

Aurora Start-up Protocol

1. Check sheath and waste tanks, replace if necessary
2. Turn ON the PC and log in:
User: My Aurora
Password: Welcome#1
Wait 3 minutes
3. Turn ON the cytometer (make sure there is a tube with H₂O installed in the SIP)
Wait 3 minutes
4. Launch the software SpectroFlo and log in:
Session: Common user
Password: Common user
5. Go to Acquisition tab and select the experiment named: Cleaning
6. Clean the instrument by running:
5 minutes RINSE
5 minutes CLEAN
5 minutes H₂O at flow rate HIGH. Put the flow rate back in LOW (as a preparation for the next steps).
7. Select the tab: QC and Set-up
8. Wait at least 15 additional minutes before running any sample. This time ensure the proper warming up of the detectors.
9. Prepare QC beads:
300ul of PBS 1X + 1 drop of Spectroflo beads (kept in the fridge of the facility)
10. Load the tube and run the beads by pressing start:
The bead lot number we are currently using is: 2003
11. Once the QC is done, a message saying, "Passed" should pop up.
12. Go to acquisition tab, select or create your experiment and start the acquisition.