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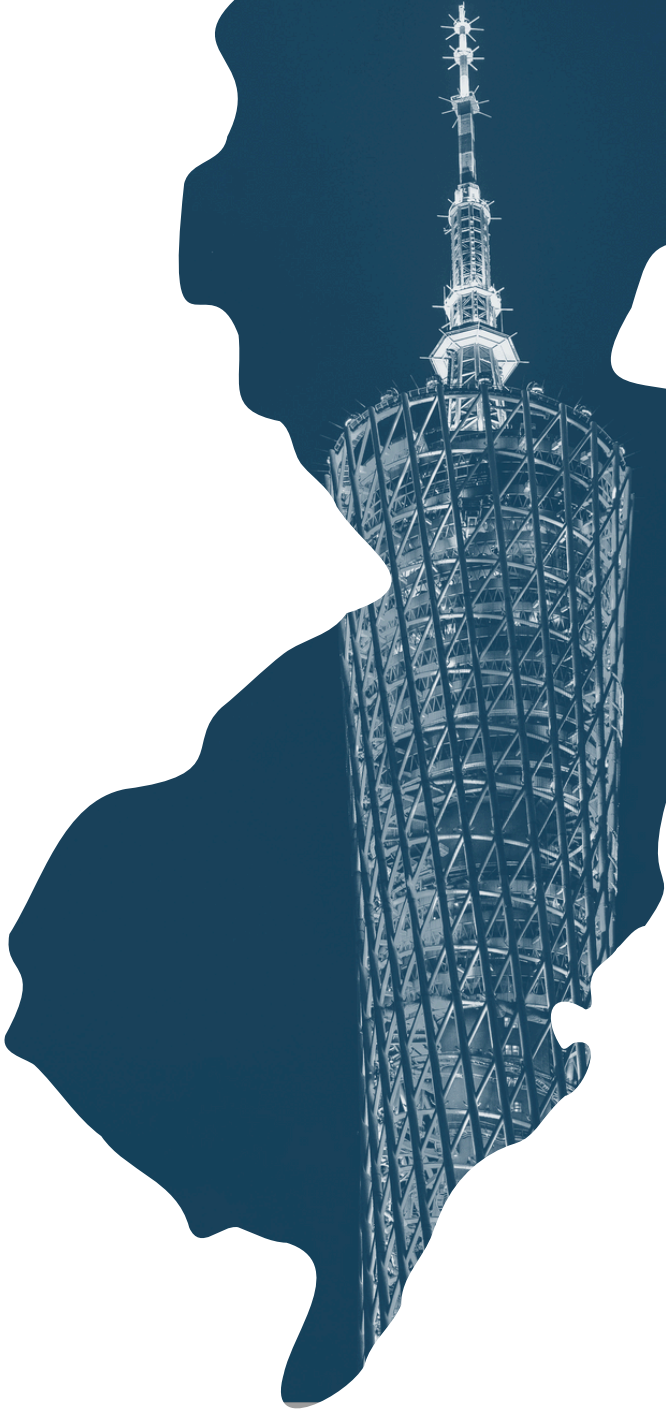

2025 SPATIAL BIOLOGY CONGRESS

26TH - 27TH JUNE 2025
DOUBLETREE BY HILTON GUANGZHOU SCIENCE CITY

CO-ORGANISERS

www.global-engage.com

WARM WELCOME

Welcome to Global Engage's 2025 Spatial Biology Congress

This prestigious event is co-organized by the **Guangzhou Institutes of Biomedicine and Health, Chinese Academy of Sciences**, and the China National Center for Bioinformation. Taking place on **June 26-27, 2025,** at the **DoubleTree by Hilton Hotel Guangzhou - Science City**, this conference will bring together leading experts from around the world to exchange scientific insights in spatial biology.

This two-day event will highlight the diversity of spatial research, covering a broad range of topics, alongside discussions on global trends and regional contributions to the field.

- 20+ speakers from academia and industry experts
- Case studies from across variety of contexts
- Interactive panel discussions session
- Early career researchers and poster exhibition to promote scientific development
- Networking opportunities

We look forward to welcoming you to Guangzhou for this insightful event!

