



STOC General Meeting

29 - 30 June

2026

Cascina Triulza, Milan, Italy



Sponsors

BGI·Tech **MGI** **STOmics**



WARM WELCOME

We are pleased to welcome you to STOC General Meeting 2026. This meeting brings together leading experts, collaborators, and partners from across the global spatiotemporal omics community to exchange ideas, share progress, and explore new opportunities for collaboration. Whether you are joining us as a contributor or exploring participation, we hope this agenda provides a clear view of the discussions and outcomes we aim to achieve together.

ORGANIZING COMMITTEE

- Ido Amit
- Jan Mulder
- Mathias Uhlen
- Piero Carninci
- Quan Nguyen
- Xun Xu

CONFERENCE THEMES

- Spatial Technologies and Data Analysis
- Spatial Biology in Cancer
- Spatial Biology in Neuroscience

CONFIRMED SPEAKERS



Ao CHEN,
Senior Vice President,
MGI, China



Jiwoon PARK
Researcher,
Cornell University,
USA



Ziqing DENG
Director,
BGI Research Beijing,
China



Jovan TANEVSKI
Group Leader,
Heidelberg University,
Germany



Lijiang FEI
Postdoc fellow,
Cambridge Stem Cell
Institute, UK



Mathias UHLEN
Professor, SciLifeLab,
KTH Royal Institute of Technology,
Sweden



Mark FIERS
Assistant Professor,
KU Leuven,
Belgium



Yanhong WANG
R&D Director, BGI Tech, China



Florent GINHOUX
Laboratory Director,
Gustave Roussy, France



Keke XIA
Chief Scientist,
State Key Laboratory of Genome
and Multi-omics Technologies,
BGI Research,
China



Jia Hui KHOO
Senior Product Manager
EUAF, MGI, Germany



Kerstin MEYER, Senior
Director, Respiratory,
Immunology and
Inflammation Research
Unit, GSK, UK

Speakers are listed in alphabetical order by last name

CHAIRS, PANELLISTS, CO-LEADS & WORKSHOP LEADERS



Ido AMIT

Professor, Weizmann
Institute of Science,
Israel



Jiwoon PARK

Researcher,
Cornell University,
USA



Piero CARNINCI

Head of Genomics,
Human Technopole &
Team Director,
RIKEN, Italy



Jan MULDER

Researcher, Karolinska
Institute, Sweden



Nicola CROSETTO

Senior Manager,
Human Technopole,
Italy



Xun XU

BGI Chief Scientist,
Director of State Key
Laboratory of Genome
and Multi-omics
Technologies, BGI
Research, China



Lipin LOO

Group Leader,
Programmable Biology,
Charles Perkins Centre,
The University of
Sydney, Australia



Quan NGUYEN

Head Genomics and
Machine Learning Lab,
Director Centre for
Immunospatial Tissue
Intelligence, University of
Queensland, Australia

Speakers are listed in alphabetical order by last name

Leveraging Multi-Omics to Accelerate Discovery

As a world-leading life science research service platform, BGI Tech has deepened its roots in the research services sector for nearly 20 years, remaining dedicated to delivering one-stop end-to-end multi-omics big data solutions to scientists worldwide.

📍 Headquarter: Shenzhen (China)

📍 Laboratories: Warsaw (Poland), Wuhan (China) and Hong Kong (China)

100+

Countries & Regions

7,000+

Collaborating Partners

40,000+

Clients Served

Sequencing Services

- ▶ Single-Cell Sequencing
- ▶ Spatial Transcriptome
- ▶ Whole Genome Resequencing
- ▶ De Novo Sequencing
- ▶ Metagenome
- ▶ Transcriptome
- ▶ Whole Genome Bisulfite Sequencing

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Mass Spectrometry Services

- ▶ Quantitative Proteome
- ▶ Nanoproteome
- ▶ Metaproteome
- ▶ PTM Proteome
- ▶ Untargeted Metabolome
- ▶ High-Throughput Targeted Metabolome
- ▶ Lipidome

.....

