

# BEFORE EVERY RUN

- 1) Use the lab's Google Calendar to **RESERVE YOUR TIME SLOT**. Log into <http://calendar.google.com> with the username "gregstep.group" and password "56422metabolism". Create an entry for the "Agilent GCMS" calendar and title it with your name. You should not reserve the calendar for more than 72 consecutive hours without speaking with Jason Walther ([jwalther@mit.edu](mailto:jwalther@mit.edu)) first.
- 2) Check the **HELIUM PRESSURE** on the right-hand gauge of the regulator on the helium tank. If the pressure is below 500 psi, you need to order a new tank of helium (HE UHP300 from Airgas). Contact Jason Walther ([jwalther@mit.edu](mailto:jwalther@mit.edu)) and let him know both that the helium is running low and that you have ordered a new tank.
- 3) Conduct an **AIR AND WATER CHECK**. From Instrument Control, go to View > Tune and Vacuum Control > Tune > Air and Water Check. A report will be sent to the printer. Place the printed report at the front of the white binder for future reference. If peak 18 (water) or peak 28 (nitrogen) is above 2%, DO NOT RUN your samples and contact Jason Walther ([jwalther@mit.edu](mailto:jwalther@mit.edu)) as soon as possible.
- 4) If you decide to run an autotune, place the printed report of the autotune at the front of the white binder for future reference. Be sure to save the autotune before returning to Instrument Control.
- 5) Check the **ELECTRON MULTIPLIER VOLTAGE** before every run. If you have run an autotune, the voltage will appear in the upper right-hand corner of the printed report next to the label "EMVolts". You can also determine the voltage by going to View > Tune and Vacuum Control > Parameters > Manual Tune and then finding the value in the "EMVolts" field. If the EMVolts value is greater than 3000, the electron multiplier horn might need to be replaced or the ion source might need to be cleaned. Contact Jason Walther ([jwalther@mit.edu](mailto:jwalther@mit.edu)) and let him know as soon as possible.
- 6) Be sure that you **SAVE YOUR DATA TO THE DATA (D:) DRIVE**. If you haven't already, create a folder in the root directory of the Data (D:) drive and name it after yourself. Create subfolders as desired. When editing a sequence, make sure that the "Data Path" directory at the top left-hand corner of the Sample Log Table points to the Data (D:) drive.
- 7) Make sure that the autosampler **SOLVENT VIALS (A11, B8)** are filled with acetone and that the autosampler **WASTE VIALS (WA2, WA3, WA4, WA5)** are empty.
- 8) Open up the **LOG.XLS SPREADSHEET** on the desktop of the GC/MS computer and create a new row describing your run. You will need to fill out the following fields:

<b>User</b>	Your name
<b>Date</b>	Date of your run
<b>Method</b>	Name of the .m method file(s) in your run
<b>Sample Type</b>	Description of the type of samples you are injecting
<b># Samples</b>	Number of different vials in your run
<b># Injections</b>	Number of overall injections in your run
<b>EMVolts</b>	Electron multiplier voltage (see #5 above)
<b>H2O %</b>	Water percent from Air and Water Check (see #3 above)
<b>N2 %</b>	Air percent from Air and Water Check (see #3 above)
<b>He Pressure</b>	Helium pressure in psi (see #2 above)
<b>Max count if &gt; 3E6</b>	The maximum ion count that occurs over your run if at any time the ion count ends up exceeding 3 million. This is filled in after your run is complete.

## AFTER EVERY RUN

- 1) Look through each of your data files and make a note of the **MAXIMUM ION COUNT**. If at any time that count exceeded the recommended maximum of 3 million, record your maximum in the log.xls spreadsheet on the desktop.
- 2) **REMOVE ALL OF YOUR VIALS** from the autosampler immediately and either store them in your personal space or discard them in the chemical sharps container, sealing the lid.