

## Curriculum Vitae

### Personal Data

Title	Jun.-Prof. Dr.
First name	Fabian
Name	Müller
Current position	Junior professor (W1 with tenure track W2)
Current institution	Universität des Saarlandes, Saarbrücken, Germany
Identifiers	Google Scholar: <a href="https://scholar.google.de/citations?user=LmY4x8oAAAAJ&amp;hl=en">https://scholar.google.de/citations?user=LmY4x8oAAAAJ&amp;hl=en</a> ORCID: 0000-0001-5809-2321

### Qualifications and Career

Stages	Periods and Details
Junior Professor	Since 2021 Saarland University, Saarbrücken, Germany
Postdoctoral researcher	2018 to 2021 William Greenleaf lab, Department of Genetics, Stanford University School of Medicine, Stanford, California, USA
PhD (Dr. rer. nat.) and postdoctoral researcher	2010 to 2017 Thesis: " <i>Analyzing DNA Methylation Signatures of Cell Identity</i> ", supervised by Prof. Dr. Dr. Thomas Lengauer and Dr. Christoph Bock, Max Planck Institute for Informatics and Saarland University, Saarbrücken, Germany
Visiting researcher	2009 to 2010 and summer 2011 Alexander Meissner lab, Department for Stem Cell and Regenerative Biology, Harvard University and Broad Institute, Cambridge, Massachusetts, USA
Master of Science	2008 to 2009 Thesis supervised by Prof. Dr. Dr. Thomas Lengauer, Max Planck Institute for Informatics and Saarland University, Saarbrücken, Germany
Bachelor of Science	2005 to 2008 Thesis supervised by Prof. Dr. Dr. Thomas Lengauer, Max Planck Institute for Informatics and Saarland University, Saarbrücken, Germany

## **Engagement in the Research System**

### ***Teaching activities***

- 2021 – 2023 “*Single-cell bioinformatics*” (Master level course)  
Course design and lead lecturer, Saarland University, Saarbrücken, Germany
- 2021 – 2023 “*Computational methods for epigenome analysis*” (Master level course)  
Course design and lead lecturer, Saarland University, Saarbrücken, Germany

### ***Organization of Scientific Meetings***

- 2022 Member of organizing committee: “*Advances in Single Cell Epigenomics 2022*”  
(approx. 70 participants), Single-Cell Omics Germany (SCOG) Workshop,  
Überherrn, Germany

### ***Institutional responsibilities***

- Since 2021 Faculty member, Saarland University, Saarbrücken, Germany
- Since 2021 Graduate student advisor, Saarland University, Saarbrücken, Germany

### ***Reviewing activity***

Journal and conference reviewer for Bioinformatics, Bioinformatics Advances,  
BMC Bioinformatics, BMC Genomics, Cell Reports Methods, Genome Biology, German  
Conference on Bioinformatics (GCB), Nature Communications, Nucleic Acids Research

### ***Memberships in Scientific Networks***

- Since 2021 Member, Research Network “*Single-Cell Omics Germany (SCOG)*”
- Since 2018 Member, Research Network “*Human Cell Atlas (HCA)*”
- Since 2012 Member, Research Network “*International Human Epigenome Consortium (IHEC)*”
- 2012 – 2017 Member, Research Network “*Deutsches Epigenom Programm (DEEP)*”
- 2011 – 2016 Member, Research Network “*BLUEPRINT Project*”

### ***Academic Distinctions***

- 2019 – 2021 Postdoctoral Fellowship, Deutsche Forschungsgemeinschaft (DFG)
- 2014 Lindau Nobel Laureate Meeting Participation
- 2009 – 2010 Rotary Ambassadorial Scholarship, Rotary International
- 2009 Günther-Hotz-Medal, Freunde der Saarbrücker Informatik, e.V., Germany

## Selected Publications

### *Selected first and corresponding author publications*

1. Trevino\*, **Müller\***, Andersen\*, Sundaram\*, Kathiria, Shcherbina, Farh, Chang, Paşca, Kundaje, Paşca#, & Greenleaf#. (2021). Chromatin and gene-regulatory dynamics of the developing human cerebral cortex at single-cell resolution. *Cell*, 184(19), 5053-5069.e23. <https://doi.org/10.1016/j.cell.2021.07.039>
2. Scherer, Nebel, Franke, Walter, Lengauer, Bock, **Müller#**, & List#. (2020). Quantitative comparison of within-sample heterogeneity scores for DNA methylation data. *Nucleic Acids Research*, 48(8), e46–e46. <https://doi.org/10.1093/nar/gkaa120>
3. **Müller\*\***, Scherer\*\*#, Assenov\*\*#, Lutsik\*\*#, Walter, Lengauer, & Bock# (2019). RnBeads 2.0: comprehensive analysis of DNA methylation data. *Genome Biology*, 20(1), 55. <https://doi.org/10.1186/s13059-019-1664-9>
4. Farlik\*, Halbritter\*, **Müller\***, Choudry, Ebert, Klughammer, Farrow, Santoro, Ciaurro, Mathur, Uppal, Stunnenberg, et al. (2016). DNA Methylation Dynamics of Human Hematopoietic Stem Cell Differentiation. *Cell Stem Cell*, 19(6), 808–822. <https://doi.org/10.1016/j.stem.2016.10.019>
5. Assenov\*, **Müller#**, Lutsik\*, Walter, Lengauer, & Bock#. (2014). Comprehensive analysis of DNA methylation data with RnBeads. *Nature Methods*, 11(11), 1138–1140. <https://doi.org/10.1038/nmeth.3115>
6. Ziller\*, **Müller\***, Liao, Zhang, Gu, Bock, Boyle, Epstein, Bernstein, Lengauer, Gnirke, & Meissner. (2011). Genomic Distribution and Inter-Sample Variation of Non-CpG Methylation across Human Cell Types. *PLoS Genetics*, 7(12), e1002389. <https://doi.org/10.1371/journal.pgen.1002389>

\* first authors # corresponding authors

### *Selected contributing author publications*

7. Andersen, Thom, Shadrach, Chen, Onesto, Amin, Yoon, Greenleaf, **Müller**, Paşca, Kaltschmidt, & Paşca (2023). Landscape of human spinal cord cell type diversity at midgestation. *Nature Neuroscience*, 26(5), 902–914. <https://dx.doi.org/10.1038/s41593-023-01311-w>
8. Calderon, Nguyen, Mezger, Kathiria, **Müller**, Nguyen, Lescano, Wu, Trombetta, Ribado, Knowles, Gao, et al. (2019). Landscape of stimulation-responsive chromatin across diverse human immune cells. *Nature Genetics*, 51(10), 1494–1505. <https://doi.org/10.1038/s41588-019-0505-9>
9. Durek, Nordström, Gasparoni, Salhab, Kressler, Almeida, Bassler, Ulas, Schmidt, Xiong, Glažar, Klironomos, ..., **Müller**, et al. (2016). Epigenomic Profiling of Human CD4+ T Cells Supports a Linear Differentiation Model and Highlights Molecular Regulators of Memory Development. *Immunity*, 45(5), 1148–1161. <https://doi.org/10.1016/j.immuni.2016.10.022>
10. Ziller, Gu, **Müller**, Donaghey, Tsai, Kohlbacher, Jager, Rosen, Bennett, Bernstein, Gnirke, & Meissner. (2013). Charting a dynamic DNA methylation landscape of the human genome. *Nature*, 500(7463), 477–481. <https://doi.org/10.1038/nature12433>