SCIENTIFIC COMMITTEE

- **Guangdun Peng**, Principal Investigator and Deputy director of Center for Cell Lineage Technology and Engineering, Guangzhou Institutes of Biomedicine and Health, Chinese Academy of Sciences
- **Lan Jiang**, Principal Investigator, China National Center for Bioinformation (CNCB)
- **Jinmiao Chen**, Associate Professor, Duke-NUS / BII A*STAR
- **Fei Sun**, Deputy Director General (Chair), Guangzhou Institutes of Biomedicine and Health, Chinese Academy of Sciences
- **Jiekai Chen**, Principal Investigator, Guangzhou Institutes of Biomedicine and Health, Chinese Academy of Sciences
- **Dali Han**, Principal Investigator, China National Center for Bioinformation (CNCB)

CONFERENCE SYNOPSIS

Spatial multi-omics technologies

- Transcriptome, proteome, genome, epigenome, metabolome
- Imaging vs spatial sequencing
- Panel-based vs whole-transcriptome
- Benchmarking new technologies
- 3D profiling
- Microbiome, host-pathogen interaction

AI and data science

- Foundation models, generative AI
- Spatial data quality and standardization
- Cell segmentation
- Cell types and neighbourhoods
- Cross-modality data integration, batch correction
- Connecting subcellular, cellular and tissue morphology to spatial omics
- Cell-cell interactions
- Scaling to massive datasets

Development and physiology

- Current applications of spatial in basic biology
- Tissue atlasing
- Human development, stem cells
- Aging
- Model organisms, organoids, cell culture
- Perturbative approaches

Disease mechanisms, diagnostics and drug discovery

- Current applications of spatial in biomarker discovery and drug development
- Spatial Biology therapeutic applications in:
  - Oncology
  - Neurobiology
  - Chronic disease
  - Infectious disease, microbiome

Panel discussion

Emerging trends and challenges in spatial omics

- What is the best technology for my question?
- How to design a spatial omics study?
- Practical tips for data analysis
- Does AI change the game?
- New possibilities enabled by new technologies

CONFERENCE FLOOR LAYOUT

1F- Grand Ballroom: Talk sessions & exhibition hall (luncheon & refreshments, and poster presentations)

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For more details contact Reuben Raj: Reuben@global-engage.com

CONFIRMED SPEAKERS

GE GAO
Professor,
Peking University

NIKOLAUS RAJEWSKY
Scientific and Founding Director, Berlin Institute for Medical Systems Biology (MDC-BIMSB)

KOK HAO CHEN
Principal Scientist II, Genome Institute of Singapore, A*STAR

KAZUMASA KANEMARU
Post-doctoral Researcher, Cambridge Stem Cell Institute, University of Cambridge

JEONGBIN PARK
Assistant Professor,
Pusan National University

ALISTAIR FORREST
Associate Director (Scientific Strategy) and Head of the Systems Biology and Genomics Lab, Harry Perkins Institute of Medical Research, University of Western Australia

NAMEETA SHAH
CEO,
Amaranth Medical Analytics

SOMPONNAT SAMPATTAVANICH
Assistant Professor,
Mahidol University

ROD DUNBAR
Director, Maurice Wilkins Centre & Professor, School of Biological Sciences, University of Auckland

RAMANUJ DASGUPTA
Professor, University of Glasgow and Cancer Research UK-Scotland Institute

LUYAO NIU
Senior Regional Marketing Manager, Bruker Spatial Biology

FANGQING ZHAO
Director and Principal Investigator, Genomic Informatics Branch, Chinese Society of Bioinformatics

HEI MING LAI
Clinical Assistant Professor, Chinese University Hong Kong

HAISHENG NIE
Senior Market Development Manager, 10x Genomics

SENIOR REPRESENTATIVE
Huapo Biotech

SENIOR REPRESENTATIVE
Standard BioTools

8:00-8:55 | Exhibition Hall (1F) | Registration I Morning Coffee

8:55-9:00 | Grand Ballroom (1F) | Global Engage's Welcome Address & Opening Remarks

9:00-9:05 | Co-organiser's Welcome Address & Opening Remarks

Chair:

9:05-9:25

GE GAO
Professor, Peking University
Multiple-scale Modeling for Cells in Tissue: Challenges and Opportunities

Human individual cells, as the basic biological units of our bodies, carry out their functions through rigorous regulation of gene expression and exhibit heterogeneity among each other in every human tissue. Recent technological advances in spatial omics have enabled the probing of regulatory maps across multiple scale, offering a unique opportunity to unveil the underlying regulatory hierarchy for various cells. Nevertheless, the disparity between feature spaces as well as the ever-increasing data volume pose serious challenge for mining these treasures. Combining massive omics data and leading-edge AI/machine learning approaches, we'd suggest that a set of generative models rationally designed with data-oriented, knowledge-based principles will bridge the gap, and further enabling a Regulatory Language Model.

