

Workshop: Single Cell Multiomics

Find out how microwell technology can make your single cell assay easier

Join us!

Thursday 7th November 2024 – 10:00

Campus de Espinardo, Universidad de Murcia. – Aula de seminarios del edificio SACE (nº 21)

“We have recently demonstrated, that—compared to other scRNASeq platforms—the **BD Rhapsody workflow** captures a notably high number of mRNA molecules per cell and may thus be particularly well suitable to depict low mRNA content cells.

Hautz et al., 2023 Nature Comm (DOI: [10.1038/s41467-023-37674-8](https://doi.org/10.1038/s41467-023-37674-8))

The BD Rhapsody system is ideal to study cell heterogeneity, being able to combine in the same assay the analysis of the gene expression of each individual cell with the protein expression of markers of interest



Maintain sample integrity

Gentle microwell technology

No sample loss due to clogging of channels

Recover cells with disparate size and morphology, including fragile cell types



Expanded throughput

Million-cell studies possible

Capable of capturing more than 320,000 cells per cartridge

Up to 80% cell capture rate (for certain cell types)



Visual workflow QC

Save time and sequencing cost

Make real-time decisions before sequencing

Be certain about your cell capture with every single-cell experiment

Agenda

- 10:00 - **BD Rhapsody™ HT Single-Cell Analysis System**: The solution to overcome limitations in single-cell analysis
- 10:20 - **CITE-Seq**: Identify intracellular and surface proteins together with RNA in the same cell
- 10:40 - **scATAC-Seq**: Epigenomic and transcriptomic characterization for the first time affordable
- **Open discussion** - Q&A Session & Project Discussion

Register here

Or scan the QR



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