

Curriculum Vitae

Benjamin Schubert Dr. rer. Nat.

d.o.b. August 30th, 1987, in Heidelberg, Germany

University Education

2017 Doctorate in Natural Sciences, University of Tübingen
2013 Master of Science in Bioinformatics, University of Tübingen
2010 Bachelor of Science in Bioinformatics, University of Tübingen

Scientific Career

Since 2021 Member of the Helmholtz International Lab on Causal Cell Dynamics
Since 2021 Member of the German Center of Lung Research (DZL)
Since 2018 Group Leader at Institute of Computational Biology, Helmholtz Center Munich, Germany
Since 2018 Guest Lecturer at 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/ Cell Biology, Harvard Medical School, Boston, USA
2013 – 2016 Academic fellow, Wilhelm-Schickard-Institute, University of Tübingen, Germany

Awards and Honors

2020 KI-Newcomer by the Gesellschaft für Informatik e.V.
2019 Independent Postdoctoral Fellowship Award, by the Helmholtz Association
2013 Masters with Honors by University of Tübingen
2012 Full-time Graduate Scholarship by the German Academic Exchange Service (DAAD)

Citation Record

Total citations: 993; h-index:14; h-index since 2017: 14 (Google Scholar July 28th, 2022)

Top-10 selected Publications

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

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.
<https://doi.org/10.1038/s41467-021-27150-6>

Fischer, D. S., Ansari, M., Wagner, K. I., Jarosch, S., Huang, Y., Mayr, C. H., ..., **Schubert, B.[•]**, Theis, F.J.[•], Busch, D.H.[•], Schiller, B.H.[•], 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.
<https://doi.org/10.1038/s41467-021-24730-4>

An, Y., Drost, F., Theis, F.[†], & Lotfollahi, M.[•], **Schubert, B.^{•†}** (2021). Jointly learning T-cell receptor and transcriptomic information to decipher the immune response. *International Conference on Machine Learning (ICML)*. <https://doi.org/10.1101/2021.06.24.449733>

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.
<https://doi.org/10.15252/msb.20199416>

Ali, M., Foldvari, Z., Giannakopoulou, E., Bösch, M.L., Yang, W., Stronen, E., **Schubert, B.**, et al. (2019). Induction Of Neoantigen Reactive T Cells From Healthy Donors. *Nature Protocols*, **14**(6), 1926.
<https://doi.org/10.1038/s41596-019-0170-6>

Schubert, B.*, Maddamsetti, R.* , Nyman, J., Marks, D. (2018). Genome-wide discovery of epistatic loci affecting antibiotic resistance using evolutionary couplings. *Nature Microbiology*, **1**.
<https://doi.org/10.1038/s41564-018-0309-1>

Hopf, T.* , Green, A.G.* , **Schubert, B.*** , Mersmann, S., Schärfe, C.P., Ingraham, J.B, et al. (2018). The EVcouplings Python framework for coevolutionary sequence analysis. *Bioinformatics*, **35**(9), 1582-1584. <https://doi.org/10.1093/bioinformatics/bty862>

Schubert, B.[†], Schärfe, C., Dönnies, P., Hopf, T., Marks, D., and Kohlbacher, O. (2018). Population-specific design of de-immunized protein biotherapeutics. *PLoS Computational Biology*, **14**(3), e1005983. <https://doi.org/10.1371/journal.pcbi.1005983>

Schubert, B.[†], and Kohlbacher, O. (2016). Designing string-of-beads vaccines with optimal spacers. *Genome Medicine*, **8**(9). <https://doi.org/10.1186/s13073-016-0263-6>

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.
<https://doi.org/10.1093/bioinformatics/btu548>