Userguide for installing the Proteogenomics MetAP finder

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To make use of this software package it is necessary to install all the third party applications on your computer. All the packages that are necessary are shown in figure 1 below.
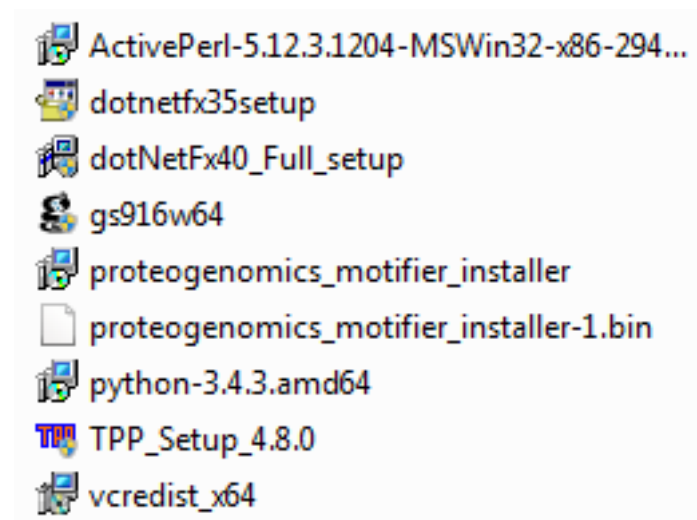

Figure 1: All the packages that the user needs for a complete installation

Now it's time to install the proteogenomics MetAP finder. This is possible to double-click on the exe-installer. The screen that is obtained after the double-click is shown on figure 2. The program asks if the user wants to continue this procedure. Click on 'Yes' to proceed.
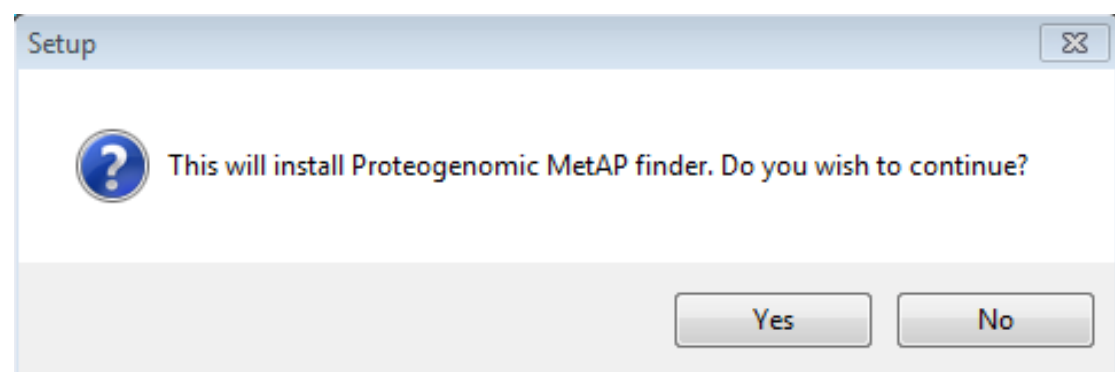

Figure 2: Question to continue with the procedure

Then the program asks which language you prefer. The user can choose between Dutch and English. This screen is shown in figure 3.
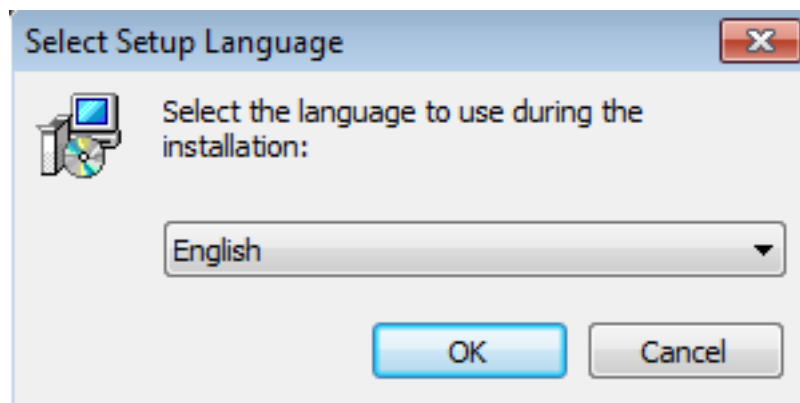

