University of Zurich UZH

Department of Molecular
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Open postdoctoral position in computational mass spec biology at the University of Zurich

A postdoctoral position in computational mass spec biology is available immediately in the group of Prof. Hottiger at the Department of Molecular Mechanisms of Disease. The postdoc will be additionally embedded in the Service and Support for Science IT group (S3IT) at the University of Zurich, Switzerland.

The main scientific interest of the Hottiger group is to understand the molecular mechanisms controlling inflammation and inflammation-associated pathologies. The group's research activity has significantly shaped the current understanding of how protein ADP-ribosylation is involved in these pathologies. For additional information visit: http://www.dmmd.uzh.ch/en/research/hottiger.html
The department is integrated within the natural sciences campus of the University of Zurich, the largest University in Switzerland and one of Europe`s leading research centers. The department is equipped with state-of-the-art infrastructure for biochemical, molecular and cell biological investigations.
S3IT is a new group in central IT with the ambitious goal of providing services in high-performance computing, data management, software development and higher-level functions related to scientific computing and data interpretation.

The successful applicant will be expected to support the ongoing research focus of the Hottiger group and will take part in ongoing activities focused on bioinformatics analysis of mass spectrometric data acquired of cultured cells or tissues (human and mouse).
The Department of Molecular Mechanisms of Disease offers a stimulating research environment and actively promotes dynamic interactions between scientists within the Department. S3IT consists of a multi-disciplinary team with different expertise and is part of the Swiss Institute of Bioinformatics network.

We are seeking a highly-motivated individual with a solid background in computational sciences (i.e. PhD in bioinformatics or computer science) who is familiar with the different software packages and analysis pipelines available for mass spectrometry data analysis, such as Mascot, TPP (including the prophets), skyline, or equivalent. Prior experience with mass spectrometry-based proteomics analysis of cells or tissues is required. Programming skills (e.g. Python, R, Java, C, C++) and experience with statistics/analytics is a prerequisite.

The applicant should be an independent thinker and problem-solver who is willing to work in a team, have a strong publication record and accept new challenges arising from working in a high-paced scientific environment. The applicant should also have good communication and writing skills, a curiosity-driven attitude and demonstrate enthusiasm and flexibility.

Please forward your application electronically (preferably as a single PDF file) with a detailed CV, a list of publications, a one-page summary of the scientific achievements, a statement of motivation and the names and addresses of two references to applications@dmmd.uzh.ch (informal and confidential inquiries should also be sent to this address).

The position is initially for 1.5 years (100 % with a salary according to the University guidelines), with the option for extension. The work place is at the Irchel campus of the University of Zurich (Winterthurerstrasse 190, 8057 Zurich). There is no formal application deadline, as the position will be filled as soon as a suitable candidate has been identified. The evaluation of applications will start immediately. Job sharing is not possible.