

Bioinformatician in computational proteomics



We are looking for a bioinformatician with experience in object oriented programming.

Mass spectrometry (MS) has emerged as a core analytical technique in protein chemistry. Driven by the rapid development of instrumentation, analysis methods and computational tools, MS based proteomics is at the forefront of techniques in modern life science research.

As MS generates huge amounts of data, sophisticated software is required for data analysis. We are offering a position for a highly motivated bioinformatician with experience in software development and curiosity to work in biological research at the interface between informatics and proteomics.

Good programming skills in object oriented and scripting languages (preferentially C# and R), as well as the motivation to acquire expertise in the field of proteomics and a keen interest to analyze biological data sets are essential prerequisites. Candidates experienced with databases or in the fields of parallel computing or data science will be preferred.

In the Protein Chemistry Facility, we are interested in developing new methods to detect and quantify proteins as well as their modifications and interaction partners. Our mission is to use these optimized methods to answer fundamental biological questions in a collaborative setting. Therefore, we are well equipped with recent computational infrastructure and latest high-resolution mass spectrometry instruments.

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 Vienna Biocenter. Our common goal is to uncover fundamental molecular and cellular mechanisms that underlie complex biological phenomena.

Please send your letter of motivation and your curriculum vitae to:

IMP - Institut für Molekulare Pathologie GmbH

Protein Chemistry Facility

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