Figure 3: Choose between English and Dutch

Now, the screen appears that gives the user some information about the program that is gonna be installed on the computer. Click 'Next >'' to continue with the procedure. This is all shown in figure 4.
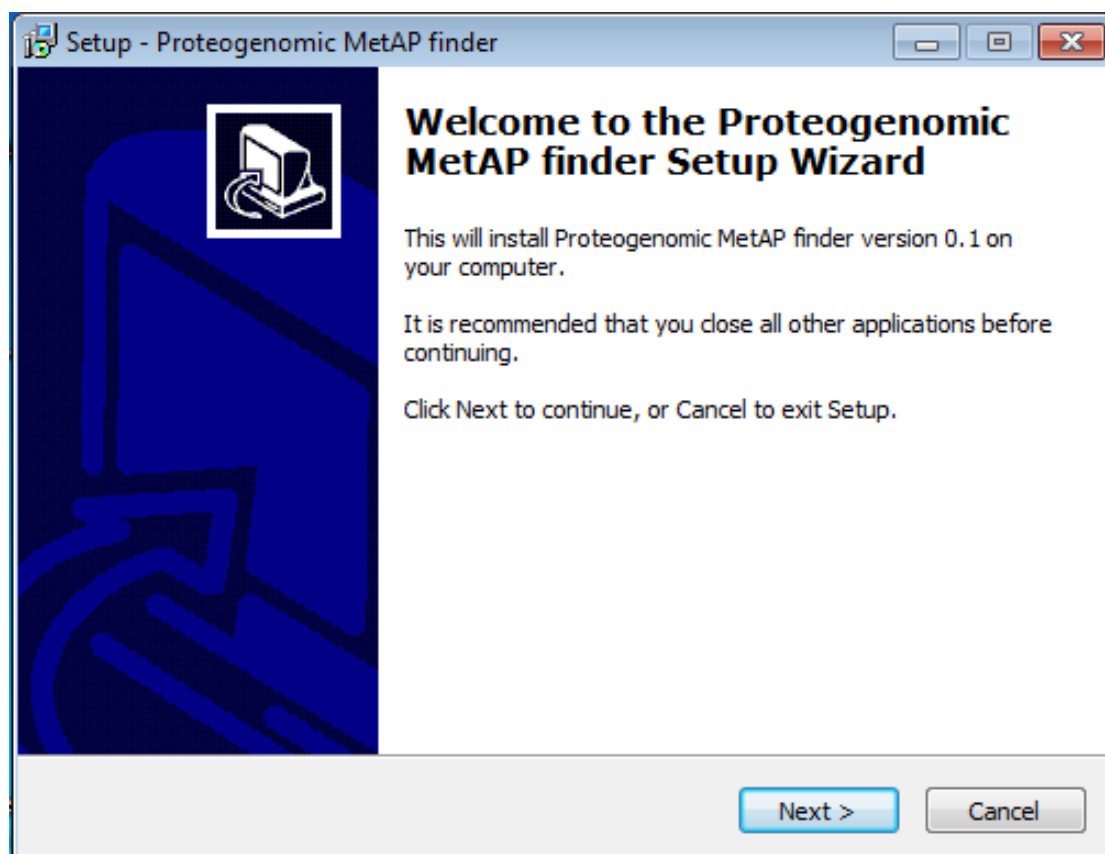

