Curriculum Vitæ

Dr. Martin Hölzer

Personal Data

Name:	Dr. rer. nat. Martin Hölzer
Gender:	Male
Nationality:	German
Family status:	Married
Place and Date of Birth:	Rudolstadt, Germany|16 March 1988
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Research focus and current role

As a bioinformatician, I work and research in a branch of science that represents a crucial interdisciplinary element of the life sciences and connects them with the help of computer science methods. In my research, I am dedicated to the comprehensive analysis of biological (sequence) data concerning infectious diseases, immunological questions, and veterinary and human medical issues. In particular, extracting information from huge (meta-) genomic and transcriptomic sequence datasets is essential for my work. I am using advances in sequencing technology to break new ground in the analysis of various pathogens, from viruses to bacteria to fungi, while also shedding light on their interactions with the host. Bioinformatics data, reproducible workflow management, and visualization tools provide the foundation for high spatial and temporal resolution data analysis methods in the life sciences.

Currently, I am leading the team "Research & Innovation" within the recently established "Genome Competence Center" (MF1) at the Robert Koch Institute (RKI), the German Institute of Public Health. I am responsible for an interdisciplinary team of four permanent and three temporary staff (TV-L 13 and 14), several students, and a technical assistant. Our team combines technology platforms and data analysis to develop, implement and apply experimental and bioinformatics approaches for future-oriented research and applications. Before, I was deputy head of the former "Bioinformatics and Systems Biology" department at the RKI. In this role, I supported a diverse and international team of ~20 scientists and was responsible for various administrative tasks and supervision. In addition to collaborations within the RKI, I work scientifically with colleagues at the European Bioinformatics Institute (EMBL-EBI), the European Virus Bioinformatics Centre (EVBC), and with various research groups at university hospitals (Jena, Leipzig, Graz, Greifswald, ...) and microbiology departments. In the past, I was responsible for experimental design and computational integration of all kinds of omics data in life sciences.

Main areas of research

- Microbial bioinformatics
- High-Throughput sequencing
- Metagenomics and -transcriptomics
- *De novo* assembly and annotation
- Transcriptomics and comparative genomics

- Genomic surveillance
- Pathogen detection and characterization
- Nanopore real-time sequencing
- Automation and visualization
- Cloud compute, containers and workflow management

Scientific Education

01/2018	**Doctorate degree**, Dr. rer. nat. (University of Jena) Grade: *summa cum laude* Doctoral thesis: *The Dark Art of Next-Generation Sequencing: fundamental approaches for genomics, transcriptomics, and differential gene expression* Prof. Dr. Manja Marz, RNA Bioinformatics and High-Throughput Analysis
01/2018–07/2020	Team lead of an associated bioinformatics research group at the University of Jena
08/2013–12/2017	PhD student at University of Jena
12/2012	**Diploma in Bioinformatics** (University of Jena) Grade: 1.4 Thesis: *Data management of mass spectra and fragmentation trees with BExIS* Prof. Dr. Sebastian Böcker, Chair of Bioinformatics, FSU Jena
10/2007–12/2012	Studies of Bioinformatics at University of Jena
2006–2007	Civilian service, Diakonisches Altenhilfezentrum, Bad Blankenburg
1998–2006	University entrance qualification, Friedrich-Fröbel-Gymnasium, Bad Blankenburg, Grade 2.0

Professional memberships

01/2020–07/2020	**iRTG AquaDiva** *Post-doc representative within the "integrated Research Training Group" (iRTG) of the CRC AquaDiva, University of Jena* Structured training program for training and education open to doctoral and postdoctoral researchers of the CRC AquaDiva, bringing together fields of hydrology, geology, and biogeochemistry with omic technologies and bioinformatics.
since 06/2019	**BioS** *Member of the external advisory board of the EU project "Digital Skills on Computational Biology for Health Professionals" (www.bios-project.eu)* BioS aims at advancing the digital skills of medical doctors through design, development and delivery of novel knowledge on Computational Biology & Bioinformatics.
since 03/2017	**EVBC** *Founding member of the "European Virus Bioinformatics Center" (EVBC), University of Jena* EVBC brings together virologists and bioinformaticians on international level to provide a platform for interdisciplinary collaborative projects.

WORK EXPERIENCE

since 04/2023

Team lead "Research & Innovation" at RKI

Genome Competence Center (MF1), Robert Koch Institute, Berlin

Build and lead an interdisciplinary team conducting research and method development to characterize infectious disease agents using genomics, transcriptomics, and proteomics. Lead a diverse team of senior researchers, postdoctoral fellows, graduate students, undergraduate students, and technical staff (n=~10).

