PEAKS Data Analysis Pipeline

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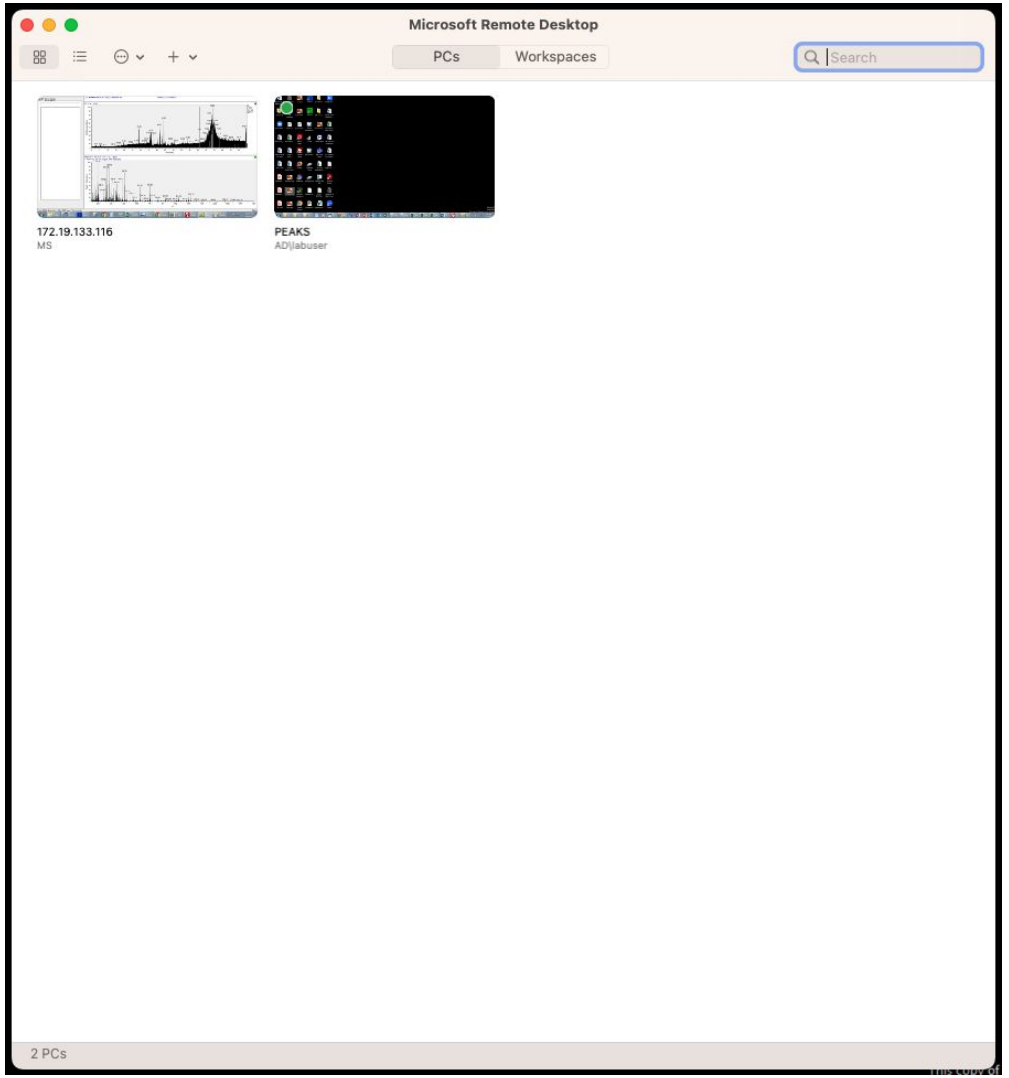
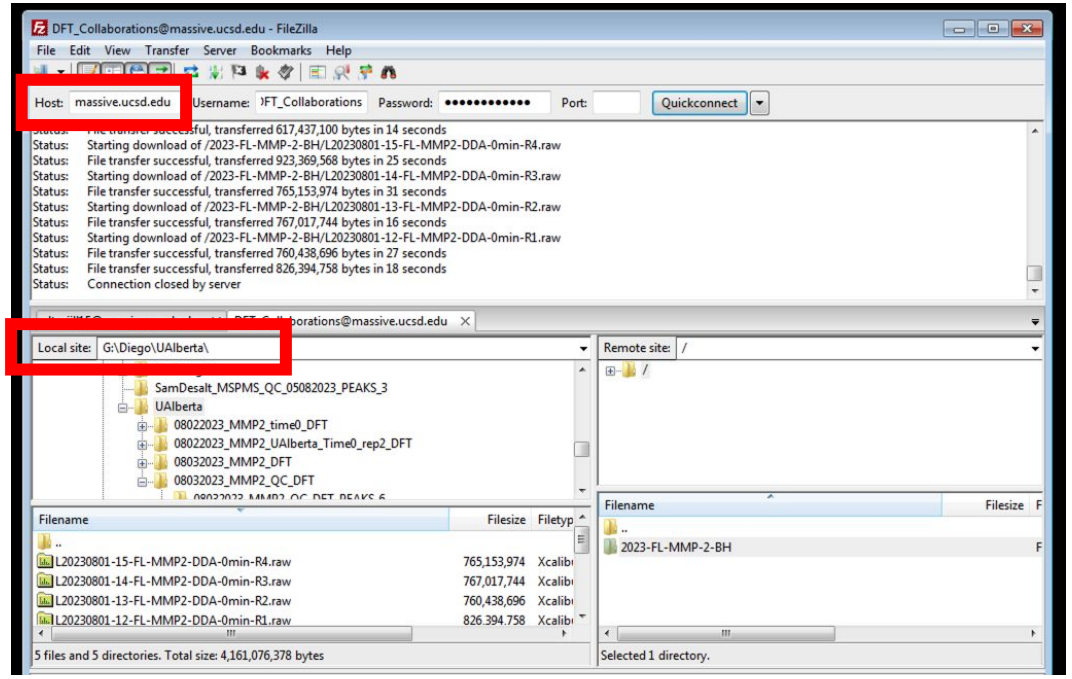
1. Go to Microsoft team viewer; Select the Peaks computer