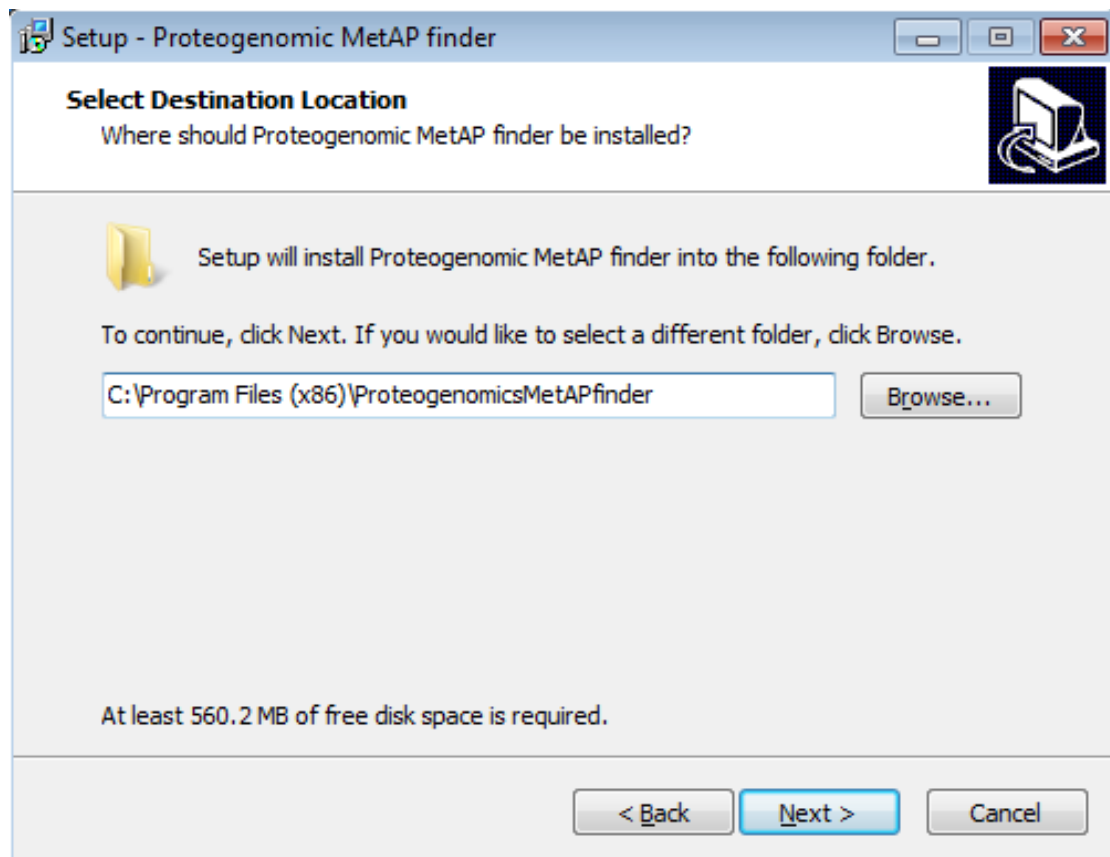
Figure 4: Welcome-message of Proteogenomic MetAP finder

Figure 5: Selecting the destination of Proteogenomic MetAP finder

Then the user gets the oppurtunity to select a different installation-folder. For this program is at least 560.2 MB of free disk space required. Keep that in mind before you proceed with the installation. If the user chose the right folder, the user can click on the 'Next >'-button to proceed with the installation. This screen is shown in figure 5.

Afterwards, the user can choose where the program shortcuts folder should be placed. Click on the 'Next >'-button to proceed. This is shown in figure 6.
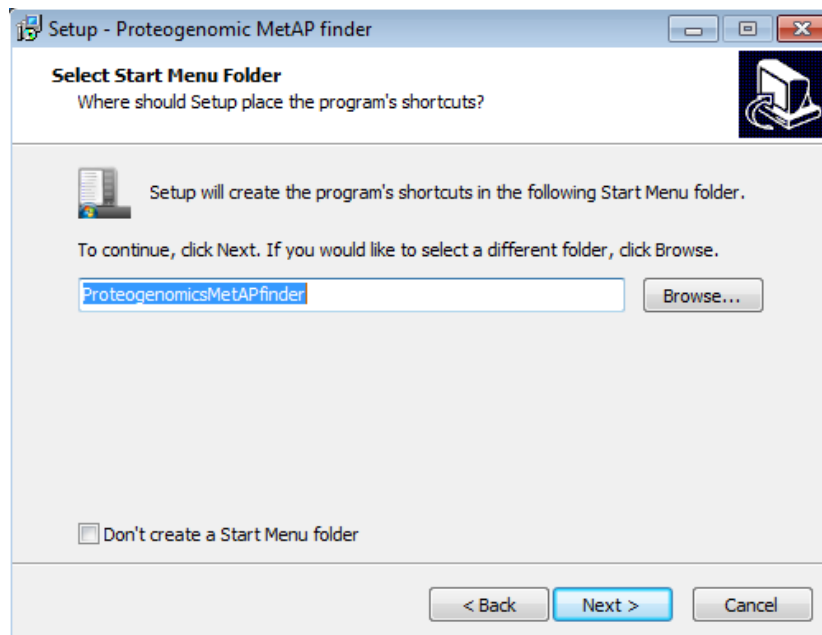