Multi-Omics Services

- ▶ Single-Cell RNA-seq+ Spatial Transcriptome
- ▶ Single-Cell RNA-seq+ Bulk RNA-seq
- ▶ Transcriptome+Proteome+ Metabolome
- ▶ Metagenome/16S+Metabolome
- ▶ Dr. Tom Visualization System

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Contact Us

✉ info@bgi.com

🌐 www.bgi.com/global

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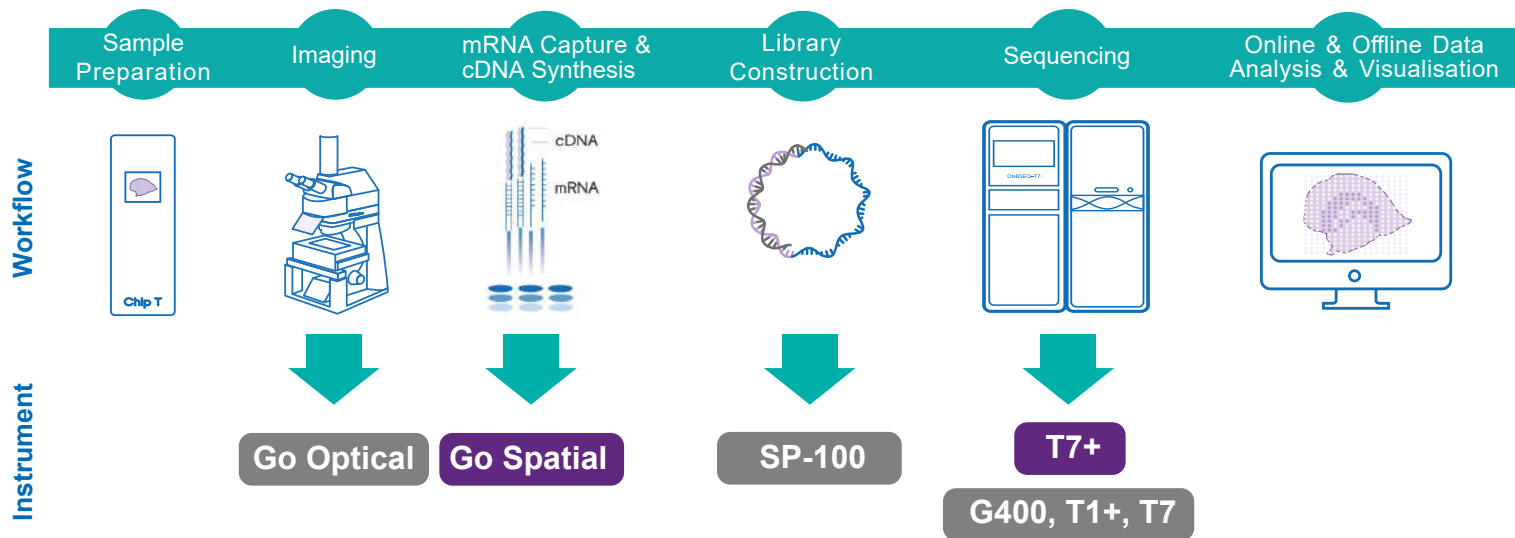


One workflow. Every Spatial Insights.

MGI Tech now delivers a fully integrated spatial transcriptomics pipeline, from tissue imaging through automated library preparation to high-throughput DNBSEQ™ sequencing.

This complete workflow enable reproducible, end-to-end spatial biology at true single-cell resolution.

The Complete Spatial Multi-Omics Platform at True Single-Cell Resolution



Go Optical

High-Resolution Microscope Designed for Stereo-seq



- 12-megapixel super-resolution imaging
- Scanning range of 100 mm x 70 mm
- Auto-focus detection function

Go Spatial-V2-24

Automation System for Sample Preparation for Stereo-seq



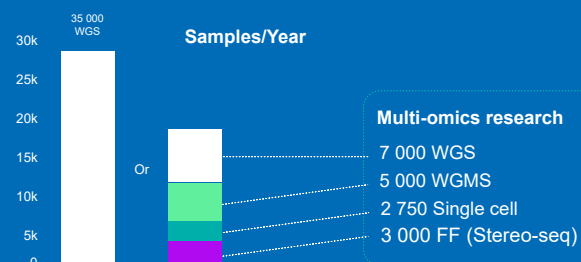
- Fully automated solution for post-imaging sample preparation
- Compatible for FF and FFPE workflow
- From mRNA capture to cDNA product
- High-throughput up to 12 reactions

T7+

Ultra-High-Throughput Sequencer



- Keep your current protocols
- Sequence mixed library types in the same run
- Support multi-omics research



Spatial Clarity. Unlimited Discovery.