04/2021–03/2023

Deputy head of the Bioinformatics unit at RKI

Methodology and Research Infrastructure, Bioinformatics MF1, Robert Koch Institute, Berlin

Mainly responsible for bioinformatics research development focusing on outbreak detection, real-time sequencing and pathogen evolution. Jointly responsible for bioinformatics work and method development for SARS-CoV-2 sequencing analysis, outbreak tracking and virus evolution during the COVID-19 pandemic. Co-supervision of a diverse team of ~20 researchers and core facility members.

since 08/2020

Researcher at RKI

Methodology and Research Infrastructure, Bioinformatics MF1, Robert Koch Institute, Berlin

Bioinformatics researcher at the RKI, computational analyses of Next-Generation Sequencing (NGS) data in the context of pathogen detection. Research focus on the application of Nanopore real-time sequencing for molecular surveillance.

01/2018–07/2020

Post-doc & team leader of an associated research group

RNA Bioinformatics/High-Throughput Analysis, Prof. Dr. Manja Marz, University of Jena

Supervision of NGS projects including the automatization of workflows for assembly, annotation, variant calling, differential gene expression, metagenomics, and visualization of results. Development of novel applications for long-read sequencing data. Team leader of an associated bioinformatics group at the University of Jena.

10/2019–03/2020

Visiting researcher

EMBL-EBI European Bioinformatics Institute, Dr. Rob Finn, Hinxton, United Kingdom

Working in the research group of Dr. Rob Finn on the analysis and classification of metagenomic samples using Nanopore long-read sequencing data and hybrid approaches.

since 06/2019

nanozoo GmbH

Co-founder of nanozoo GmbH, Jena, Germany

Founded in mid-2019, nanozoo is a bioinformatics start-up providing end-to-end services for the production and analysis of microbial data. *nanozoo* has set itself the goal of removing barriers in bioinformatic data analysis to provide up-to-date standards and analyses to a broad mass of researchers.

08/2013–12/2017

PhD student

RNA Bioinformatics and High-Throughput Analysis, Prof. Dr. Manja Marz, University of Jena

Management of various NGS projects comprising experimental design, data analysis, visualization and interpretation. Development of pipelines for downstream bioinformatical analyses. Examination of (meta-)genomic/transcriptomic data with a special focus on *de novo* assembly, annotation, and identification of differential expressed protein- and non-coding genes. Contributions to the emerging field of virus bioinformatics.

09/2009–05/2012

Student assistant

Chair of Bioinformatics, Prof. Dr. Sebastian Böcker, University of Jena

Integration of algorithms, data management and visualization for phylogenetic analyses and clustering.

ORGANIZATION OF CONFERENCES AND WORKSHOPS (SELECTION)

08/2022 | *Training*: SARS-CoV-2 SEQUENCING AND DATA ANALYSIS Harare, Zimbabwe
NEXT-GENERATION SEQUENCING USING NANOPORE TECHNOLOGY
Responsibilitites: Joined an official mission as part of the "German Epidemic Prepardness Team" (SEEG) to support SARS-CoV-2 genomic surveillance in Zimbabwe and teach participants about the corresponding bioinformatics data analysis.

10/2021 | *Workshop*: FROM DNA TO GENOME: HANDS-ON NANOPORE RKI, Berlin, Germany
ANALYSIS OF BACTERIAL GENOMES
Responsibilitites: Prepared the bioinformatics workshop part including all necessary material and code. Supervised students from diverse backgrounds in a two-day practical course on the topics Nanopore sequencing, genome assembly and comparison with Illumina data.

11/2019 | *Workshop*: HANDS-ON NANOPORE SEQUENCING: ADVENTURES IN IIT, New Delhi, India
METAGENOMICS AND ANTIMICROBIAL RESISTANCE
Responsibilitites: Prepared workshop. Co-supervised and assisted students in a one-week practical course on the topic of Nanopore sequencing and metagenomics data analysis.

10/2018 | *Workshop*: BIOINFORMATICS ANALYSIS OF NANOPORE Doubice, Czech Republic
SEQUENCING DATA: AN INTRODUCTION
Responsibilitites: Co-prepared workshop and assisted students in a two-day practical course on the topic of Nanopore sequencing data analysis.

