5890 Series II Gas Chromatograph/5971 Mass Selective Detector

Operation Instructions <Manual Injection>

1. Turn computer on and click on icon that says HP5890_5971 GC_MSD.
2. Go under **View** at the top of the screen and select **Instrument Control**
3. Go under **Method** at the top of the screen where you can either **Load** a previous method or edit the one that is already there.
4. Save the method under a different name if you edited entire method.
5. If you **Edit Entire Method**, it goes through step by step and asks you for the parameters.
6. If you only want to change a few things you can do it from the main instrument control screen by clicking on the OVEN or MS icons and changing the temperatures or scan ranges.

Note At this point you can manually inject by removing the autosampler and following directions 7-12. Or, you can follow the Autosampler directions.

7. Either go under **Method** at the top of the screen and select **Run**, or click on the icon at the top of the instrument control panel with the green arrow.
8. Type in your name, a name for the data file, and the name of the sample you are running.
9. Press START RUN
10. Wait until the red light on the instrument goes on and a screen comes up that says it is ready.
11. Inject your sample into the injection port and press the start button on the keypad of the GC.
12. If you had a solvent delay, click "no" when it asks if you would like to override it.
13. Wait until the run is over and then go to **View** at the top of the screen and select **Data Analysis**
14. Go to **File** at the top of the screen and select **Load**
15. Type in the file name or browse for it to get your data file
16. To determine area under the peak and retention time go under **Chromatogram** at the top of the screen and click on **Percent Report** . If the peak is too small for the computer to obtain a percent report this can be done manually

    - Zoom in by making a box around the area by clicking with your left mouse button and dragging over the area
    - Manually integrate by clicking with the right mouse button at the point you wish to start measuring the area and dragging until you wish to stop measuring. A red line should appear and you can find the results of this by going to **List Results** under **Chromatogram**.

1. To determine the identity of the peak, double click on the point with your right mouse button and a mass spectrum should appear. With your mouse pointing to the mass spectrum, double click with the right mouse button and a library match(es) will appear for this spectrum.
2. **Library Search Report** under **Spectrum** will provide library match(es) for all peaks that the instrument finds. If you would rather compare on your own, you can obtain mass spectra of any substance in the library by selecting **Parametric Retrieval** in the **Spectrum** menu and search for the substance by a variety of parameters.

Last Update: 17 February 2000 Christina Moore and Eric Williamsen