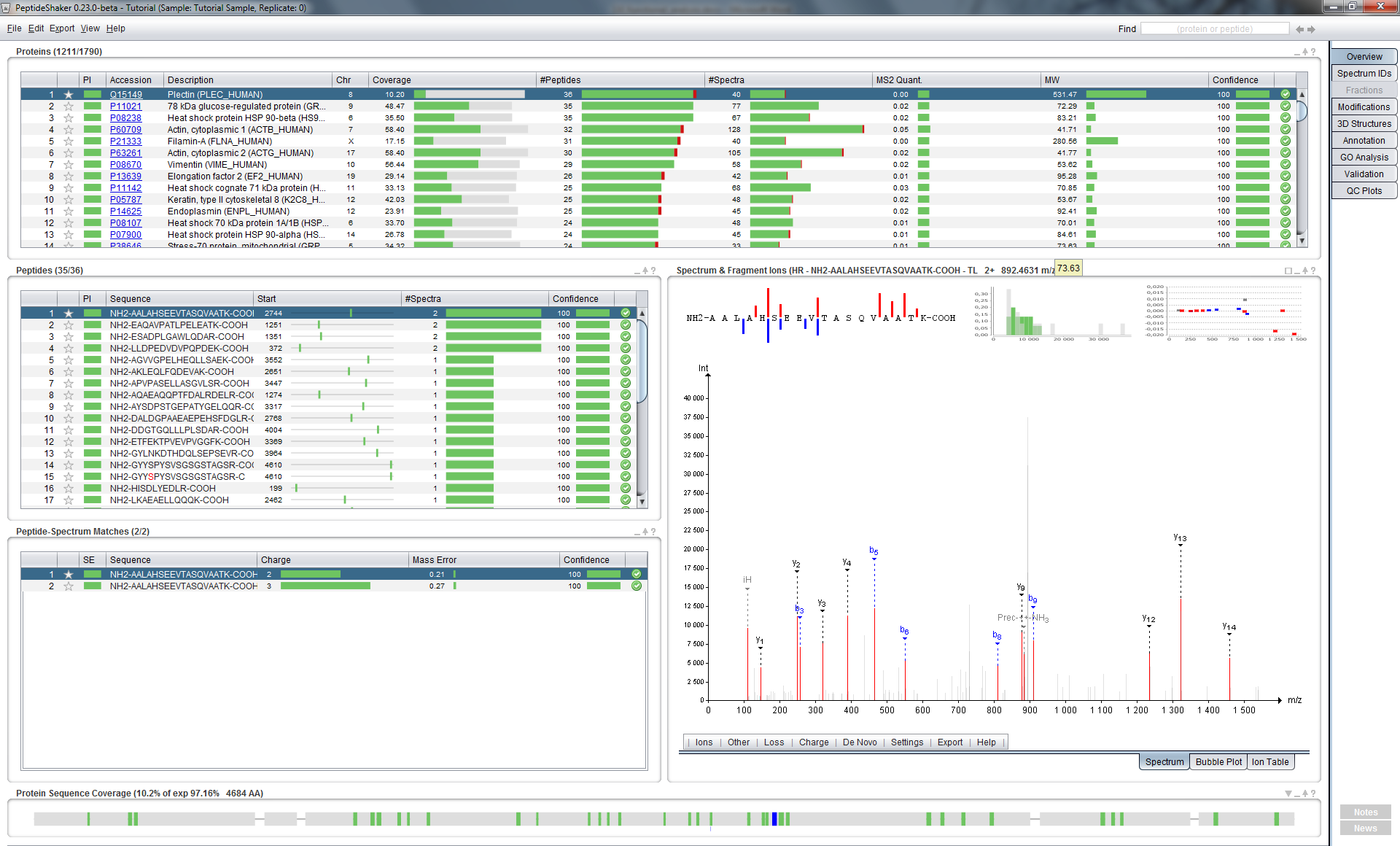
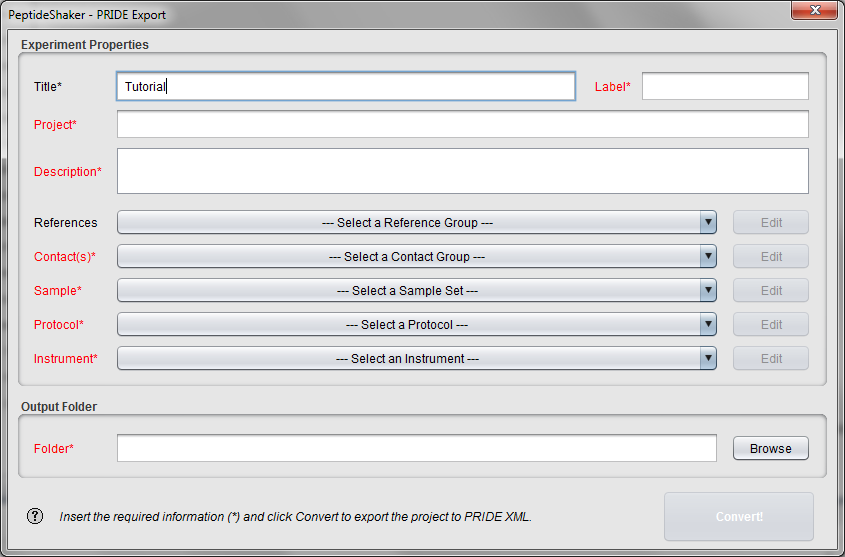
Submitting to Online Repositories

