

Moritz Schlapansky

Bioinformatician | Multi-Omics Analysis | Reproducible Workflows
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PROFESSIONAL SUMMARY

Computational and experimental genome biologist and data scientist with more than five years of experience across high-dimensional genomics, single-cell biology and genome engineering. Expert in developing reproducible Python, R and Bash workflows for data processing, quality control, multimodal integration, statistical modelling, machine learning and visualisation. Proven leader in end-to-end method development, international interdisciplinary collaborations and mentoring junior researchers. Secured more than CHF 300,000 in competitive funding and co-authored work in *Nature*, *Nature Biotechnology*, *Nature Communications*, *Cell* and *Science*, alongside a first-author bioRxiv preprint. Combines computational and wet-lab expertise to translate complex biological data into clear, decision-relevant conclusions.

TECHNICAL EXPERTISE

Programming & Compute: Python, R, Bash, Linux, Pandas, SQL (basic), Git, workflow automation and documentation, HPC, Slurm, AWS.

Single-Cell & Multi-Omics: scRNA-seq, scATAC-seq, sgRNA capture, Seurat, Scanpy, 10x Genomics, BD Rhapsody, Parse Biosciences, multimodal integration, limited spatial-transcriptomics exposure.

Genomics & Genome Engineering: targeted amplicon and RNA sequencing, long-read sequencing, NGS analysis and library preparation, CRISPR screens, prime and base editing, AAV vectors, editing-outcome analysis.

Statistics & Machine Learning: exploratory and high-dimensional analysis, data modelling, biostatistics, differential expression, logistic regression, gradient boosting, predictive modelling, scikit-learn, model validation.

Experimental & Communication: human primary-cell culture, flow-cytometric analysis, high-throughput screening, Opentrons automation, data visualisation, IBCS, Adobe Illustrator, reports, grants, mentoring and stakeholder communication.

PROFESSIONAL EXPERIENCE

ETH Zürich – Jacob Corn Lab

Zürich, Switzerland

PhD Researcher / Postdoctoral Researcher

July 2020–July 2026

- Developed *scOUT-seq*, an end-to-end experimental and computational method linking genome-editing outcomes with transcriptomes at single-cell and single-nucleotide resolution; led conception, assay development, sequencing, pipeline development, analysis, interpretation and publication.
- Built reproducible Python, R and Bash workflows for scRNA-seq, targeted amplicon-sequencing, long-read and CRISPR-screen datasets; established quality controls, multimodal integration and publication-quality reporting.
- Applied differential-expression analysis, statistical modelling, logistic regression, gradient boosting and interpretable machine learning to identify cell-state-specific DNA-repair mechanisms in primary human cells and other systems.
- Served as a bioinformatics and genomics resource across collaborative projects, advising on study design, platform selection, analysis strategy and biological interpretation; contributed to manuscripts, figures, grants, reports and international presentations.
- Investigated clinically relevant large genomic alterations caused by genome editing; supported genome-wide and dual-sgRNA screens of DNA-damage-response networks and synthetic-lethal cancer vulnerabilities; established Opentrons laboratory automation for NGS workflows.

University of California, San Francisco – Michael McManus Lab

San Francisco, USA

Visiting Scientist / Master's Researcher

October 2018–September 2019

- Developed a high-throughput functional-genomics approach combining targeted RNA sequencing, complex ORF libraries and computational analysis to detect and quantify rare cell-state transitions.
- Led a four-person undergraduate team and coordinated library generation, screening implementation, experimental execution, data interpretation and communication.

Center for Molecular Medicine (CeMM) - Andreas Bergthaler Lab

Vienna, Austria

Research Project – Immunology

March–September 2018

- Investigated the interaction between chronic viral infection and liver metabolism in mouse models within a BSL-3 laboratory environment; contributed to work subsequently published in *Immunity*.

Austrian Agency for Health and Nutrition Safety

Vienna, Austria

Research Intern

September–October 2017

- Validated and optimised a PCR method for identifying THC-containing variants of *Cannabis sativa*.

Research Institute of Molecular Pathology – Johannes Zuber Lab

Vienna, Austria

Bachelor's Researcher – Cancer Biology

March–August 2017

- Performed genome-wide pooled screens in human cancer and leukaemia cell lines to identify synthetic-lethal dependencies and generated knockout and inducible-degron models for functional validation.
- Adapted the auxin-inducible degron system for *in vitro* and prospective *in vivo* use and contributed to work subsequently published in *Science*.

