

Curriculum vitae: MANUELA MARZ

PERSONAL DETAILS

Name: Prof. Dr. Manuela Marz (née Lindemeyer)
Gender: Female
Place and Date of Birth: 06.05.1981, Leipzig, Germany
Nationality: German
Email: manja@uni-jena.de
URL: rna.uni-jena.de

WORK EXPERIENCE

since 2026	Spokesperson of CRC 1768 VirusREvolution
2018–2026	Scientific advisory board member of RNA Central and Rfam
since 03/2017	Founding member, board member and managing director of “European Virus Bioinformatics Center” (EVBC)
since 07/2015	Full Professorship for High Throughput Sequencing Analysis at Friedrich Schiller University Jena
since 04/2015	Founding and board member of FIFI (<i>Fördervereinverein des Instituts für Informatik</i>)
04/2015	Founding member of MSCJ (<i>Michael Stifel Zentrum Jena for Data-Driven and Simulation Science</i>)
since 01/2015	Associated Research Group at Leibniz Institute on Aging – Fritz Lipmann Institute
10/2014	Call for a Professorship at Friedrich Schiller University Jena
06/2014	Call for a Professorship at University of Lübeck
since 07/2013	Founding and board member of ZAJ (<i>Aging Research Center Jena</i>)
02/2012–06/2015	Junior-Professorship for “High Throughput Sequencing Analysis” at Friedrich Schiller University Jena
01/2010–01/2012	Group Leader of “RNA Bioinformatics” at Philipps-University Marburg

RESEARCH ASSISTANCIES

02/2006–12/2009	Computer Science Department, University of Leipzig
12/2005–01/2006	Computer Science Department, University of Leipzig
08/2003–09/2003	Computer Science Department, University of Leipzig
10/2002–12/2002	Biology Department, University of Leipzig
05/2002–06/2002	Biology Department, University of Leipzig
08/2001–09/2001	Computer Science Department, University of Leipzig
01/2001–03/2001	Biology Department, University of Leipzig
10/2000–12/2000	Biology Department, University of Leipzig

SCIENTIFIC EDUCATION

2006–2009	DOCTORATE DEGREE: Dr. rer. nat. University of Leipzig Doctoral Thesis: <i>Strategies of Homology-Based Identification of Non-Coding RNA Genes</i> Prof. Dr. Peter F. Stadler, Bioinformatics, Faculty of Mathematics and Computer Science
2006	DIPLOMA IN COMPUTER SCIENCE Specialism: Bioinformatics University of Leipzig Diploma Thesis: <i>Evolution of Spliceosomal RNAs in Metazoan Animals</i> Prof. Dr. Peter F. Stadler, Bioinformatics, Faculty of Mathematics and Computer Science
2001–2006	Studies of Computer Science at the University of Leipzig
2002–2003	Studies of Computer Science at the University of Edinburgh
2005	DIPLOMA IN BIOLOGY University of Leipzig Diploma Thesis: <i>Arbeiten zur evolutiven Optimierung des HI-Virus: Erzeugung, funktionelle Bewertung und Sequenzierung von Enzymvarianten</i> Prof. Dr. Martin Schlegel, Faculty of Biology, Pharmacy and Psychology
1999–2005	Studies of Biology at the University of Leipzig
2004	Studies of Biology at TU Darmstadt
2002–2003	Studies of Biology at the University of Edinburgh

FELLOWSHIP AND AWARDS

04/2009–12/2009	PhD Scholarship from “Landestipendium Sachsen” at the University of Leipzig
02/2006–12/2008	PhD Scholarship from “Graduiertenkolleg Wissensrepräsentation” at the University of Leipzig in cooperation with “Deutsche Forschungs-Gemeinschaft”

CAREER BREAKS

2006–2007	9 month break – parental leave
2011	6 month break – parental leave
2013	6 month break – parental leave

COMMISSIONS OF TRUST

I am editor of a special issue “Virus Bioinformatics” which is published yearly in parallel to the Annual EVBC Meeting (2018 in Virus Research; since 2019 in Viruses).