9:25-9:45

TECHNOLOGY PARTNER PRESENTATION

SENIOR REPRESENTATIVE
Huapo Biotech
Sony ID7000 and FP7000: High-Dimensional Flow Cytometry Solutions for Cell Lineage Research

The SONY ID7000 and FP7000 full-spectral flow cytometers constitute a comprehensive solution for cell lineage research. The ID7000,as an ultra-high-dimensional full-spectral analyzer, is equipped with up to 7 lasers and 186 detectors. It enables precise multi-parameter detection, including the accurate identification of rare cell subpopulations, through spectral optimization algorithms. The FP7000 cell sorter, which seamlessly integrates with the ID7000,features real-time resolution technology. It maintains high-purity sorting while enhancing experimental efficiency through an intelligent operating system. The entire system covers the needs of multiple disciplines, including immunology and tumor research, and combines high-sensitivity analysis with high-speed sorting capabilities, providing a reliable technical platform for the study of complex cell populations.

9:45-10:25

KEYNOTE ADDRESS

NIKOLAUS RAJEWSKY
Scientific and Founding Director, Berlin Institute for Medical Systems Biology (MDC-BIMSB)
TBD

10:25-11:25 | Morning Refreshments I Poster Sessions I 1-2-1 Partnering Meetings

Spatial Multi-omics Technologies

Chair:

11:25-11:45

KOK HAO CHEN
Principal Scientist II, Genome Institute of Singapore, A*STAR
Discovering Cell Type and Tissue Architecture with Imaging-based Spatial Transcriptomics

Spatially resolved omics analysis of tissue sample promises to transform biomedical research and diagnostic. In this talk, I will introduce a spatial clustering algorithm called BANKSY. BANKSY is a fast and accurate software for cell type identification and domain finding. It is applicable for spatial RNA (e.g. Visium, MERSCOPE, CosMx) and protein (e.g. MIBI, CODEX) datasets. It is also compatible with widely used bioinformatics pipelines, like Seurat and SCANPY. For the second part of my talk, I will introduce a sensitive and cost-effective multiplexed FISH assay for spatial cell typing called FISHnCHIPs. By labeling gene programs, FISHnCHIPs can rapidly profile whole-slide tissue sections and robustly analyze clinical tissue samples. I hope that these and other spatial omics tools can bring us closer to solving the complexities of human diseases.

11:45-12:05

KAZUMASA KANEMARU
Post-doctoral Researcher, Cambridge Stem Cell Institute, University of Cambridge
Spatially Resolved Multiomics of Human Cardiac Niches

The function of a cell is defined by its intrinsic characteristics and niche. Here, we combine paired single-nucleus RNA and ATAC sequencing with spatial transcriptomics data to discover cellular niches in the human heart. We profile cells of the cardiac conduction system, revealing that the pacemaker cells exhibit distinct characteristics in both the adult and developing heart, including gene expressions involved in innervation. In the ventricle, spatiotemporal transition along the transmural axis demonstrates the morphological process of cardiomyocyte compaction. By generating data from Trisomy 21 hearts and comparing it with the euploid atlas, we reveal a reduced abundance of specific cell types, including compact cardiomyocytes. Overall, we provide a comprehensive map of the human heart, both in adults and during development.

12:05-12:20

CONTRIBUTED TALK

Authors of accepted abstracts will be notified on the first week of June

12:20-12:35

TECHNOLOGY PARTNER PRESENTATION

LUYAO NIU
Senior Regional Marketing Manager, Bruker Spatial Biology
Expanding the Limits of Spatial Biology: Comprehensive Integrated Technologies for Spatial Multiomics

Tissue heterogeneity and complex microenvironments are one of the major challenges in clinical and translational medicine research. In order to reveal the cellular composition and function of complex tissues, as well as the molecular mechanisms of interactions between cell populations, spatial in situ analysis technologies based on tissue background information have been developing rapidly in recent years. GeoMx Digital Spatial Profiler System provides regional basis spatial proteomic and transcriptomic expression profiling; CosMx Single Cell Molecular In Situ Imaging System it provides quantification of ultra-high plex RNAs and proteins at single-cell and subcellular resolution. It allows researchers to comprehensively map single cells in their native environment and extract deeper biological insights from a single experiment. CellScape super-resolution spatial in situ single-cell protein imaging system is compatible with open-source reagents, enabling flexible and scalable spatial single-cell proteomics exploration.

