

Instructions for online submission of VITEK MS MALDI-TOF MS spectra for comparison with the Mabriteccentral database

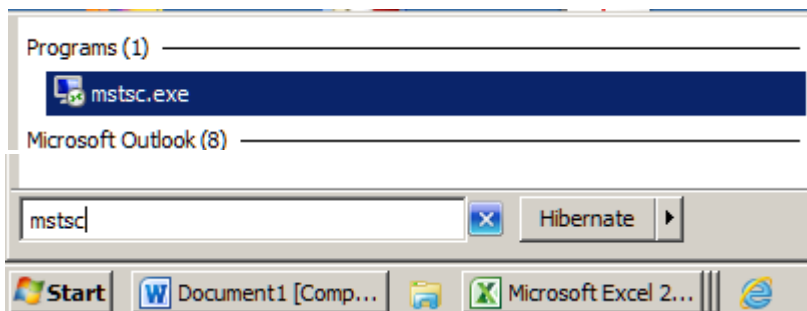
1. How to retrieve MZML files from Myla

All spectra are stored on the Myla-server connected to the VITEK MS instrument.

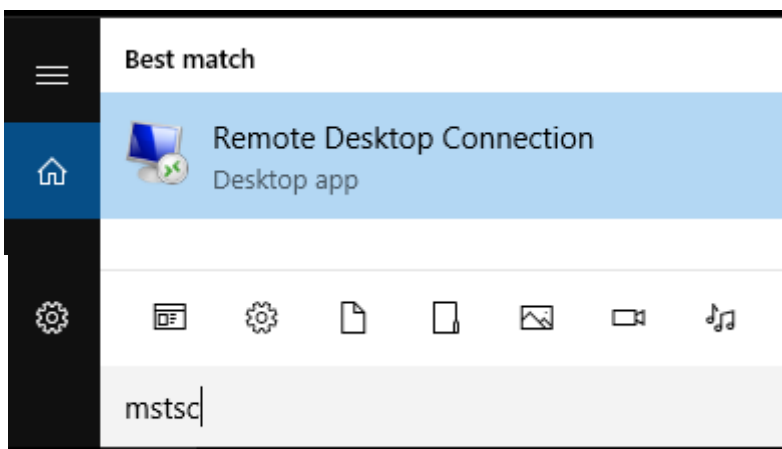
To retrieve selected spectra, at first a connection to the Myla-server must be established.

This is done with **mstsc.exe** that can be accessed through the Windows menu bar at the bottom. Depending on the version of Windows this may vary:

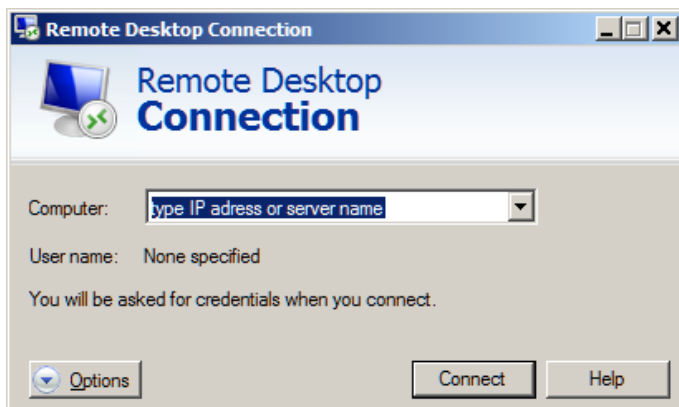
click on the Start button and type **mstsc** in the search field and click on **mstsc.exe** listed in the search results



- a) click on the search command, type **mstsc** in the search field, and click on **Remote Desktop Connection** in the search results.



In the new window of Remote Desktop Connection type in the **server's name or its IP-address** and click Connect



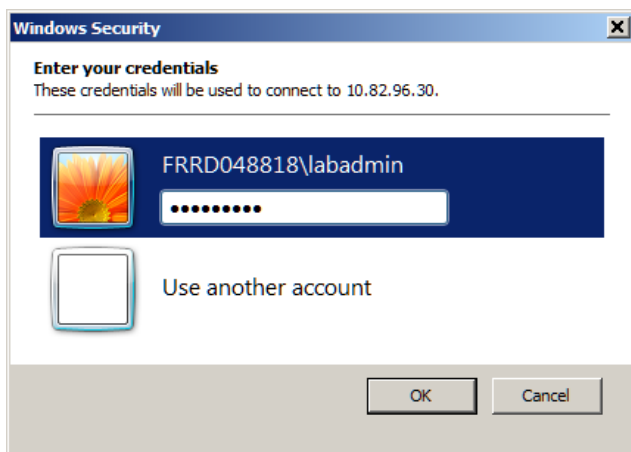
The credentials to connect to the Myla server are by default:

user: labadmin

password: Lab_Admin

Note that the location of special character keys (underscore) depends on the keyboard layout that isn't necessarily the same as the physical keyboard's layout.

