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
Work Address:	RKI, Nordufer 20, 13353 Berlin
Twitter:	@martinhoelzer
Code:	github.com/hoelzer
Web:	hoelzer-lab.github.io

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 Faculty of Mathematics and Computer Sciences
01/2018–07/2020	Team leader 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 Faculty of Mathematics and Computer Sciences
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

MAIN AREAS OF RESEARCH

- Bioinformatics
- High-Throughput Sequencing
- Metagenomics and -transcriptomics
- *De novo* assembly and annotation
- Transcriptomics and comparative genomics

- Non-coding RNAs
- Microbes and viruses
- Oxford Nanopore Sequencing
- Automation and visualization
- Containerization and workflow management

WORK EXPERIENCE

since 08/2020	**Researcher at RKI** *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, Wellcome Trust Genome Campus, Hinxton, Cambridge, 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, Leipzig, 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/High-Throughput Analysis, Prof. Dr. Manja Marz, University of Jena* Management of various NGS projects comprising 1) experimental design, 2) selection of appropriate sequencing parameters, and 3) 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.

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
	The iRTG provides a structured training program for training and education open to doctoral and postdoctoral researchers of the CRC AquaDiva. It offers courses that bring together the 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 the design, development and delivery of new modular vocational curricula on Computational Biology & Bioinformatics. As a member of the advisory board I am supporting the project by giving advice on the main outcomes of the project.
since 03/2017	**EVBC**
	Founding member of the "European Virus Bioinformatics Center" (EVBC), University of Jena
	The EVBC is intended to bring together virologists and bioinformaticians across Europe and provide a platform for interdisciplinary collaborative projects. My expertise covers sequencing, design and high-throughput analysis of virus-enriched and -infected biological samples.

Organization of conferences and workshops

11/2019	*Workshop*: Hands-on Nanopore sequencing: Adventures in metagenomics and antimicrobial resistance	IIT, New Delhi, India
	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 sequencing data: an introduction	Doubice, Czech Republic
	Responsibilitites: Co-prepared workshop and assisted students in a two-day practical course on the topic of Nanopore sequencing data analysis.	
08/2018	*Workshop*: 23rd International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology (VEME)	RKI, Berlin
	Responsibilitites: Supporting organizer. Logistical tasks.	
05/2017	*Hackathon*: Aging-related RNA-Seq data analysis Stay Young or Die Trying	University of Jena
	Responsibilitites: Supporting organizer of this one-week hackathon. Logistical tasks.	
01/2017	*Conference*: First Meeting of the European Virus Bioinformatics Center	University of Jena
	Responsibilitites: Supporting organizer. Logistical tasks.	
04/2014	*Hackathon*: Virus-infected RNA-Seq data analysis Fight against Ebola – in silico	University of Jena
	Responsibilitites: Prepared a one-week collaborative workshop as a main organizer and assisted participants in data analysis.	

Further tasks beyond own research

- **Sequencing project management**
  Management of more than 60 Next-Generation Sequencing projects, including the design of experimental set-ups and the definition of sequencing parameters. Calculation of project costs and communication between the wet lab partners and the sequencing facility. Organization of data handling and computational analysis.

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

- **Peer-reviews for journals**
  Briefings in Bioinformatics (2020), MDPI Viruses (2020), Nature Communications (2019), Microbiome (2019), Genome Biology (2019), BMC Supplements (2019), Scientific Reports (2019), Frontiers in Microbiology (2019), Virus Research (2018), Molecular Ecology Resources (2018)   publons.com/author/1521002

Supervision

Master theses:	4
Bachlor theses:	2
Practical works/ research internships:	4

- **Master theses**
    - 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)

- **Bachlor 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**
    - Kunaphas Kongkitimanon, *Detection of antimicrobial peptides from large RNA-Seq collections.* (started 09/2020)

    - 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
2020 – 2025	Thuringian Ministry of Science	–
	"Digitisation of the life sciences: Ways into the future". The University of Jena received €1.35 million to advance the digitization of life sciences. I was jointly responsible for the application and significantly involved in the compilation of the contents and the writing. Co-supervision of work packages and project partner (digleben.uni-jena.de/projektpartner).	
DEC. 2018 – MAR. 2020	Program of the University of Jena to support junior researchers in obtaining third-party funding	€9,930