12:35-13:45 | Lunch I Poster Sessions I 1-2-1 Partnering Meetings

AI & Data Science

Chair:

13:45-14:05

JEONGBIN PARK
Assistant Professor, Pusan National University
Cell segmentation-free Inference of Cell Types from Spatial Transcriptomics Data

The recent advances in multiplexed fluorescence in situ hybridization show how gene expression varies, and eventually allow the identification of different cell types in a spatial context. However, due to the limitation of cell segmentation, it is difficult to identify cell types and understand tissue structure at the single-cell level. To this end, we developed a novel method called SSAM that identifies cell types and tissue regions in both 2D and 3D without cell segmentation. We tested SSAM on three different mouse brain regions imaged by different techniques: the somatosensory cortex (SSp), the hypothalamus preoptic region (POA), and the primary visual cortex (VISp). Our results show that SSAM accurately identifies the location of known cell types and can discover new cell types that were not reported before.

14:05-14:25

NAMEETA SHAH
CEO, Amaranth Medical Analytics
Understanding Glioblastoma Vasculature Using Spatial Transcriptome Data

Glioblastoma (GBM) is characterized by complex and aberrant vasculature that critically influences tumor growth, immune interactions, and therapeutic resistance. Using spatial transcriptomic analysis of 39 glioma cases with over 3.8 million single-cell profiles obtained via the 10x Xenium platform, we dissected the molecular landscape underlying GBM vascular architecture. A customized gene panel facilitated the identification of distinct subtypes of endothelial cells, pericytes, and fibroblasts. Our analysis revealed specific communication networks between vascular and immune cell populations, highlighting critical ligand-receptor interactions involved in immunosuppression and angiogenesis. Additionally, we investigated correlations between genomic alterations and vascular cell gene expression patterns, uncovering novel biomarkers and therapeutic targets. By integrating spatial localization with genomic data, we illustrate the intricate interplay between genetic events and tumor microenvironment remodeling in glioblastoma. These findings provide comprehensive molecular insights into GBM vascular biology, informing the development of targeted therapies aimed at disrupting vascular signaling pathways to improve therapeutic outcomes.

14:25-14:45

TECHNOLOGY PARTNER PRESENTATION

HAISHENG NIE
Senior Market Development Manager, 10x Genomics
Revving Up Insights in Spatial Exploration

Spatial biology provides unprecedented insights into tissue organization and cellular function, revealing complex cellular interactions and distributions. 10x Genomics is advancing the field of spatial biology through their cutting-edge platforms, Visium and Xenium. Elevating spatial biology to new heights, Xenium In Situ technology offers ultra-precise spatial imaging at sub- cellular resolutions, studying thousands of genes across entire tissue sections in a single experiment. Combining spatial transcriptomics with histological stains and immunofluorescence, Xenium in situ technology will enable a deeper understanding of tissue complexity and biomolecular interactions within their native contexts, empowering research areas including immunology, neuroscience, and oncology. In this talk, we will share the latest updates on 10x Genomics's 2025 roadmap and some recent groundbreaking discoveries enabled by Xenium in situ technology.

14:45-15:00

CONTRIBUTED TALK

Authors of accepted abstracts will be notified on the first week of June

15:00-15:50 | Afternoon Refreshments I Poster Sessions I 1-2-1 Partnering Meetings

AI & Data Science

Chair:

15:50-16:10

FANGQING ZHAO
Director and Principal Investigator, Genomic Informatics Branch, Chinese Society of Bioinformatics
TBD

16:10-17:00

PANEL DISCUSSION
Emerging Trends and Challenges in Spatial Omics

- What is the best technology for my question?
- How to design a spatial omics study?
- Practical tips for data analysis
- Does AI change the game?
- New possibilities enabled by new technologies

17:00-17:05 | Group Photo Session

17:05 | End of Day 1

8:30-9:00 | Exhibition Hall (1F) | Registration I Morning Coffee

Chair:

