

Curriculum vitae Prof. Dr. Manja Marz

Name Manja Marz

Work address RNA Bioinformatics and High-Throughput Analysis
Faculty of Mathematics and Computer Science
Friedrich Schiller University Jena
Leutragraben 1
07743 Jena
fon: +49 3641 9 46480
E-mail: manja@uni-jena.de

Academic Education	1999–2005	Studies of Biology at the University of Leipzig
	2001-2006	Studies of Computer Science at the University of Leipzig
	2002-2003	Studies of Biology and Computer Science at the University of Edinburgh
	2004	Studies of Biology at TU Darmstadt
	2006-2009	Doctoral Degree Dr. rer. nat., University of Leipzig
Professional Career	2010–2012	Group Leader of “RNA Bioinformatics” at Philipps-University Marburg
	2012–2015	Junior-Professorship for “High Throughput Sequencing Analysis” at Friedrich Schiller University Jena
	since 2013	Founding and board member of ZAJ (Aging Research Center Jena)
	since 2015	Group leader at Leibniz Institute for Age Research – Fritz Lipmann Institute
	2015	Founding member of MSCJ (Michael Stifel Zentrum Jena for Data-Driven and Simulation Science)
	since 2015	Full Professorship for High Throughput Sequencing Analysis at Friedrich Schiller University Jena
	since 2015	Founding and board member of FIFI (Fördervereinverein des Instituts für Informatik)
	since 2017	Founding member, board member and managing director of “European Virus Bioinformatics Center”
	since 2018	Scientific advisory board member of RNA Central and Rfam
	since 2020	Head of Bioinformatics Core Facility Jena

Funding (last 5 years)

Landesprogramm „ProDigital“ des Freistaats Thüringen	2020–2024	Digitalisierung der Lebenswissenschaften: Wege in die Zukunft
Carl Zeiss Stiftung	2019–2022	Eine virtuelle Werkstatt für die Digitalisierung in den Wissenschaften: Datengetriebene Virusdiagnostik auf multiplen Ebenen II (Anwendung)
International Max Planck Research School for the Science of Human History	2019–2022	A comprehensive analysis of microorganisms and viruses from ancient samples using minion sequencing techniques
BMBF	2019–2021	DBT Cooperative Science Program: Development of metagenomics assisted surveillance tools for tracking antibiotic resistance in river bodies — A study in the Ganges river valley (NANOLOG)
DFG	2017–2021	CRC 1076 — AquaDiva: Viral diversity, viral de novo assembly, and viral decay in groundwater
DFG	2017–2019	SFB/TR124 Pathogenic fungi and their human host: The role of human microbiota for the development of fungal infectious diseases – <i>Candida albicans</i> as a case study
DFG	2017–2019	Forschungszentrum 118 — iDiv: All-in-one Multiplex-Sequencing
EU	2016–2019	Zwanzig20 – InfectControl 2020, Subproject: STIKO-Serologie: Molekulare Serologie zur schnellen Bestimmung der Impftiter gegen impf-präventable Infektionskrankheiten (STIKO-Liste) bei Migranten und anderen Patientengruppen
DFG	2016–2019	Embryonale nicht-kodierende RNAs in der menschlichen Plazenta und dem mütterlichen Blutkreislauf (MA 5082/9-1)
DFG	2016–2019	SPP 1596: Ecology and Species Barriers in Emerging Viral Diseases

Publications (max. 10 most relevant)

1. M. Fricke, N. Dünnes, M. Zayas, R. Bartenschlager, M. Niepmann, and M. **Marz**. “Conserved RNA secondary structures and long-range interactions in hepatitis C viruses”. In: *RNA (New York, N.Y.)* 21.7 (2015), pp. 1219–1232. DOI: 10.1261/rna.049338.114
2. M. **Marz**, M. Ferracin, and C. Klein. “MicroRNAs as biomarker of Parkinson disease? Small but mighty”. In: *Neurology* 84.7 (2015), pp. 636–638. DOI: 10.1212/WNL.0000000000001275
3. M. **Marz**, N. Beerenwinkel, C. Drosten, M. Fricke, D. Frishman, I. L. Hofacker, D. Hoffmann, M. Middendorf, T. Rattei, P. F. Stadler, and A. Töpfer. “Challenges in RNA virus bioinformatics”. In: *Bioinformatics (Oxford, England)* 30.13 (2014), pp. 1793–1799. DOI: 10.1093/bioinformatics/btu105
4. M. Lechner, A. I. Nickel, S. Wehner, K. Riege, N. Wieseke, B. M. Beckmann, R. K. Hartmann, and M. **Marz**. “Genomewide comparison and novel ncRNAs of Aquificales”. In: *BMC genomics* 15 (2014), p. 522. DOI: 10.1186/1471-2164-15-522
5. S. Wehner, A. K. Dörrich, P. Ciba, A. Wilde, and M. **Marz**. “pRNA: NoRC-associated RNA of rRNA operons”. In: *RNA biology* 11.1 (2014), pp. 3–9. DOI: 10.4161/rna.27448
6. X. Qi, Y. Li, S. Honda, S. Hoffmann, M. **Marz**, A. Mosig, J. D. Podlevsky, P. F. Stadler, E. U. Selker,

- and J. J.-L. Chen. "The common ancestral core of vertebrate and fungal telomerase RNAs". In: *Nucleic acids research* 41.1 (2013), pp. 450–462. DOI: 10.1093/nar/gks980
7. Y. Huang, Y. Li, D. W. Burt, et al. "The duck genome and transcriptome provide insight into an avian influenza virus reservoir species". In: *Nature genetics* 45.7 (2013), pp. 776–783. DOI: 10.1038/ng.2657
 8. B. M. Beckmann, P. G. Hoch, M. **Marz**, D. K. Willkomm, M. Salas, and R. K. Hartmann. "A pRNA-induced structural rearrangement triggers 6S-1 RNA release from RNA polymerase in *Bacillus subtilis*". In: *The EMBO journal* 31.7 (2012), pp. 1727–1738. DOI: 10.1038/emboj.2012.23
 9. M. **Marz**, A. Donath, N. Verstraete, T. van Nguyen, P. F. Stadler, and O. Bensaude. "Evolution of 7SK RNA and its protein partners in metazoa". In: *Molecular biology and evolution* 26.12 (2009), pp. 2821–2830. DOI: 10.1093/molbev/msp198
 10. E. Birney, J. A. Stamatoyannopoulos, A. Dutta, et al. "Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project". In: *Nature* 447.7146 (2007), pp. 799–816. DOI: 10.1038/nature05874