

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
Address: Anton-Bruckner-Weg 45, 07743 Jena
Phone: +49 177 8458312
Family status: Married to Dr. Michael Marz
Son Ferdinand Marz, born 24.06.2006
Son Leopold Marz, born 05.05.2011
Daughter Larissa Marz, born 04.02.2013

WORK EXPERIENCE

since 07/2015	Full Professorship for “High Throughput Sequencing Analysis” at Friedrich Schiller University Jena
since 01/2015	Group leader at Leibniz Institute for Age Research – Fritz Lipmann Institute
since 04/2015	Founding and board member of FIFI (<i>Fördervereinverein des Instituts für Informatik</i>)
since 07/2013	Board member of ZAJ (<i>Aging Research Center Jena</i>)
04/2015	Founding member of MSCJ (<i>Michael Stifel Zentrum Jena for Data-Driven and Simulation Science</i>)
10/2014	Call for a Professorship at Friedrich Schiller University Jena
06/2014	Call for a Professorship at University of Lübeck
07/2013	Founding 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 Forschungsgemeinschaft”

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 associate editor of *Frontiers of non-coding RNAs*, and *Frontiers in Microbiology* and part of the editorial board of *RNA Biology*, and *Biology direct*.

Ad hoc reviewer of *Nucleic Acids Research*, *Bioinformatics*, *Biological Chemistry*, *Journal of Heredity*, *BMC Genomics*, *EMBO*, *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.

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

Program Committee of *German Conference of Bioinformatics (2012–2015)*, *Central German Meeting of Bioinformatics (2015)*, *RECOMB-Seq (2014–2015)*.

Organisation committee of *International Study Group on Systems Biology (2016)*

NONSCIENTIFIC ACTIVITIES

since 2014	Advisory board of European Go Congress (EGC)
since 2005	Boardmember 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 2 nd Place: 2008,2012 3 rd Place: 2006
European Female Championship	3 rd Place: 2010,2013
World Female Championship	Participation: 2013
German Pairgo Championship	1 st Place: 2012 2 nd Place: 2005,2009–2010 3 rd Place: 2007,2013–2014
European Pairgo Championship	2 nd Place: 2005,2008,2010,2014
Open European Pairgo Championship	1 st Place: 2012,2014,2016 2 nd Place: 2015
World Pairgo Championship	Participation: 2012,2014
European Female Student Championship	1 st Place: 2005–2009
World Student Championship	Participation: 2008
MLILY Cup	Participation: 2013
World Mind Sport Games	Participation: 2008

MAJOR COLLABORATIONS

- 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
- Kirsten Küsel, Institute of Ecology, Friedrich Schiller University of Jena
Accessing key players, genes and pathways in aqueous habitats using metagenomics and -transcriptomics
- Aria Bani Ahmad, Institute of Human Genetics, Universitätsklinikum Jena
Evolution of COP9 signalosome in unicellular and multicellular organisms
- Lenhard Rudolph, Leibniz Institute for Age Research - Fritz Lipmann Institute, Jena
Irregular genome structures associated with human aging
- Oliver Kurzai, Fungal Septomics, Leibniz Institute for Natural Product Research and Infection Biology – Hans Knöll Institute, Jena
*Analysis of transcriptomic *Candida glabrata* data*
- Konrad Sachse, Institute of Molecular Pathogenesis, Friedrich Loeffler Institute, Jena
Antibody detection via peptides
- 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
- Rolf Backofen, Chair for Bioinformatics, Department of Computer Science, Albert-Ludwigs-University Freiburg
RNA secondary structures
- 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
- Christian Berens, Chair for Microbiology, Department Biology, Friedrich-Alexander-University Erlangen-Nuremberg
Transcription start site discovery in Coxiella
- 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**