EDUCATION

Doctor of Philosophy – ETH Zürich, Switzerland

November 2025

Biology: Computational & Experimental Genomics / Genome Biology

Master of Science – University of Vienna, Austria
Molecular Biology / Molecular Medicine; with Distinction, GPA 1.08

April 2020

Bachelor of Science – University of Vienna, Austria
Molecular Biology; with Distinction, GPA 1.31

August 2017

SELECTED PUBLICATIONS (Full list available)

- Schlapansky MF**, Schröder MS, Santinha AJ, et al. Cell-stereotyped DNA repair outcomes are widespread during genome editing. *bioRxiv* (2025). <https://doi.org/10.1101/2025.10.23.684114>
- Fielden J, Siegner SM, Gallagher DN, et al. Comprehensive interrogation of synthetic lethality in the DNA damage response. *Nature* (2025). <https://doi.org/10.1038/s41586-025-08815-4>
- Cullot G, Aird EJ, **Schlapansky MF**, et al. Genome editing with the HDR-enhancing DNA-PKcs inhibitor AZD7648 causes large-scale genomic alterations. *Nature Biotechnology* (2024). <https://doi.org/10.1038/s41587-024-02488-6>
- DeWitt M, Wong J, Wienert B, **Schlapansky MF**, Aird E. “In vitro transcription of guide RNAs and 5'-triphosphate removal.” *protocols.io* (2023). [protocols.io](https://doi.org/10.1038/s41587-024-02488-6)
- Lercher A, Bhattacharya A, Popa AM, et al. Type I interferon signaling disrupts the hepatic urea cycle and alters systemic metabolism to suppress T cell function. *Immunity* (2019). [https://www.cell.com/immunity/fulltext/S1074-7613\(19\)30458-3](https://www.cell.com/immunity/fulltext/S1074-7613(19)30458-3)
- Muhar M, Ebert A, Neumann T, et al. SLAM-seq defines direct gene-regulatory functions of the BRD4-MYC axis. *Science* (2018). <https://doi.org/10.1126/science.aao2793>

AWARDS AND FELLOWSHIPS

PhD Fellowship ; Boehringer Ingelheim Fonds <i>Award value: CHF 180,000</i>	2021–2024
NOMIS Foundation Grant ; NOMIS Foundation <i>Award value: CHF 100,000</i>	2021–2026
Marshall Plan Scholarship ; Austrian Marshall Plan Foundation <i>Award value: € 20,000</i>	2018–2019
Advancement Scholarship / Research Grant ; University of Vienna <i>Award value: € 20,000</i>	2018-2019
Merit Scholarship ; University of Vienna <i>Award value: € 4,000</i>	2015-2018

LEADERSHIP AND SERVICE

- Board Member, Institute for Molecular Health Sciences, ETH Zürich** 2023 – 2025
Represented more than 100 PhD students and postdoctoral researchers on a 12-member executive board; launched and led a speaker series for 50 attendees, raised CHF 3,000 and secured two high-profile keynote speakers.
- Committee Member, Molecular Life Sciences Graduate School (ETH Zürich / UZH)** 2020 – 2025
Managed a six-person team that delivered two professional and personal development events for more than 200 students; organised or moderated workshops and retreats and secured CHF 10,000 in funding.
- Mentoring and Teaching**: Mentored three Master's student projects, led a four-person undergraduate screening team, taught exactly three ETH biology block courses/practicals, and advised researchers on experimental design, genomics platforms, bioinformatics, visualisation and interpretation.

RIGHT TO WORK AND LANGUAGES

Switzerland; C permit holder
Austria / European Union; Austrian citizen
Languages: German (native), English (professional / business fluent), Swiss German (passive understanding)

ADDITIONAL SKILLS AND INTERESTS

Hobbies: Soccer, Brazilian Jiu-Jitsu, kickboxing, biking.

Home Server Infrastructure: Built and maintain an Ubuntu-based personal compute server, including user and permission management, networking, databases, drivers, software environments, system monitoring, command-line troubleshooting, and routine maintenance.

Custom Carbon Gravel Bike: Built a carbon gravel bike from individually sourced components, including frame preparation, drivetrain and hydraulic brake installation, wheel and cockpit setup, internal cable routing, component compatibility checks, fine-tuning, and ongoing maintenance.