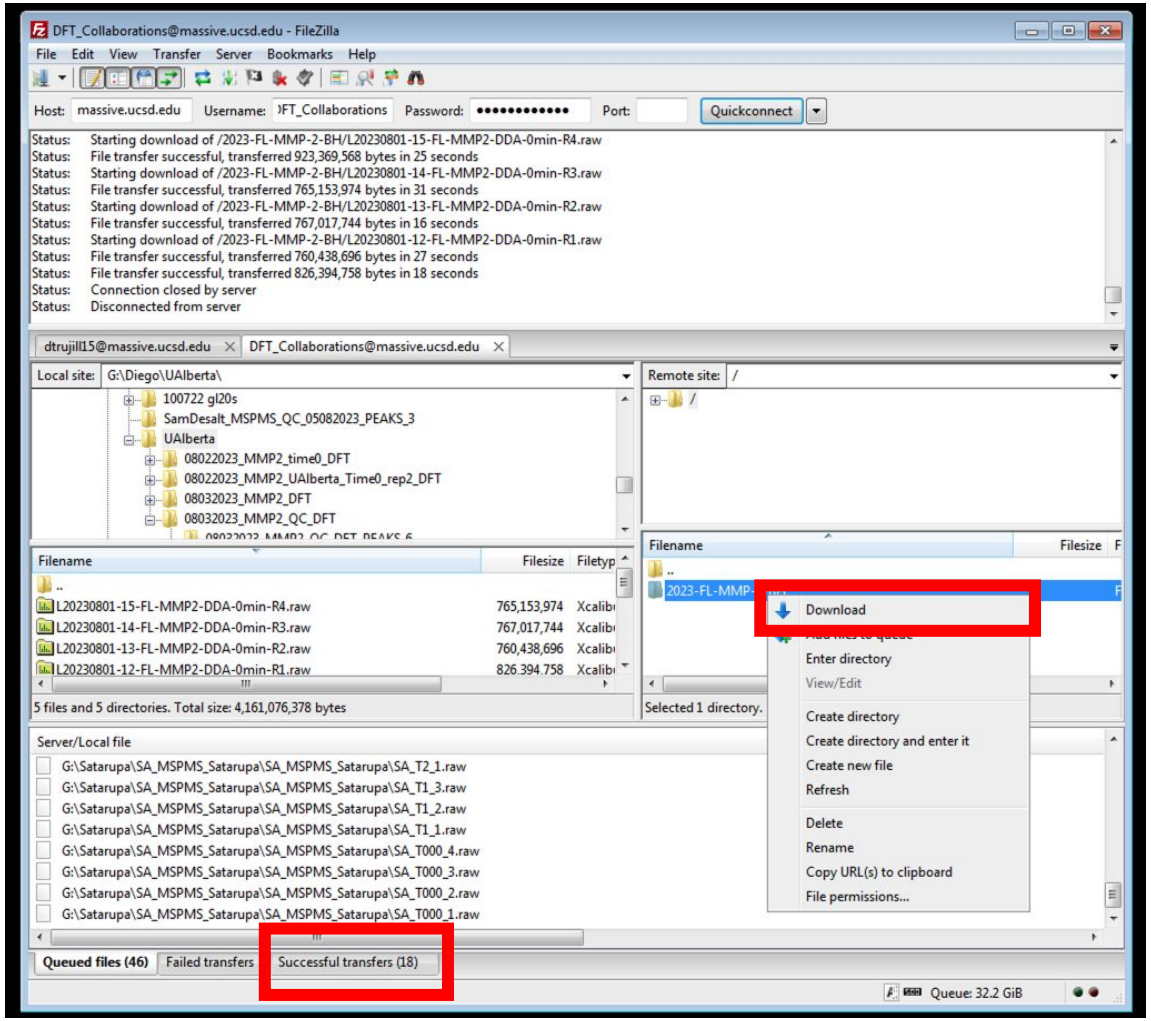
To remote in to the MS computer and PEAKS computer (3rd floor, Hook Lab), use UCSD Wifi or UCSD VPN with Cisco AnnyConnect (Icon above)