05/2017 | *Hackathon*: AGING-RELATED RNA-SEQ DATA ANALYSIS University of Jena
STAY YOUNG OR DIE TRYING
Responsibilitites: Supporting organizer of this one-week hackathon. Logistical tasks.

01/2017 | *Conference*: FIRST MEETING OF THE EUROPEAN VIRUS University of Jena
BIOINFORMATICS CENTER
Responsibilitites: Supporting organizer. Logistical tasks.

04/2014 | *Hackathon*: VIRUS-INFECTED RNA-SEQ DATA ANALYSIS University of Jena
FIGHT AGAINST EBOLA – IN SILICO
Responsibilitites: Prepared a one-week collaborative workshop as a main organizer and assisted participants in data analysis.

FURTHER TASKS BEYOND OWN RESEARCH

- **Committee work at RKI**
  Active participation in the SARS-CoV-2 working groups "Diagnostics" and "Evolution" at the Robert Koch Institute. Contribution of expertise in bioinformatics, virus evolution and computational method development to these committees during the COVID-19 pandemic and beyond. Co-organization of the "Diagnostics and Pathogen Evolution" working group.

- **Editorial board tasks**
  - Research topic editor for *Frontiers in Genetics*: "The Transition Era to New Sequencing Technologies and Their Application to Integrative Omics in Molecular Surveillance" (2020/21)
  - Editorial board member for the "Bioinformatic and Predictive Virology" section in *Frontiers in Virology* (since 2021)

- **Peer-reviews for journals** (Selection)
  BMC Biology (2023), iScience (2022), Frontiers in Genetics (2022), PeerJ (2021), GigaScience (2021), PLOS Comp Biol (2021), Bioinformatics (2021), Briefings in Bioinformatics (2023, 2021, 2020), MDPI Viruses (2022, 2021, 2020), Nature Communications (2019), Microbiome (2019), Genome Biology (2019), BMC Supplements (2019), Scientific Reports (2021, 2019), Frontiers in Microbiology (2019), Virus Research (2018), Molecular Ecology Resources (2018) publons.com/author/1521002

- **Peer-reviews for international conferences** (Selection)
  Annual International Conference on Research in Comp. Molecular Biology (RECOMB 2018),
  Annual International Conference on Intelligent Systems for Molec Bio (ISMB 2017, 2022, 2023),
  German Conference on Bioinformatics (GCB 2014, 2015, 2017)

Supervision

PhD theses:	2
Master theses:	10
Bachelor theses:	2
Practical works & research internships:	6

Plus supervision of several research assistants and co-supervised PhD students.

- **PhD theses**
  - Stefan Frank, *Contextual genomics and detection of positive selection in AMR genes.* (started 01/2022)
  - Marie Lataretu, *Usable, scaleable and reproducible workflows for Next-Generation Sequencing Data.* (completion planned in 2023)

- **Master theses**
  - Namuun Battur, *Evaluation of an universal primer design for amplicon-based short- and long-read sequencing and detection of poliovirus.* (started 04/2023)
  - Ashkan Ghassemi, *Calculation of an minimal signature mutation set for SARS-CoV-2 lineage characterization and detection.* (started 04/2023)
  - Julius Tembrockhaus, *Positive selection detection in SARS-CoV-2 genes and sampling bias comparison in a German sequence data collection.* (started 10/2022)
  - Eva Aßmann, *Development of an approach for detection and quantification of known and cryptic SARS-CoV-2 variants from wastewater using nanopore sequencing data of the spike gene.* (completed 03/2023)
  - Charlotte Reuschel, *Comparative genome analysis of five strains of the recently defined genus Chlamydiifrater.* (completed 07/2022)
  - Kunaphas Kongkitimanon, *An improved deep learning model for the prediction of antimicrobial peptides.* (completed 09/2021)
  - Lisa-Marie Barf, *Bioinformatic and in vitro comparison among Chlamydia spp. to elucidate chlamydial host specificity and phylogeny.* (completed 06/2019), co-supervised
  - Lasse Faber, *Effective clustering of de novo transcriptome assemblies.* (completed winter 2019)
  - Marie Lataretu, *Spotting fungal mitogenomes in de novo assemblies of short-read NGS data.* (completed summer 2018)
  - Ruman Gerst, *PCAGO: An interactive web service to analyze RNA-Seq data with principal component analysis.* (completed fall 2017)

