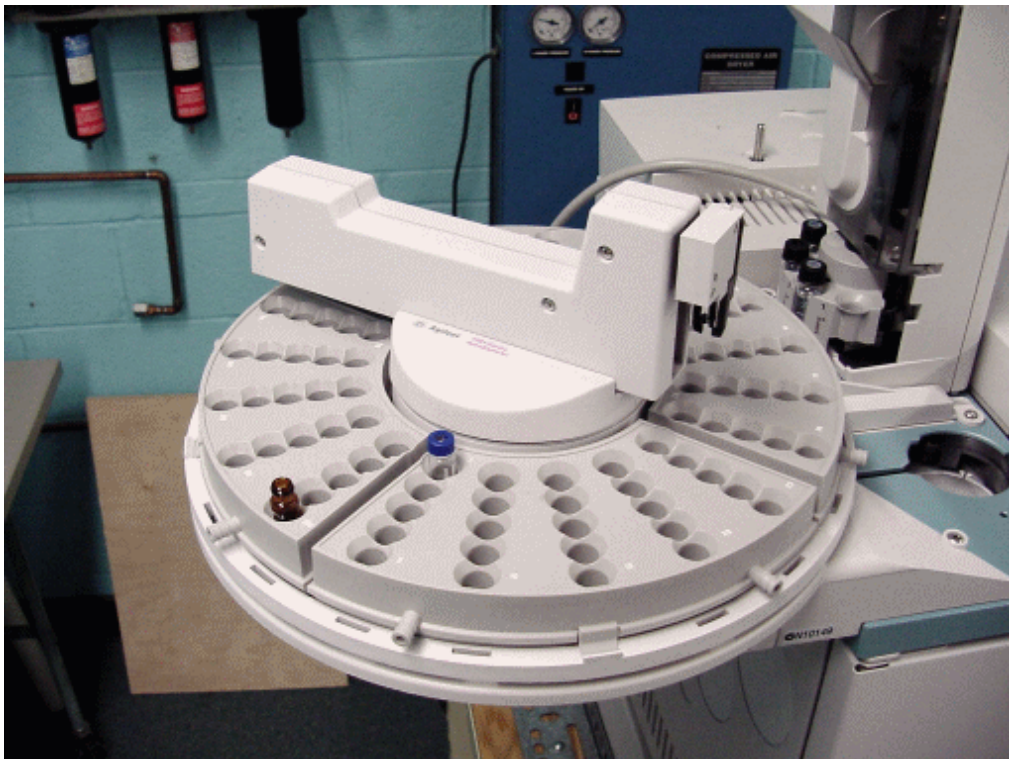


MicroGC Operating Instructions



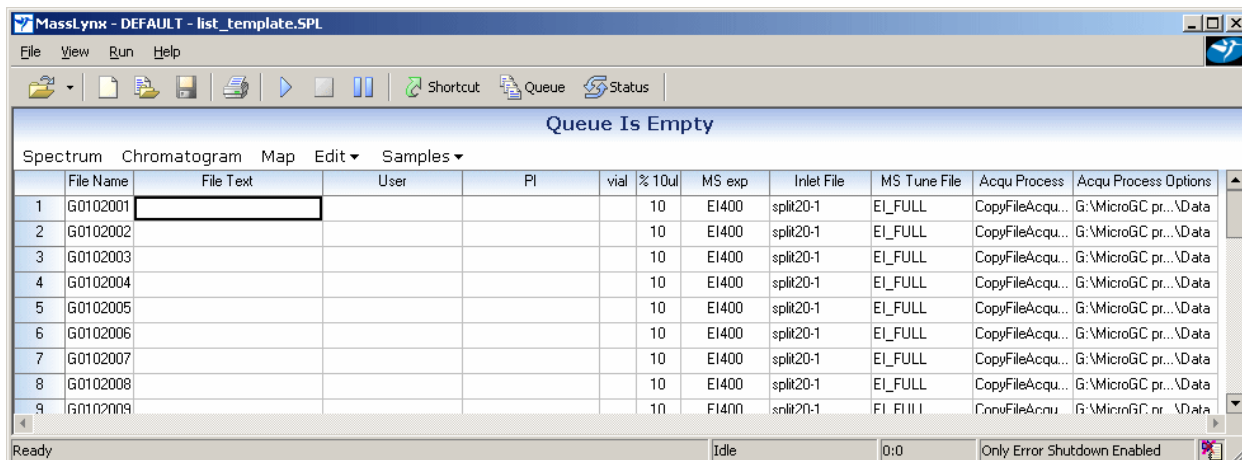
Sample preparation:

1. Dissolve your sample in a compatible solvent.
2. Fill the auto-sampler vial with 0.5 to 1.5 ml of Hexane.
3. Put around 5 μ l of your diluted sample into the auto-sampler vial. (Use only Teflon caps on the vials). **IT IS VERY IMPORTANT THAT YOU DO NOT INJECT TOO MUCH SAMPLE AS IT CONTAMINATES THE SYSTEM FOR EVERYONE ELSE.** You want to inject approximately 10 to 100 pmole/ μ l or 0.5 to 10 ng/ μ l of sample.
4. Place your vial in the auto sampler (shown below) in the next open spot. Remember the location number(s) for entry into the MassLynx software (the instrument control software) software.