I am associate editor of Frontiers in Genetics (RNA Section), and Frontiers in Microbiology and part of the editorial board of PLoS Computational Biology, RNA Biology, and Biology direct.

I am *ad hoc* reviewer of Nature Genetics, Nature Methods, EMBO, Nucleic Acids Research, Bioinformatics, Biological Chemistry, Journal of Heredity, BMC Genomics, Journal of theoretical Biology, Journal of Microbiology, Genome Research, Molecular Biology and Evolution, PLoS ONE, PLoS Computational Biology, RNA, Frontiers of Microbiology, and many more.

I am regular advisor for Deutsche Forschungsgemeinschaft (DFG), Bundesministerium für Bildung und Forschung (BMBF), Deutscher Akademischer Austauschdienst (DAAD), German-Israeli Foundation for Scientific Research and Development (GIF), and Agence nationale recherche (ANR-France).

I have been part of the Program Committee of German Conference of Bioinformatics (2012–2018), Central German Meeting of Bioinformatics (2015, 2017, 2018), RECOMB-Seq (2014–2016), and Intelligent Systems for Molecular Biology (2016, 2017).

I have been part of the Organisation committee of International Study Group on Systems Biology (2016), and Annual Meeting of the European Virus Bioinformatics Center (2017, 2018, 2019, 2020).

NON-SCIENTIFIC ACTIVITIES

since 2018	Managing director of Jena International Go School
since 2014	Advisory board of European Go Federation (EGF)
2005–2017	Board member of German Go Federation (DGoB)
since 2004	President of Go Federation Brandenburg-Saxony-Thuringia (LV-BST)

ACHIEVEMENTS IN GO

German Female Championship	1 st Place: 2007, 2009–2010, 2013–2016, 2018 2 nd Place: 2008, 2012, 2017 3 rd Place: 2006
European Female Championship	1 st Place: 2017 3 rd Place: 2010, 2013
World Female Championship	Participation: 2013, 2017
German Pairgo Championship	1 st Place: 2012, 2018 2 nd Place: 2005, 2009–2010 3 rd Place: 2007, 2013–2014
European Pairgo Championship	2 nd Place: 2005, 2008, 2010, 2014 3 rd Place: 2016
Open European Pairgo Championship	1 st Place: 2012, 2014, 2016 2 nd Place: 2015
World Pairgo Championship	Participation: 2012, 2014, 2016
European Female Student Championship	1 st Place: 2005–2009
World Student Championship	Participation: 2008
MLILY Cup	Participation: 2013
World Mind Sport Games	Participation: 2008, 2017