- **Bachelor theses**
  - Sandra Triebel, *A comparison of short-read, long-read, and hybrid de novo genome assembly tools for the reconstruction of Mycoplasma bovis strains.* (completed autumn 2019)
  - Jannes Spangenberg, *Analysis of host-virus transcriptome data: exploring the unmapped.* (completed autumn 2019), co-supervised

- **Practical works/ research internships**
  - Ashkan Ghassemi, *Mutation frequency calculator – a covsonar utility.* (completed spring 2023)

  - David Fischer, *Evaluation of assembly and polishing methods for the reconstruction of fungi genomes from short- and long-read sequencing data.* (completed autumn 2021)

  - Kunaphas Kongkitimanon, *Detection of antimicrobial peptides from large collections of publicly available RNA-Seq data.* (completed winter 2020)

  - Anne Muriel Christin Ritsch, *Transcribed endogenous viral elements in Myotis lucifugus.* (completed summer 2019), co-supervised

  - Lasse Faber, `Transcripto` *– A Snakemake de novo transcriptome assembly pipeline.* (completed spring 2019)

  - Daria Meyer, *Endogenous Viral Elements (EVEs).* (completed winter 2018), co-supervised

Scholarships

Mar. 2020 – Mar. 2021	"Google for Education" Google Cloud Platform research credits for cloud calculations for a research proposal	€5,000
Dec. 2018 – Jan. 2022	"Add-on Fellowship for Interdisciplinary Life Science" of the Joachim Herz Stiftung, Hamburg, Germany	€12,500

GRANTS

		Amount
APR. 2024 – MAR. 2027	**JPIAMR (MARRES)** Non-funded project partner: "One health surveillance approach on marine mammal, marine environmental and human antimicrobial resistance on the North and Baltic Seas", to support with metagenome sequencing using Illumina and Nanopore and subsequent bioinformatics analyses for taxonomic classification and AMR annotation.	–
JAN. 2024 – DEC. 2024	**Sonderforschungsmittel, Robert Koch Institute** 1-year PostDoc position woking on "MetagenomeWatch: Harnessing Big Data for Pathogen Surveillance and Genome Discovery", to set up a new system, using k-mer and MinHash-based algorithmics, to search for genomic sequences of interest in all publicly available metagenome sequencing data sets in real-time. (*co-supervised*)	€ 96.000
JAN. 2024 – DEC. 2026	**Sonderforschungsmittel, Robert Koch Institute** 3-year PhD student position woking on "Decoding Bacterial Secrets: Unraveling DNA Modifications through Nanopore Sequencing for Public Health Insights". Computer-aided detection of DNA modifications in bacterial pathogens using Nanopore sequencing and involving three expert units at the RKI (working on *Mycobacteria* and *Acinetobacter baumanii* and machine learning algorithms for identifying specific patterns in large datasets).	€ 230.000
JAN. 2022 – DEC. 2024	**Sonderforschungsmittel, Robert Koch Institute** 3-year PhD student position woking on "Contextual genomics and detection of positive selection in antibotic resistant bacteria". Interdisciplinary project involving four units at the RKI (monitoring *Enterococcus, L. monocytogenes, N. gonorrhoeae* infections in Germany) as well as international cooperations to develop computational methods for AMR screening in bacteria.	€ 230.000
DEC. 2018 – MAR. 2020	Program of the University of Jena to support junior researchers in obtaining third-party funding	€ 9,930

Teaching instructor

2022, 2023 (at FU Berlin)	*Practical course*: SARS-CoV-2 data science *Responsibilitites*: Prepared, supervised, and assisted students in a two-week practical course on genome reconstruction and outbreak detection using SARS-CoV-2 as an example. Co-organized together with Prof. Dr. Max von Kleist.
2018, 2019	*Practical course*: VIROINFORMATICS *Responsibilitites*: Prepared, supervised, and assisted students in a two-week practical course on the topic of virus detection from meta-transcriptomic NGS data.
2017, 2017/18 2018	*Lecture* & *Practical course*: LATEX basics for the Life Sciences *Responsibilitites*: Presented lectures on the document preparation system LATEX. Supervised and assisted 30 undergraduate students in a one-week full-time course. Graded daily assignments, excercises, and exams.
2017/18	*Practical course*: HIGH-THROUGHPUT BIOINFORMATICS *Responsibilitites*: Prepared, supervised, and assisted students in a two-week practical course on the topic of RNA-Seq data analysis.