Stereo-seq — The Complete Spatial Multi-Omics Platform

Single-Cell Resolution

Scalable Field of View

Species Agnostic

True Multi-Omics

Stereo-seq SOLUTIONS

Stereo-seq Transcriptomics FF V1.3

Sample Type: Fresh Frozen

Detection: mRNA

Staining: ssDNA / H&E / mIF

Chip Sizes: 0.5 cm × 0.5 cm / 1 cm × 1 cm

Key Highlights: 500 nm nanoscale resolution; mRNA & protein co-detection (mIF).

Stereo-seq OMNI V1.1

NEW!

Sample Type: FFPE

Detection: Coding and Non-coding RNA

Staining: ssDNA / H&E

Chip Sizes: 0.5 cm × 0.5 cm / 1 cm × 1 cm

Key Highlights: 1×–3× higher capture efficiency & 2× data usability; enhanced diffusion control.

Stereo-CITE Proteo-Transcriptomics

Sample Type: Fresh Frozen

Detection: mRNA + Protein (100+ markers)

Staining: DAPI

Chip Sizes: 1 cm × 1 cm

Key Highlights: Highly multiplexed (100+) protein co-detection; ideal for studying tissue heterogeneity in complex diseases.

Stereo-seq Large Chip Designs (LCD)

Sample Type: Fresh Frozen / FFPE (coming soon)

Detection: mRNA

Staining: ssDNA / H&E

Chip Sizes: 1 cm × 2 cm / 2 cm × 2 cm / 2 cm × 3 cm

Key Highlights: Supports whole-organ profiling and co-embedded tissue sections for high-throughput parallel experiments.

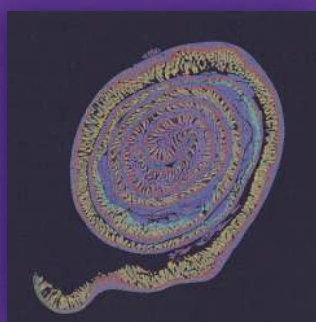
Stereo-seq OMNI V1.1 DEMO DATA



Whole-Organ Developmental Profiling

Sample: Rat Embryo (E12)

High-resolution spatial mapping of intricate developmental structures and whole-organ architecture.



Complex Tissue Microenvironment

Sample: Mouse Small Intestine

Precise spatial clustering revealing the distinct layers and cellular heterogeneity of the intestinal spiral structure.

CREDIBILITY & CONTACT

500+ Peer-Reviewed Publications — Empowering global spatial biology research with discoveries published in top-tier journals:

[Nature](#) • [Cell](#) • [Science](#) • [Cancer Cell](#) • [Neuron](#)

Manufactured by

STOmics

Reach out to us to learn more:

Email: info_global@stomics.tech

Website: <https://en.stomics.tech/>



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STOmics X



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MGI Website

DAY 1 CONGRESS SCHEDULE

Welcome & STOC Vision Recap

8:30-9:15



Quan Nguyen, Head Genomics and Machine Learning Lab, Director Centre for Immunospacial Tissue Intelligence, University of Queensland, Australia



Xun Xu, BGI Chief Scientist, Director of State Key Laboratory of Genome and Multi-omics Technologies, BGI Research, China

STOC Working Group Progress & European Perspectives

9:15-10:15



Ido Amit, Professor, Weizmann Institute of Science, Israel



Jan Mulder, Researcher, Karolinska Institute, Sweden

10:15-10:45

Coffee break/Networking

Spatial Technologies and Data Analysis

Chairperson: Quan Nguyen, Head Genomics and Machine Learning Lab, Director Centre for Immunospacial Tissue Intelligence, University of Queensland, Australia