Teaching

at the University of Jena

Teaching instructor

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 NATURAL SCIENTISTS
	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
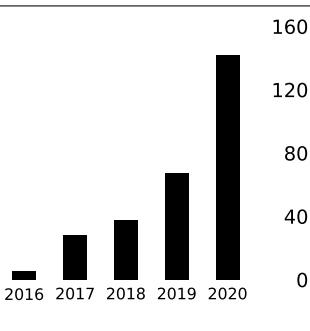
03/2019	3rd annual meeting of the European Virus Bioinformatics Center (EVBC), Glasgow, Scotland *Virus- and interferon alpha-induced transcriptomes of the microbat* Myotis daubentonii.
03/2019	29th Annual Meeting of the Society for Virology, Düsseldorf, Germany *Virus- and interferon alpha-induced transcriptomes of the microbat* Myotis daubentonii.
09/2018	German Conference on Bioinformatics, Vienna, Austria *Long reads matter: The advantages of nanopore long-read sequencing.*
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

(selection)	slideShare
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*
02/2015	30. Winterseminar der Bioinformatik, Bled, Slovenia *Fight against Ebola – in silico –*

CITATION ANALYSIS

Total number of publications:	39
No. of peer rev. publications:	26
No. of submissions & preprints:	11
No. of book chapters:	2
h-index:	11
Citations:	292
Average impact factor:	5.0
Three most cited publications	No. 18 (45); No. 4 (40); No. 13 (36)
ORCID	0000-0001-7090-8717
Google Scholar	goo.gl/CY4352

PUBLICATIONS

Peer-reviewed journal publications
Ψ These authors contributed equally

26   **M. Hölzer**$^\Psi$, L. Barf$^\Psi$, K. Lamkiewicz, F. Vorimore, M. Lataretu, A. Favaroni, C. Schnee, K. Laroucau, M. Marz, K. Sachse. Comparative genome analysis of 33 *Chlamydia* strains reveals characteristic features of *Chlamydia psittaci* and closely related species. *MDPI Pathogens*, 2020.   **IF: 3.4**

25   **M. Hölzer**. A decade of *de novo* transcriptome assembly: Are we there yet? *Molecular Ecology Resources*, 2020.   **IF: 7.0**

24   Hufsky F., Lamkiewicz K., Almeida A., Aouacheria A., Arighi C., Bateman A., Baumbach J., Beerenwinkel N., Brandt C., Cacciabue M., Chuguransky S., Drechsel O., Finn R.D., Fritz A., Fuchs S., Hattab G., Hauschild A., Heider D., Hoffmann M., **Hölzer M.**, Hoops S., Kaderali L., Kalvari I., von Kleist M., Kmiecinski R., Kühnert D., Lasso G., Libin P., List M., Löchel H.F., Martin M.J., Martin R., Matschinske J., McHardy A.C., Mendes P., Mistry J., Navratil V., Nawrocki E., O'Toole Á.N., Palacios-Ontiveros N., Petrov A.I., Rangel-Piñeros G., Redaschi N., Reimering S., Reinert K., Reyes A., Richardson L., Robertson D.L., Sadegh S., Singer J.B., Theys K., Upton C., Welzel M., Williams L., and Marz M. Computational strategies to combat COVID-19: Useful tools to accelerate SARS-CoV-2 and coronavirus research. *Briefings in Bioinformatics*, 2020.   **IF: 8.9**

23   D. C. Flores, M. Fricke, V. Wesp, D. Desirò, A. Kniewasser, **M. Hölzer**, M. Marz, and M. Mittag. A marine *Chlamydomonas* sp. emerging as an algal model. *Journal of Phycology*, 2020.   **IF: 2.3**

22   M. Collatz, F. Mock, **M. Hölzer**, E. Barth, K. Sachse, and M. Marz. EpiDope: A Deep neural network for linear B-cell epitope prediction. *OUP Bioinformatics*, 2020.   **IF: 5.6**