Teaching assistant

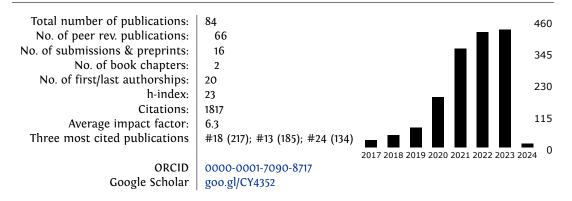|	
2016/17, 2017/18 2018/19	*Lecture*: BASIC BIOINFORMATIC APPLICATIONS *Responsibilities*: Prepared and taught four 1.5-hour lectures on the topic of high-throughput data analysis and assembly (*From raw read data to differential expressed genes*). Prepared and supervised practical examples. Graded assignments and course exams.
2014/15, 2015, 2016, 2017	*Lecture*: VIRUS BIOINFORMATICS *Responsibilitites*: Developed and taught hour-long lessons on viral replication, assembly, and sequencing.
2014/15, 2015/16, 2016/17, 2017/18	*Lecture*: HIGH-THROUGHPUT BIOINFORMATICS *Responsibilitites*: Developed and taught hour-long lessons on sequencing technologies and protocols, Next-Generation Sequencing design, quality control and data processing, *de novo* and reference-based assembly, read quantification, normalization, and differential gene expression analysis.
2015/16, 2018/19	*Practical course*: HIGH-THROUGHPUT BIOINFORMATICS *Responsibilitites*: Prepared, supervised, and assisted students in a one-week practical course on the topic of RNA-Seq data analysis.

Scientific poster presentations

04/2022	31st Annual Meeting of the Society for Virology, Online *Integrated Molecular Surveillance of SARS-CoV-2: Fix the bioinformatics bottleneck.*
09/2021	73th Annual meeting of the German society for Hygiene and Microbiology (DGHM), Online *From raw sequences to alert: bioinformatics infrastructure and targeted method development in response to SARS-CoV-2.*
03/2019	3rd Annual meeting of the European Virus Bioinformatics Center (EVBC), Glasgow, Scotland *Virus- and interferon alpha-induced transcriptomes of the microbat* Myotis daubentonii.
03/2019	29th Annual Meeting of the Society for Virology, Düsseldorf, Germany *Virus- and interferon alpha-induced transcriptomes of the microbat* Myotis daubentonii.
09/2018	German Conference on Bioinformatics, Vienna, Austria *Long reads matter: The advantages of nanopore long-read sequencing.*
03/2018	28th Annual Meeting of the Society for Virology, Würzburg, Germany *PCAGO: An interactive web service to analyze RNA-Seq data with principal component analysis.* R. Gerst, M. Marz, and M. Hölzer
05/2017	Bioinformatics Mittelerde Meeting, Leipzig, Germany *PoSeiDon: a web server for the detection of evolutionary recombination events and positive selection.*
03/2017	27th Annual Meeting of the Society for Virology, Marburg, Germany *PoSeiDon: a web server for the detection of evolutionary recombination events and positive selection.*
04/2016	26th Annual Meeting of the Society for Virology, Münster, Germany *A method pipeline for the detection of positively selected sites in silico – exemplarily shown for bat Mx1.*

Scientific oral presentations

03/2023	32nd Annual Meeting of the Society for Virology, Ulm, Germany *Establishing SARS-CoV-2 genomic surveillance at the national level*
05/2021	Viruses *in silico*, the EVBC lecture series, Online *Genomic surveillance of SARS-CoV-2 at the Robert Koch Institute: an overview and bioinformatics edge cases*
09/2020	RKI research meeting, Berlin, Germany *Workflow Management Systems & Containers: Reproducible computational pipelines with Nextflow & Docker*
09/2020	Joachim Herz Foundation, Königstein im Taunus, Germany *A journey from the source of the Ganges to the national health institute in Germany: a nanopore story*
01/2020	EMBl-EBI research talk, Hinxton, Cambridge, UK *Nanopore long-read metagenomics: How long reads improve microbial and phage genomes from a complex aquifer system*
11/2018	Institut für Mikrobiologie der Bundeswehr, Munich, Germany *A short and a long sequencing story about Ebola and Coronaviruses*
07/2018	11th International Conference on Virology/Microbiology, Vancouver, Canada *An Interface between Bioinformatics and Virology* (Keynote Speaker)
02/2018	33. Winterseminar der Bioinformatik, Bled, Slovenia *PCAGO: An interactive web service to analyze RNA-Seq data with principal component analysis*
02/2017	32. Winterseminar der Bioinformatik, Bled, Slovenia *PoSeiDon: A web server for the detection of evolutionary recombination events and positive selection*
10/2016	14. Herbstseminar der Bioinformatik, Doubice, Czech Republic *Fun with PCA: Insights into RNA-Seq based principal component analysis*
02/2016	31. Winterseminar der Bioinformatik, Bled, Slovenia *Evolutionary analyses of positively selected sites in the interferon-induced innate immunity factor Mx1 of bats*
03/2015	25th Annual Meeting of the Society for Virology, Bochum, Germany *Differential transcriptional responses to Ebola and Marburg virus infection in cells from bats and humans*