pwd for MS comptuer = Cathep$inV

2. Use Massive/Filezilla to transfer MS/PEAKS data to eachother and to home CPU

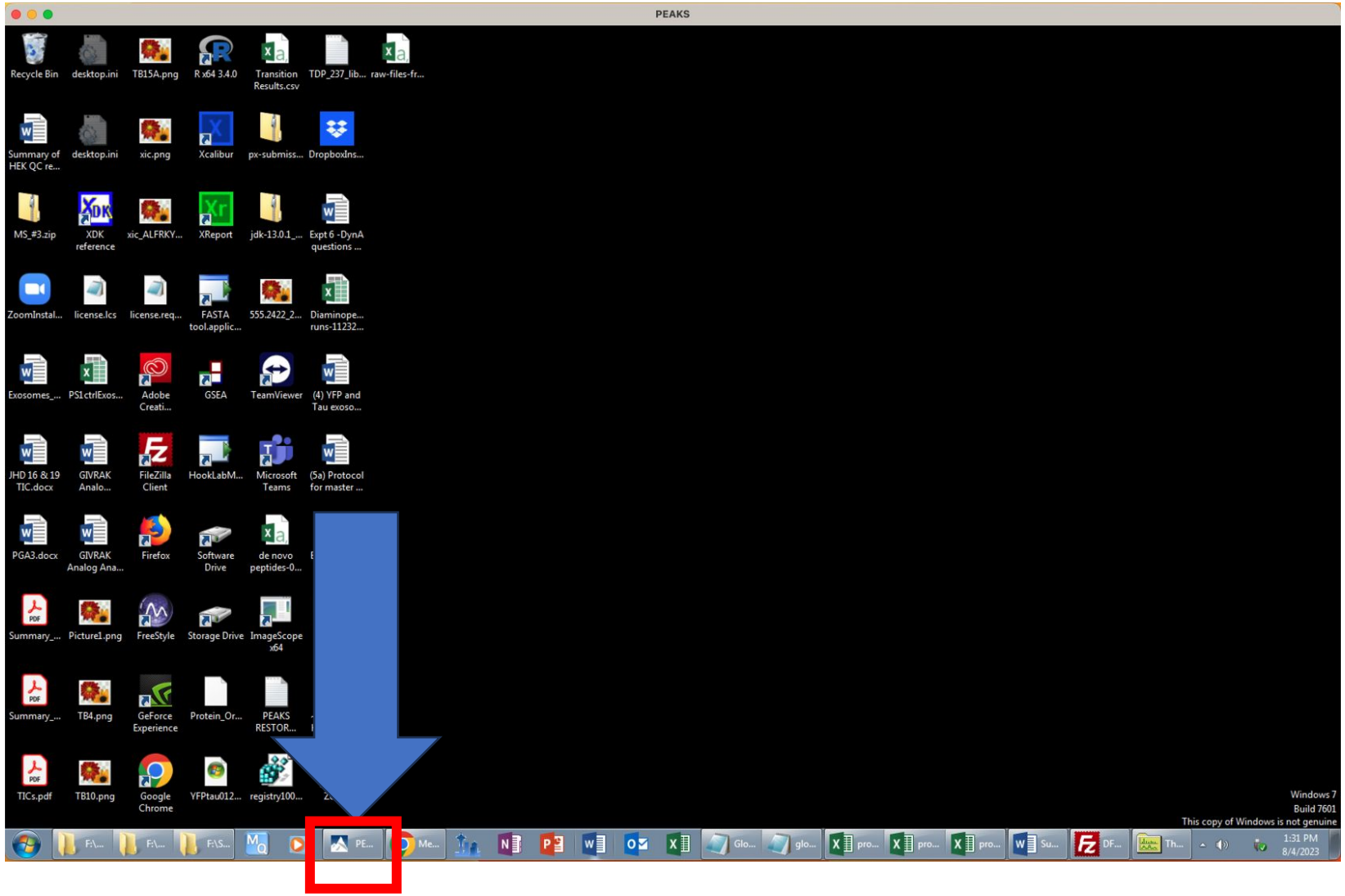


- Sign in using the host “massive.ucsd.edu” (shown above) and with personal massive credentials
  - For this step, we will want the data to be on our remote site already; this means it should have been placed on massive/filezilla from the MS computer prior to this protoocol
- Find local directory where you want your data on the left side; this is usually in the G drive (easystore)

