTATIVESanofi
Topic TBC

15:30

End of Conference

POSTER PRESENTATIONS**MAKING A POSTER PRESENTATION**

Poster presentation sessions will take place in breaks and alongside the other breakout sessions of the conference. Your presentation will be displayed in a dedicated area, with the other accepted posters from industry and academic presenters. We also issue a poster eBook to all attendees with your full abstract in and can share your poster as a PDF after the meeting if you desire (optional). Whether looking for funding, employment opportunities or simply wanting to share your work with a like-minded and focused group, these are an excellent way to join the heart of this Congress. In order to present a poster at the forum you need to be registered as a delegate. Please note that there is limited space available and poster space is assigned on a first come first served basis (subject to checks and successful registration).

MAKING A POSTER PRESENTATION

We will require the form to be submitted by the 21st June 2024. This is the formal deadline however space is another limiting factor so early application is recommended. Therefore, please contact us with any questions you have as soon as possible.

POSTER COMPETITION - CLOSING DATE 21st June 2024

1. Submit your entry prior to the closing deadline (1 entry per person)
2. Two entries for the 3rd International Spatial Biology Congress: Europe will be selected by the judges
3. The 2 winners of the poster presentation will be each be given a 15-minute speaking position on the conference agenda and will be notified in advance of the meeting
4. The judge(s) will make the decision based on the abstract(s) submitted
5. The winner will also receive a certificate from the organisers
6. Representatives from solution provider organisations or experts already speaking on the program are not eligible to enter the competition but are welcome to present posters at the meeting as normal



SUSTAINABILITY

Venues with Sustainability Goals

We are committed to selecting venues with more sustainable practices. These will cover energy supply, food & waste, water use, recycling and plastics.

Catering

You will have some great food choices while you are with us. We have worked with the caterer to increase the proportion of plant-based items. We have also built a plan with the venue to avoid waste through how they serve meals and how any leftovers are processed. Our aim is that you have some great meals, whilst with us, but with less environmental impact by the time you leave.

Travel

An international meeting does involve travel but where it is practical, please consider more sustainable alternatives to flying. The app will also have a discussion space to arrange ride shares.

