

Bioinformatician in Cancer Biology

The Research Institute of Molecular Pathology (IMP) and the Medical University of Vienna (MUW) in Vienna, Austria, are recruiting a highly motivated and well-organized **bioinformatician** for a collaborative translational research project focused on **investigating the molecular basis of cancer** and **discovering new targets for innovative therapeutic approaches**.

The successful candidate will contribute to experimental design, perform method development, and integrative data analysis on large (epi)genomic datasets produced by cutting-edge sequencing technologies (e.g. SLAMseq¹, single cell sequencing) and standard sequencing approaches (whole genome sequencing, exome sequencing, RNA-seq and ChIP-seq) from patient samples and experimental model systems. The candidate will work closely with a dynamic and ambitious group of cancer biologists led by Anna Obenaus and Johannes Zuber (IMP), and physician-scientists led by Thomas Wiesner (MUW).

Successful candidates should:

1. have profound experience in NGS data analysis and deep knowledge of standard tools and data formats.
2. have a sound knowledge of statistics.
3. have excellent knowledge of at least one scripting language and hands-on expertise with R/Bioconductor.
4. have experience with mining and integrative analysis of large data.
5. have excellent communication skills in English, an ability to translate and communicate results, and a basic understanding of cancer biology.
6. hold an academic degree such as a BSc, MSc, PhD in Bioinformatics, Biostatistics, or Life Sciences.

As bioinformatician in our team you will:

1. interpret and integrate comprehensive sequencing datasets (variant calling from whole genome and exome sequencing, RNAseq, ChIPseq), generated by our team with support from our NGS facility (with access to all state-of-the-art sequencing platforms (Illumina, PacBio, Nanopore) and single cell sequencing <http://www.vbcf.ac.at/facilities/next-generation-sequencing/>).
2. develop methods for cutting-edge technologies (e.g. SLAMdunk²) and design and analyze complex libraries for large scale CRISPR screens³.
3. be in charge of data mining from publicly available datasets (e.g. TCGA, ICGC, datasets on GEO) to identify gene signatures of disease progression, features of the tumor microenvironment etc., to formulate hypotheses which will then be tested in our experimental systems^{3,4}.
4. become an integral member of our cancer biology team with deep intellectual project involvement and close interactions with wet lab scientists and physician scientists.
5. be embedded in a group of experienced computational biologists/bioinformaticians with complementary expertise affiliated with different research groups at the IMP and the MUW, ensuring constant interactions, support, and training.

The salary is commensurate with qualifications/experience and includes a comprehensive benefits package. Applications, including a letter of motivation describing your particular interest in this position and past research experiences, a CV, GitHub account if available, and the names and contact details of referees should be sent to tobias.neumann@imp.ac.at. The application deadline is **May 25th, 2018**.

Further information:

<https://www.imp.ac.at/groups/anna-obenaus/>
<https://www.imp.ac.at/groups/johannes-zuber/>

¹Muhar M, et al., Science, 2018, ²<http://t-neumann.github.io/slamdunk/>,

³Rathert P, et al. Nature, 2015, ³Obenaus AC et al., Nature, 2015, ⁴Wiesner T et al., Nature, 2015