9:00-9:20

ALISTAIR FORREST
Associate Director (Scientific Strategy) and Head of the Systems Biology and Genomics Lab, Harry Perkins Institute of Medical Research, University of Western Australia

Studying Tumour Subclones and the Tumour Microenvironment Using Spatial Transcriptomics

The tumour microenvironment (TME) plays a pivotal role in tumour progression, treatment response, and patient outcomes. Comprised of diverse immune cells, fibroblasts, and stromal components, the TME's composition is strongly linked to clinical outcomes, with several immune infiltrates, such as tumour-infiltrating T cells, B cells, plasma cells, and tertiary lymphoid structures, showing positive correlations with survival. Recent advances in spatial transcriptomics provide high-resolution profiling of cellular neighbourhoods within the TME, offering unparalleled insights into tumour-immune interactions, autocrine signalling, and chemotherapy resistance mechanisms. In our work, we apply spatial transcriptomics to map the TMEs of high-grade serous ovarian carcinoma (HGSOC), breast cancer, uveal melanoma, and mesothelioma. I will present findings from our recent study of ovarian cancer, where we identified subclones expressing distinct ligands and receptors. Our analysis suggests that these subclone-specific ligands drive differences in TME composition and may underlie treatment resistance. Additionally, I will discuss our tools for predicting cell-to-cell communication networks.

9:20-9:40

TECHNOLOGY PARTNER PRESENTATION

SENIOR REPRESENTATIVE
Standard BioTools
TBD

9:40-10:20

KEYNOTE ADDRESS

ROD DUNBAR
Director, Maurice Wilkins Centre & Professor, School of Biological Sciences, University of Auckland
TBD

10:20-11:20 | Morning Refreshments I Poster Sessions I 1-2-1 Partnering Meetings

Development and Physiology

Chair:

11:20-11:40

HEI MING LAI
Clinical Assistant Professor, Chinese University of Hong Kong
Resolving the Technological Obstacles to Stereophenotyping

Biology is three-dimensional. Stereophenotypes-based biomarkers can potentially empower precise patient selection for therapeutics. We first describe the physical barriers towards accessible stereophenotyping, followed by reporting our latest iteration on INSIHGT - a foundational chemistry that enables highly multiplexed, deeply penetrating immunostaining in centimeter-scale tissue volumes. INSIHGT has been proven to be compatible with >300 off-the-shelf antibodies, up to 28-plex profiling using multi-round immunostaining can be achieved in 1mm-thick samples preserved only with conventional formalin fixation. Same species multiplexing is also possible. The whole pipeline requires no specialized machines, techniques, or custom reagents. Samples after 3D analyses are indistinguishable from non-processed controls by pathology specialists, RNA and DNA sequencing, and spatial proteomics profiling by mass spectrometry. We also report our epitope rescue technology, enabling 3D IHC on paraffin-embedded samples archived for 30 years at room temperature, opening the path towards clinical studies and deployment.

11:40-12:00

INVITATION OUT

12:00-12:15

CONTRIBUTED TALK

Authors of accepted abstracts will be notified on the first week of June

12:15-12:35

TECHNOLOGY PARTNER PRESENTATION

For sponsorship opportunities, please contact Reuben Raj (reuben@global-engage.com)

12:35-13:45 | Lunch I Poster Sessions I 1-2-1 Partnering Meetings

Disease Mechanisms, Diagnostics, and Drug Discovery

Chair:

13:45-14:05

RAMANUJ DASGUPTA
Professor, University of Glasgow and Cancer Research UK-Scotland Institute
Spatially Resolved Single Cell Analysis of Bevacizumab-induced Enhancement of anti-PD1 Response in Nasopharyngeal Cancer