GRANTS

		Amount Marz Group:
2016–2019	Zwanzig20 – InfectControl 2020 – Molekulare Serologie zur schnellen Bestimmung der Impftiter gegen impf-präventable Infektionskrankheiten (STIKO-Liste) bei Migranten und anderen Patientengruppen; Subproject: STIKO-Serologie – TV1 One PostDocc (1x24 months) and one doctoral student (1x12 months)	317 662€
2016–2019	DFG MA 5082/9-1, Embryonale nicht-kodierende RNAs in der menschlichen Plazenta und dem mütterlichen Blutkreislauf One doctoral student (1x36 months E13/100%)	269 500€
2016–2017	MGH, CCXDP Exploring Non-coding RNAs in X-linked Dystonia-Parkinsonism (XDP) using High-Throughput Sequencing (RNA-Seq) in Various Endogenous Models Co-PI with Christine Klein and Aloysius Domingo. Supervision of a PhD student	121 400 €
2016–2019	DFG SPP-1596 Ecology and Species Barriers in Emerging Viral Diseases, 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	–
2015–2018	ZAJ RegenerAging – Analyzing the regulation of aging One doctoral student (1x36 months E13/50%)	90 000 €
2013–2017	CRC 1076 – AquaDiva BIODIV4 – Elucidation of microbial nutrient cycling using key functional genes and proteins One shared doctoral student (1x36 months E13/50%), associated member	–
2013–2017	DFG SFB/TR124 Pathogenic fungi and their human host: Networks of interaction (FungiNet), Speaker: Axel Brakhage One doctoral student (1x36 months E13/65%)	139 500 €
2011–2016	DFG MA 5082/1-1 Automated Genomewide Annotation of Non-coding RNAs Two doctoral students (2x36 months E13/50%)	220 000 €

EXPIRED GRANTS

		Amount Marz Group:
2013–2016	DFG SPP-1596 Ecology and Species Barriers in Emerging Viral Diseases, Speaker: Christian Drosten One doctoral student (1x24 months E13/50%), associated member	57 596 €
2014–2016	Carl-Zeiss-Stiftung Lücken im Kraftwerk der Zukunft – Kombinierte Metabolom- und Transkriptomanalyse des Hell/Dunkel-Zyklus bei Cyanobakterien One doctoral student (1x24 months E13/50%) and one PostDoc (1x24 months E13/100%)	200 000 €
2011–2015	DFG GRK-1384 International Research Training Group – Enzymes and multienzyme complexes acting on nucleic acids One doctoral student (1x54 months E13/50%)	208 440 €
2010–2013	DFG - SPP 1258 Sensory and regulatory RNAs in Prokaryotes Associated member	–

INVITED TALKS

- 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

2009	<i>Strategies for Homology-Based Identification of Eukaryotic Non-Coding RNA Genes</i> Zhejiang University, Hangzhou, China
2009	<i>Homology Search in Biological Networks</i> German Conference of Bioinformatics, Halle, Germany
2009	<i>A transdisciplinary attempt to represent structured data by sonification.</i> Institut de Biologie de l'Ecole Normale Supérieure, Paris, France
2005	<i>Prediction and Secondary Structure of 7SK RNA</i> Math/Chem/Comp, Dubrovnik, Croatia
	<i>snRNA search without a magnifying glass</i>

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</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
Practical Course <i>High Throughput Bioinformatics</i>	U Jena	2012, 2013, 2014/15, 2015/16, 2016/17
Lecture <i>RNA Bioinformatics</i>	U Jena	2012/13, 2013/14, 2015, 2016
Practical Course <i>RNA Bioinformatics</i>	U Jena	2012/13, 2013/14, 2015, 2016
Literature Seminar	U Jena	2014, 2014/15, 2015, 2015/16, 2016/17
Practical Course <i>Scripting Languages</i>	U Jena	2014, 2015, 2015/16, 2016, 2016/17
Lecture <i>Virus Bioinformatics</i>	U Jena	2014/15, 2015, 2016
Lecture <i>Gene Expression Analysis</i>	U Jena	2016
Lecture <i>Basic bioinformatic applications</i>	U Jena	2016/17

* – shared with other lecturer

GROUP COMPOSITION

PostProf

- Konrad Sachse, *Bacterial annotation and vaccination*

PostDocs:

- Franziska Hufsky, *Correlation of Transcriptomic and Metabolomic Data*
- Holger Bierhoff, *Genomewide detection of triplexes and quadruplexes*
- Diana Morales, *Exosome extraction*
- Wittaya Chaiwangyen, *Microparticle extraction*
- Alejandro Nabor Lozada Chavez, *Evolution of the genome structure in RNA viruses under selective pressure*
- Markus Fricke, *Viral Bioinformatics*

PhD students:

- Konstantin Riege, *Automated genomewide annotation of non-coding RNAs and comparative genomics*, since 2012
- Martin Hölzer, *Ecology and Species Barriers in Emerging Viral Diseases*, since 2013
- Michael Gaspar, *Elucidation of key players and functional genes in the subsurface microbial nutrient cycling using metagenomics and -transcriptomics*, since 2014
- Emanuel Barth, *Regulation of Aging*, since 2014
- 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