MAJOR COLLABORATIONS

- Rolf Backofen, Chair for Bioinformatics, Department of Computer Science, Albert-Ludwigs-University Freiburg
RNA secondary structures
- Lenhard Rudolph, Leibniz Institute for Age Research - Fritz Lipmann Institute, Jena
Irregular genome structures associated with human aging
- Kirsten Küsel, Institute of Ecology, Friedrich Schiller University of Jena
Assessing key players, genes and pathways in aqueous habitats using metagenomics and -transcriptomics
- Otto Witte, Department of Neurology, Universitätsklinikum Jena
*Regulatory non-coding RNAs involved in murine aging,
Cross-disease analysis of ncRNAs in exosomes and microvesicles from blood, CSF, and iPS-derived neurons of patients with different neurodegenerative disorders via RNA-Seq of transcriptomes; preliminary data available*
- Udo Markert, Placenta-Labor, Universitätsklinikum Jena
*Embryonal non-coding RNAs in exosomes and microvesicles derived from human placenta and the maternal circulation; preliminary data available
Non-coding RNAs in human ovarian follicles*
- Christine Klein, Institute of Neurogenetics, University of Lübeck
Non-coding RNAs in X-linked Dystonia-Parkinsonism (XDP)
- Kerstin Voigt, Jena Microbial Resource Collection (JMRC), Institute of Microbiology, Friedrich Schiller University of Jena
Evolutionary genomics of ancient mucorales
- Sebastian Böcker, Chair of Bioinformatics, Faculty of Mathematics and Computer Science, Friedrich Schiller University of Jena
Combined metabolome and transcriptome analysis of the light/dark cycle of cyanobacteria
- Aria Baniahmad, Institute of Human Genetics, Universitätsklinikum Jena
Evolution of COP9 signalosome in unicellular and multicellular organisms
- Oliver Kurzai, Institut für Hygiene und Mikrobiologie, Universitätsklinikum Würzburg
*Analysis of transcriptomic *Candida glabrata* data*
- Stephan Becker, Institute for Virology, Philipps-Universität Marburg, Marburg
Differential transcriptional responses to Ebola and Marburg virus infection in cells from bats and humans
- Friedemann Weber, Institute for Virology, Veterinary Medicine, Justus-Liebig-University Giessen
Examination of Rift Valley fever virus infection of bats
- John Ziebuhr, Institute for Medical Virology, Justus-Liebig-University Giessen
RNA structure analysis of alphacoronavirus terminal genome regions
- Michael Niepmann, Biochemical Institute of the Medical Faculty, Justus-Liebig-University Giessen
Conserved RNA secondary structures and long range interactions in HCV
- Christian Drosten, Institute for Virology, Universitätsklinikum Bonn
Non-coding RNAs in emerging viral infections
- Annegret Wilde, Molekulare Genetik (Genetik der Prokaryoten), Albert-Ludwigs-University Freiburg
Combined metabolome and transcriptome analysis of the light/dark cycle of cyanobacteria
- Georg Kochs, Institute of Virology, Universitätsklinikum Freiburg
Evolution of Mx proteins.
- Martin Schwemmle, Institute of Virology, Universitätsklinikum Freiburg
Packaging of influenza virus
- Peter Stadler, Chair of Bioinformatics, Faculty of Mathematics and Computer Science, University of Leipzig
Evolution of non-coding RNAs

- Martin Middendorf, Parallel Computing and Complex Systems, Faculty of Mathematics and Computer Science, University of Leipzig
Virus-host-coevolution
- Norbert Tautz, Institute of Virology and Cell Biology, University of Lübeck
Secondary structures of Pestivirus genomes
- Martin Beer, Institute of Diagnostic Virology, Friedrich Loeffler Institute, Greifswald
Annotation of Pox-virus genome
- Ivo Hofacker, Theoretical Biochemistry Group, Institute for Theoretical Chemistry, University of Vienna, Austria
Prediction of triplex and quadruplex structures
- Paul Gardner, School of Biological Sciences, University of Canterbury, Christchurch, New Zealand
Non-coding RNAs and Rfam
- Julian Chen, School of Molecular Sciences, Arizona State University, Arizona, USA
Discovery of telomerase RNA in various organisms
- Alessandro Cellerino, Neurobiology Laboratory, Scuola Normale Superiore Pisa, Italy
MicroRNA catalog in Nothobranchius furzeri
- Richard Scheuermann, Craig Venter Institute, San Diego, USA