Figure 6: Select the start menu folder

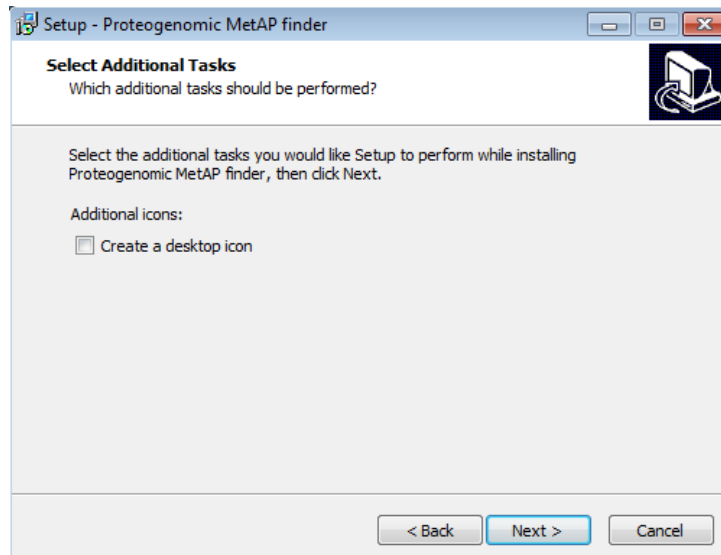Then, the user can choose to have an addional desktop icon. This is shown in figure 7.

Figure 7: Select additional icons on the desktop

After setting the needs and settings of the user, the user gets an overview of all the chosen locations. This is shown in figure 8. The user can now click on the 'Install'-button to install the Proteogenomic MetAP finder.
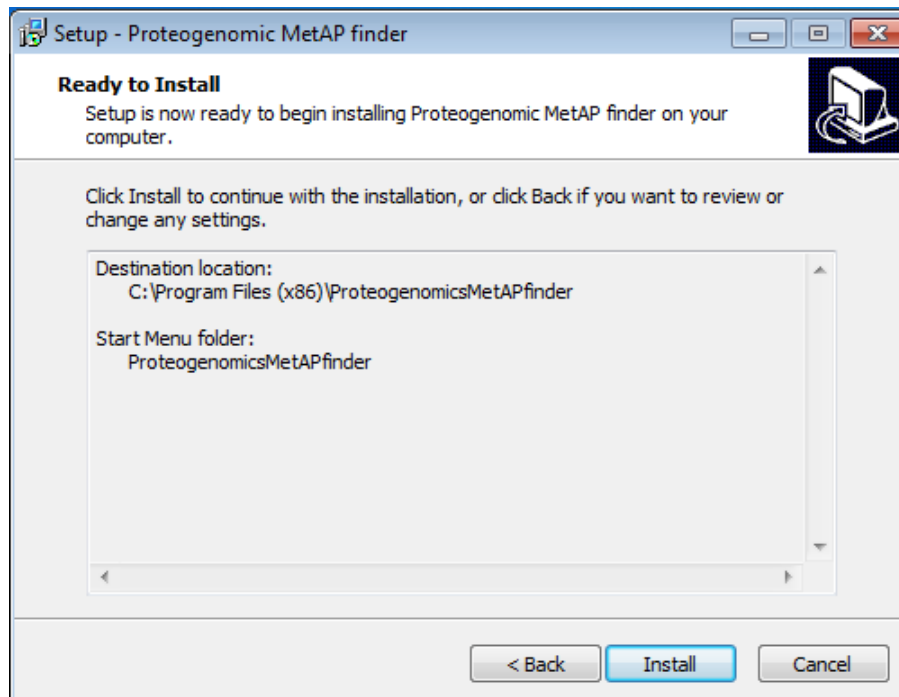
Figure 8: Overview of the chosen destination folders