In case you have changed or disabled the default account select Use other account and type in the valid credentials.

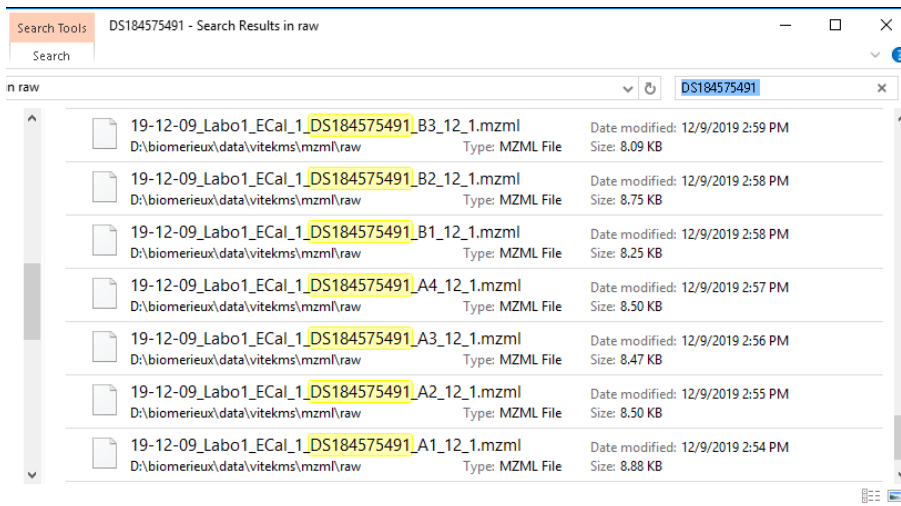
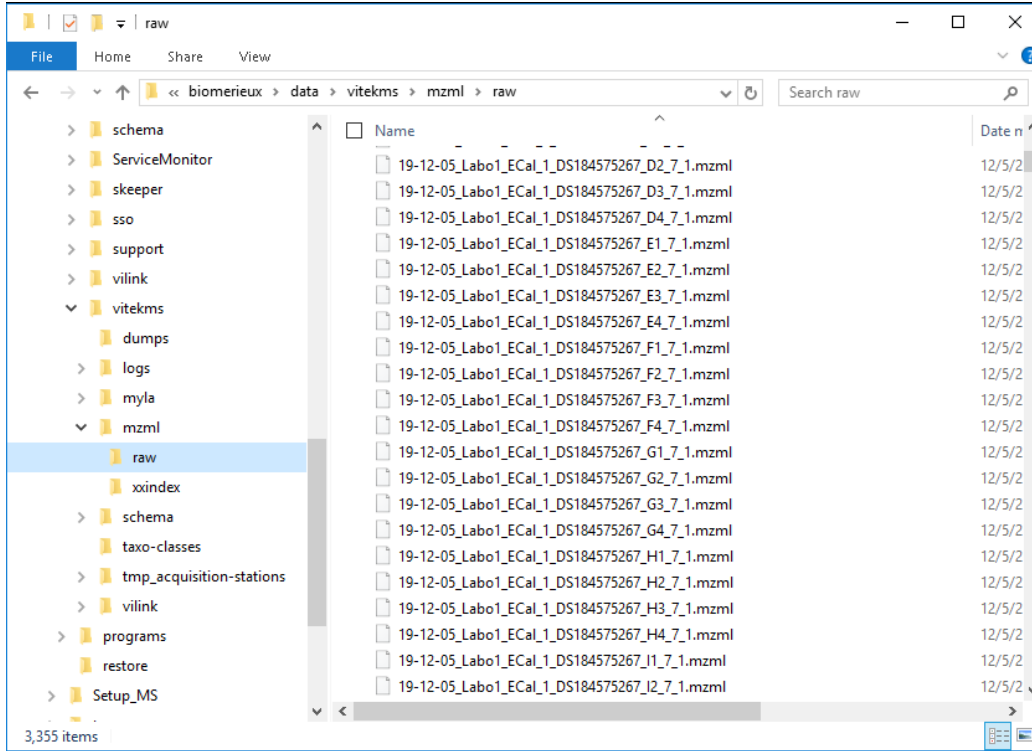


Once connected to the Myla-server, open Windows Explorer.