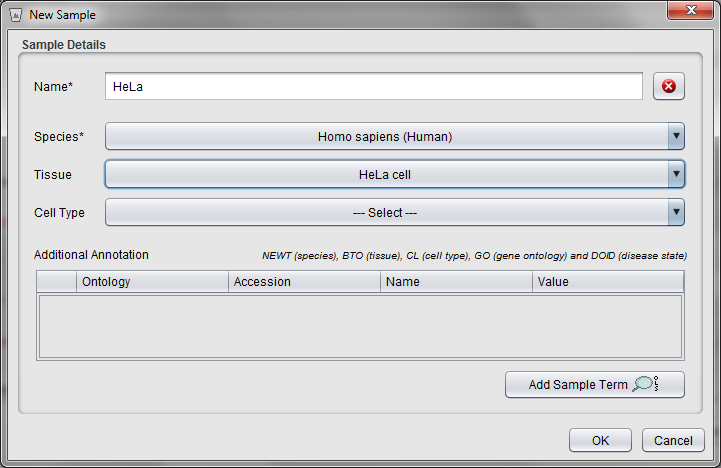
In this section, we will generate a PRIDE XML file from the previously used HeLa dataset. Load the example project into PeptideShaker:



Now click on ‘Save As...’ in the ‘File’ menu and select ‘Export to PRIDE’. The following dialog appears:



The information needed here will be used to annotate your dataset in PRIDE1. Using the respective fields, create or select a Contact, a Sample, a Protocol and an Instrument for our dataset. Note that all terms are standardized, creating a HeLa Sample as illustrated below will thus help other scientists working with HeLa cells to find your results.