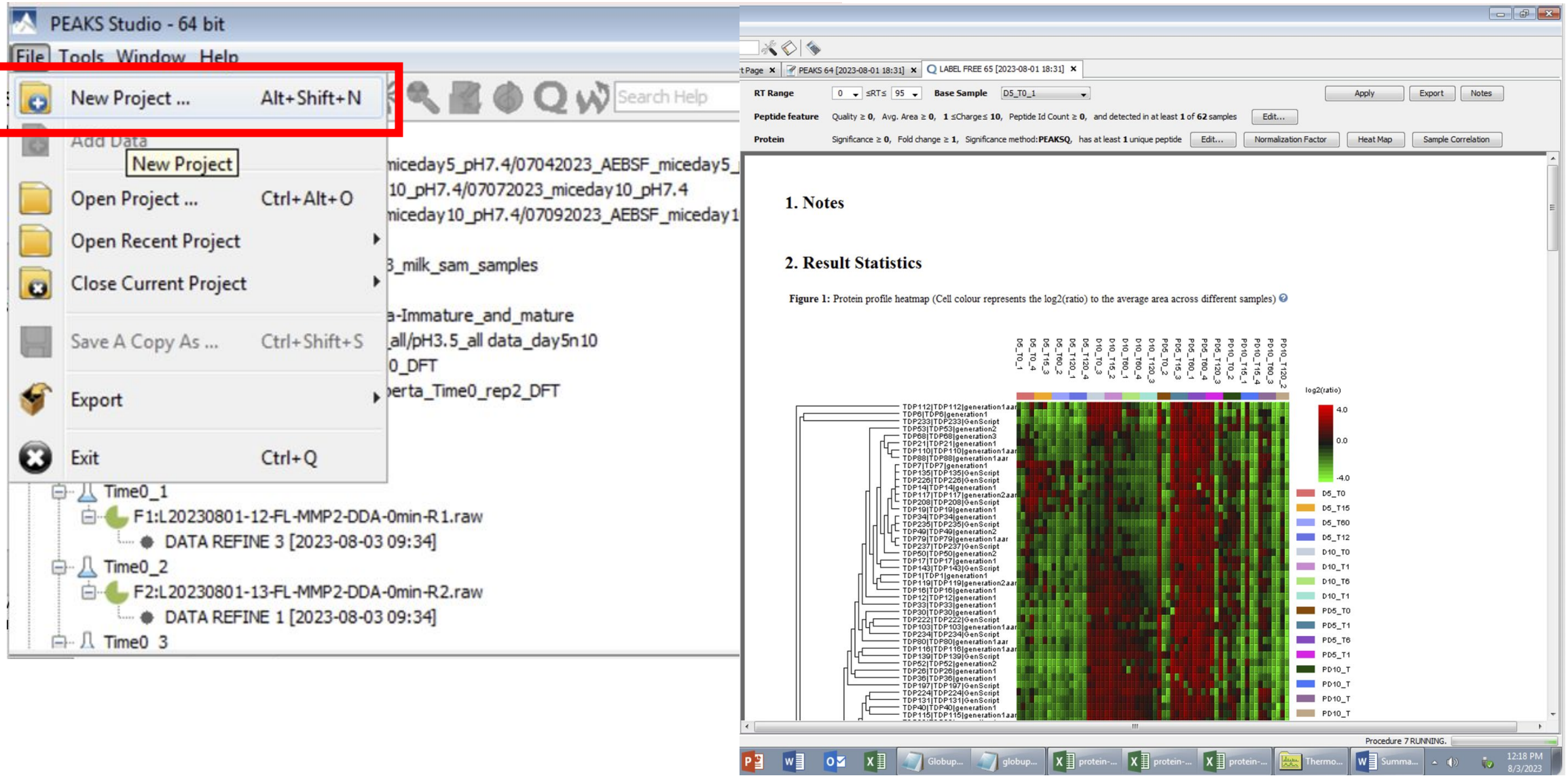


- Double/Right click to get a menu selection; Download from the remote site to the local site on the PEAKS computer
- Find local directory to ensure transfers were made succesfully. Can also check the tab at the bottom in peaks

3. Open Up PEAKS Software

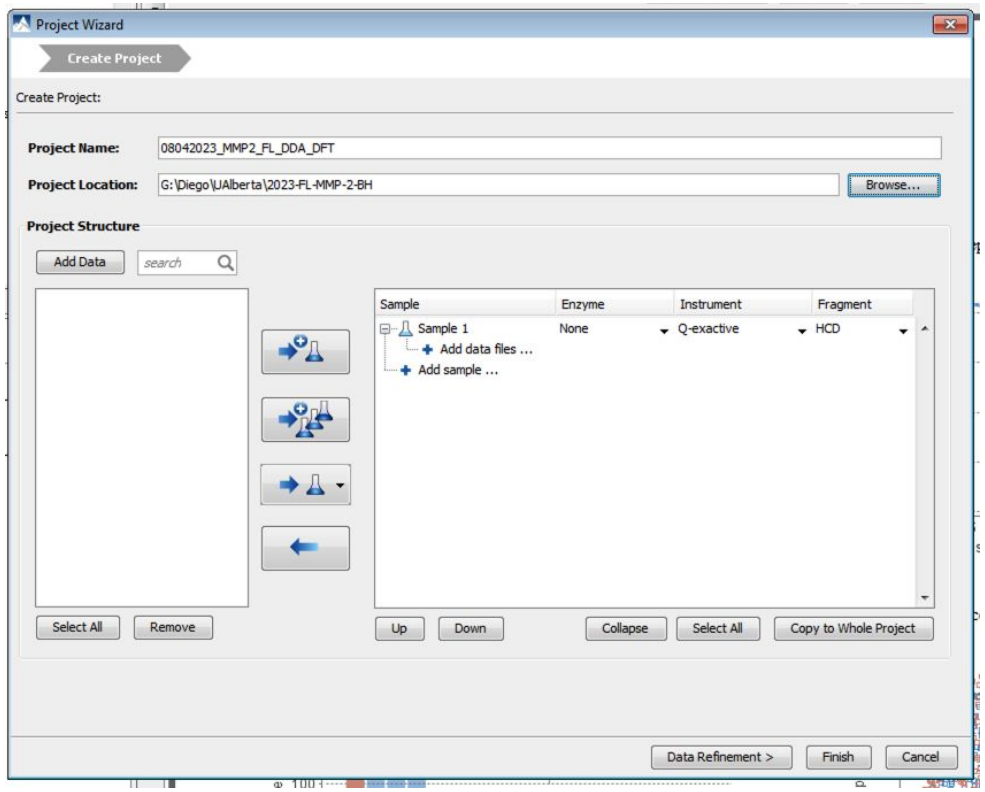


4. Create a New Project in PEAKS



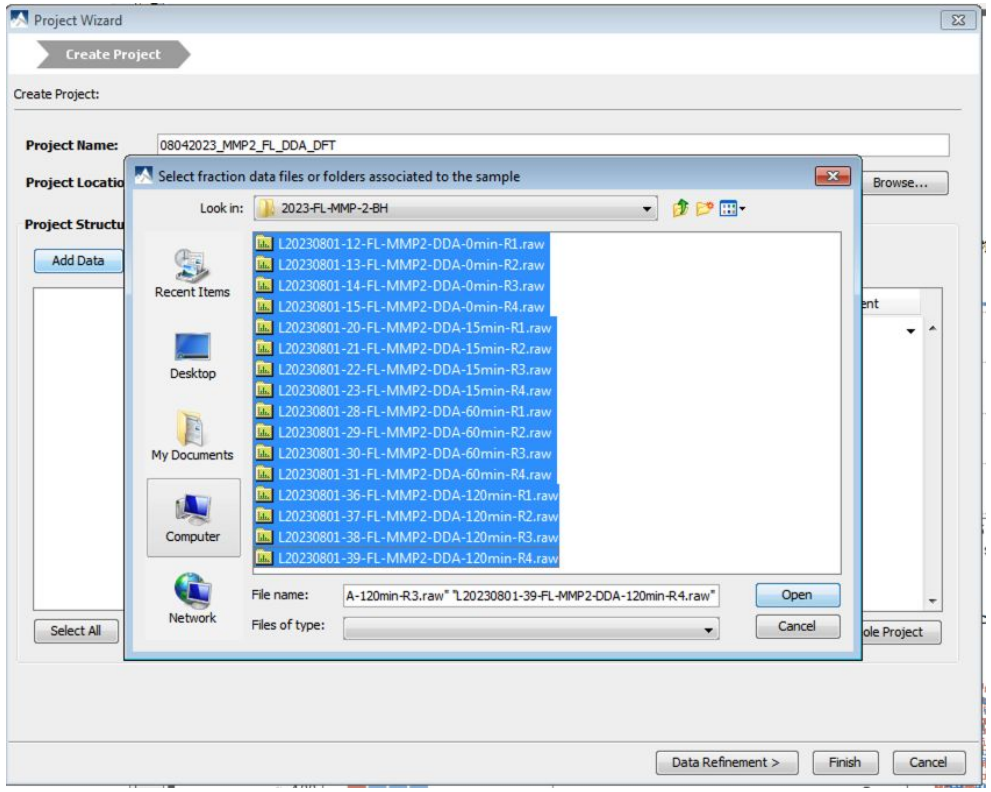
5. Select data to add to PEAKS project

A.