CURRENT GRANTS

		Amount Marz Group:
2020–2024	Landesprogramm „ProDigital“ des Freistaats Thüringen <i>Digitalisierung der Lebenswissenschaften: Wege in die Zukunft</i> , Speaker: Manja Marz involvement in five different projects one doctoral students (60 months E13/75%), one PostDoc (60 months E13/100%)	1 350 000 € (total funding amount)
2019–2022	Carl Zeiss Stiftung <i>Eine virtuelle Werkstatt für die Digitalisierung in den Wissenschaften – Datengetriebene Virusdiagnostik auf multiplen Ebenen II (Anwendung)</i>	145 000 €
2019–2022	International Max Planck Research School for the Science of Human History <i>A comprehensive analysis of microorganisms and viruses from ancient samples using minion sequencing techniques</i> one doctoral student	99 000 €
2019–2021	BMBF – DBT Cooperative Science Program <i>Development of metagenomics assisted surveillance tools for tracking antibiotic resistance in river bodies — A study in the Ganges river valley (NANOLOG)</i> one doctoral student (24 months E13/25%), one doctoral student (12 months E13/50%)	150 000 €
2017–2021	DFG CRC 1076 – AquaDiva A6: <i>Viral Diversity, Viral de novo Assembly, and Viral Decay in Groundwater</i> , Speaker: Kirsten Küsel One doctoral student (1x48 months E13/75%)	242 000 €
2017–2019	DFG SFB/TR124 <i>Pathogenic fungi and their human host; B5: The role of human microbiota for the development of fungal infectious diseases – Candida albicans as a case study</i> , Speaker: Axel Brakhage One doctoral student (1x48 months E13/65%)	139 500 €
2017–2019	DFG iDiv – All-in-one Multiplex-Sequencing Two PostDocs (2x24 months) and Consumables	128 000 €
2016–2019	Zwanzig20 – InfectControl 2020 – Molekulare Serologie zur schnellen Bestimmung der Impftiter gegen impf-präventable Infektionskrankheiten (STIKO-Liste) bei Migranten und anderen Patientengruppen ; Subproject: <i>STIKO-Serologie – TV1</i> One PostDocs (1x24 months) and one doctoral student (1x12 months)	317 662 €
2016–2019	DFG MA 5082/9-1 , <i>Embryonale nicht-kodierende RNAs in der menschlichen Plazenta und dem mütterlichen Blutkreislauf</i> One doctoral student (1x36 months E13/100%)	269 500 €
2016–2019	DFG SPP-1596 <i>Ecology and Species Barriers in Emerging Viral Diseases</i> , second funding period, Speaker: Christian Drosten One doctoral student (1x36 months E13/75%) and one PostDoc (1x36 months E13/50%), associated member	375 750 €
since 2015	DFG Forschungszentrum 118 iDiv – German Centre for Integrative Biodiversity Research Associated member	–

EXPIRED GRANTS

		Amount Marz Group:
2018	DFG MA5082/13-1 <i>VEME: International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology</i>	24 400 €
2016–2018	MGH, CCXDP <i>Exploring Non-coding RNAs in X-linked Dystonia-Parkinsonism (XDP) using High-Throughput Sequencing (RNA-Seq) in Various Endogenous Models</i> Co-PI with Christine Klein and Aloysius Domingo. Supervision of a PhD student	121 400 €
2015–2018	ZAJ <i>RegenerAging – Analyzing the regulation of aging</i> One doctoral student (1x36 months E13/50%)	90 000 €
2013–2017	DFG SFB/TR124 <i>Pathogenic fungi and their human host: Networks of interaction (FungiNet)</i> , Speaker: Axel Brakhage One doctoral student (1x36 months E13/65%)	139 500 €
2013–2017	CRC 1076 – AquaDiva BIODIV4 <i>Elucidation of microbial nutrient cycling using key functional genes and proteins</i> One shared doctoral student (1x36 months E13/50%), associated member	–
2011–2016	DFG MA 5082/1-1 <i>Automated Genomewide Annotation of Non-coding RNAs</i> Two doctoral students (2x36 months E13/50%)	220 000 €
2013–2016	DFG SPP-1596 <i>Ecology and Species Barriers in Emerging Viral Diseases</i> , Speaker: Christian Drosten One doctoral student (1x24 months E13/50%), associated member	57 596 €
2014–2016	Carl-Zeiss-Stiftung <i>Lücken im Kraftwerk der Zukunft – Kombinierte Metabolom- und Transkriptomanalyse des Hell/Dunkel-Zyklus bei Cyanobakterien</i> One doctoral student (1x24 months E13/50%) and one PostDoc (1x24 months E13/100%)	200 000 €
2011–2015	DFG GRK-1384 <i>International Research Training Group – Enzymes and multienzyme complexes acting on nucleic acids</i> One doctoral student (1x54 months E13/50%)	208 440 €
2010–2013	DFG - SPP 1258 <i>Sensory and regulatory RNAs in Prokaryotes</i> Associated member	–