Citation Analysis

Total number of publications:	84
No. of peer rev. publications:	66
No. of submissions & preprints:	16
No. of book chapters:	2
No. of first/last authorships:	20
h-index:	23
Citations:	1817
Average impact factor:	6.3
Three most cited publications	#18 (217); #13 (185); #24 (134)

ORCID	0000-0001-7090-8717
Google Scholar	goo.gl/CY4352

Publications

Peer-reviewed journal publications

Ψ These authors contributed equally

66 **M. Hölzer**. POCP-nf: an automatic Nextflow pipeline for calculating the percentage of conserved proteins in bacterial taxonomy. *OUP Bioinformatics*, 2024.   **IF: 5.8**

65 C. Kohler, J. King, L. Stacker, KV. Goller, J. Moritz, A. Pohlmann, N. Nath, A. Tzvetkova, M. Rieck, S. Paraskevopoulou, D. Beslic, **M. Hölzer**, S. Fuchs, J. Ziemann, L. Kaderali, M. Beer, NO. Hübner, and K. Becker. Neighbourhood watch: genomic epidemiology of SARS-CoV-2 variants circulating in a German federal state, Mecklenburg-Western Pomerania, in 2020–2022. *Emerging Microbes & Infections*, 2023.   **IF: 13.2**

64 S. Triebel, K. Sachse, M. Weber, M. Heller, C. Diezel, **M. Hölzer**, C. Schnee, and M. Marz. *De novo* genome assembly resolving repetitive structures enables genomic analysis of 35 European *Mycoplasma bovis* strains. *BMC Genomics*, 2023.   **IF: 4.4**

63 N. Bollen, SL. Hong, BI. Potter, R. Lienhard, ML. Tritten, N. Sierro, E. Guedj, R. Dulize, D. Bornand, M. Auberson, M. Berthouzoz, P. Duvoisin, NV. Ivanov, MC. Peitsch, V. Hill, COVID-19 Genomics Belgium Consortium, V. Matheeussen, S. Bontems, B. Verhasselt, J. Degosserie, L. Waumans, G. Bayon-Vicente, M. Reynders, L. Cattoir, V. Coste, H. Valgaeren, JV. Weyenbergh, L. Cuypers, E. Andre, K. Durkin, P. Maes, K. Khan, C. Huber, MA. Suchard, MM. Foudi, C. Godwe, MHM. Yifomnjou, M. Landry, R. Njouom, PM. Kingebeni, P. Oluniyi, IB. Olawoye, C. Happi, A. Ayouba, M. Peeters, S. Behillil, E. Simon-Loriere, **M. Hölzer**, S. Dellicour, G. Dudas, and G. Baele. Tracking down the origin and subsequent spread of SARS-CoV-2 lineage B.1.619. *OUP Virus Evolution* 2023.   **IF: 7.9**

62 K. Sachse, **M. Hölzer**, F. Vorimore, LM. Barf, C. Sachse, K. Laroucau, M. Marz, and K. Lamkiewicz. Genomic analysis of 61 *Chlamydia psittaci* strains reveals extensive divergence associated with host preference. *BMC Genomics*, 2023.   **IF: 4.4**

61 J. Linde, H. Brangsch, **M. Hölzer**, C. Thomas, M. C Elschner, F. Melzer, and H. Tomaso. Comparison of Illumina and Oxford Nanopore Technology for genome analysis of *Francisella tularensis*, *Bacillus anthracis*, and *Brucella suis*. *BMC Genomics*, 2023.   **IF: 4.4**

60 A. Schoen, **M. Hölzer**, M. Müller, C. Drosten, M. Marz, B. Lamp, and F. Weber. Functional comparisons of the virus sensor RIG-I from humans, the microbat *Myotis daubentonii*, and the megabat *Rousettus aegyptiacus*, and their response to SARS-CoV-2 infection. *Journal of Virology*, 2023.   **IF: 5.1**