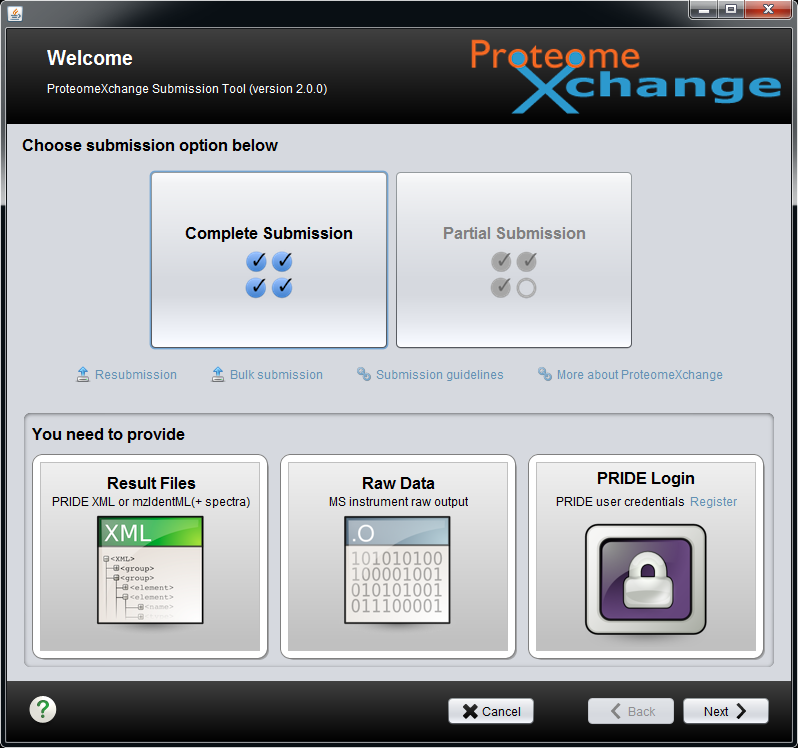


*Why is it important to annotate our data? How can to find the proper annotation?* *[3.1a]*

Selecting an output folder and clicking on the 'Convert!' button will start the creation of the PRIDE XML file. In order to save time, the corresponding file has already been generated for you and is located in the resources folder.

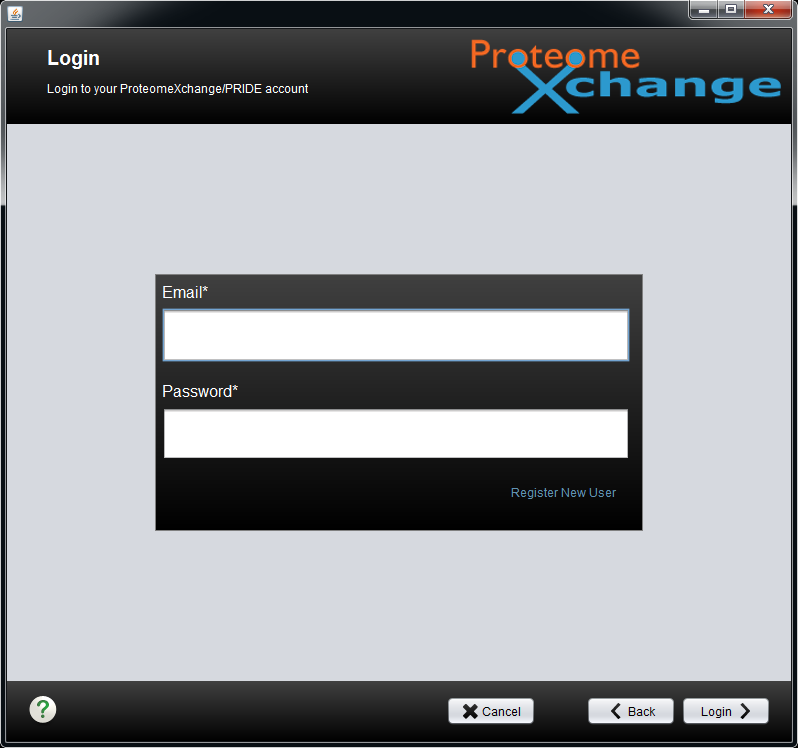
Start the ProteomeXchange submission tool located in the software folder (PX\_Submission). The tool can also be downloaded or launched directly from <http://www.proteomexchange.org> after clicking on “Submit Data”.

