

Michael Hackenberg

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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|-------------------|-------------------------|----------------|-----------------|
| 78 papers | 3,112 citations | 28 h-index | 55 g-index |
| 84 ext. papers | 3,801 ext. citations | 7.2 avg, IF | 5.17 L-index |

| # | Paper | IF | Citations |
|----|---|------|-----------|
| 78 | The limits of human microRNA annotation have been met.. <i>Rna</i> , 2022 , | 5.8 | 3 |
| 77 | sRNAbench and sRNAtoolbox 2022 update: accurate miRNA and sncRNA profiling for model and non-model organisms.. <i>Nucleic Acids Research</i> , 2022 , | 20.1 | 2 |
| 76 | MirGeneDB 2.1: toward a complete sampling of all major animal phyla. <i>Nucleic Acids Research</i> , 2021 , | 20.1 | 9 |
| 75 | genomC: A Database to Explore the Association between Genetic Variation (SNPs) and CpG Methylation in the Human Genome. <i>Journal of Molecular Biology</i> , 2021 , 433, 166709 | 6.5 | 0 |
| 74 | In Silico Analysis of Micro-RNA Sequencing Data. <i>Methods in Molecular Biology</i> , 2021 , 2284, 231-251 | 1.4 | |
| 73 | Extracellular vesicle miRNA predict FDG-PET status in patients with classical Hodgkin Lymphoma. <i>Journal of Extracellular Vesicles</i> , 2021 , 10, e12121 | 16.4 | 5 |
| 72 | mirnaQC: a webserver for comparative quality control of miRNA-seq data. <i>Nucleic Acids Research</i> , 2020 , 48, W262-W267 | 20.1 | 6 |
| 71 | Transcriptional Dynamics and Candidate Genes Involved in Pod Maturation of Common Bean (L.). <i>Plants</i> , 2020 , 9, | 4.5 | 1 |
| 70 | Unification of miRNA and isomiR research: the mirGFF3 format and the mirtop API. <i>Bioinformatics</i> , 2020 , 36, 698-703 | 7.2 | 23 |
| 69 | MirGeneDB 2.0: the metazoan microRNA complement. <i>Nucleic Acids Research</i> , 2020 , 48, D132-D141 | 20.1 | 105 |
| 68 | Emerging roles of non-coding RNAs in vector-borne infections. <i>Journal of Cell Science</i> , 2020 , 134, | 5.3 | 1 |
| 67 | On the Need of Interpretability for Biomedical Applications: Using Fuzzy Models for Lung Cancer Prediction with Liquid Biopsy 2019 , | | 5 |
| 66 | sRNAbench and sRNAtoolbox 2019: intuitive fast small RNA profiling and differential expression. <i>Nucleic Acids Research</i> , 2019 , 47, W530-W535 | 20.1 | 71 |
| 65 | Noncoding RNAs in Parasite-Vector-Host Interactions. <i>Trends in Parasitology</i> , 2019 , 35, 715-724 | 6.4 | 13 |
| 64 | GENE-60. THE EPITRANSCRIPTOMIC CODE IN LGG: METABOLICALLY REPROGRAMMED IDH-MUTANT GLIOMAS ALTER tRNA MODIFICATION LANDSCAPE. <i>Neuro-Oncology</i> , 2019 , 21, vi110-vi111 [†] | | 78 |
| 63 | liqDB: a small-RNAseq knowledge discovery database for liquid biopsy studies. <i>Nucleic Acids Research</i> , 2019 , 47, D113-D120 | 20.1 | 6 |
| 62 | Identification and characterisation of a previously unknown drought tolerance-associated microRNA in barley. <i>Plant Journal</i> , 2018 , 95, 138-149 | 6.9 | 16 |

