

# Standard Operation Procedure

## Agilent 7890B GC-MS system



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1. PC Workstation Access.  
Username = admin  
Password = 3000hanover
2. Hardwares.  
The hardware of the GCMS system includes three major parts, the GC, the MSD, and PAL3 autosampler. Gases connected to the system are, He as the carrier gas, H<sub>2</sub> and Air for FID detector.
3. Precautions
  - a. DO NOT turn off the power button on the MS detector without venting the system.
  - b. DO NOT use the remote of the PAL3 autosampler.
  - c. DO NOT expose the end of the column in air without a stopper.
4. Sample preparation.
  - a. The autosampler supports standard size 2ml GC vials and 1ml glass wells in 96 well plates.
  - b. Samples can be prepared in most organic solvents. Water, inorganic acid, inorganic base, and involatile salts should be avoid in GCMS samples.
  - c. Samples should be pre-filtered before bring in for analysis.
  - d. Recommended sample concentration range is from 15ug/ml to 10mg/ml.
5. Method preparation.
  - a. Load a template method with “Method” -> “Load Method”.
  - b. Modify the template method with “Instruments” options. The setup of the method includes “Inlet”, “Autosampler”, “GC” and “MS”. Go through these setups and save the method as a new method.
6. Edit sequence.
  - a. Use “Sequence”  “Load sequence” to load an existing sequence, then use “Sequence”  “Edit sequence” to open the sequence setup page.
  - b. Add the sample information into the sequence table. Click “OK” to quit the sequence editing.

- c. Use “Run sequence” button to submit the sequence to run the sequence from the first sample, or use “Sequence” □ “Position and Run sequence” to starting running the sequence from the middle of a sequence.
  - d. When a sequence is running, use the “Edit” button in the status bar to get into the sequence setup page and add new samples or insert samples into the running sequence.
7. Data analysis.
- a. All the raw data should be saved under D:/MassHunter/GCMS/1/data folder. This folder will be uploaded to the server and the data will be available online.
  - b. Use “MassHunter WorkStation” for data analysis. Use “File”□ “Load” to open the raw data. The TIC trace will be displayed in the “Chromatogram” window. Double click on a time point, and the MassSpec of this time point will be displayed in the “Spectrum” window.
  - c. Right click and use “integrate chromatogram” for automatic integration, or use the “Manual Integration” tool to add peaks manually. Right click and select “Integration Peak List” to view the integration result.
  - d. Use “File”  “Report”  “Print Report” to generate a report file in .pdf or .csv.
  - e. Right click on the chromatogram or spectrum window, use “Export” to create the data table file.
8. Instrument reservation.
- a. Users will get access to the instrument calendar after taking the instrument training. The schedule of the instrument will be displayed on the calendar, and users can book the instrument time on the calendar.
  - b. The maximum time for one reservation is for one whole 96 well plate. Between two plates, users must leave at least 8 hours for other users.
9. Data server information.

To connect to the catalysis center data server:

In the explorer window, display "this PC", then choose "add a network location", Input "\\128.32.246.30\catalytic center data" when you are asked for the network address. (If you are using a Mac, there is a similar setup in the Finder.)

Username: catcenter

Password: c@t@lys1s