- Akash Srivastava, *Healthy aging*, since 2015
- Maximilian Collatz, *Expression analysis of high throughput data under various conditions in bats*, since 2016

Assistancies:

- Marie Lataretu, student assistant
- Florian Mock, student assistant
- Sabrina Eichwald, technical assistant
- Mara Sanai, technical assistant

Completed PhD theses:

- 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:

- Emanuel Barth, bachelor thesis (2012), master thesis (2014)
- Luise Modersohn, bachelor thesis (2012)
- Franziska Klincke, master thesis (2012)
- Cornelia Mühlich, bachelor thesis (2012)
- Silvia Müller, bachelor thesis (2013)
- Stephan Kanter, bachelor thesis (2014)
- Eugen Bauer, master thesis (2014)
- Nelly Fernanda Mostajo Berrospi, master thesis (2014)
- Ralf Schmidt, master thesis (2014)
Award for best student 2014 from Faculty of Mathematics and Informatics, Friedrich Schiller University Jena
- Alexandra Morscher, bachelor thesis (2015)
- Ruman Gerst, bachelor thesis (2015)
- Bastian Seelbinder, bachelor thesis (2015)

Completed assistencies:

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

CITATION ANALYSIS

Total number of publications:	62
No. of peer rev. publications:	58
No. of first/last authorships:	31
No. of book chapters:	4
h-index	19
Citations	5564
Three most cited publications	No. 5 (3826); No. 19 (271); No. 3 (262)

LIST OF PEER-REVIEWED PUBLICATIONS IN REVERSE CHRONOLOGICAL ORDER

- 58 M. Hölzer, V. Krähling, 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, **M. Marz**. Differential transcriptional responses to Ebola and Marburg virus infection in bat and human cells. *Sci Rep* 6:34589, 2016.
- 57 M. Fricke, **M. Marz**. Prediction of conserved long-range RNA-RNA interaction in full viral genomes. *Bioinformatics*, 32(19):2928-35, 2016.
- 56 The Computational Pan-Genomics Consortium. Computational pan-genomics: status, promises and challenges. *Brief Bioinform*, Epub ahead of print, 2016.
- 55 S. Winter, K. Jahn, S. Wehner, L. Kuchenbecker, J. Stoye, **M. Marz**, S. Böcker. Finding approximate gene clusters with Gecko3. *Nucleic Acids Res*, Epub ahead of print, 2016.
- 54 G. K. Gerresheim, N. Dünnes, A. Nieder-Röhrmann, L. A. Shalamova, M. Fricke, I. Hofacker, C. Höner zu Siederdisen, **M. Marz**, M. Niepmann. microRNA-122 target sites in the hepatitis C virus RNA NS5B coding region and 3' untranslated region: function in replication and influence of RNA secondary structure. *Cell Mol Life Sci*, Epub ahead of print, 2016.
- 53 M. Hölzer, K. Laroucau, H. H. Creasy, S. Ott, F. Vorimore, P. M. Bavoil, **M. Marz**, K. Sachse. Whole-genome sequence of *Chlamydia gallinacea* type strain 08-1274/3. *Genome Announc*, 4(4):e00708-16, 2016.
- 52 E. Barth, R. Hübler, A. Baniahmad, **M. Marz**. The evolution of COP9 signalosome in unicellular and multicellular organisms. *Genome Biol Evol*, 8:1279-1289, 2016.
- 51 L. Graf, F. Sendker, A. Dick, E. Barth, **M. Marz**, O. Daumke, G. Kochs. ID: 187: Allelic variations in the interferon-induced human MxA protein affect its antiviral activity against influenza A virus *Cytokine*, 76(1):98, 2015.
- 50 P. Möbius, M. Hölzer, M. Felder, G. Nordsiek, M. Groth, H. Köhler, K. Reichwald, M. Platzer, **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.
- 49 A. H. Sahyoun, M. Hölzer, F. Jühling, C. Höner Zu Siederdisen, M. Al-Arab, K. Tout, **M. Marz**, M. Middendorf, P. F. Stadler, M. Bernt. Towards a comprehensive picture of alloacceptor tRNA remodeling in metazoan mitochondrial genomes. *Nucleic Acids Res*, 43(16):8044-8056 2015.
- 48 M. Fricke, N. Dünnes, M. Zayas, R. Bartenschlager, M. Niepmann, **M. Marz**. Conserved RNA secondary structures and long-range interactions in hepatitis C viruses. *RNA*, 21(7):1219-1232, 2015.