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| 61 | Exosome-Mediated Pathogen Transmission by Arthropod Vectors. <i>Trends in Parasitology</i> , 2018 , 34, 549-552 | 16 |
| 60 | Mesenchymal stem cell secretome promotes selective enrichment of cancer stem-like cells with specific cytogenetic profile. <i>Cancer Letters</i> , 2018 , 429, 78-88 | 9.9 18 |
| 59 | Prediction of CpG Islands as an Intrinsic Clustering Property Found in Many Eukaryotic DNA Sequences and Its Relation to DNA Methylation. <i>Methods in Molecular Biology</i> , 2018 , 1766, 31-47 | 1.4 5 |
| 58 | Herpes simplex virus 1 miRNA sequence variations in latently infected human trigeminal ganglia. <i>Virus Research</i> , 2018 , 256, 90-95 | 6.4 2 |
| 57 | Identification of tomato miRNAs responsive to root colonization by endophytic <i>Pochonia chlamydosporia</i> . <i>Applied Microbiology and Biotechnology</i> , 2018 , 102, 907-919 | 5.7 11 |
| 56 | In silico target network analysis of de novo-discovered, tick saliva-specific microRNAs reveals important combinatorial effects in their interference with vertebrate host physiology. <i>Rna</i> , 2017 , 23, 1259-1269 | 5.8 29 |
| 55 | sRNAtoolboxVM: Small RNA Analysis in a Virtual Machine. <i>Methods in Molecular Biology</i> , 2017 , 1580, 149-174 | 2 |
| 54 | Thiourea priming enhances salt tolerance through co-ordinated regulation of microRNAs and hormones in <i>Brassica juncea</i> . <i>Scientific Reports</i> , 2017 , 7, 45490 | 4.9 28 |
| 53 | NGSmethDB 2017: enhanced methylomes and differential methylation. <i>Nucleic Acids Research</i> , 2017 , 45, D97-D103 | 20.1 11 |
| 52 | On the presence and immunoregulatory functions of extracellular microRNAs in the trematode <i>Fasciola hepatica</i> . <i>Parasite Immunology</i> , 2017 , 39, e12399 | 2.2 31 |
| 51 | Viral Ubiquitin Ligase Stimulates Selective Host MicroRNA Expression by Targeting ZEB Transcriptional Repressors. <i>Viruses</i> , 2017 , 9, | 6.2 7 |
| 50 | Error Correction in Methylation Profiling From NGS Bisulfite Protocols 2017 , 167-183 | 1 |
| 49 | Generation of different sizes and classes of small RNAs in barley is locus, chromosome and/or cultivar-dependent. <i>BMC Genomics</i> , 2016 , 17, 735 | 4.5 6 |
| 48 | Sensing of latent EBV infection through exosomal transfer of 5'pppRNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, E587-96 | 11.5 99 |
| 47 | Non-invasive prostate cancer detection by measuring miRNA variants (isomiRs) in urine extracellular vesicles. <i>Oncotarget</i> , 2016 , 7, 22566-78 | 3.3 85 |
| 46 | The revised microRNA complement of <i>Fasciola hepatica</i> reveals a plethora of overlooked microRNAs and evidence for enrichment of immuno-regulatory microRNAs in extracellular vesicles. <i>International Journal for Parasitology</i> , 2015 , 45, 697-702 | 4.3 44 |
| 45 | sRNAtoolbox: an integrated collection of small RNA research tools. <i>Nucleic Acids Research</i> , 2015 , 43, W467-73 | 20.1 161 |
| 44 | Differential expression of microRNAs and other small RNAs in barley between water and drought conditions. <i>Plant Biotechnology Journal</i> , 2015 , 13, 2-13 | 11.6 107 |

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| 43 | Integrated microRNA, mRNA, and protein expression profiling reveals microRNA regulatory networks in rat kidney treated with a carcinogenic dose of aristolochic acid. <i>BMC Genomics</i> , 2015 , 16, 365 | 4.5 | 24 |
| 42 | A systems level analysis reveals transcriptomic and proteomic complexity in Ixodes ricinus midgut and salivary glands during early attachment and feeding. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 2725-35 | 7.6 | 61 |
| 41 | DNA clustering and genome complexity. <i>Computational Biology and Chemistry</i> , 2014 , 53 Pt A, 71-8 | 3.6 | 6 |
| 40 | Sources of individual variability: miRNAs that predispose to neuropathic pain identified using genome-wide sequencing. <i>Molecular Pain</i> , 2014 , 10, 22 | 3.4 | 37 |
| 39 | Expression of herpes simplex virus 1 microRNAs in cell culture models of quiescent and latent infection. <i>Journal of Virology</i> , 2014 , 88, 2337-9 | 6.6 | 27 |
| 38 | Nontemplated nucleotide additions distinguish the small RNA composition in cells from exosomes. <i>Cell Reports</i> , 2014 , 8, 1649-1658 | 10.6 | 379 |
| 37 | NGSmethDB: an updated genome resource for high quality, single-cytosine resolution methylomes. <i>Nucleic Acids Research</i> , 2014 , 42, D53-9 | 20.1 | 18 |
| 36 | sRNAbench: profiling of small RNAs and its sequence variants in single or multi-species high-throughput experiments 2014 , 1, | | 30 |
| 35 | Surface analysis of Dicrocoelium dendriticum. The molecular characterization of exosomes reveals the presence of miRNAs. <i>Journal of Proteomics</i> , 2014 , 105, 232-41 | 3.9 | 83 |
| 34 | Characterization of phosphorus-regulated miR399 and miR827 and their isomirs in barley under phosphorus-sufficient and phosphorus-deficient conditions. <i>BMC Plant Biology</i> , 2013 , 13, 214 | 5.3 | 78 |
| 33 | A comprehensive expression profile of microRNAs and other classes of non-coding small RNAs in barley under phosphorous-deficient and -sufficient conditions. <i>DNA Research</i> , 2013 , 20, 109-25 | 4.5 | 82 |
| 32 | CpGislandEVO: a database and genome browser for comparative evolutionary genomics of CpG islands. <i>BioMed Research International</i> , 2013 , 2013, 709042 | 3 | 4 |
| 31 | MethylExtract: High-Quality methylation maps and SNV calling from whole genome bisulfite sequencing data. <i>F1000Research</i> , 2013 , 2, 217 | 3.6 | 25 |
| 30 | MethylExtract: High-Quality methylation maps and SNV calling from whole genome bisulfite sequencing data. <i>F1000Research</i> , 2013 , 2, 217 | 3.6 | 20 |
| 29 | Clustering of DNA words and biological function: a proof of principle. <i>Journal of Theoretical Biology</i> , 2012 , 297, 127-36 | 2.3 | 19 |
| 28 | Segmentation of time series with long-range fractal correlations. <i>European Physical Journal B</i> , 2012 , 85, 1 | 1.2 | 19 |
| 27 | Whole transcriptome analysis of a reversible neurodegenerative process in Drosophila reveals potential neuroprotective genes. <i>BMC Genomics</i> , 2012 , 13, 483 | 4.5 | 10 |
| 26 | Bioinformatics for High Throughput Sequencing 2012 , | | 9 |