10:45-11:15



Jiwoon Park, Researcher, Cornell University, USA

Consortium Science, AI Integration, and the Path to Clinical Spatial Omics

The rapid maturation of spatial omics technologies has created an unprecedented opportunity to map human tissue architecture at single-cell resolution. Yet realizing this potential demands coordinated, large-scale efforts that go beyond any single lab or platform. In this talk, I present the Spatial Atlas of Human Anatomy (SAHA), a global consortium building standardized, clinical-grade spatial reference atlases across multiple organs and technology platforms. I discuss the consortium's organizational architecture, cross-platform harmonization strategies across technologies such as CosMx, Xenium, and MERFISH, and our approach to multi-scale data integration from subcellular to tissue level. I then describe how AI and computational tools, including hierarchical multi-modal cell typing, automated marker-driven classification, and the STAMP analysis platform, serve as the engine enabling atlas construction at this scale. Finally, I show how reference atlases translate into clinical impact through SPOT-Met, a 1,000-patient spatial transcriptomics and proteomics study predicting metastatic organotropism in colorectal cancer. Together, these efforts illustrate a roadmap from consortium-scale atlas building to AI-powered clinical spatial omics.

11:15-11:45



Jovan Tanevski, Group Leader, Heidelberg University, Germany

Context-Aware Framework for Multimodal Integration and Tissue Dynamics

Spatial omics provides detailed molecular snapshots of tissues, but integrating these into a coherent, functional view remains challenging. We present a computational framework for context-aware tissue modeling using Optimal Transport and Flow Matching. This approach bridges static data, disparate modalities, and temporal progression, offering a scalable path to decode how cellular environments drive biological function. We map cellular information across modalities to enrich molecular coverage and spatial resolution, including imputing unmeasured markers and reconstructing continuous cell states. We then align datasets across samples while preserving local tissue architecture and extend the model temporally to infer cellular trajectories constrained by signaling and neighborhood context. The framework provides a path to reconstruct dynamic, context-aware maps of tissue organization and function.

DAY 1 CONGRESS SCHEDULE

Platinum Partner Presentation



Yanhong Wang, R&D Director, BGI Tech, China

Spatial Multi-Omics at Scale: BGI's Solutions for Deciphering Tissue Ecosystems

11:45-12:00

The advent of spatially resolved transcriptomics has transformed our understanding of tissue organization, yet capturing both cellular resolution and molecular coverage remains challenging. Here, we present BGI's Stereo-seq technology, a spatially resolved transcriptomics platform that achieves nanoscale resolution combined with centimeter-level field of view. We demonstrate how Stereo-seq, integrated with single-cell RNA sequencing and multi-omics approaches, enables comprehensive mapping of cellular ecosystems, dissection of cell-cell communication networks, and identification of spatially restricted molecular niches. Through case studies in development and disease, we illustrate analytical frameworks that leverage these integrated modalities to uncover biologically contextual insights. Our discussion highlights how Stereo-seq-based multi-omics solutions accelerate translational research and precision medicine applications.

12:00-13:00

Lunch Welcome Reception

Spatial Biology in Cancer

Chairperson: Ido Amit, Professor, Weizmann Institute of Science, Israel



Lijiang Fei, Postdoc fellow, Cambridge Stem Cell Institute, UK

From Development to Disease: Multi-omic Atlases of Human Skeletal Development and Endocrine Regulation

13:00-13:30

Multi-omic atlases provide a powerful framework for understanding how cellular states, regulatory programs and signalling environments are established in human tissues, and how these processes may be altered in disease. In this talk, I will present approaches integrating single-cell multi-omics and spatial profiling to map human developmental and systemic signalling landscapes. In human embryonic skeletal development (5-11 weeks), we define spatially resolved osteoprogenitor trajectories and regulatory networks underlying intramembranous and endochondral ossification and uncover progenitor zonation using in situ sequencing. These data further enable links to disease through genetic perturbation modelling and trait association. Extending beyond development, we construct a cross-tissue Human Hormone Cell Atlas to map hormone production and responses across human tissues, revealing underappreciated endocrine signalling in immune cells for viral infection. Together, these atlases highlight how multi-omic integration can resolve cell states, tissue context and inter-tissue communication relevant to development, disease and cellular plasticity.