The installation takes a few minutes and then you are ready to go. The user can click on the 'Finish'-button to finish the installation. It is not possible to launch the program directly, so the user needs to uncheck this. This is shown in figure 9.
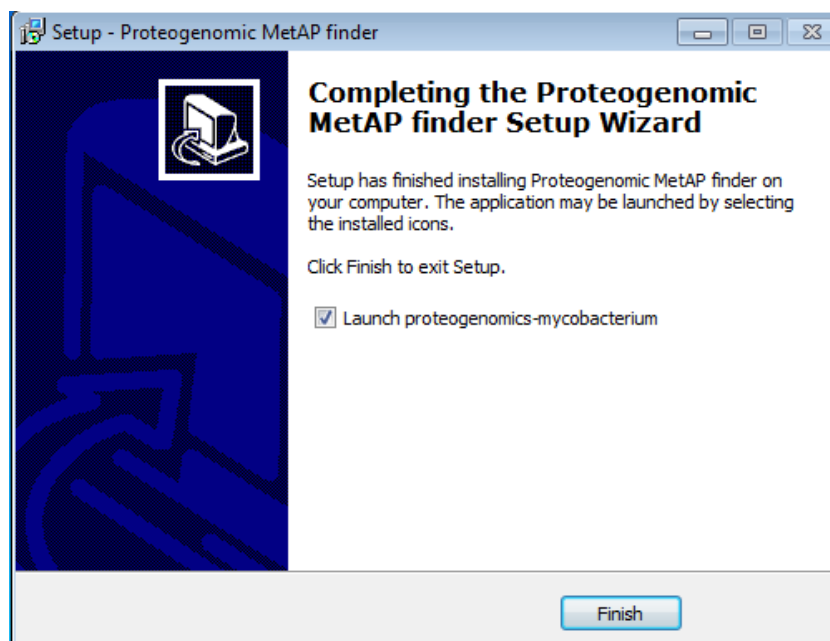
Figure 9: Completing the installation