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| 25 | Discovery of novel microRNAs in rat kidney using next generation sequencing and microarray validation. <i>PLoS ONE</i> , 2012 , 7, e34394 | 3.7 | 17 |
| 24 | MicroRNA Expression Profiling and Discovery 2012 , 191-208 | | |
| 23 | A transgenic transcription factor (TaDREB3) in barley affects the expression of microRNAs and other small non-coding RNAs. <i>PLoS ONE</i> , 2012 , 7, e42030 | 3.7 | 26 |
| 22 | High-level organization of isochores into gigantic superstructures in the human genome. <i>Physical Review E</i> , 2011 , 83, 031908 | 2.4 | 18 |
| 21 | WordCluster: detecting clusters of DNA words and genomic elements. <i>Algorithms for Molecular Biology</i> , 2011 , 6, 2 | 1.8 | 13 |
| 20 | NGSmethDB: a database for next-generation sequencing single-cytosine-resolution DNA methylation data. <i>Nucleic Acids Research</i> , 2011 , 39, D75-9 | 20.1 | 45 |
| 19 | miRanalyzer: an update on the detection and analysis of microRNAs in high-throughput sequencing experiments. <i>Nucleic Acids Research</i> , 2011 , 39, W132-8 | 20.1 | 222 |
| 18 | TargetSpy: a supervised machine learning approach for microRNA target prediction. <i>BMC Bioinformatics</i> , 2010 , 11, 292 | 3.6 | 117 |
| 17 | Prediction of CpG-island function: CpG clustering vs. sliding-window methods. <i>BMC Genomics</i> , 2010 , 11, 327 | 4.5 | 35 |
| 16 | Algorithms and methods for correlating experimental results with annotation databases. <i>Methods in Molecular Biology</i> , 2010 , 593, 315-40 | 1.4 | 2 |
| 15 | ContDist: a tool for the analysis of quantitative gene and promoter properties. <i>BMC Bioinformatics</i> , 2009 , 10, 7 | 3.6 | 6 |
| 14 | Level statistics of words: finding keywords in literary texts and symbolic sequences. <i>Physical Review E</i> , 2009 , 79, 035102 | 2.4 | 55 |
| 13 | miRanalyzer: a microRNA detection and analysis tool for next-generation sequencing experiments. <i>Nucleic Acids Research</i> , 2009 , 37, W68-76 | 20.1 | 244 |
| 12 | Phylogenetic distribution of large-scale genome patchiness. <i>BMC Evolutionary Biology</i> , 2008 , 8, 107 | 3 | 7 |
| 11 | Annotation-Modules: a tool for finding significant combinations of multisource annotations for gene lists. <i>Bioinformatics</i> , 2008 , 24, 1386-93 | 7.2 | 25 |
| 10 | Identifying characteristic scales in the human genome. <i>Physical Review E</i> , 2007 , 75, 032903 | 2.4 | 39 |
| 9 | CpGcluster: a distance-based algorithm for CpG-island detection. <i>BMC Bioinformatics</i> , 2006 , 7, 446 | 3.6 | 124 |
| 8 | The biased distribution of Alus in human isochores might be driven by recombination. <i>Journal of Molecular Evolution</i> , 2005 , 60, 365-77 | 3.1 | 37 |

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| 7 | IsoFinder: computational prediction of isochores in genome sequences. <i>Nucleic Acids Research</i> , 2004 , 32, W287-92 | 20.1 | 64 |
| 6 | Isochore chromosome maps of the human genome. <i>Gene</i> , 2002 , 300, 117-27 | 3.8 | 48 |
| 5 | Interplay of disorder and tunneling in coupled quantum well structures Tuning the intersubband line shape by an electric field. <i>Physica E: Low-Dimensional Systems and Nanostructures</i> , 2000 , 7, 722-725 | 3 | 1 |
| 4 | Intersubband transitions in coupled wells with disorder. <i>Physica E: Low-Dimensional Systems and Nanostructures</i> , 2000 , 6, 606-610 | 3 | 1 |
| 3 | Subband selective disorder in a quasi-2D system and its effect on the intersubband spectrum. <i>Physica E: Low-Dimensional Systems and Nanostructures</i> , 2000 , 7, 216-219 | 3 | |
| 2 | DNA Methylation Profiling from High-Throughput Sequencing Data | | 3 |
| 1 | MirGeneDB 2.0: The metazoan microRNA complement | | 7 |