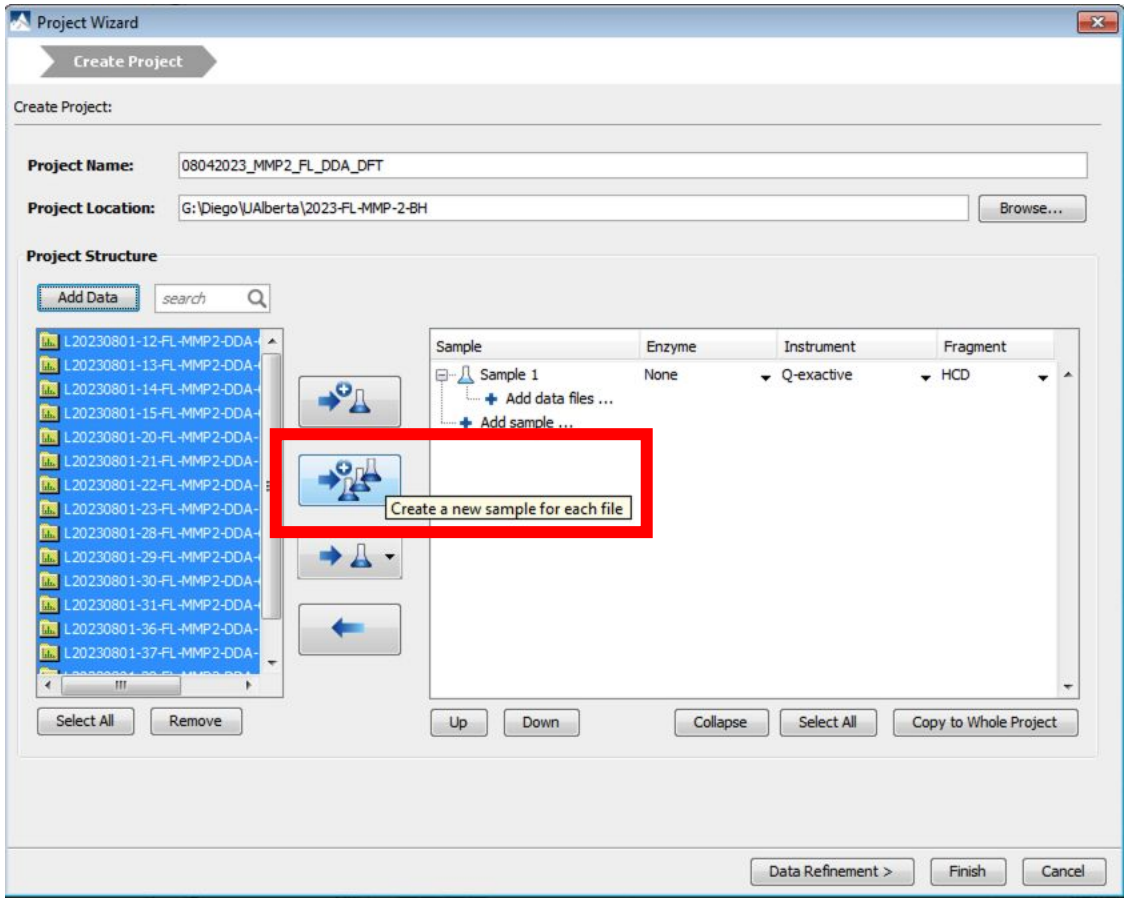
- First, create a project name, and select a project location
  - i.e. Easy Store; G:\Diego

B.