You should now see the following screen:



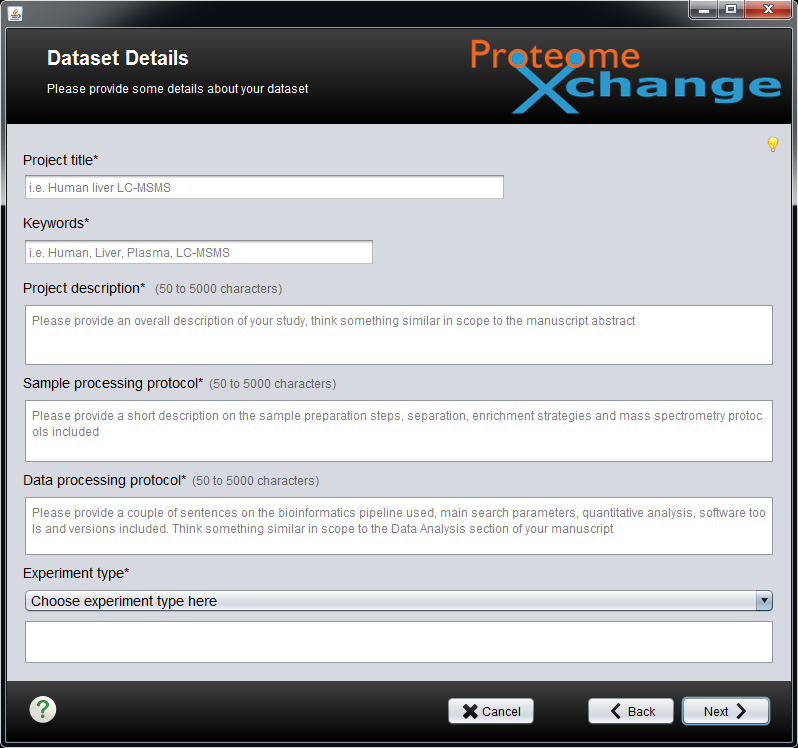
Note that a complete tutorial is available in the folder of the submission tool. The following is an example on the data we generated.

Click on ‘Complete Submission’ then ‘Next’. You will be asked to register using your PRIDE credentials:



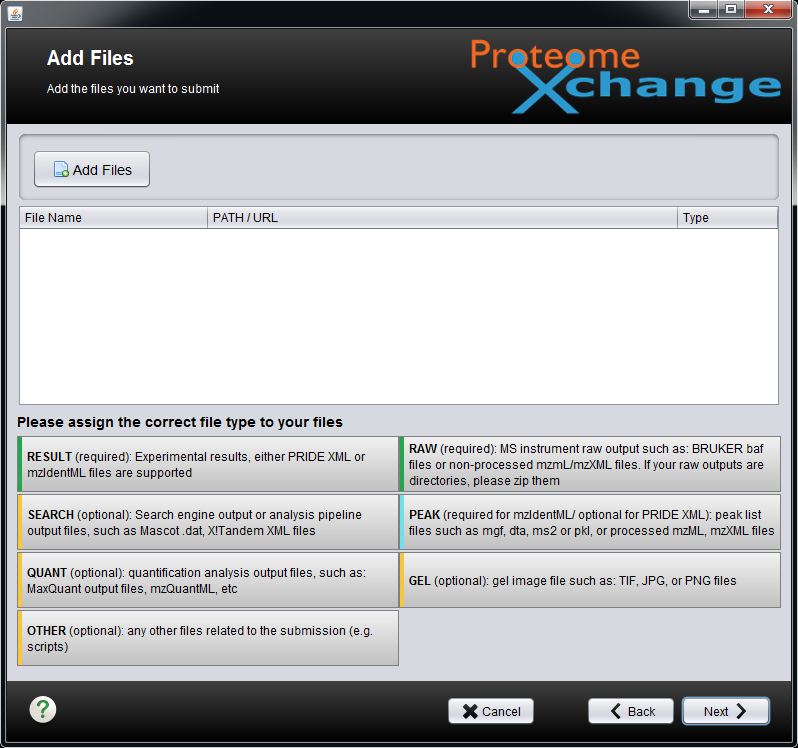
If you don’t have an account, click on “Register New User”.