59 TE. Klassert, **M. Hölzer**, C. Zubiria-Barrera, J. Bethge, E. Klaile, MM . Müller, M. Marz, and H. Slevogt. Differential Transcriptional Responses of Human Granulocytes to Fungal Infection with *Candida albicans* and *Aspergillus fumigatus*. *MDPI Journal of Fungi*, 2023.   **IF: 4.7**

58 M. Lataretu, O. Drechsel, R. Kmiecinski, K. Trappe, **M. Hölzer**, and S. Fuchs. Lessons learned: overcoming common challenges in reconstructing the SARS-CoV-2 genome from short-read sequencing data via CoVpipe2. *F1000Research*, 2023.   **IF: –**

57 G. Rangel-Pineros, A. Almeida, M. Beracochea, E. Sakharova, M. Marz, A. Reyes, **M. Hölzer**, and RD. Finn. VIRify: an integrated detection, annotation and taxonomic classification pipeline using virus-specific protein profile hidden Markov models. *PLOS Comp Biol*, 2023.   **IF: 4.3**

56 M. Jundzill, R. Spott, M. Lohde, **M. Hölzer**, A. Viehweger, and C. Brandt Managing and monitoring a pandemic: showcasing a practical approach for the genomic surveillance of SARS-CoV-2. *OUP Database*. **Supp.**: SOP SARS-CoV-2 sequencing and data administration. 2023.   **IF: 5.8**

55   A. Viehweger, M. Marquet, **M. Hölzer**, N. Dietze, M. Pletz, and C. Brandt. Nanopore-based enrichment of antimicrobial resistance genes – a case-based study. *GigaByte*. 2023.   **IF: –**

54   A. Erkes, R. Grove, M.   arkovi , S. Krautwurst, R. Koebnik, RD. Morgan, GG. Wilson, **M. Hölzer**, M. Marz, J. Boch, and J. Grau. Assembling highly repetitive *Xanthomonas* TALomes using Oxford Nanopore sequencing. *BMC Genomics*. 2023.   **IF: 4.5**

53   GC. Martín-Hernández, M. Chmielarz, B. Müller, C. Brandt, A. Viehweger, **M. Hölzer**, V. Passoth. Enhanced glycerol assimilation and lipid production in *Rhodotorula toruloides* CBS14 upon addition of hemicellulose primarily correlates with early transcription of energy-metabolism-related genes. *Biotechnology for Biofuels and Bioproducts*. 2023.   **IF: 7.6**

52   M. Marquet, **M. Hölzer**, M. W. Pletz, A. Viehweger, O. Makarewicz, R. Ehricht, and C. Brandt. What the Phage: A scalable workflow for the identification and analysis of phage sequences. *GigaScience*. 2022.   **IF: 7.6**

51   F. Song, R. Kotolloshi, M. Gajda, **M. Hölzer**, M. Grimm, and D. Steinbach. Reduced IQGAP2 Promotes Bladder Cancer through Regulation of MAPK/ERK Pathway and Cytokines. *MDPI Int. J. Mol. Sci.*. 2023.   **IF: 6.2**

50   DY. Oh[Ψ], **M. Hölzer**[Ψ], S. Paraskevopoulou, M. Trofimova, F. Hartkopf, M. Budt, M. Wedde, H. Richard, B. Haldemann, T. Domaszewska, J. Reiche, K. Keeren, A. Radonic, JPR. Calderon, MR. Smith, AA. Brinkmann, K. Trappe, O. Drechsel, K. Klaper, S. Hein, E. Hildt, W. Haas, S. Calvignac-Spencer, T. Semmler, R. Dürrwald, A. Thürmer, C. Drosten, S. Fuchs, S. Kröger, Mv. Kleist, T. Wolff. Advancing Precision Vaccinology by Molecular and Genomic Surveillance of SARS-CoV-2 in Germany, 2021. *Clinical Infectious Diseases*. 2022.   **IF: 9.0**

49   T. Kaleta, L. Kern, S. Hong, **M. Hölzer**, G. Kochs, J. Beer, D. Schnepf, M. Schwemmle, N. Bollen, P. Kolb, M. Huber, S. Ulferts, S. Weigang, G. Dudas, A. Wittig, L. Jaki, A. Padane, A. Lagare, M. Salou, E. Ozer, N. Nnaemeka, J. Odoom, R. Rutayisire, A. Benkahla, C. Akoua-Koffi, AS. Ouedraogo, E. SIMON-LORIERE, V. Enouf, S. Kröger, S. Calvignac-Spencer, G. Baele, M. Panning, J. Fuchs. Antibody escape and global spread of SARS-CoV-2 lineage A.27. *Nature Communications*. 2022.   **IF: 17.7**

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M. Hölzer and M. Marz. Chapter Nine – Software Dedicated to Virus Sequence Analysis "Bioinformatics Goes Viral". *Adv Virus Res.* (ed. M. Beer), 99:233-257, Academic Press, 2017.