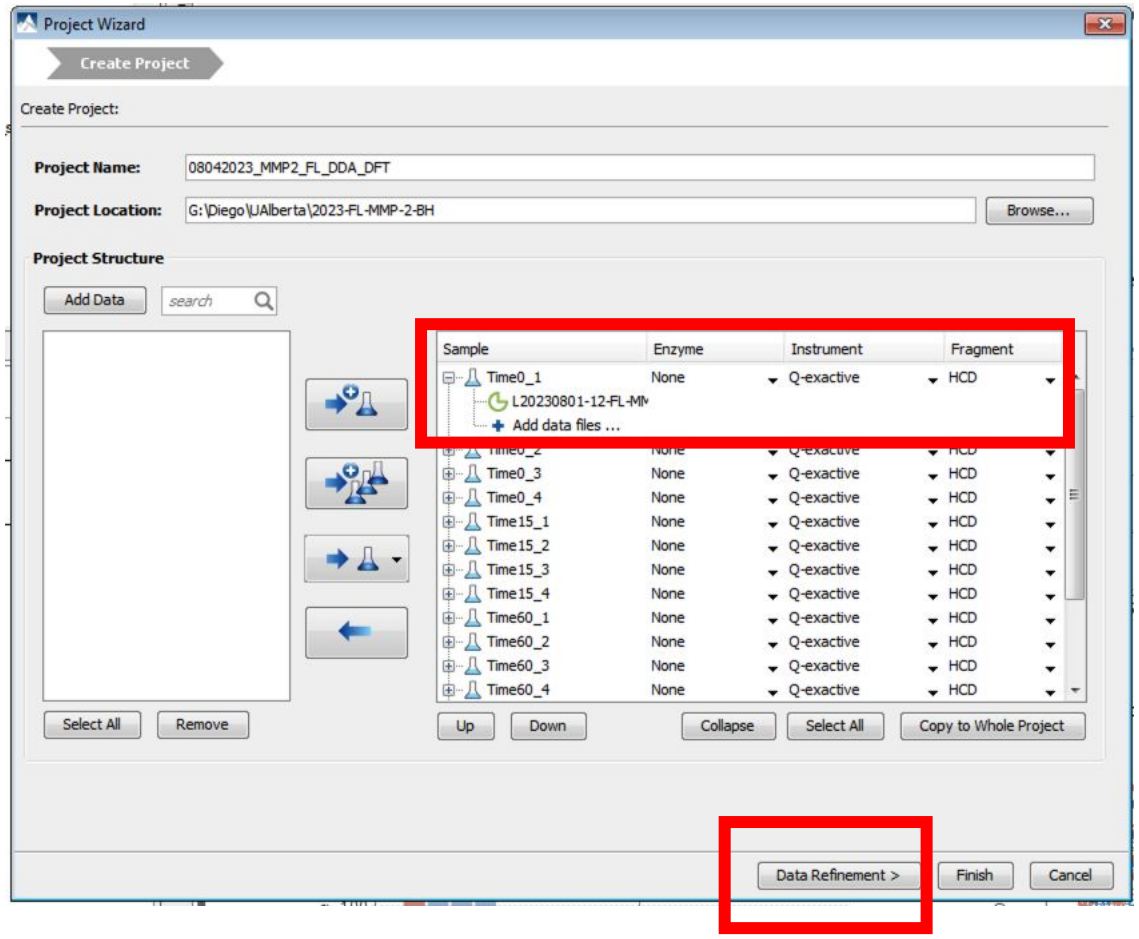


- Select the files you would like to analyze

6. Add data, rename samples, set correct parameters

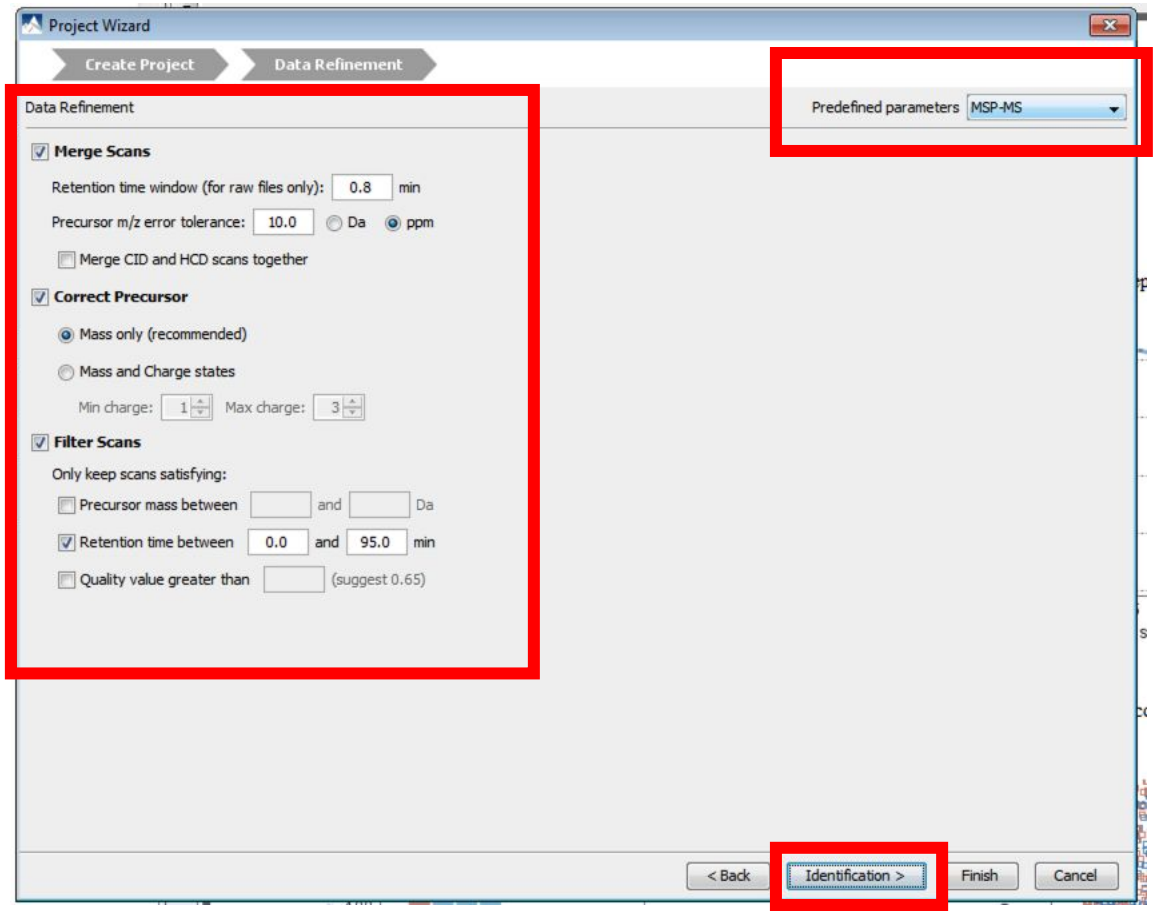


- Highlight all the added data.
- Select Create new sample for each file



- Select appropriate instrument and fragmentation method
- Set Enzyme to “None”
- Rename samples according to enzymes, time points, and replicates
  - Can also ensure appropriate data is selected for these
- Select “Data Refinement” to continue

