

Omics Discovery Day

14 MAY 2025 | 9:30 AM | HOLIDAY INN, OXFORD, UNITED KINGDOM



Join us this May 14th at the Holiday Inn in Oxford for a day of learning, networking, and innovation. Unlock new insights during our full-day event dedicated to the latest advancements in genomics, transcriptomics, and proteomics, beginning with talks covering **key technologies**.

Program Agenda

Arrival and Registration	8:30 AM
Scientific Talks	9:30 AM
Lunch	12:30 PM
Workshops	1:45 PM – 3:45 PM

WEDNESDAY, 14 MAY 2025

Secure your spot.
Register today!

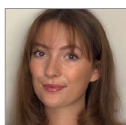
WORKSHOP 1

Low Input Library Prep: Considerations and Tips

Max and Beth will cover tips and considerations, focusing on the Illumina® Oncology 500 solid and ctDNA assays and NEBNext® kits.

WHAT YOU WILL LEARN ABOUT:

- Sample extraction and preparation best practices
- Quality control metrics for sample input
- Sample input requirements for Illumina's TSO500 solid and ctDNA assays
- High level overview of TSO500 assays including workflow, sequencing, and analysis
- Library preparation and multiplexing with NEBNext
- Overview of library prep and multiplexing with NEBNext
- Sample requirements at Azenta/GENEWIZ for NEBNext kits
- Sample extraction and purification requirements for DNA and RNA
- Library prep workflows with NEBNext kits



Beth Russell,
Field Application
Scientist, Illumina



Dr. Max Fritsch,
Field Application
Scientist, NEB

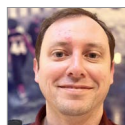
WORKSHOP 2

ONT Bacterial Whole Genome/ Methylation/Plasmid Sequencing

John Townes will delve into theory and workflow from applications through experimental design and analysis.

WHAT YOU WILL LEARN ABOUT:

- Introduction to workflows:
 - Nanopore theory
 - Applications
 - Experimental design
 - Library preparation
 - Data analysis
- Practical: Flow cell loading
- Demo: wf-metagenomics analysis
- Conclusion: Moving forward with Nanopore Sequencing



John Townes, Field Applications Scientist,
Oxford Nanopore Technologies



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PROGRAM AGENDA CONTINUED

WORKSHOP 3

Bioinformatics for Transcriptomics and Single-Cell

Chris and Claudia will discuss the bioinformatics pipeline and common challenges in RNA-seq bioinformatics analysis, then follow with an introduction to 10x/single-cell analysis with an overview of analysis options and your choice to follow along with a live demo.

WHAT YOU WILL LEARN ABOUT:

- Evaluating sequence quality
- Trimming reads
- Mapping reads to a genome
- Generating hit counts for gene/exons
- Comparing gene hit counts
- Analyzing gene ontology
- 10x/single-cell analysis including:
 - Introduction to single-cell workflow
 - Overview of Cell Ranger algorithm for 10x single-cell analysis
 - 10x Cloud demo
 - Loupe Browser tutorial for data visualization and exploration, with option to follow along.



Dr. Chris Bauser,
Team Lead,
Bioinformatics



Claudia Tamburini, Ph.D.,
Field Application Scientist,
10x Genomics

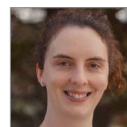
WORKSHOP 4

Olink®: Approaching Your First Proteomics Experiment

Janet Kenyon will dive into main considerations and workflow for Olink experiments with a case study walkthrough.

WHAT YOU WILL LEARN ABOUT:

- A recipe for success: sample choice, experimental design and analysis
- Publicly available tools to support your journey with Olink
- Taking biomarkers from discovery to clinical with Olink's Next Generation Sequencing proteomics
- Case study walkthrough



Janet Kenyon, D.Phil, Field Support
Manager for UKI, Nordics and
MEA Regions, Olink Proteomics

Drinks & Mingling

4:00 PM

Event Accommodations

Venue location & where to stay:

Holiday Inn, Oxford, United Kingdom

Contact

Reach out to Dora Quest via email for any questions or concerns.

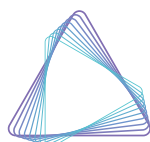
dora.quest@azenta.com

REGISTER NOW TO SAVE YOUR SEAT

Please note: registration spots are limited and will be allocated on a first-to-register basis. If your plans change, please let us know



SCAN OR CLICK to register for the
UK Omics Discovery Day Event



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