INVITED TALKS

- 2018 Computational Approaches to RNA Structure and Function, Benasque, Spain
RNA Viruses
- 2018 Seminar Talks, Braunschweig, Germany
Software Dedicated to Virus Sequence Analysis
- 2018 Workshop, Bielefeld, Germany
Nanopore sequencing and Quasispecies reconstruction
- 2018 The European Bioinformatics Center, Utrecht, The Netherlands
Challenges in 2018 of the European Virus Bioinformatics Center
- 2018 28th Annual Meeting of the Society for Virology, Würzburg, Germany
Viral host prediction with deep learning
- 2018 33rd TBI Winterseminar, Bled, Slovenia
Medley: Interaction of Virology and Bioinformatics
- 2018 SciencePub, Jena, Germany
Wie man echte Viren mit dem Computer identifiziert
- 2018 Schülertag (Schools Day), Jena, Germany
Das älteste Brettspiel der Welt
- 2018 Craig Venter Institute Series, San Diego, USA
Analysis of Omics-Data
- 2018 SFB 1021, Marburg, Germany
Virus Bioinformatics
- 2017 CIBB2017 Keynote Computational Intelligence methods for Bioinformatics and Biostatistics, Calgliari, Italy
Virus Bioinformatics
- 2017 Keynote, 22nd International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology (VEME), Lissabon, Spain
Virus Bioinformatics
- 2017 Micom, 6th International Conference on Microbial Communication for Young Scientists, Jena, Germany
Fight infections in silico
- 2017 Bionection, Jena, Germany
Virology – Bioinformatics – Diagnostics
- 2017 Leibniz Institut for Aging Retreat, Luisenthal, Germany
Aging in silico
- 2016 National Workshop on Metagenomics, Robert-Koch-Institute, Berlin, Germany
Transcriptome data analysis and interpretation
- 2016 Preparation for foundation of the European Virus Bioinformatics Center, Jena, Germany
Virology – Bioinformatics – Diagnostics
- 2016 XDP Data Blitz, Lübeck, Germany
Identification of noncoding RNAs using RNA-Seq
- 2016 AquaDiva Retreat, Dornburger Schlösser, Germany
Identification, Assembly, Annotation and Comparison of unknown viruses in groundwater
- 2016 ZAJ Symposium, Leibniz Institute on Aging – Fritz Lipmann Institute, Jena, Germany
Non-coding RNAs involved in aging
- 2016 Friedrich-Loeffler-Cross-Talk, Insel Riems, Germany
Challenges in Virus Genomics
- 2015 Tag der Fakultät, Friedrich Schiller University Jena, Germany