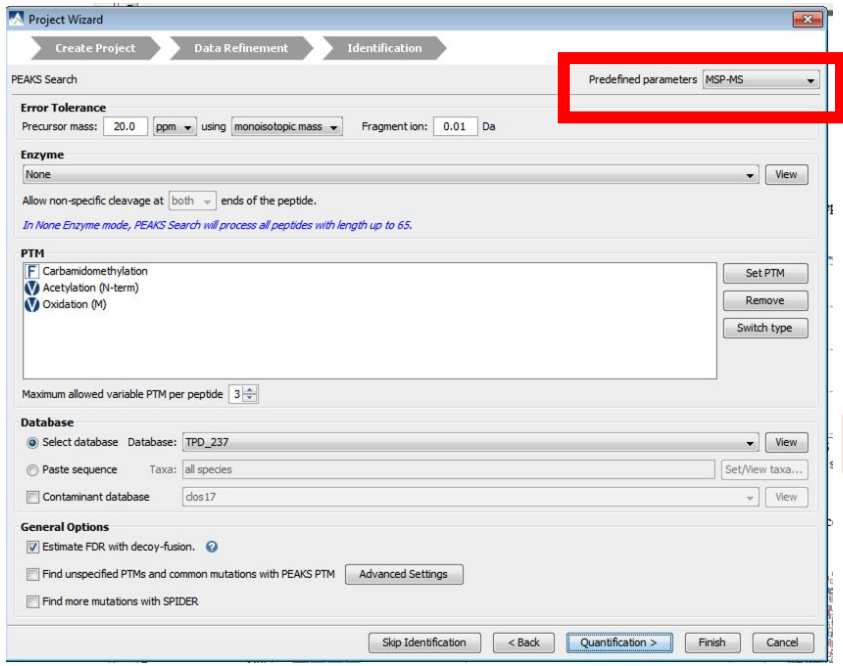
7. Data Refinement



- On the top right, select MSP-MS as the predefined parameters
- Parameters shown are what should be used for MSP-MS data analysis
- Select “Identification” to continue

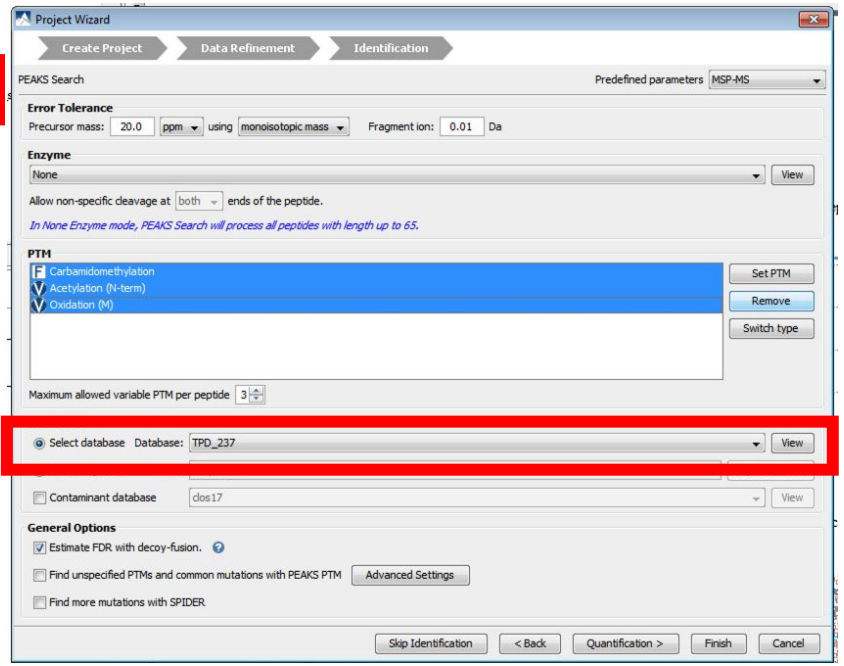
8. Peptide Identification

A.



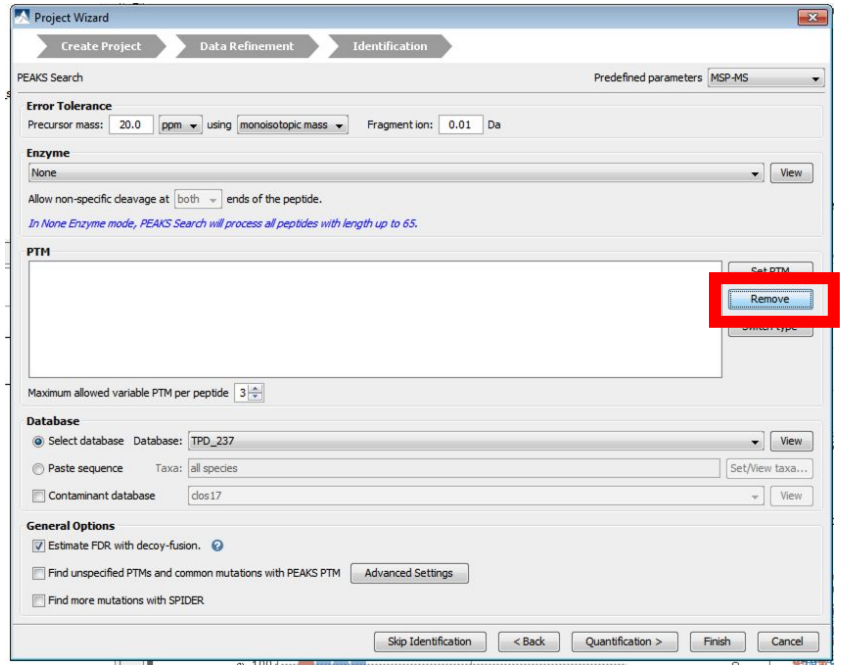
- On the top right, select MSP-MS as the predefined parameters
- Parameters shown are what should be used for MSP-MS data analysis

B.



