

## Staff Bioinformatician / Computational Biologist

<b>Employer</b>	<b>Institute of Microbiology, ETH Zurich</b>
<b>Location</b>	<b>ETH Zürich</b> Vladimir-Prelog-Weg 4 8093 Zürich Switzerland
<b>Description:</b>	<p>The Institute of Microbiology at ETH Zurich is seeking a highly qualified and experienced staff bioinformatician / computational biologist who is motivated to support and stimulate collaborative work between its members.</p> <p>The institute is composed of interdisciplinary research groups that work under the unifying theme of microbial interactions. We study host-microbe and microbiome interactions in diverse systems at all scales of biological organization including the ocean, humans, mice, plants, sponges, and fungi. By developing and applying cutting-edge technology in the area of next generation sequencing, mass spectrometry, imaging, multi-parameter flow cytometry and single-cell approaches, our institute provides a unique opportunity for data-integrative research and collaborations.</p> <p>More detailed information can be found at: <a href="http://www.micro.biol.ethz.ch/">http://www.micro.biol.ethz.ch/</a>.</p> <p>The motivation of the candidate is to provide strong support for ongoing research projects, and to foster bioinformatic skills among the institute's students and research staff. The candidate has excellent organisational skills and is able to effectively communicate results to individuals with diverse scientific backgrounds.</p> <p>The post holder will be embedded in the Microbiome Research group at the Institute of Microbiology providing an environment of complementary expertise and infrastructure for high-performance computational analysis.</p>
<b>Qualifications:</b>	<p>Essential qualifications include:</p> <ul style="list-style-type: none"><li>- postgraduate degree in bioinformatics or related field</li><li>- excellent communication, teamwork and organisational skills</li><li>- excellent skills biological / statistical data analysis (including machine learning)</li><li>- experience in NGS data analysis: (meta)genomics, (meta)transcriptomics</li><li>- advanced programming skills (e.g., Python/Perl, R, UNIX/bash scripting)</li></ul> <p>The following additional qualifications will be advantageous:</p> <ul style="list-style-type: none"><li>- background in population genetics / microbial ecology / phylogenetics</li><li>- experience in analysis of antibody sequence libraries (Ig-seq)</li><li>- experience in image data analysis</li><li>- experience in metabolomics/proteomics data analysis</li><li>- experience in web/database development (HTML, PHP, JavaScript, CSS, SQL)</li></ul>
<b>Comments:</b>	Applications will be considered until 31/12/2017 and reviewed on an on-going basis. Therefore, the post may be filled before the deadline. Informal inquiries should be directed by email to Prof. Dr. Shinichi Sunagawa ( <a href="mailto:ssunagawa@ethz.ch">ssunagawa@ethz.ch</a> ).