21   W. A. Overholt, **M. Hölzer**, P. Geesink, C. Diezel, M. Marz, and K. Küsel. Inclusion of Oxford Nanopore long reads improves all microbial and viral metagenome assembled genomes from a complex aquifer system. *Environmental Microbiology*, 2020.   **IF: 4.0**

20   **M. Hölzer** and M. Marz. PoSeiDon: a Nextflow pipeline for the detection of evolutionary recombination events and positive selection. *OUP Bioinformatics*, 2020.   **IF: 5.6**

19   N. F. Mostajo$^\Psi$, M. Lataretu$^\Psi$, S. Krautwurst, F. Mock, D. Desirò, K. Lamkiewicz, M. Collatz, A. Schoen, F. Weber, M. Marz$^\Psi$, and **M. Hölzer**$^\Psi$. A comprehensive annotation and differential expression analysis of short and long non-coding RNAs in 16 bat genomes. *NAR Genomics and Bioinformatics* 2(1):lqz006, 2019.   **IF: na**

18   A. Viehweger, S. Krautwurst, K. Lamkiewicz, R, Madhugiri, J. Ziebuhr, **M. Hölzer**, and M. Marz. Direct RNA nanopore sequencing of full-length coronavirus genomes provides novel insights into structural variants and enables modification analysis. *Genome Research*, 2019.   **IF: 10.1**

17   **M. Hölzer**$^{\Psi}$, A. Schoen$^{\Psi}$, J. Wulle, MA. Müller, C. Drosten, M. Marz, and F. Weber. Virus- and interferon alpha-induced transcriptomes of cells from the microbat *Myotis daubentonii*. *iScience*, 2019.   **IF: 4.4**

16   K. Laroucau, F. Vorimore, R. Aaziz, L. Solmonson, RC. Hsia, PM. Bavoil, P. Fach, **M. Hölzer**, A. Wuenschmann, and K. Sachse. *Chlamydia buteonis*, a new *Chlamydia* species isolated from a red-shouldered hawk. *Systematic and Applied Microbiology* 2019.   **IF: 3.2**

15   R. Kallies, **M. Hölzer**, R. Brizola Toscan, U. Nunes da Rocha, J. Anders, M. Marz, and A. Chatzinotas. Evaluation of sequencing library preparation protocols for viral metagenomic analysis from pristine aquifer groundwaters. *Viruses* 11(6):484, 2019.   **IF: 3.7**

14   S. Peter, **M. Hölzer**, K. Lamkiewicz, P. Speroni di Fenizio, HA. Hwaeer, M. Marz, S. Schuster, P. Dittrich, and B. Ibrahim. Structure and hierarchy of influenza virus models revealed by reaction network analysis. *Viruses* 11(5), 2019.   **IF: 3.7**

13   **M. Hölzer** and M. Marz. *De novo* transcriptome assembly: A comprehensive cross-species comparison of short-read RNA-Seq assemblers. *GigaScience* 8(5), 2019.   **IF: 7.3**

12   Z. Chen, E. Amro, F. Becker, **M. Hölzer**, S. Rasa, S. Njeru, B. Han, S. Di Sanzo, Y. Chen, D. Tang, S. Tao, R. Haenold, M. Groth, V. Romanov, J. Kirkpatrick, J. Kraus, H. Kestler, M. Marz, A. Ori, F. Neri, Y. Morita, and K. L. Rudolph. Cohesin-mediated NF-κB signaling limits hematopoietic stem cell self-renewal in aging and inflammation. *J. Exp. Med.* 216(1):152–175, 2018.   **IF: 10.8**

11   D. Desirò, **M. Hölzer**, B. Ibrahim, and M. Marz. SilentMutations (SIM): a tool for analyzing long-range RNA-RNA interactions in viral genomes and structured RNAs. *Virus Res.*, 2018.   **IF: 2.5**