- Invadierende Partikel*
- 2015 Central German Meeting on Bioinformatics, Halle, Germany
Challenges in virus genomics
- 2015 Moscow Conference on Computational Molecular Biology, Moskow, Russia
Challenges in Virus Genomics
- 2015 DFG, SPP 1596, Bonn, Germany
Non-coding RNAs as barriers in emerging viral infections
- 2015 Center for non-coding RNA in technology and health, Copenhagen, Denmark
Viruses go bioinformatics
- 2015 IRTG (GRK 1384), Justus-Liebig University, Giessen, Germany
Challenges in Virus Bioinformatics
- 2015 Future Perspectives in Computational Pan-Genomics, Leiden, The Netherlands
Pan-viruses, Haplotypes and Quasispecies
- 2015 30th TBI Winterseminar, Bled, Slovenia
The Evolution of The TBI WS
- 2014 AquaDiva, CRC 1076, Jena, Germany
What we can (not) expect from transcriptomic data? A bioinformatical survey.
- 2014 12th Herbstseminar der Bioinformatik, Doubice, Czech Republic
Fight against Ebola!
- 2014 XDP Workshop Itinerary, Lübeck, Germany
Are ncRNAs involved in XDP?
- 2014 DFG, Preparation SPP, Bonn, Germany
Long-range RNA interactions that are critically involved in the replication and expression of large-size RNA virus genomes
- 2014 DFG, Preparation SPP, Frankfurt, Germany
Correlation of RNA degradation, secondary structures and transcriptome profiles
- 2014 Molecular Evolution and Bioinformatics, Münster, Germany
Bioinformatics of RNA viruses
- 2013 Bundesinnenministerium, "Frauen machen neue Länder", Jena, Germany
Frauen machen neue Länder
- 2013 Professorship application, Lübeck, Germany
Gen oder nicht Gen? Moderne Genomanalytik
- 2013 Friedrich-Loeffler Institut, Jena, Germany
Genomsequenzierung für alle - Was kann Bioinformatik leisten?
- 2011 Rolf Backofen Retreat, Freiburg, Germany
Wet RNA Bioinformatics
- 2011 Technische Universität, Bielefeld, Germany
Genome Annotation: Plain or Pain?
- 2010 EBI, Hinxton, UK
Abnormal non-coding RNAs
- 2009 NanKai University, Tianjin, China
Use and Complexity of existing RNA-tools
- 2009 CAS-MPG PICB, Shanghai, China
Strategies for Homology-Based Identification of Eukaryotic Non-Coding RNA Genes
- 2009 Zhejiang University, Hangzhou, China
Homology Search in Biological Networks
- 2009 German Conference of Bioinformatics, Halle, Germany
A transdisciplinary attempt to represent structured data by sonification.
- 2009 Institut de Biologie de l'Ecole Normale Supérieure, Paris, France
Prediction and Secondary Structure of 7SK RNA

2005 | Math/Chem/Comp, Dubrovnik, Croatia
snRNA search without a magnifying glass

TEACHING ACTIVITIES

Lecture	Institute	Terms
Practical Course <i>Bioinformatics</i> *	U Leipzig	2004/05, 2005/06
Lecture <i>Mathematical Game Theory</i>	WU Vienna	2008/09
Lecture <i>Clinical Chemistry for Pharmacists</i>	U Marburg	2010, 2010/11, 2011, 2011/12
Practical Course <i>Bioinformatics for Pharmacists</i>	U Marburg	2010, 2010/11, 2011, 2011/12
Ring Lecture <i>Fundamentals of Bioinformatics</i>	U Marburg	2010/11, 2011/12
Lecture <i>High Throughput Bioinformatics</i>	U Jena	2012, 2013, 2014/15, 2015/16, 2016/17, 2017/18, 2018/19
Practical Course <i>High Throughput Bioinformatics</i>	U Jena	2012, 2013, 2014/15, 2015/16, 2016/17, 2017/18, 2018/19
Lecture <i>RNA Bioinformatics</i>	U Jena	2012/13, 2013/14, 2015, 2016, 2017, 2018, 2019
Practical Course <i>RNA Bioinformatics</i>	U Jena	2012/13, 2013/14, 2015, 2016, 2017, 2018, 2019
Literature Seminar	U Jena	2014, 2014/15, 2015, 2015/16, 2016/17, 2017, 2017/18
Practical Course <i>Scripting Languages</i>	U Jena	2014, 2015, 2015/16, 2016, 2016/17, 2017/18, 2018/19
Lecture <i>Virus Bioinformatics</i>	U Jena	2014/15, 2015, 2016, 2017, 2018, 2019
Practical Course <i>Virus Bioinformatics</i>	U Jena	2019
Lecture <i>Gene Expression Analysis</i>	U Jena	2016, 2017, 2018
Lecture <i>Basic bioinformatic applications</i>	U Jena	2016/17, 2017/18, 2018/19
Seminar <i>L^AT_EX basics for scientists</i>	U Jena	2016/17, 2017/18, 2018/19, 2019