13:30-14:00



Florent Ginhoux, Laboratory Director, Gustave Roussy, France

Tumor Macrophage Heterogeneity

Platinum Partner Presentation



Jia Hui Khoo, Senior Product Manager EUAF, MGI, Germany

Go Spatial: Automation Meets Total, Unbiased Insight at Centimeter-Scale FOV

14:00-14:20

Stereo-seq enables unbiased, whole-transcriptome spatial gene expression profiling using DNA nanoball arrays, delivering single-cell resolution at unprecedented scale. MGI's Go Spatial is a powerful, robust automation system that streamlines sample preparation through a fully automated post-imaging workflow, processing samples from RNA capture to cDNA with minimal hands-on time across both fresh frozen (FF) and FFPE workflows. It can process up to 12 cm² of FF tissue or 8 cm² of FFPE tissue per day. Stereo-seq OMNI Large Chip Design expands spatial analysis to centimeter-scale fields of view, enabling high-efficiency profiling of larger and more complex tissues. The FFPE Tissue Transfer Device streamlines tissue transfers onto Stereo-seq chips, enhancing workflow simplicity and reliability. Together, Go Spatial and early access to the latest Stereo-seq innovations deliver next-generation spatial profiling with unmatched automation, scalability, and precision.

DAY 1 CONGRESS SCHEDULE

Spatial Biology in Neuroscience

Chairperson: Jan Mulder, Researcher, Karolinska Institute, Sweden



Mark Fiers, Associate Professor, VIB Center for Brain and Disease, KU Leuven, Belgium

Spatial Transcriptomics Dissects the Neuroinflammatory Inflection Point in Alzheimer's Disease

14:20-14:50

Alzheimer's disease is a dynamic process in which cell state response to amyloid- β , including neuroinflammation and the induction of Tau phosphorylation and aggregation, drive disease progression rather than a fixed consequence of pathology. We profiled the superior frontal cortex using single-nucleus transcriptomics integrated with Visium and Xenium spatial transcriptomics in octogenarians and centenarians with and without dementia. Multimodal computational integration defined six Tissue Domains that map a spatial continuum of pathology. A key inflection point separated amyloid-linked inflammatory programs from tau-associated cellular states. This transition coincided with a shift in microglial phenotypes from early inflammatory to late antigen-presenting plaque-induced gene programs. Resilience showed distinct molecular signatures: dementia-free octogenarians lacked late PIGs, while centenarians exhibited late PIG activation, but uncoupled from tau. These results position microglial state transitions at the amyloid-tau interface as tractable targets for intervention.

14:50-15:20

Coffee break & Networking

STOC Updates

Chairperson: Xun Xu, BGI Chief Scientist, Director of State Key Laboratory of Genome and Multi-omics Technologies, BGI Research, China



Ziqing Deng, Director, BGI Research Beijing, China

STOC Infection: Advancement and Future Directions of the STOC Infection Working Group

15:20-15:40

Co-chaired by Professors George Fu Gao and Andrea Cossarizza, the STOC Infection Working Group comprises 54 researchers from 39 institutions across 14 countries. By bringing together international experts in microbiology, immunology, molecular biology, bioinformatics, and biological mapping, we aim to accelerate mechanistic research on infectious diseases and optimize prevention and treatment strategies through the application of spatiotemporal omics technologies. The STOC Infection Working Group was formally established with an inauguration ceremony in September 2025 in Beijing, China. At the International Symposium on Spatiotemporal Omics for Infectious Diseases 2025 (ISSOID 2025), our group members exchanged the latest progress on spatiotemporal omics in infectious diseases. In the future, we will strive to advance the implementation of international large-scale scientific initiatives to decipher the pathogen-host interaction mechanisms of major infectious diseases.