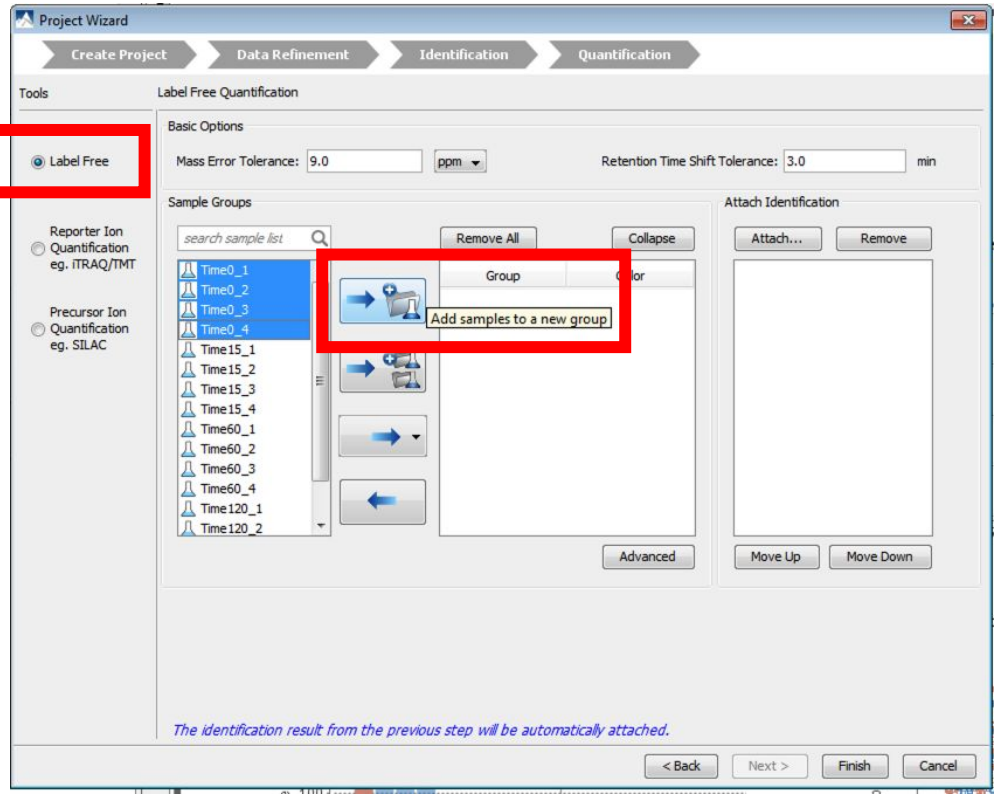
- Identification -> Select Database -> TPD_237

C.

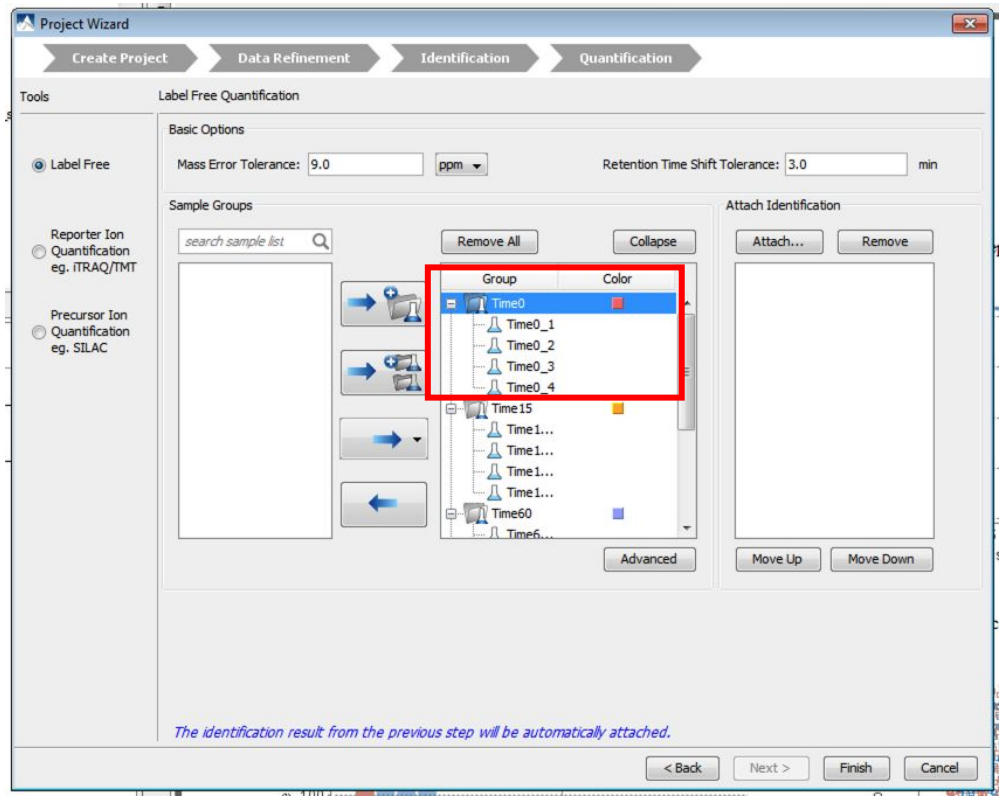


- Identification -> no PTMs
  - Can remove the PTMs by highlighting them and selecting Remove

9. Label Free Quantification



- Make sure Label Free is selected
- Group samples -> add quadruplicates of samples to new group
  - Note: I never really play with the Basic option on the top, I just leave these as is



- Rename samples according to time points
- Select Finish. Let PEAKS finish running the analysis
  - Usually takes at least 4 hours for MSP-MS data
- Once complete, use R scripts to further process data
  - See “MSP-MS Data Analysis” protocol for R scripts