* – shared with other lecturer

GROUP COMPOSITION

PostProf

- Konrad Sachse, *Bacterial annotation and vaccination*

PostDocs:

- Franziska Hufsky, *European Virus Bioinformatics Center – Coordinator*
- Diana Morales, *Exosome extraction*
- Wittaya Chaiwangyen, *Microparticle extraction*
- Martin Hölzer, *Genome Assembly, Transcriptome assembly*
- Emanuel Barth, *Regulation of Aging*

PhD students:

- Lisa-Marie Barf, *Minion Sequencing Protocols*, since 2019
- Marie Lataretu, *Virus bioinformatics*, since 2018
- Florian Mock, *Omics of Fungi and Mycoviruses*, since 2018
- Daniel Desiro, *RNA secondary structure, RNA-RNA Interactions*, since 2017
- Dr. Adrian Viehweger, *De novo virus detection with NGS Methods*, since 2017
- Kevin Lamkiewicz, *Viral miRNAs*, since 2017
- Sebastian Krautwurst, *Tools for Minion Sequencing*, since 2017
- Maximilian Collatz, *Expression analysis of high throughput data under various conditions in bats*, since 2016
- Akash Srivastava, *Healthy aging*, since 2015
- Nelly Fernanda Mostajo Berrospi, *ncRNAs expression analysis in human infected cell lines with Zaire Ebola virus (pathogenic) and Reston Ebola virus (non pathogenic)*, since 2014

Bachelor/master students:

- Rebekka Köhl, bachelor thesis
- Sarah Krautwurst, bachelor thesis
- Sandra Triebel, bachelor thesis
- Kirsten Göbel, bachelor thesis
- Jannes Spangenberg, bachelor thesis
- Daria Meyer, master thesis
- Michele Kayser, master thesis
- Lasse Faber, master thesis

Assistancies:

- Celia Diezel, technical assistant
- Sabrina Eichwald, technical assistant
- Muriel Ritsch, student assistant
- Michele Kayser, student assistant
- Sarah Krautwurst, student assistant

Completed PhD theses:

- Emanuel Barth, *The regulation of aging by RNAs* (to be defended)

- Konstantin Riege, *Automated genomewide annotation of non-coding RNAs and comparative genomics* (2019)
- Martin Hölzer, *The Dark Art of Next-Generation Sequencing, summa cum laude* (2018)
- Markus Fricke, *Structural analysis of full viral genomes, summa cum laude* (2016)
- Stefanie Wehner, *Prediction and analysis of challenging non-coding RNAs, magna cum laude* (2015)
- Marcus Lechner, *Orthology-based approaches and applications for comparative genomics, magna cum laude* (2014)

Completed bachelor/master theses:

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- Christian Blumenscheit (master thesis 2018)
- Marie Lataretu, master thesis (2018)
- Andreas Goral, master thesis (2018)
- Ruman Gerst, bachelor thesis (2015), master thesis (2018)
- Daniel Loos, master thesis (2018)
- Valentin Wesp, bachelor thesis (2017)
- Muriel Ritsch, bachelor thesis (2017)
- Fleming Kretschmer, bachelor thesis (2017)
- Stefan Koch, master thesis (2017)
- Adrian Viehweger, master thesis (2017)
- Florian Mock, master thesis (2017)
- Simone Wälde, bachelor thesis (2016)
- Bastian Seelbinder, bachelor thesis (2015)
Award for best bachelor thesis 2015 from Institute of Informatics, Friedrich Schiller University Jena
- Alexandra Morscher, bachelor thesis (2015)
- Ralf Schmidt, master thesis (2014)
Award for best student 2014 from Faculty of Mathematics and Informatics, Friedrich Schiller University Jena
- Nelly Fernanda Mostajo Berrospi, master thesis (2014)
- Eugen Bauer, master thesis (2014)
- Stephan Kanter, bachelor thesis (2014)
- Silvia Müller, bachelor thesis (2013)
- Cornelia Mühlich, bachelor thesis (2012)
- Franziska Klincke, master thesis (2012)
- Luise Modersohn, bachelor thesis (2012)
- Emanuel Barth, bachelor thesis (2012), master thesis (2014)