- 47 I. Althoefer, S. Kaitschick, **M. Marz**. Computer-aided Go on high-dan level. *IGGSC Proceedings*, 2015.
- 46 **M. Marz**, M. Ferracin, C. Klein. MicroRNAs as biomarker of Parkinson disease? Small but mighty. *Neurology*, 84(7):636–638, 2015.
- 45 J. Linde, S. Duggan, M. Weber, F. Horn, P. Sieber, D. Hellwig, K. Riege, **M. Marz**, R. Martin, R. Guthke, O. Kurzai. Defining the transcriptomic landscape of *Candida glabrata* by RNA-Seq. *Nucleic Acids Res*, 43(3):1392–1406, 2015.
- 44 E. Bauer, H. Salem, **M. Marz**, H. Vogel, M. Kaltenpoth. Transcriptomic immune response of the cotton stainer *Dysdercus fasciatus* to experimental elimination of vitamin-supplementing intestinal symbionts. *PLoS One*, 9(12):e114865, 2014.
- 43 R. Madhugiri, M. Fricke, **M. Marz**, J. Ziebuhr. RNA structure analysis of alphacoronavirus terminal genome regions. *Virus Res*, 194:76–89, 2014.
- 42 H. Salem, E. Bauer, A. S. Strauss, H. Vogel, **M. Marz**, M. Kaltenpoth. Vitamin supplementation by gut symbionts ensures metabolic homeostasis in an insect host. *Proc Biol Sci*, 281(1796):20141838, 2014.
- 41 J. Qin, M. Fricke, **M. Marz**, P. F. Stadler, R. Backofen. Graph-distance distribution of the Boltzmann ensemble of RNA secondary structures. *Algorithms Mol Biol*, 9:19, 2014.
- 40 C. Beckstein, S. Böcker, M. Bogdan, H. M. B. H. Bruelheide, J. Denzler, P. Dittrich, I. Grosse, A. Hinneburg, B. König-Ries, F. Löffler, **M. Marz**, M. Müller-Hannemann, M. Winter, W. Zimmermann. Explorative analysis of heterogeneous, unstructured, and uncertain data: A computer science perspective on biodiversity research. In M. Helfert, A. Holzinger, O. Belo, C. Francalanci, editors, *Proceedings of the 3rd International Conference on Data Management Technologies and Applications (DATA 2014)*, Vienna, Austria, pages 251–257, 2014.
- 39 S. Wehner, K. Damm, R. K. Hartmann, **M. Marz**. Dissemination of 6S RNA among bacteria. *RNA Biol*, 11(11):1467–1478, 2014.
- 38 **M. Marz**, N. Beerenwinkel, C. Drosten, M. Fricke, D. Frishman, I. L. Hofacker, D. Hoffmann, M. Middendorf, T. Rattei, P. F. Stadler, A. Töpfer. Challenges in RNA virus bioinformatics. *Bioinformatics*, 30(13):1793–1799, 2014.
- 37 M. Lechner, A. I. Nickel, S. Wehner, K. Riege, N. Wieseke, B. M. Beckmann, R. K. Hartmann, **M. Marz**. Genomewide comparison and novel ncRNAs of *Aquificales*. *BMC Genomics*, 15:522, 2014.
- 36 S. Wehner, G. K. Mannala, X. Qing, R. Madhugiri, T. Chakraborty, M. A. Mraheil, T. Hain*, **M. Marz***. Detection of very long antisense transcripts by whole transcriptome RNA-Seq analysis of *Listeria monocytogenes* by semiconductor sequencing technology. *PLoS One*, 9(10):e108639, 2014.
- 35 K. Sachse, K. Laroucau, K. Riege, S. Wehner, M. Dilcher, H. H. Creasy, M. Weidmann, G. Myers, F. Vorimore, N. Vicari, S. Magnino, E. Liebler-Tenorio, A. Ruettger, P. M. Bavoil, F. T. Hufert, R. Rosselló-Móra, **M. Marz**. Evidence for the existence of two new members of the family *Chlamydiaceae* and proposal of *Chlamydia avium* sp. nov. and *Chlamydia gallinacea* sp. nov. *Syst Appl Microbiol*, 37(2):79–88, 2014.

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- 33 J. Vierna, S. Wehner, C. Höner zu Siederdisen, A. Martínez-Lage, **M. Marz**. Systematic analysis and evolution of 5S ribosomal DNA in metazoans. *Heredity (Edinb)*, 111(5):410–421, 2013.
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