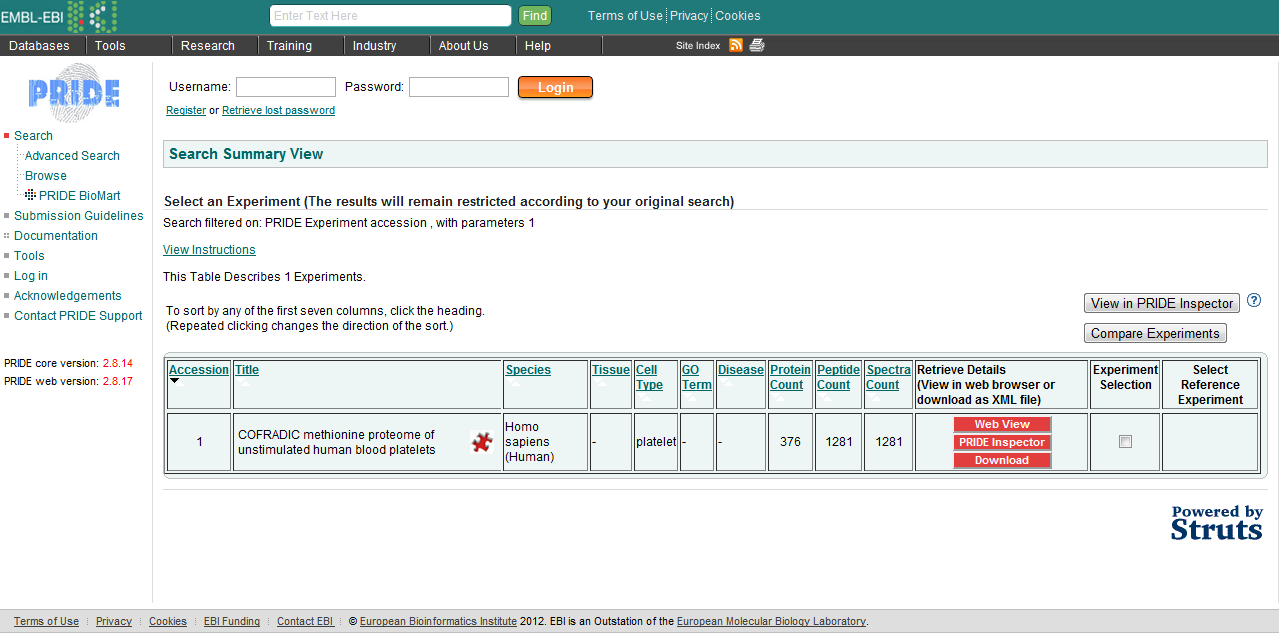
Browse Online Repositories

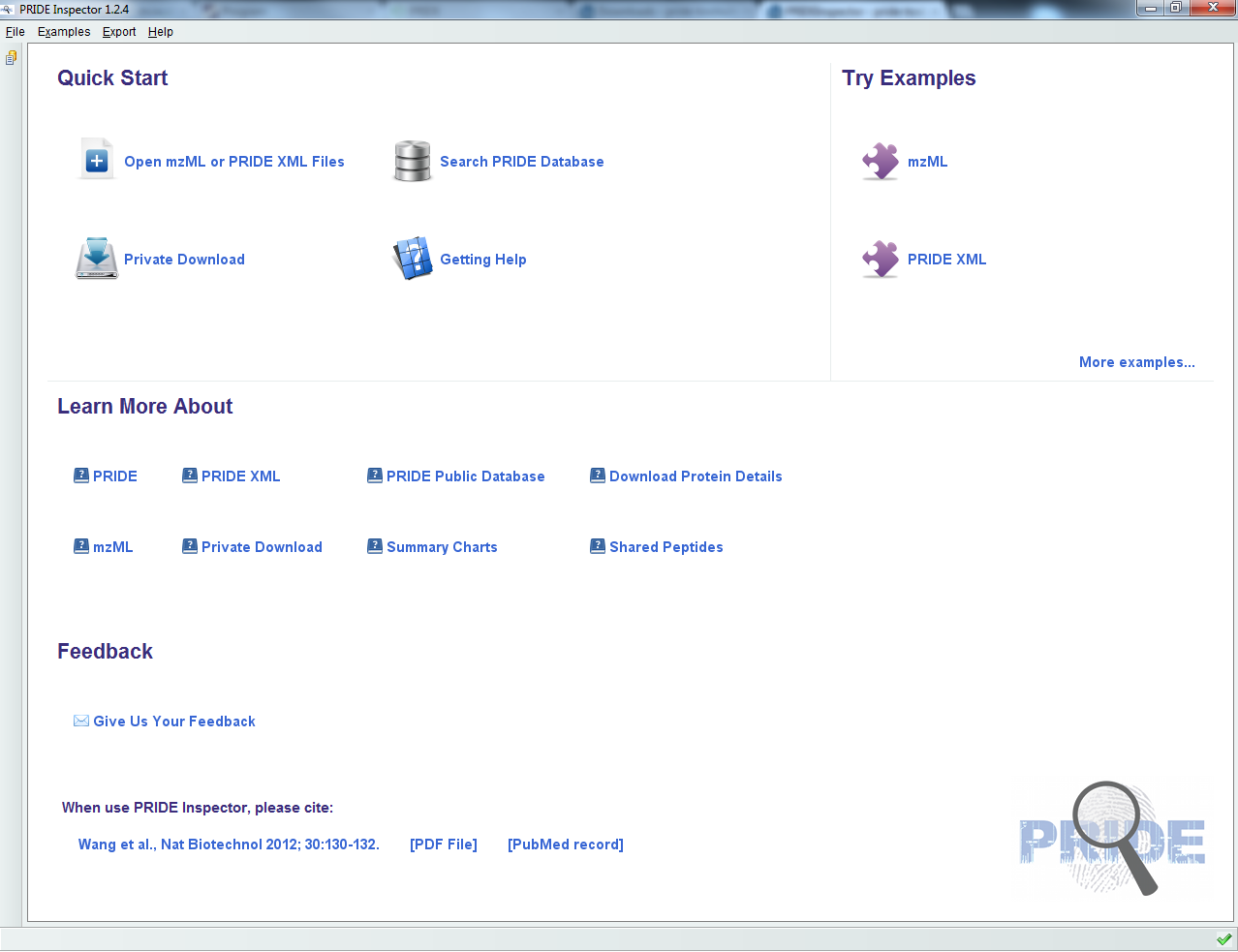
The vast amount of data stored in the public repositories can be accessed via the web interface or viewed in the PRIDE Inspector[1](#_ENREF_1) viewer. Go on the PRIDE website (<http://www.ebi.ac.uk/pride>) and search PRIDE project number 1, you should see the following screen:



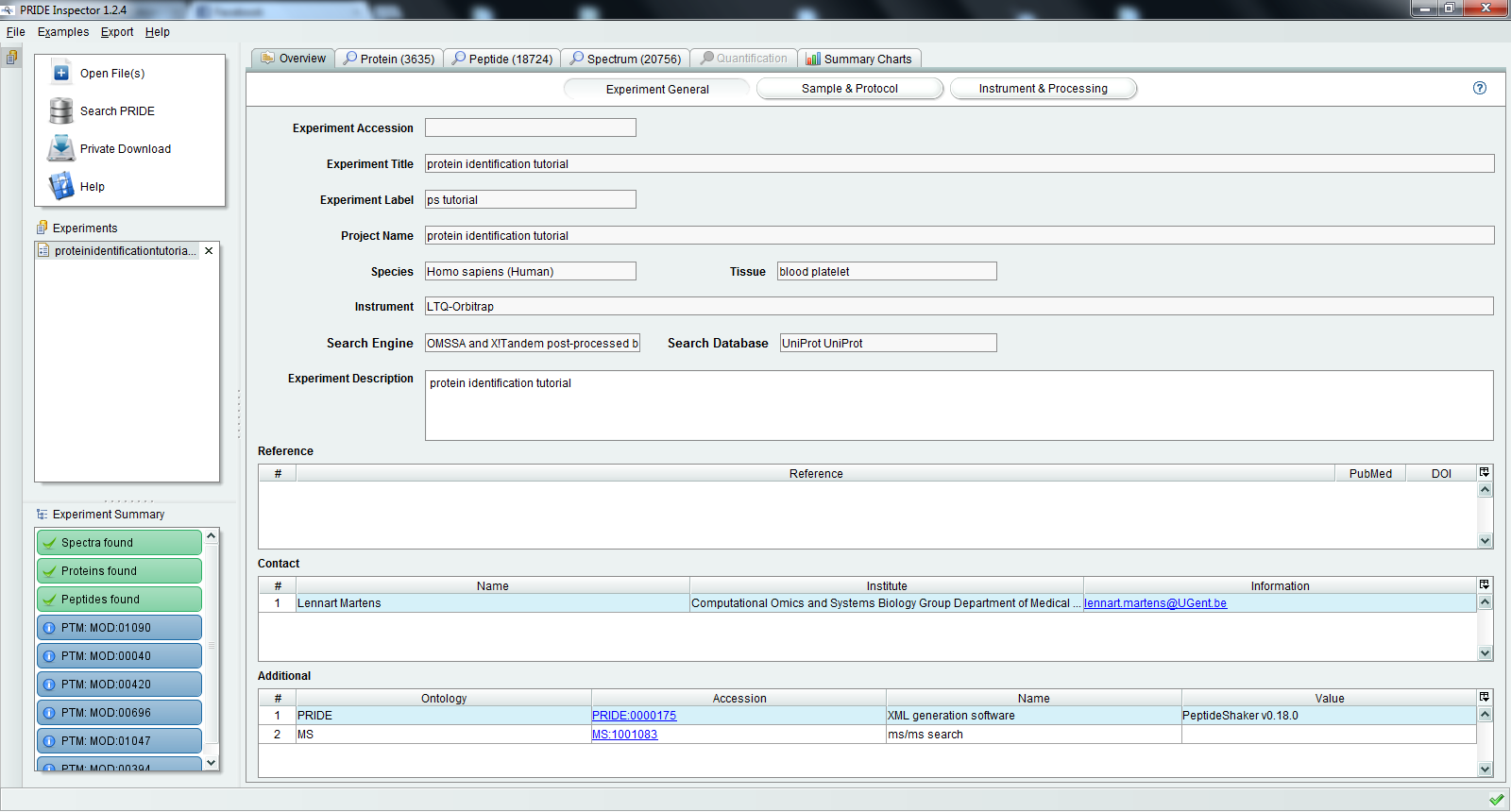
Click on ‘Web View’ to browse this project. *What information can you access on this experiment? What is your opinion about making all data available?*

*You can see detailed information about the project, notably, the publication it is attached to, contacts of the authors, type of sample, protocol used and statistics about the spectra and their identification. You see here how crucial it is to annotate your data in a comprehensible way in order to make it comprehensible by others when viewing.*

It is possible to browse all online PRIDE datasets using PRIDE Inspector (<http://pride-toolsuite.googlecode.com>), available in the software folder. Starting PRIDE Inspector, you should see the following:



Select ‘Open mzML or PRIDE XML Files’ and open tutorial.xml located in the resources folder. You should see the following:



Note that all spectrum annotation (modifications, ions, etc.) have been passed by PeptideShaker to PRIDE Inspector as standardized terms and will thus be available for all other online resources. *What difference do you see compared to the PeptideShaker results?*

*One of the main differences with PeptideShaker is that PRIDE Inspector does not support the groups inferred during protein inference. Also, the interface does not display the result of the validation process. PeptideShaker yet added all the available information as additional parameters for the matches which you can access at the end of every line. Note also that the m/z differences you see in the tables do not correspond to the ones used by the search engines so do not panic!*

*Finally, it is impossible to interact with external resources. This viewer is hence a rudimentary interface allowing you to verify that you file was generated correctly but not really make sense out of the data. For this, we will reprocess the data ourselves in the next chapter.*

References

1. Wang, R. et al. PRIDE Inspector: a tool to visualize and validate MS proteomics data. *Nature biotechnology* **30**, 135-137 (2012).