Completed assistencies:

-
- Marie Lataretu (2016)
- Nelly Fernanda Mostajo Berrospi (2015)
- Daria Meyer (2015)
- Stephan Koch (2015)
- Marc Kriegbaum (2015)
- Abdullah Sahyoun (2015)
- Jana Jaeck (2014)
- Martin Hölzer (2013)
- Luise Modersohn (2012/2013)
- Markus Fricke (2012)
- Emanuel Barth (2012–2014)
- Marco Blickensdorf (2012/2013)

CITATION ANALYSIS

(incl. journal publications, conference publications & book chapters)

Total no. of peer rev. publications	84
Last author publications	20
First author publications	11
Citations	7862
h-index	25
i10-index	46
Three most cited publications	No. 3 (4809); No. 20 (512); No. 17 (352)
Google Scholar	https://bit.ly/2MGdLEq

LIST OF PEER-REVIEWED PUBLICATIONS AND PREPRINTS

IN REVERSE CHRONOLOGICAL ORDER

- 80 M. Hölzer, A. Schoen, J. Wulle, M. A. Müller, C. Drosten, **M. Marz**, and F. Weber. Virus- and interferon alpha-induced transcriptomes of cells from the microbat *Myotis daubentonii*. *iScience*, 2019.
- 79 A. Dukhovny, K. Lamkiewicz, Q. Chen, M. Fricke, N. Jabrane-Ferrat, **M. Marz**, J. U. Jung, and E. H. Sklan. A CRISPR activation screen identifies genes protecting from Zika virus infection. *J Virol*, 2019.
- 78 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, 2019.
- 77 S. Peter, M. Hölzer, K. Lamkiewicz, P.S. di Fenizio, H.A. Hwaer, **M. Marz**, S. Schuster, P. Dittrich, and B. Ibrahim. Structure and hierarchy of influenza virus models revealed by reaction network analysis. *Viruses*, 11(5):449, 2019.
- 76 M. Hölzer and **M. Marz**. *De novo* transcriptome assembly: a comprehensive cross-species comparison of short-read RNA-seq assemblers. *GigaScience*, 8(5):giz039, 2019.
- 75 G. Gerresheim, J. Bathke, A. Michel, D. Andreev, L. Shalamova, O. Rossbach, P. Hu, D. Glebe, M. Fricke, M. Marz, A. Goesmann, S. Kiniry, P. Baranov, I. Shatsky, and M. Niepmann. Cellular gene expression during hepatitis C virus replication as revealed by ribosome profiling. *Int J Mol Sci*, 20(6):1321, 2019.
- 74 CE. Wegner, M. Gaspar, P. Geesink, M. Herrmann, **M. Marz**, K. Küsel. Biogeochemical regimes in shallow aquifers reflect the metabolic coupling of elements of nitrogen, sulfur and carbon. *Appl Environ Microbiol*, 85(5):e02346-18, 2019.
- 73 Z. Chen, EM. Amro, F. Becker, M. Hölzer, SMM. Rasa, SN. Njeru, B. Han, S. Di Sanzo, Y. Chen, D. Tang, S. Tao, R. Haenold, M. Groth, VS. Romanov, JM. Kirkpatrick, JM. Kraus, HA. Kestler, **M. Marz**, A. Ori, F. Neri, Y. Morita, KL. Rudolph. Cohesin-mediated NF- κ B signaling limits hematopoietic stem cell self-renewal in aging and inflammation. *J Exp Med*, 216(1):152–175, 2018.

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