

Curriculum Vitae

Benjamin Schubert Dr. rer. Nat.
d.o.b. August 30th, 1987, in Heidelberg, Germany

University Education

2017 Doctorate in Bioinformatics, University of Tübingen
2013 M.Sc. in Bioinformatics, University of Tübingen
2010 B.Sc. in Bioinformatics, University of Tübingen

Scientific Career

2022 – 2024 Working Group Coordinator for *AI and Computational Tools* of the German Center for Lung Research (DZL)
2021 – present Principal Investigator at the German Center for Lung Research (DZL)
2021 – present Principal Investigator, Helmholtz International Lab on Causal Cell Dynamics (MILA Canada)
2021 – present Biomedical Data Warehouse Coordinator, Comprehensive Pneumology Center Munich, German Center of Lung Research
2018 – present Group Leader, Institute of Computational Biology, Helmholtz Center Munich, Germany
2018 – 2023 Guest Lecturer, Department of Mathematics, Technical University Munich, Germany
2017 – 2018 Research Fellow, cBio Center, Dana-Farber Cancer Research Center, Boston, USA
2016 – 2018 Postdoctoral Fellow, Department of Systems Biology, Harvard Medical School, Boston, USA

Awards and Honors

2021 KI-Newcomer 2021 by the Gesellschaft für Informatik e.V.
2019 Postdoctoral High-Potentials Fellowship Award, awarded by Helmholtz Center, Munich, Germany
2013 Master's with Honors, awarded by the Institute of Informatics, University of Tübingen
2012 Full-time Graduate Scholarship, awarded by German Academic Exchange Service (DAAD), Germany

Citation Record

Total citations: 3976; h-index:21; h-index since 2019: 19 (Google Scholar Mar. 04th, 2026)

Top-10 selected Publications

* Joint first authors, • Joint last authors, † Corresponding author

Kocher, K., Drost, F., Tesfaye, A. M., Moosmann, C., Schüle, C., Grotz, M., ... **Schubert, B.*** & Schober, K.* (2025). Vaccination-induced T cell responses maintain polyclonality with high antigen receptor avidity. *Science Immunology*, 10(112), eadu6730.

Drost, F., Chernysheva, A., Albahah, M., Kocher, K., Schober, K., & **Schubert, B.**† (2025). Benchmarking of T cell receptor-epitope predictors with ePytope-TCR. *Cell Genomics*, 5(8).

Drost, F., An, Y., Bonafante-Pardàs, I., Dratva, L. M., Lindeboom, ..., M., Lotfollahi*, & **Schubert, B.***† (2024). Multi-modal generative modeling for joint analysis of single-cell T cell receptor and gene expression data. *Nature Communications*, 15(1), 5577.

Drost, F., Dorigatti, E., Straub, A., Hilgendorf, P., Wagner, K. I., Heyer, K., ... & **Schubert, B.**† (2024). Predicting T cell receptor functionality against mutant epitopes. *Cell Genomics*, 4(9).

Buettner, M., Ostner, J., Mueller, C. L., Theis, F. J.* & **Schubert, B.***. (2021). scCODA is a Bayesian model for compositional single-cell data analysis. *Nat. Commun* 12(1), 1-10.

Fischer, D. S., Ansari, M., Wagner, K. I., Jarosch, S., Huang, Y., Mayr, C. H., ..., **Schubert, B.***, Theis, FJ*, Busch, DH*, Schiller, BH*, Schober, K*. (2021). Single-cell RNA sequencing reveals in vivo signatures of SARS-CoV-2-reactive T cells through 'reverse phenotyping'. *Nat Commun* 12, 4515.

Dorigatti, E., & **Schubert, B.*** (2020). Graph-theoretical formulation of the generalized epitope-based vaccine design problem. *PLoS Computational Biology*, 16(10), e1008237.

Fischer, D. S., Wu, Y., **Schubert, B.**, and Theis, F. J. (2020). Predicting antigen-specificity of single T-cells based on TCR CDR3 regions. *Molecular Systems Biology* *Molecular systems biology*, 16(8), e9416.

Schubert, B.*, and Kohlbacher, O. (2016). Designing string-of-beads vaccines with optimal spacers. *Genome Medicine*, 8(9).

Szolek, A. *, **Schubert, B.***, Mohr, C. *, Sturm, M., Feldhahn, M., and Kohlbacher, O. (2014). OptiType: precision HLA typing from next-generation sequencing data. *Bioinformatics*, 30(23), 3310-3316.