Clinical outcome data from our recent Phase II randomized study aimed at interrogating the benefit of combining anti-VEGF therapy (Bevacizumab) with immune checkpoint blockade (ICB, Pembrolizumab) in advanced nasopharyngeal cancer (NPC) showed a ~4x increase in overall survival rate (ORR) in the combinatorial arm compared to anti-PD1 monotherapy (REF). In this study, we employed single cell RNA-seq and spatial transcriptomic analyses on longitudinal, serial biopsies from patients with matched clinical outcome data, to explore the underlying molecular mechanisms and prognostic biomarkers associated with how anti-angiogenic therapy may regulate anti-PD1 response. Notably, our single cell-spatiotemporal analyses revealed that one week of Bevacizumab monotherapy alone can remarkably alter and prime the tumour ecosystem into an immune-activated state. Specifically, we elucidate the anti-VEGFA-induced alterations in cell types, cell states, and spatial neighbourhoods that promote vascular normalization, and a proinflammatory switch in myeloid cells as well as cancer-associated fibroblasts (CAFs), which facilitate reversal of immune tolerance, and restoration ICB response. Additionally, gene regulatory network analysis and interrogation of spatially-aware cell-cell interactions associated with emergence cell-states, and dynamic alterations in response-associated spatial niches, revealed potential pathways and cross-regulatory interactions that may control therapy response. Altogether, our study reveals a critical role for vascular normalization and stromal remodelling in promoting immunotherapy response, while opening new avenues of investigation into alternative targets for combinatorial interventions to enhance immunotherapy response.

14:05-14:25

SOMPONNAT SAMPATTAVANICH
Assistant Professor, Mahidol University
Advancing Precision Medicine with Spatial Biology: Insights from Rare Cancer Applications

Spatial biology enables high-dimensional tissue analysis while preserving the spatial context of cellular architecture, offering unprecedented insight into tumor microenvironments and therapeutic response. At the Siriraj Center of Research Excellence for Cancer Precision Medicine and Systems Pharmacology, we deploy advanced tissue-based multiplex immunofluorescence platforms, such as t-CyCIF, to explore spatial immune phenotypes and cellular neighborhood structures in challenging cancer types. In this talk, I will highlight three case studies demonstrating the power of spatial biology in driving precision oncology. First, we examine tumor microenvironment (TME) heterogeneity in pancreatic ductal adenocarcinoma (PDAC), integrating spatial immune profiling with molecular subtyping to identify immune-hot and immune-cold tumor variants. Second, in non-small cell lung cancer (NSCLC), we explore the spatial determinants of response to immune checkpoint inhibitors by comparing TME features between superresponders and non-responders, focusing on tertiary lymphoid structures and cellular neighborhood analysis. Lastly, we present early findings from tumor-induced osteomalacia (TIO), a rare paraneoplastic syndrome, using spatial markers to improve diagnostic precision and uncover pathophysiological mechanisms driven by FGF23-expressing mesenchymal tumors. These examples illustrate how spatial biology can uncover clinically actionable insights and refine personalized treatment strategies for rare and complex cancers.

14:25-14:40

CONTRIBUTED TALK
Authors of accepted abstracts will be notified during the first week of June

14:40-15:00

INVITATION OUT

15:00-15:05	Closing Remarks
15:05	End of Day 2

VENUE INFORMATION

DOUBLETREE BY HILTON GUANGZHOU SCIENCE CITY

18 Shuixi Rd, Huangpu, Guangzhou,
Guangdong Province, China, 510530

CALL FOR **ABSTRACT**

SUBMISSION DEADLINE: 27TH MAY 2025

This is an excellent opportunity to showcase your groundbreaking research at the congress. Selected abstracts will be allocated a 15-minute oral presentation in the program, along with complimentary registration. We welcome submissions in the following areas (but not limited to):

- Spatial multi-omics technologies (Transcriptome, proteome, genome, epigenome, metabolome)
- Spatial data quality and standardization
- Cross-modality data integration and batch correction
- AI application in spatial biology
- Development and physiology
- Disease mechanism, diagnostic and drug discovery
- Spatial imaging and spatial sequencing
- Single-cell spatial analysis

SUBMISSION INSTRUCTIONS

Click **HERE** to submit an abstract for consideration.
For any inquiries, please contact **Wen Fang** at **wenfang@global-engage.com**

POSTER PRESENTATIONS

MAKING A POSTER PRESENTATION – CLOSING DATE: 27TH MAY 2025

Poster presentations will take place during 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. 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). Representatives from solution provider organizations are not eligible to enter the competition but are welcome to present posters at the meeting.

SUBMISSION INSTRUCTIONS

Download poster presentations form: **HERE**
For any inquiries, please contact **Haley** at **haley@global-engage.com**

We will require the form (downloadable from the event website) to be submitted by **27th May 2025**. This is the formal deadline however space is another limiting factor so early application is recommended.

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