10   D. Steinbach, **M. Hölzer**, M. Marz, M. Gajda, F. C. Von Rundstedt, and M. O. Grimm. Analysis of molecular mechanism of progression of non-muscle-invasive bladder cancer (NMIBC) by genome-wide exome and UTR mutation analysis. *Eur Urol Suppl.* 17(2):e1523, 2018.   **IF: 3.5**

9   P. Möbius, G. Nordsiek, **M. Hölzer**, M. Jarek, M. Marz, and H. Köhler. Complete Genome Sequence of JII-1961, a Bovine *Mycobacterium avium* subsp. *paratuberculosis* Field Isolate from Germany. *Genome Announc.* 5(34), 2017.   **IF: 1.2**

8   J. Fuchs, **M. Hölzer**, M. Schilling, C. Patzina, A. Schoen, T. Hoenen, G. Zimmer, M. Marz, F. Weber, M. A. Müller, and G. Kochs. Evolution and Antiviral Specificities of Interferon-Induced Mx Proteins of Bats against Ebola, Influenza, and Other RNA Viruses. *J Virol.* 12; 91(15), 2017.   **IF: 4.7**

7   P. Möbius, E. Liebler-Tenorio, **M. Hölzer**, and H. Koehler. Evaluation of associations between genotypes of *Mycobacterium avium* subsp. *paratuberculsis* and presence of intestinal lesions characteristic of paratuberculosis. *Veterinary microbiology.* 201:188-194, 2017.   **IF: 2.6**

6   K. Riege$^{\Psi}$, **M. Hölzer**$^{\Psi}$, T. Klassert, E. Barth, J. Bräuer, M. Collatz, F. Hufsky, N. Mostajo, M. Stock, B. Vogel, H. Slevogt, and M. Marz. Massive Effect on LncRNAs in Human Monocytes During Fungal and Bacterial Infections and in Response to Vitamins A and D. *Sci Rep.* 7:40598, 2017.   **IF: 4.8**

5   T. E. Klassert, J. Bräuer, **M. Hölzer**, M. Stock, K. Riege, C. Zubiría-Barrera, M. M. Müller, S. Rummler, C. Skerka, M. Marz, and H. Slevogt. Differential Effects of Vitamins A and D on the Transcriptional Landscape of Human Monocytes during Infection. *Sci Rep.* 7:40599, 2017.   **IF: 4.8**

4   **M. Hölzer**$^{\Psi}$, V. Krähling$^{\Psi}$, F. Amman, E. Barth, S. H. Bernhart, V. A. O. Carmelo, M. Collatz, G. Doose, F. Eggenhofer, J. Ewald, J. Fallmann, L. M. Feldhahn, M. Fricke, J. Gebauer, A. J. Gruber, F. Hufsky, H. Indrischek, S. Kanton, J. Linde, N. M. Berrospi, R. Ochsenreiter, K. Rieger, L. Rivarola-Duarte, A. H. Sahyoun, S. J. Saunders, S. E. Seemann, A. Tanzer, B. Vogel, S. Wehner, M. T. Wolfinger, R. Backofen, J. Gorodkin, I. Grosse, I. Hofacker, S. Hoffmann, C. Kaleta, P. F. Stadler, S. Becker, and M. Marz. Differential transcriptional responses to Ebola and Marburg virus infection in bat and human cells. *Sci Rep.* 6:34589, 2016.   **IF: 4.8**

3   **M. Hölzer**, K. Laroucau, H. H. Creasy, S. Ott, F. Vorimore, P. M. Bavoil, M. Marz, and K. Sachse. Whole-genome sequence of *Chlamydia gallinacea* type strain 08-1274/3. *Genome Announc.* 4(4):e00708–16, 2016. **IF: 1.2**

2   P. Möbius[Ψ], **M. Hölzer**[Ψ], M. Felder, G. Nordsiek, M. Groth, H. Köhler, K. Reichwald, M. Platzer, and M. Marz. Comprehensive insights in the *Mycobacterium avium* subsp. *paratuberculosis* genome using new WGS data of sheep strain JIII-386 from Germany. *Genome Biol Evol.* 7(9):2585-2601, 2015. **IF: 3.9**