The mzml-files of individual spectra can be found following the path:

D:\biomerieux\data\vitekms\mzml\raw

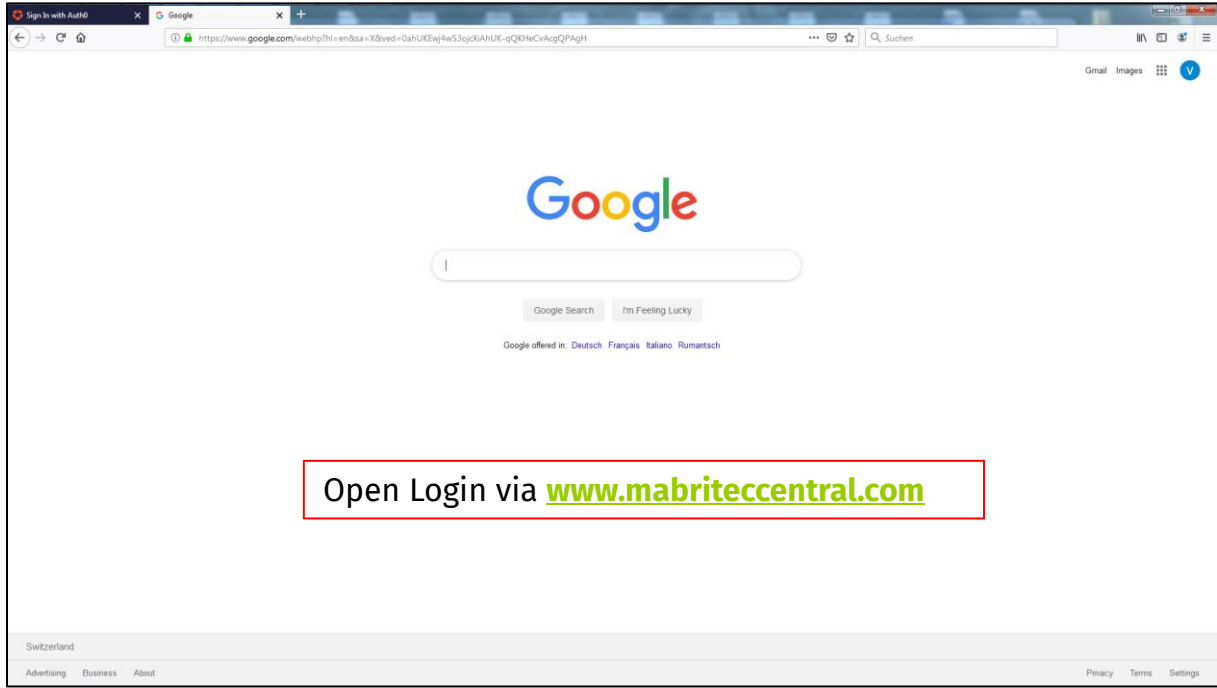
Select the spectra you want to retrieve. If spectra of a full slide were to be selected, these can be filtered by typing the slide number in the search field. The folder containing the mzml-files (raw) can be mapped as network drive or pinned to the Quick access directory for easier access.