The user can now click on the start button to search for the folder with the shortcut. It should looks like figure 10.
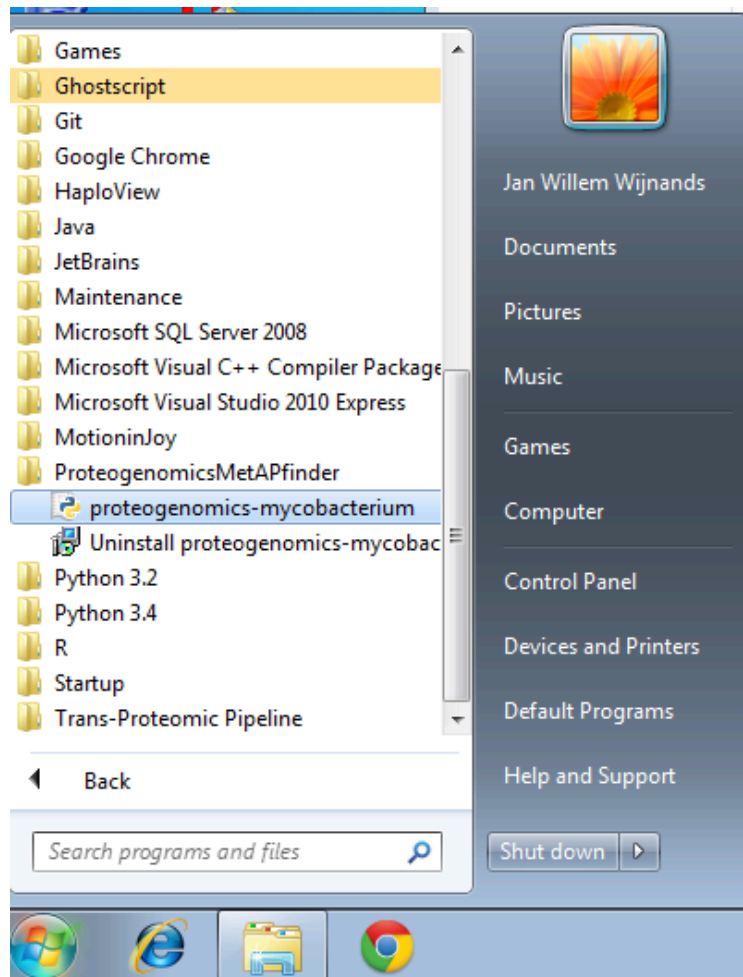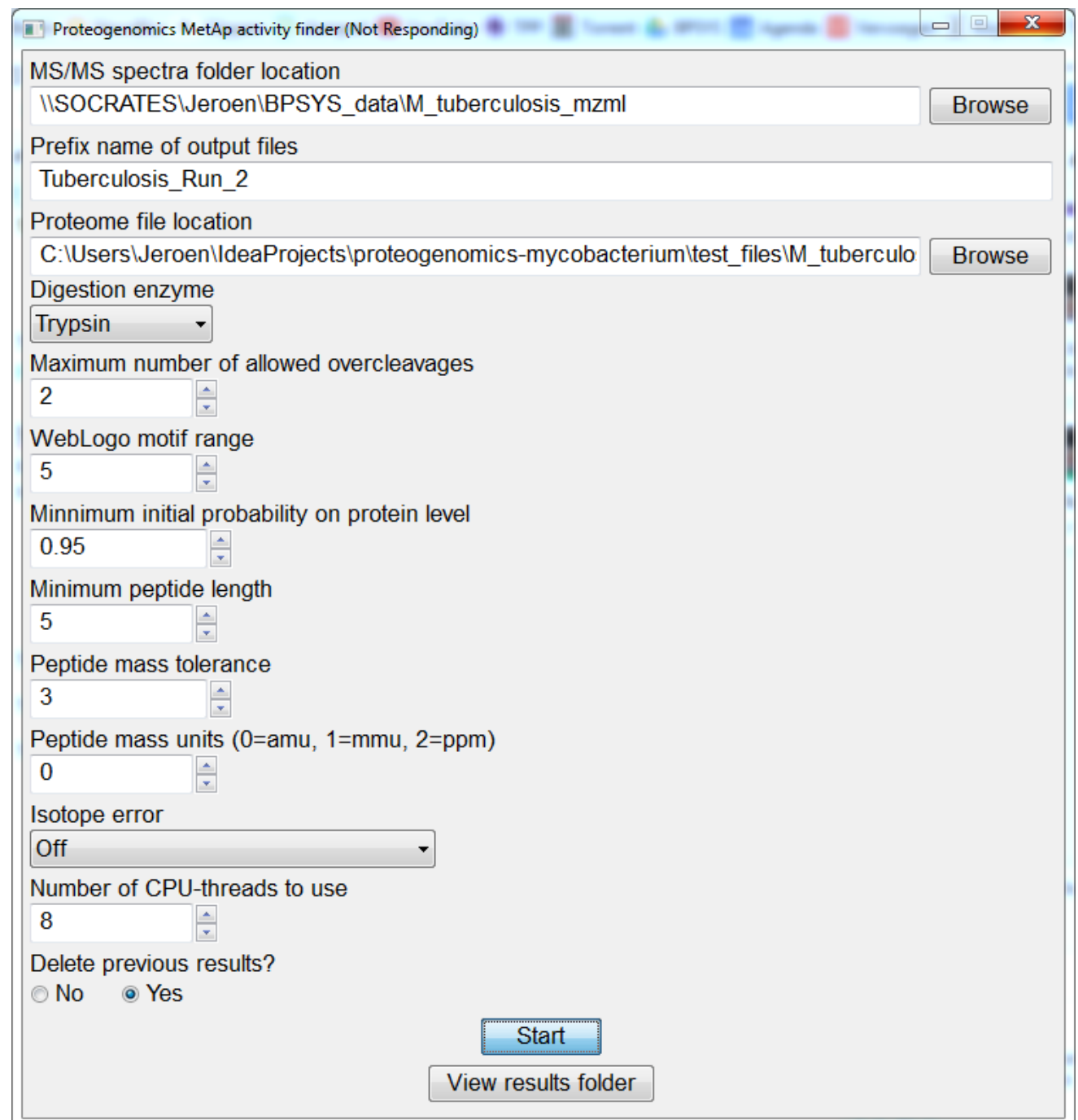
Finally, there is the main page of the Proteogenomics MetAP finder. The user can adjust all the parameters himself. This is all shown in figure 11.

Figure 11: Proteogenomics MetAP finder