How to use the GC-MS: A short introduction.

For the use of the GC-MS you need an instruction! Please ask **Lisa (1926)** for your instruction. If you have any questions, please feel free to ask Lisa.

The instrument is suitable for samples **up to 550 Da**.

1. Prepare your sample. (Do not use screw cap bottles, they don't match with the autosampler.) Your sample should not exceed a concentration of **1 mg / mL**. Do not use high boiling solvents like water, DMF or DMSO. Close the cap using the tool you find in the top drawer. Place your sample into the autosampler.

2. Before you start your measurements, please check the solvent level of the **solvents A (ethylacetate, blue)** and **B (methanol, red)** at the autosampler. Refill the solvents if necessary.

3. Enter yourself into the list (date, time, name, phone number, solvents used in your sample, number of samples).

4. Start your measurement:

4a: GC-MS **is not** running:

- go to: „**5971 – Instrument1**" (desktop or via „Programm-Manager" → „5971 – Instrument1" → „MS Top #1"

- select „Sequence" → „**Edit Sample Log Table**"

    - delet („cut") all entries

    - write your entry:

„Type"	Sample
„Vial"	position of your Vial (1 to 100)
„Data File"	name of your file, up to 8 characters
„Method"	select your method (standard: AKSTAU2)
„Sample Name"	additional information about your sample

    - exit with „OK"

- select „Sequence" → „**Run**"

- „Operator“ your name

- „Data File Directory“ your files will be saved here (standard: c:/data/files)

- start your measurement with „**Run Sequence**“

4b: GC-MS **is** running:

- go to window: „**5971 – Instrument1 – xxx**“

- select „Edit Sample Log Tbl“

- **do not delete anything**

- add your sample at the end of the list

- write your entry:

„Type“ Sample

„Vial“ position of your Vial (1 to 100)

„Data File“ name of your file, up to 8 characters

„Method“ select your method (standard: AKSTAU2)

„Sample Name“ additional information about your sample

- exit with „OK“

Your sample will be measured automatically.

5. Open your files:

- go to: „**Standalone Data Analysis**“ (desktop or via „Programm-Manager“ → „5971 – Instrument1“ → „MS Data Analysis #1“)

- select „File“ → „**Load**“

-Select your file (standard: c:/data/files)

- **upper half** of the window shows your **chromatogram**.

- zoom with left click and drag

- right click and drag shows the **mass spectrum** of the selected area in the **lower half** of the window.

6. Remember to **remove your vials** after you’re finished. If you don’t want to keep them, feel free to use the canister provided.