Instrument operation:

1. Find the MassLynx sample list page (shown below) on the acquisition computer next to the Quatro Micro GC, it should always be up on the computer.






	File Name	File Text	User	PI	vial	% 10ul	MS exp	Inlet File	MS Tune File	Acqu Process	Acqu Process Options
1	G0102001					10	EI400	split20-1	EI_FULLL	CopyFileAcqu...	G:\MicroGC pr...\Data
2	G0102002					10	EI400	split20-1	EI_FULLL	CopyFileAcqu...	G:\MicroGC pr...\Data
3	G0102003					10	EI400	split20-1	EI_FULLL	CopyFileAcqu...	G:\MicroGC pr...\Data
4	G0102004					10	EI400	split20-1	EI_FULLL	CopyFileAcqu...	G:\MicroGC pr...\Data
5	G0102005					10	EI400	split20-1	EI_FULLL	CopyFileAcqu...	G:\MicroGC pr...\Data
6	G0102006					10	EI400	split20-1	EI_FULLL	CopyFileAcqu...	G:\MicroGC pr...\Data
7	G0102007					10	EI400	split20-1	EI_FULLL	CopyFileAcqu...	G:\MicroGC pr...\Data
8	G0102008					10	EI400	split20-1	EI_FULLL	CopyFileAcqu...	G:\MicroGC pr...\Data
9	G0102009					10	EI400	split20-1	EI_FULLL	CopyFileAcqu...	G:\MicroGC pr...\Data

2. The "File Name" column should already be filled in and should not be altered. The file name includes the date and sample number. The page shown is for January 2nd. A directory with the same name as the "File Name" will be created and will hold your data.
3. Enter the sample code in the "File Text" column. The "File Text" entry will be printed on hard copies of your data, so you should put your name there also.
4. Enter your name and the principle investigator in the "User" and "PI" columns.
5. The "vial" column selects which vial the auto sampler picks up and should correspond to where you placed your samples.
6. The "MS exp" column should be either EI400 or EI600, depending on the expected mass of your compound. The numbers stand for the highest masses scanned during the experiment. Other types of experiments are possible but you need to ask Mass Spec. Lab. permission to perform any other type of analysis.
7. The "Inlet File" column is used to set the GC temperature program and the inlet conditions. Unless you know what you are doing use either split20-1, split10-1 or splitless. The split methods flush most of the vaporized sample so that the injected sample fills a reasonably small length of column.
8. The "MS Tune File", "Acqu Process" and "Acqu Process Options" columns should not be changed. If the columns are accidentally changed, paste them back in from adjacent rows.
9. Save the sample list page after you have entered the proper information by selecting File>Save from the menu or clicking the shortcut icon .
10. To run the samples, highlight the desired entries by dragging over the row numbers at the far left on the sample list page and then click the blue arrow  at the top of the page. There may be a waiting period before your sample is injected due to other samples in the queue or initial temperature setup.
11. Please use one of the work station computers to analyze your data, not the data acquisition computer. The data will be accessible from the workstations as soon as it is complete.

Notes: Copy and paste cells with "ctrl insert" and "shift insert"
Edit cells by double clicking inside them.

Data Analysis on Mass Spec. Lab. Work Station Computers

In order to use all the functions available in MassLynx, you need to copy your data to the local hard drive from the network drive, proceed as follows:

1. Double click on the Archived MSdata icon on the desktop as a shortcut to the G: drive.
2. Navigate the directories for the proper instrument and month. Finally open the data folder.
3. Copy your data (the entire folder) to the corresponding "Retrieved data" folder on the desktop.
4. Click the "Chromatogram" menu found just above the table in MassLynx. This will display the chromatogram window which will probably display the last file accessed, ignore this file for now.
5. Click on the file>open menu and navigate to the local "Retrieved data" folder and select which file you want. This may remove the unwanted file that opened when the chromatogram window was opened, if not select the unwanted file with the up and down arrow keys and then press the delete key to remove the unwanted file.
6. Click the crossed arrows icon  to see more of the chromatogram, drag with the left mouse button to expand a selected area.
7. Click or drag across peaks with the right mouse button to see the mass spectra of one or several averaged acquisitions. LCT users need to check that they have not saturated the detector by single right clicking the chromatograph peak at its highest point and then checking the mass spectra for peaks labeled with a question mark indicating saturation. If saturation has occurred it may be possible to use lower positions on the peak for to obtain unsaturated mass spectra.
8. To perform background subtraction, first click the summation tool . Peaks and background are selected by dragging with the right mouse button, the peak must be selected first and then the background must be selected.
9. To switch from replace graph to add graph mode (display more than one graph at a time), click the add or replace icon .