

G-JAM Proteome Informatics Training

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Proteomics technologies such as LC-MS/MS (liquid chromatography coupled with tandem mass spectrometry) are a natural fit for the biology of ageing because these technologies powerfully detect changes in protein turnover and modification. This hands-on training will introduce the key steps required to identify tandem mass spectra by matching them to potential peptide sequences, selecting a set of putative identifications by controlling false discovery rate (FDR), and inferring the proteins that would result in the identified peptides. The training will then detect differentially expressed proteins in a simple cohort versus cohort study with three replicates in each.

The emphasis of the training will be the use of software tools, but the program will start with a short overview of protein identification for new researchers in the field. The tools to be used in the training will include *ProteoWizard* to convert Thermo RAW files to mzML, the *MSFragger* search engine to match database protein sequences to tandem mass spectra, and the *OpenMS* tools to process the identification and quantification data from these experiments.

Participants should bring laptops for the training; for best results, we suggest that the computers feature at least 8GB of RAM and at least quad-core processors.

The MSFragger and OpenMS tools can be used in MS Windows, macOS, and Linux.

Prior to the training, we recommend that students install the *Java Runtime Environment* (such as <https://learn.microsoft.com/en-us/java/openjdk/>) and *OpenMS* (<https://openms.readthedocs.io/en/latest/about/installation.html>).