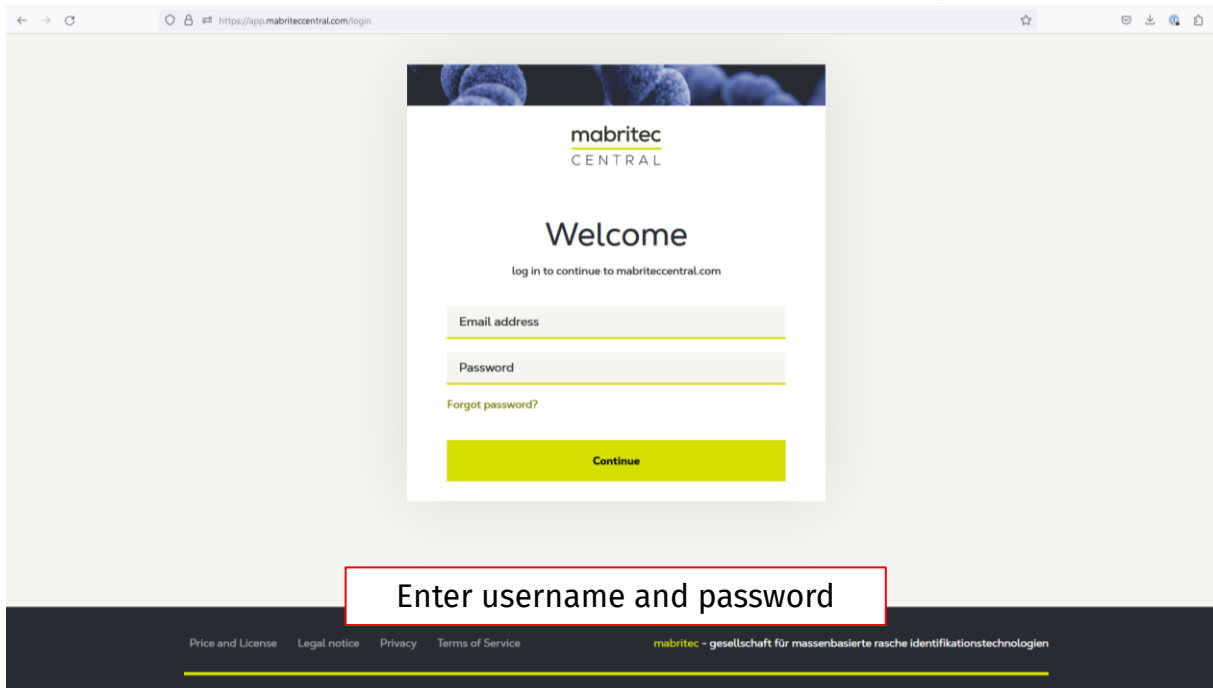
Select the spectra you want to retrieve and right-click on the selection.
Copy the files to a destination of choice (upload folder)
Spectra can now be uploaded from your “upload folder”.

2. How to upload MZML files from Myla to mabriteccentral.com

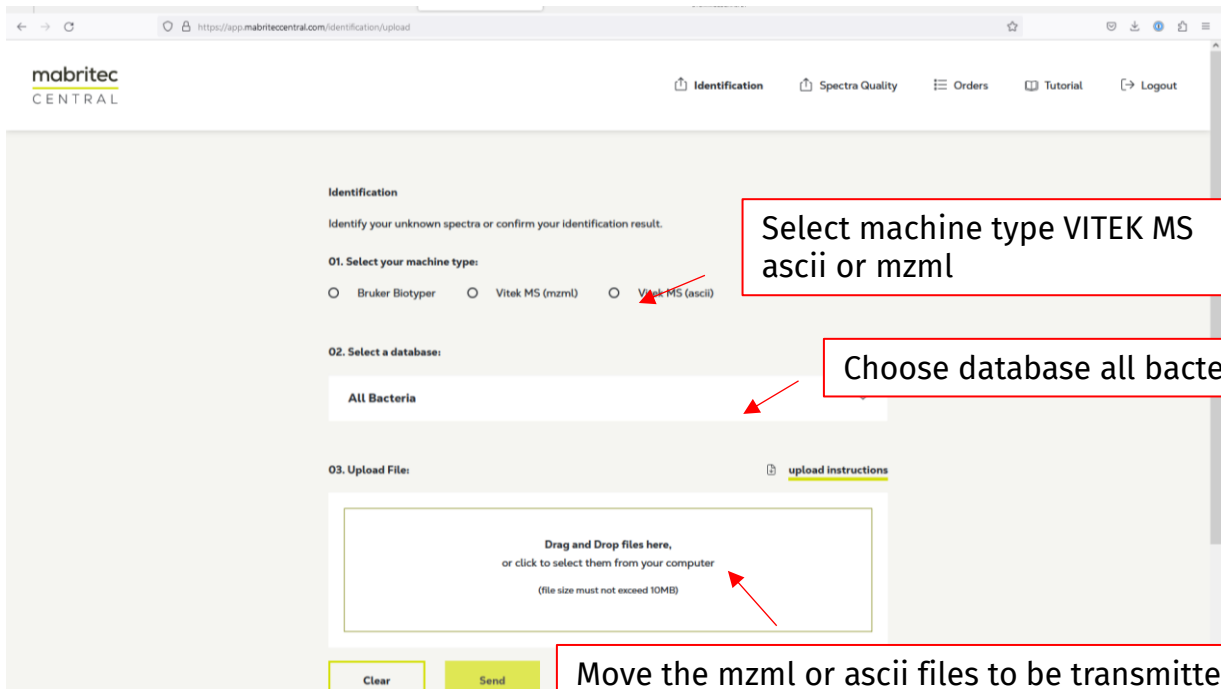
2.1 Access mabriteccentral.com via browser



