

Getting ready for mass cytometry

If you are **new to mass cytometry**, you will need to:

- Register your project by submitting the **Helios Registration Form**.
- Request a project meeting with the IMC Platform team to discuss your study.
- Attend the Introduction to Helios course (under the **Training** tab) which includes information on how mass cytometry works, antibody panel design, and how to validate and establish antibody panels.
- Attend a machine introduction (this will usually occur the first time you run samples on the Helios).

Planning and booking:

- Once the IMC Platform team receives a completed registration form, we will add you and your research group to the IRIS booking calendar so you have access to the service.
- Sign in to the IRIS booking calendar (under the **Reservation** tab).
- Please check the booking calendar at <https://iris.science-it.ch> for free slots and to request a booking (titled Service request in IRIS) as outlined in the **Reservation** tab.
- Long-term longitudinal experiments should be discussed in advance to guarantee instrument availability.
- Please place your Service request at least 5 working days in advance. The response time is generally within 24h.
- Cancellation is possible up to 24h before the booking free of charge. Cancellation is not possible less than 24h before the booking slot due to inability to recover fees.
- Time for sample acquisition will be calculated based on your project details, number of cells to be measured and number of samples. As a general rule, 1 million cells can be acquired per hour. So, acquisition time can be planned based on this.

Sample preparation:

- On acquisition day, please bring samples on ice in Iridium Fix-Perm Buffer.
- Please bring a completed copy of your uploaded **Sample Template** excel from the IRIS Service request and if possible, an CSV file of your panel from the MaxPar Panel Designer online tool for direct upload into the CyTOF software.

- Please complete the three wash steps before sample acquisition upon arrival, unless instructed otherwise.
- After the washes, samples will be filtered (40µm blue-capped FACS tubes), counted and put in CAS solution with 10% EQ normalization beads for acquisition (CAS and beads are provided by the IMC Platform).
- Fees due to extra troubleshooting from low quality samples (e.g. cells not staying in single cell suspension, improperly fixed material, residues of sticky material, etc.) are the sole responsibility of the users.
- Any samples with possible environmental contaminants that can be measured by the instrument (Cisplatin, from cancer treatments, Gadolinium from MRI contrast agent, Iodine from Ficoll, Barium from detergents, lead from glass containers) should be discussed with the team before acquisition.

Quality control (QC)

- The instrument will be tuned and EQ calibration beads will be run at the start of each day and in between users.
- For normalization, EQ calibration beads will be added to the sample to adjust for time dependent decrease of signal and day-to-day variations of the instrument.
- The use of reference samples with positive and negative controls for every target in a panel should be included with each run except for titrations. This is to control for the staining on a given day.

Data management

- For each acquisition, two files will be created: a raw data FCS file, and raw data IMD file. These files will be transferred to your storage device. Please be aware that mass cytometry IMD files are very large files therefore, they will not be saved on the computer hard drive after acquisition. All FCS files will be deleted from the computer hard drive 3 months after your sample acquisition.
- Please indicate to the IMC Platform team if you would like us to normalize, and/or concatenate, and/or debarcode your samples with the CyTOF software before you take them off the machine hard drive.