1   A. H. Sahyoun, **M. Hölzer**, F. Jühling, C. Höner Zu Siederdissen, M. Al-Arab, K. Tout, M. Marz, M. Middendorf, P. F. Stadler, and M. Bernt. Towards a comprehensive picture of alloacceptor tRNA remolding in metazoan mitochondrial genomes. *Nucleic Acids Res.* 43(16):8044–8056, 2015. **IF: 11.5**

Submitted journal publications & preprints

F. Voimore, **M. Hölzer**, E. Liebler-Tenorio, LM. Barf, S. Delannoy, M. Vittecoq, R. Wedlarski, A. Lécu, S. Scharf, Y. Blanchard, P. Fach, RC. Hsia, P. Bavoil, R. Rosselló-Móra, K. Laroucau, and K. Sachse. Evidence for the existence of a new genus *Chlamydiifrater* gen. nov. inside the family *Chlamydiaceae* with two new species isolated from flamingo (*Phoenicopterus roseus*) specimens: *Chlamydiifrater phoenicopteri* sp. nov. and *Chlamydiifrater volucris* sp. nov. Submitted to *Systematic and Applied Microbiology*. 2020.

A. Viehweger, C. Brandt, and **M. Hölzer**. DarkQ: Continuous genomic monitoring using message queues. *bioRxiv.* 10.1101/2020.11.12.379560, 2020.

K. Heinze, **M. Hölzer**, M. Ungelenk, M. Gerth, J. Thomale, R. Heller, CR. Morden, KJ. McManus, A. Mosig, M. Dürst, IB. Runnebaum, and N. Häfner. RUNX3 transcript variants have dichotomous roles in ovarian carcinoma and influence platin sensitivity and angiogenesis. Submitted to *Cellular Oncology*. 2020.

M. Lataretu and **M. Hölzer**. RNAflow: An effective and simple RNA-Seq differential gene expression pipeline using Nextflow. Submitted to *MDPI Genes*. 2020.

G. C. Martín-Hernández, B. Müller, M. Chmielarz, C. Brandt, **M. Hölzer**, A. Viehweger, and V. Passoth. The genome of the oleaginous yeast *Rhodotorula toruloides* CBS 14 assembled and annotated by a combined approach of long- and short-read sequencing. Submitted to *Genome Biology and Evolution*. 2020.

S. S. Kashaf, D. Proctor, C. Deming, **M. Hölzer**, Comparative Sequencing Program NISC, M. Taylor, H. Kong, A. Almeida, and R. Finn. Integrating bacterial cultivation and genome-resolved metagenomics to uncover new skin microbiome diversity and functions. Submitted to *Nature Microbiology*. 2020.

R. Kotolloshi, **M. Hölzer**, M. Gajda, MO. Grimm, and D. Steinbach. SLC35F2, a transporter sporadically mutated in the UTR, promotes growth, migration and invasion of bladder cancer cells. Submitted to *MDPI Cells*. 2020.

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. *bioRxiv.* 10.1101/2020.07.24.219899v1, 2020.

R. Van Damme, **M. Hölzer**, A. Viehweger, M. Bettina, E. Bongcam-Rudloff, and C. Brandt. Metagenomics workflow for hybrid assembly, differential coverage binning, transcriptomics and pathway analysis (MUFFIN). *bioRxiv.* 10.1101/2020.02.08.939843v1, 2020.

A. Viehweger, **M. Hölzer**, and C. Brandt. Addressing dereplication crisis: Taxonomy-free reduction of massive genome collections using embeddings of protein content. *bioRxiv.* 10.1101/855262v2, 2019.

R. Gerst and **M. Hölzer**. PCAGO: An interactive web service to analyze RNA-Seq data with principal component analysis. *bioRxiv.* doi.org/10.1101/433078, 2018.

Book chapter

N. Pappas, S. Roux, **M. Hölzer**, K. Lamkiewicz, F. Mock, M. Marz, B. E. Dutilh. Virus Bioinformatics. *Reference Module in Life Sciences*, Elsevier, 2020.

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

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
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. Konrad K. W. Sachse

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