Keke Xia, Chief Scientist, State Key Laboratory of Genome and Multi-omics Technologies, BGI Research, Beijing

STOC Plant: Building the Plant Comprehensive Spatiotemporal Cellular Big Data to Drive Smart Breeding

15:40-16:00

This report will highlight the rapid expansion and strategic vision of the STOC Plant consortium since 2024. By uniting an expansive international network of scientists, the consortium champions a "Big Science" model to democratize spatial omics technologies and establish comprehensive, open-access foundational databases. A flagship initiative is the pioneering Wheat Spatiotemporal Atlas Project, which maps the crop's entire life cycle at single-cell resolution to address critical food security challenges. Ultimately, STOC Plant aims to extend these multi-omics atlases across major staple crops, leveraging massive spatiotemporal datasets to construct AI-driven "Virtual Plant Cells" and pioneer a new era of in silico smart breeding for climate-resilient agriculture.

DAY 1 CONGRESS SCHEDULE

Working Group Breakout Sessions

Spatial Omics Tools and Technologies

Working Group Leader:



Nicola Crosetto
Senior Manager,
Human
Technopole, Italy

16:00-17:45

In this work group session, the participants can expect a focused discussion on efforts to standardize oligo-based FISH probe design and establish validated reference probe sets, enabling more consistent, scalable, and comparable spatial transcriptomics across platforms.

Infectious Diseases & Cancer

Working Group Leader:



Ido Amit
Professor,
Weizmann Institute
of Science, Israel

In this work group session, the participants will identify the major knowledge gaps and the opportunities to bridge these gaps with spatial omics approaches. The focus will be on pan-disease approach to extract both disease-specific and shared pathological processes. These efforts should overall improve diagnostics, patient stratification and increase treatment options for patients.

Neuroscience & Diseases of the Brain

Working Group Leader:



Jan Mulder
Researcher,
Karolinska
Institute, Sweden

In this work group session, the participants will identify what is needed to understand the brain and how spatial omics approaches could provide these insights. They will decide on flagship projects that require global collaborative efforts that can be achieved with currently available resources and can be completed in the next 5 years.

End of Day 1

DAY 2 CONGRESS SCHEDULE

8:30-9:00 Registration | Morning Coffee

Chairperson: Jan Mulder, Researcher, Karolinska Institute, Sweden

Spotlight Session



Mathias Uhlen, Professor, SciLifeLab, KTH Royal Institute of Technology, Sweden

The Human Protein Atlas - Creating an Open Access Pan-disease Blood Atlas Based on Next Generation Blood Profiling

9:00-10:00

As part of the Human Protein Atlas (www.proteinatlas.org), we present the creation of an open access resource to allow the exploration the protein profiles in blood across patients in a pan-disease manner (www.proteinatlas.org). We have performed comprehensive analysis of blood from patients across 60 diseases using a multiplex assay allowing high sensitivity and specificity based on "next generation blood profiling". Several proteins correlating with age, sex, BMI and diseases were identified. The analyzed protein levels are visualized together with differential expression results based on patients diagnosed with a particular disease and compared to (i) a cohort of healthy individuals, (ii) all other diseases and (iii) all other diseases within the same class.

Innovation and Industry (Academic/Commercial Partnerships)

10:00-10:20



Ao Chen, Senior Vice President, MGI, China

TBD

10:20-10:40



Kerstin Meyer, Senior Director, Respiratory, Immunology and Inflammation Research Unit, GSK

Cell Atlases and Spatial Technologies in R&D at GSK

- Why do we want to use single cell and spatial transcriptomics (SpTx) ?
- Cross modality data integration to support the drug discovery pipeline
- In house capabilities of single cell & SpTx at GSK and what does the ideal technology look like?
- Data landscape being generated at GSK
- An example of target discovery in hepatology

Working Group Breakout Reconnect Sessions

Spatial Omics Data Analysis

Working Group Leaders:



Quan Nguyen
Head Genomics and Machine Learning Lab,

Director Centre for Immunospacial Tissue Intelligence, University of Queensland, Australia,

10:40-11:10

In this work group session, the participants identify technical and practical needs and will decide on STOC action plan to facilitate global collaborative efforts in the field of spatial omics.

