



Bachelor Thesis at the interface between Informatics and Proteomics

The Research Institute of Molecular Pathology (IMP) and the Institute of Molecular Biotechnology of the Austrian Academy of Science (IMBA) are highly renowned basic biomedical research institutes located at the Campus Vienna Biocenter. Our common goal is to uncover fundamental molecular and cellular mechanisms that underlie complex biological phenomena. Within the IMP/IMBA, the Protein Chemistry Facility uses mass spectrometry¹⁾ to identify, characterize and quantify proteins and protein complexes in cells.²⁾ Since proteins constitute cellular “machines” that perform specific tasks in cells, their analysis helps understand cellular processes in health and disease.

We are looking for a highly motivated informatics student with good object-oriented programming skills, as well as an interest to work in research at the interface between informatics and proteomics (the science of studying proteins in cells). As mass spectrometry generates huge amounts of data, sophisticated software is required to analyze and process it. The offered Bachelor project aims at the integration of existing algorithms into our modular downstream bioinformatics workflow. Possible topics are listed as follows:

- *Determination of the charge state of fragment ions of peptides based on the ¹³C isotope pattern, removal of ¹³C isotopic peaks from the MS/MS spectrum (de-isotoping) and subsequent transformation into singly-charged values (deconvolution).*
- *Integration of known spectrum search algorithms into our bioinformatics pipeline.*

Good programming skills in C# and Java, as well as the motivation to acquire expertise in the area of proteomics, are both essential prerequisites. Payment will be available for qualified Bachelor students. If you are interested, please send your letter of motivation and your curriculum vitae to

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1) Aebersold R., Mann M. Mass spectrometry-based proteomics. Nature 2003.

2) Hutchins J.R., et al. Systematic analysis of human protein complexes identifies chromosome segregation proteins. Science. 2010