2.2 Enter your credentials



2.3 Upload your mzml or ascii files

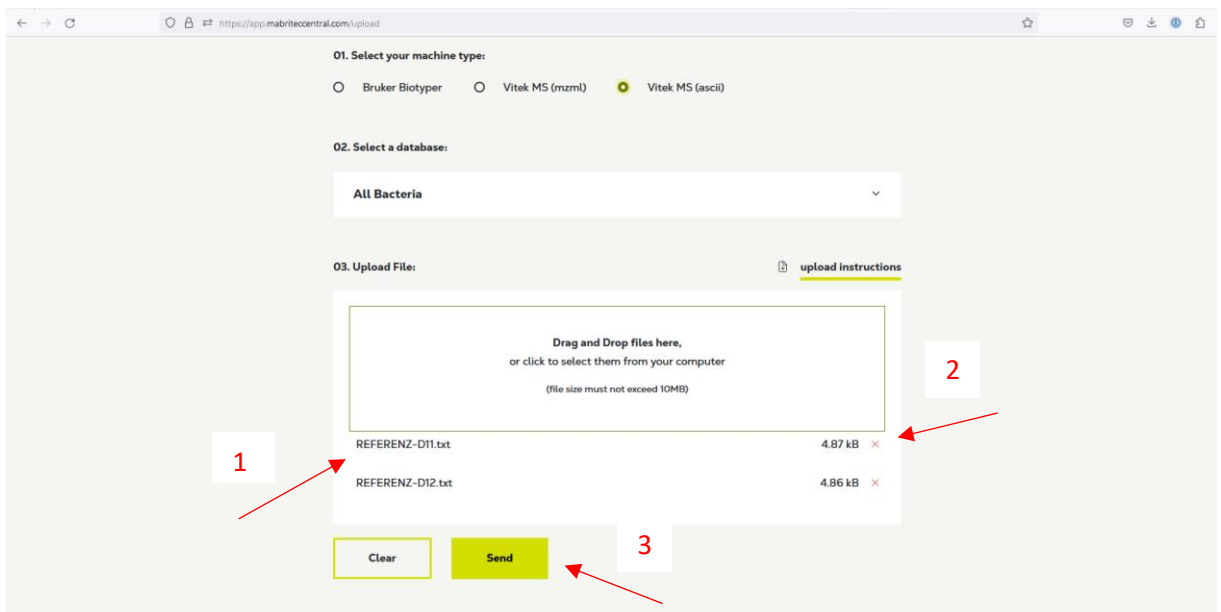


Select machine type VITEK MS
ascii or mzml

Choose database all bacteria

Move the mzml or ascii files to be transmitted into the "Drag and Drop" field. Or navigate to the corresponding folder by "clicking" on the "Drag and Drop" field and select all mzml or ascii files.

2.4 Select/Deselect



1. The selected files are displayed.
2. Files that were selected by mistake can be deleted by means of "delete".
3. Otherwise launch upload and identification by pressing "send".

2.5 Results / PDF and CSV export

The screenshot shows the mabritec CENTRAL web interface. At the top left is the logo. The top right has navigation links: Upload, Orders, Tutorial, and Logout. The main content area displays order information: Order ID: 561f4c7e-b041-4af7-892a-f7f9d5a9a651, Order date: 20.3.2023, 11:33:24, Number of spectras uploaded: 8, and Database used: All. To the right of this information are links for 'CSV export' and 'PDF export'. Below this is a table with two rows of results. Each row has a 'more details' button.

Filename	Sample Name	Qualified result	Non qualified result
042_Mabritec_AXIMA_I09.mabr_E QA20_0002.2J1.txt	042_Mabritec_AXIMA_I09.mabr_E QA20_0002.2J1	● Escherichia coli	● ---
more details			
042_Mabritec_AXIMA_I09.mabr_E QA20_0002.2J2.txt	042_Mabritec_AXIMA_I09.mabr_E QA20_0002.2J2	● Escherichia coli	● ---
more details			

Results are displayed as a list and can be exported as a PDF or a CSV file