You should now see the following dialog:



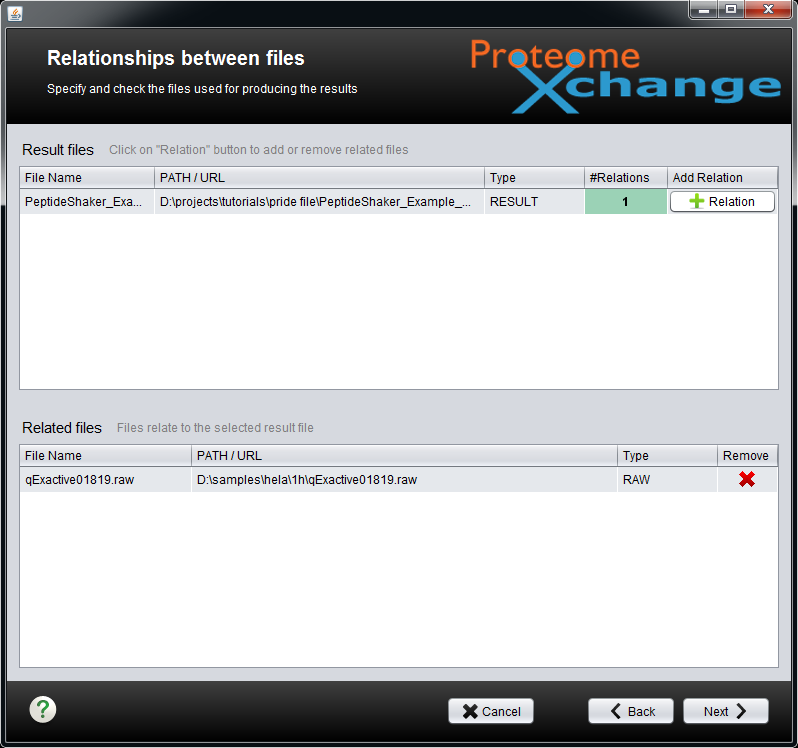
Here you are asked to fill the description of your project. While the annotation conducted during the conversion was standardized for automatic recognition, here the input is user oriented. You can thus simply reuse parts of your manuscript.

After clicking on “Next”, you will be able to load your files:



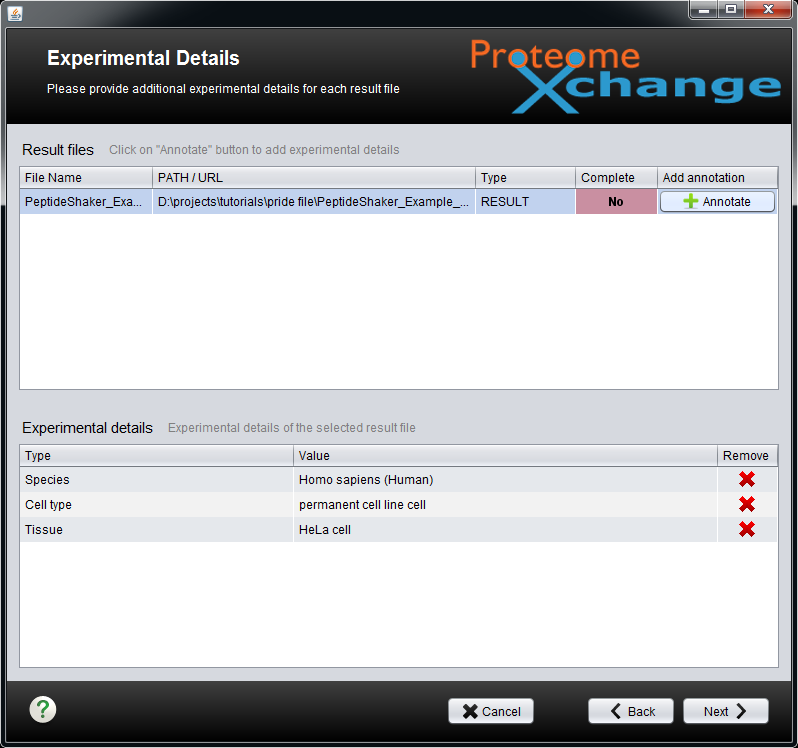
Here, load the raw file (available in the resources folder) and the PRIDE XML file we just created. Note that the submission tool recognizes the different file formats.