Infectious Diseases & Cancer

Working Group Leader:



Ido Amit
Professor, Weizmann Institute of Science, Israel

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DAY 2 CONGRESS SCHEDULE

11:10-11:40 Coffee break & Networking

Working Group Breakout Sessions

Spatial Omics Data Analysis

Working Group Leader:



Lipin Loo
Group Leader,
Programmable
Biology, Charles
Perkins Centre, The
University of
Sydney, Australia

11:40-13:30

In this work group session, the participants identify technical and practical needs and will decide on STOC action plan to facilitate global collaborative efforts in the field of spatial omics.

Infectious Diseases & Cancer

Working Group Leader:



Ido Amit
Professor,
Weizmann Institute
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13:30-14:30 Lunch

Chairperson: Ido Amit, Professor, Weizmann Institute of Science, Israel

Panel Discussion

Building a Sustainable Global Spatio-Temporal Omics Ecosystem

Some of the key points to be addressed at the panel:

- Funding
- Data policies
- Training
- Industry engagement
- Long-term sustainability

14:30-15:15



Ido Amit, Professor, Weizmann Institute of Science, Israel (**moderator**)



Mathias Uhlen, Professor, SciLifeLab, KTH Royal Institute of Technology, Sweden



Jovan Tanevski, Group Leader, Heidelberg University, Germany



Mark Fiers, Associate Professor, VIB Center for Brain and Disease, KU Leuven, Belgium

DAY 2 CONGRESS SCHEDULE

Synthesis, Key Takeaways & Next Steps for STOC

Some of the key points to be addressed:

- Summary of key decisions, proposed projects
- Outline for the closed-door meeting

15:15-15:45



Ido Amit, Professor, Weizmann Institute of Science, Israel



Jan Mulder, Researcher, Karolinska Institute, Sweden

Closing Remarks | End of Day 2



Global Leaders in
Single-Cell and Spatial

Stereo-seq Spatial Transcriptomics Service

Subcellular-resolution spatial profiling
for tissue-scale biology



Technology Highlights

Subcellular-Scale
Spatial Resolution

Large Capture Area

Standard Stereo-seq chip formats support 1 cm × 1 cm and 0.5 cm × 0.5 cm capture areas, with custom sizes available based on project needs

High Molecular
Capture per Unit Area

Available Services

	Resolution	Sample Type
Stereo-seq FF V1.3	Subcellular-scale	Frozen
Stereo-seq FFPE V1.1	Subcellular-scale	FFPE

Project Support in Europe

- 👤 Dedicated project coordination for European research teams
- 🧪 Guidance on frozen and FFPE tissue sample preparation
- 📄 Streamlined communication from sample evaluation to data delivery
- 🔗 End-to-end support including sequencing and bioinformatics analysis



OMICS EMPOWER GMBH

✉ info@omicsempower.com

📍 Arnold-Graffi-Haus / D85, Robert-Rössle-Straße 10, 13125 Berlin, Germany

ADDITIONAL INFORMATION



VENUE INFORMATION

Cascina Triulza

Fondazione Triulza, Via
Cristina Belgioioso, 171,
20157, Rho (MI)

HOTEL RECOMMENDATION

UNA Hotels Expo Fiera Milan

Via Giovanni Keplero
12, 20016 Milan, Italy



SHUTTLE INFORMATION

A complimentary shuttle service will be provided between UNA Hotels Expo Fiera Milano to Cascina Triulza. Please arrive at the pick-up point at least 5 minutes before departure. The shuttle will wait for a maximum of 10 minutes before leaving.

Date	Hotel → Cascina Triulza	Hotel → Cascina Triulza
29th June 2026	07:45	18:40
30th June 2026	08:15	16:15

ADDITIONAL INFORMATION

"Beware of Fraud"

Please be aware of fraudulent third parties claiming to offer registration, accommodation, or other services related to this event. These companies are not affiliated with the organisers and may attempt to mislead participants using unofficial communication or unauthorized use of event branding.

To protect yourself, only engage with our official channels and partners. We will never request sensitive information such as login credentials via email.

If you receive any suspicious communication, please disregard it and contact the STOC General Meeting 2026 Team via email at events@sto-consortium.org

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www.stocgeneralmeeting.com

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