SOP.UCF.050 – CYTEK AURORA OPERATION

On Weekdays, if there is a slot available at 9am, the UCF staff will switch the machine ON and perform the Quality Control.

On Weekends, Holidays and outside weekly working hours (9am to 6pm), if you are the 1st user of the day you must turn ON the machine 30 minutes prior acquisition and perform the Start-up Cleaning Procedure and a Quality Control check.

STARTING UP

- **(if you are the first user of the day and the machine is OFF)**

1. Check the sheath and waste tanks; fill and/or empty, if necessary.
2. Turn on the computer.
3. Login on windows:

   Username: **MyAurora**

   Password: **Welcome#1**
4. Turn on the cytometer. **IMPORTANT**: please ensure that a DI water tube is loaded, before launching the software, for proper SIT depth calibration.
5. Launch SpectroFlo and log in. Note that:
   - SpectroFlo controls the LASERs, meaning that exiting SpectroFlo will turn off the LASERs. On the other hand, logging in and out, will not turn the LASERs off.
   - The LASERs take **30-45 minutes to fully warm up**.
   - When launching the SpectroFlo software, a SIT calibration is automatically performed.
     Username – **Your User**

     Password - **Your Diva/SpectroFlo password**
6. Check the status indicator in the lower-right corner of the screen and confirm the indicator for Connected is a green checkmark.
7. Wait 30 minutes to allow the cytometer to warm up before running Daily QC, **while performing the daily cleaning procedure**:
8. Remove the tube with Water.
9. Run a new tube with WATER+AZIDE on HIGH for 30 min
10. Run Daily QC.
11. Run your samples.

- **(if the machine is ON)**

1. Launch SpectroFlo and log in.

   Username – **Your User**

   Password - **Your Diva/SpectroFlo password**
2. Run your samples.

FINISHING ACQUISITION AND DATA HANDLING

After you finish recording your last sample, you can now export your data.

Important Notes

- The long-term storage of all data generated by the independent usage of Aurora is the responsibility of the researchers/groups who have collected the data.

- It is strongly recommended to export experiments from the SpectroFlo to your Lab folder on the **iMM server** (shortcut on the desktop). To access the iMM server you must use your email credentials.

- If you want to analyze your data in one of our Analysis Stations, you can also **export your experiments directly to them.** To access these stations, right click on the shortcuts on the desktop (MacFlow 1 and 2) and use the following credentials:

  User- **flowcytometryuser** **Password**- **BDIS**

- The local folder that should be used to store temporarily data exported from SpectroFlo is located in the Desktop (**Export – Exported Experiments**). Any files or folders outside this folder will be deleted without notice.

- The use of USB pens or external drives in the Aurora computer is not allowed.

- On the Aurora computer: on the first work day of each month, anything in the “My Experiments” window in SpectroFlo that is older than 30 days will be deleted from the software.

- The Flow Cytometry Unit is not liable for any loss of data on the local hard disks.

EXPORT YOUR DATA

1. If your experiment is open, first close the experiment clicking the “**x**” in the experiment tab.
2. **Right click** on the experiment in SpectroFlo Acquisition module > **Experiment tab** > **My Experiments** and click **Export.**
3. Select a folder, type an export file name, and click **Save.**
4. **Click OK** to close the export pop-up window.
5. **Right click** on the experiment in SpectroFlo Acquisition module > Experiment tab > My Experiments and click **Delete.**
6. Click **Delete** to remove the experiment from SpectroFlo.

To open your saved experiment on another computer:

1. In the acquisition tab, select Import.
2. Locate your experiment on the computer (exported file is a zip folder)
3. The experiment should automatically open and you can run your samples

NOTE: Experiments will be then saved in “My Experiments”.

Experiment Templates

Use the **Save As** option above the experiment’s tube/group (hierarchy) list to save the current experiment as a template, which can then be used for running similar experiments. Experiment templates include fluorescent tags used in the experiment, reference controls, groups/tubes, labels, worksheets, and stopping criteria. Templates are saved in the library. To open and use a template, select Template from the Acquisition Experiment menu.

FCS Files

FCS files generated from an experiment are stored in the Export folder by default, or the folder you set as the default. Experiments can contain the following types of FCS data files for each tube run:

• raw data files only (for samples that were acquired in an experiment)

• raw data files + unmixed data files (for samples that were acquired and unmixed live during acquisition)

• unmixed data files only (for samples that were unmixed post acquisition)

1. **Clean the cytometer according the protocol indicated on the top of the table. DO NOT FORGET TO RECORD IT**

2. **Refill the Sheath tank.**

3. If during your acquisition, **the waste container gets full,** you should put the cytometer in **Standby**, and **close** the container with the red cap that is on top of it and replace the container with a new one.

TURNING OFF THE MACHINE

After you end your experiment, please confirm in Agendo if anyone has made a reservation for Aurora after you. If you are the **last user of the day after 5pm on weekdays or the last user on weekends and holidays**, the system should be turned off. To shutdown Aurora, please follow these steps:

1. In SpectroFlo, either on the QC & Setup or Acquisition module menu, select **Fluidics Shutdown**.
2. Follow the prompts to load a tube with 3 mL of FACSClean, followed by a tube with 3 mL of DI water, followed by 3 mL of 30% contrad, followed by 3 mL of DI water. The entire procedure takes about 6 minutes.
3. Leave the tube of DI water on the SIP. Make sure the SIT is submerged in the DI water.
4. Turn off the cytometer, exit the SpectroFlo software and shutdown the workstation.