In the next step, we will indicate that the PRIDE XML file results from the processing of the raw file. Add a relation between the raw file and the PRIDE XML file. You should see the following:



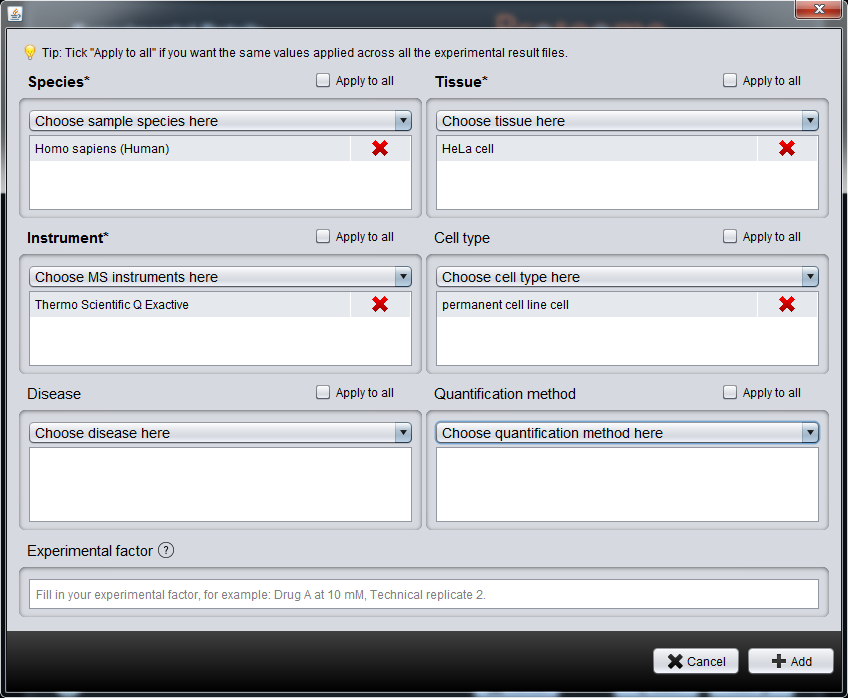
*In which case will you have different PRIDE XML files with different relations? [3.1b]*

After clicking on “Next”, you will be asked to annotate your result files:



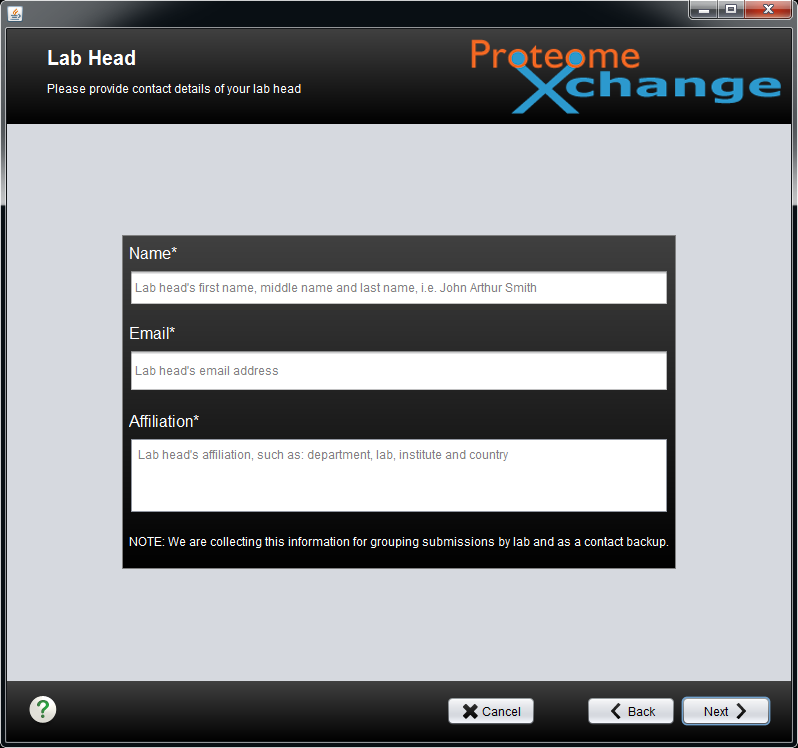
As you can see, the uploader already picked the sample details selected in PeptideShaker.

Clicking on “Annotate” will allow you to add more information. Under instrument, select Thermo Scientific Q Exactive:

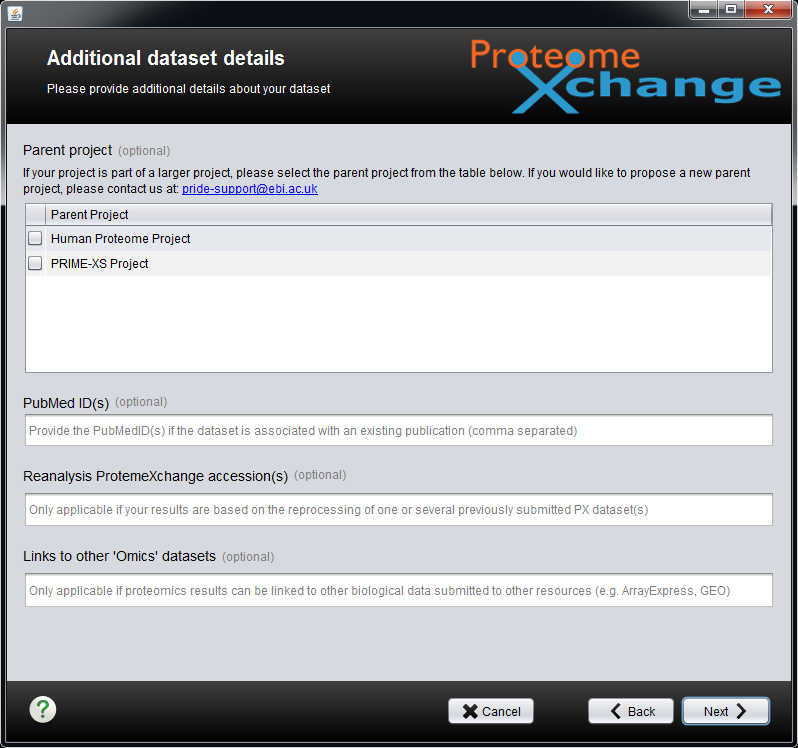


*What else can we add? [3.1c]*

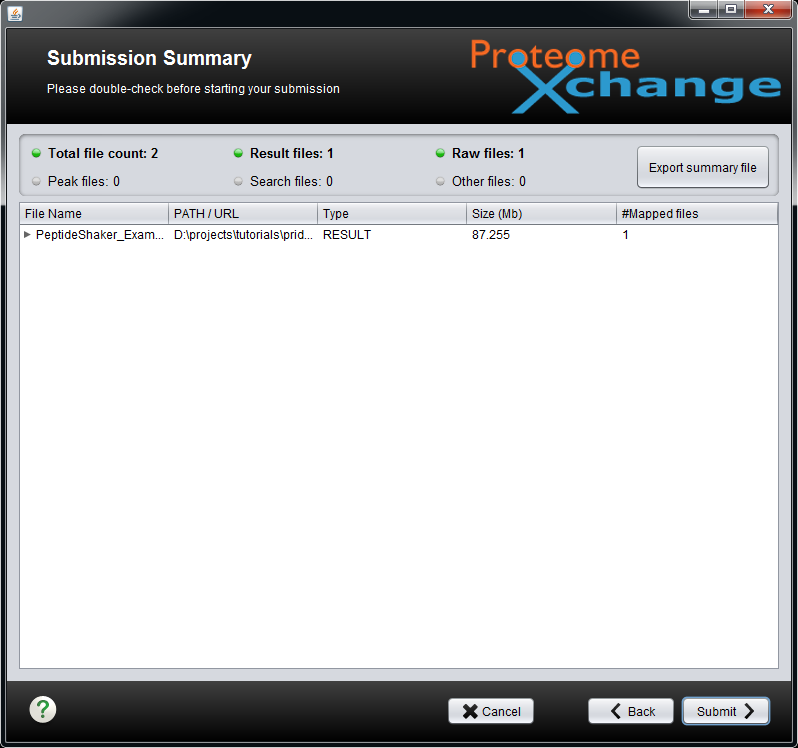
Finally, you will be asked to provide the lab head contact details:



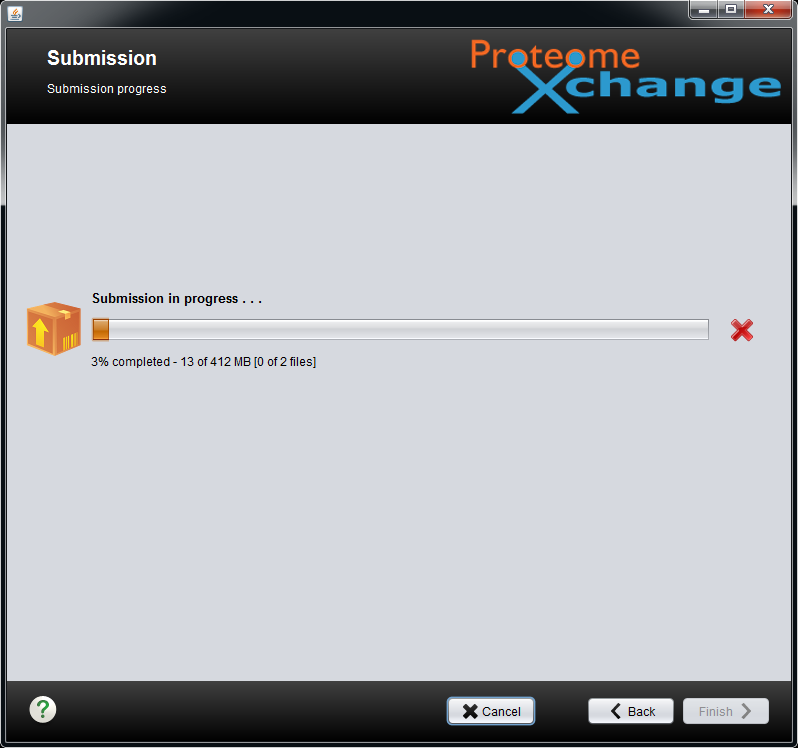
Next, you can link your identification results to parent projects and other datasets:



When all these steps are completed, a summary of your submission is displayed:



The tutorial data is already online so we will not upload it again, but clicking on “Submit” would have started the upload automatically.



Once the upload is finished, the PRIDE team will contact you at the address used to log in and will provide you with the accession details of your dataset. Note that your dataset will be kept private until you notify the PRIDE team that it should be made publicly available.

*What is the difference between a public and a private dataset? Can I give a reviewer access to my data? [3.1d]*

References

1. Martens, L. et al. PRIDE: the proteomics identifications database. *Proteomics* **5**, 3537-3545 (2005).