Theses

M. Hölzer. The Dark Art of Next-Generation Sequencing: fundamental approaches for genomics, transcriptomics, and differential gene expression. *PhD thesis*, University of Jena, 2018.

M. Hölzer. Data management of mass spectra and fragmentation trees with BExIS. *Diploma thesis*, in German, University of Jena, 2012.

SOFT SKILLS

12/2022	*Web seminar, Bioterrorism: Relevant pathogens, diagnostics and management*, STAKOB, Berlin
02/2020	*Nextflow: reproducible containerised scientific workflows across clusters and cloud*, Dr. Paolo Di Tommaso & Dr. Evan Floden, FU Berlin
06/2019	*Managing a Bioinformatics Core Facility*, European Bioinformatics Institute (EMBL-EBI), Hinxton, UK
07/2018	*Fördermöglichkeiten für exzellente Nachwuchswissenschaftler/innen*, Dr. Mareile Knees, Jena
05/2018	*Workshop "Drittmittel einwerben"*, Jana Dümmler, Graduate Academy, Jena
04/2018	*Workshop "Gute wissenschaftliche Praxis und der Umgang mit Konflikten im Forschungsalltag"*, Dr. Dorit Schmidt & Dr. Andrea Kliewer, Graduate Academy, Jena
02/2018	*Patente als Chance für meine Forschung*, Dr. Christian Liutik, Patentinformationszentrum FSU, Jena
02/2018	*Pursuing an Academic Career in Germany: Pros and Cons*, Dr. Hanna Kauhaus, Graduate Academy, Jena
02/2018	*Proposal Writing Workshop*, Frank Lauterbach, iRTG AquaDiva, Jena
03/2014	*Mitteldeutscher Fundraisingtag*, Crowdfunding: Chancen und Grenzen, FundraisingForum e.V., Jena
04/2013	*Jugendgruppenleiter Card (JuLeiCa)*, nationwide uniform identity card for voluntary people in youth work, VTPV e.V., Bad Blankenburg
03/2012	*Mitteldeutscher Fundraisingtag*, Fundraising und Freiwillige: wie passt das zusammen? FundraisingForum e.V., Jena
09/2010	*Web 2.0 – für Vereine, Initiativen & Parteien*, Thomas Mergen, Friedrich-Naumann-Stiftung für die Freiheit, Erfurt
since 2002	Various workshops, seminars, and advanced trainings about time and group management, group dynamics, self-motivation, project planning, association and employment law, speech, presentation, administration, and building management.

Non-scientific Leadership Experiences & Activities

Scout association "Bund der Pfadfinderinnen und Pfadfinder" (BdP)

since 2019	*Management board member of "VTPV" registered society*
	Administrative tasks and representation of the scout activities in Thuringia.
since 2012	*Management board member of "Scoutactive" registered society*
	Administrative tasks and writing of proposals for staff funding.
since 2008	*Assistant manager of BdP scouting center of Thuringia*
	Administrative tasks, coordination of staff and volunteers, realization of adventure activities for kids and youths, technical support, web site and hardware supervision.
since 2007	*Assistant leader of BdP "Landesverband Thüringen e.V."*
	Organization of activities in Thuringia and across national borders. Organized events and elections.
2005–2015	*Group leader of BdP scout tribe "Falken vom Greifenstein"*
	Administration of the association. Management of scout camps, international cooperations, regular meetings. Represented the association at national and international events.
since 1998	*Member of BdP*

Water of Life

2019/20	*Member of the Cambridge University Whisky Appreciation Society*
since 2017	*Co-Founder and organizer of the Bad Blankenburger "Kessel-Treffen"*
	Coordination of Scottish events and whisky tastings, kessel-treffen.de.
since 2014	*Whisky tastings*
	Preparation and execution of whisky tastings for beginner and advanced

Music

since 1999	*Piano*

Languages

German	Native language
English	Written and spoken fluently

References

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Dr. rer. nat. Martin Hölzer   Leipzig, May 15, 2024