**SOP: RAMPT start**

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**Initial Version created on:** 30.01.25

**Version Number:** 1

**Last modification date:** 30.01.25  
**Last modified by** Josua Carl

1. **Purpose**

Explaining the operation of the raw to annotation metabolomic pipeline tool (RAMPT).

1. **Procedure**
   1. **Introduction**

RAMPT is a tool for combining mass-spectrometry data analysis with mzmine and following annotation with SIRIUS and GNPS into one program. The program is accessible through the command line (albeit in separate steps) and through a graphical user interface (GUI).

* 1. **Material / Preparations**

To follow along, you need:

* + 1. RAMPT installed (See SOP\_rampt\_installation)
  1. **Methods / Procedure**

After installing RAMPT and moving the shortcut / symbolic link to your desired location you may

* + 1. Start the application by opening the shortcut / symbolic link. This will cause a command-line window to be opened. The first start will maybe take a short while (~1-5min), cause by preparations by python and taipy. This will cause two folders to be created at your startup location. You may delete them after usage, but keep in mind that the startup time is significantly faster (a few seconds) while the remain.
    2. The command-line window is your application! If you close this window, you will close the application. If you only close the tab in the browser, the application will remain unaffected.
    3. The application will automatically detect installed browsers and open a window at the address <http://127.0.0.1:5001/configuration>. If taipy is unable to detect a sufficient browser, you can access RAMPT by entering this address into a browser of your choosing.
  1. **Results**

You should now have an open window in a browser, which displays RAMPT.

* 1. **Troubleshooting**

If there is any trouble during these steps, please post an issue at <https://github.com/JosuaCarl/RAMPT/issues>.

1. **References**

<https://github.com/JosuaCarl/RAMPT>

<https://github.com/JosuaCarl/RAMPT/blob/main/Manual.md>