

Michael Hackenberg

List of Publications by Citations

Source: <https://exaly.com/author-pdf/8257542/michael-hackenberg-publications-by-citations.pdf>
Version: 2024-04-09

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.
The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Nontemplated nucleotide additions distinguish the small RNA composition in cells from exosomes. <i>Cell Reports</i> , 2014 , 8, 1649-1658	10.6	379
77	miRanalyzer: a microRNA detection and analysis tool for next-generation sequencing experiments. <i>Nucleic Acids Research</i> , 2009 , 37, W68-76	20.1	244
76	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
75	sRNAtoolbox: an integrated collection of small RNA research tools. <i>Nucleic Acids Research</i> , 2015 , 43, W467-73	20.1	161
74	CpGcluster: a distance-based algorithm for CpG-island detection. <i>BMC Bioinformatics</i> , 2006 , 7, 446	3.6	124
73	TargetSpy: a supervised machine learning approach for microRNA target prediction. <i>BMC Bioinformatics</i> , 2010 , 11, 292	3.6	117
72	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
71	MirGeneDB 2.0: the metazoan microRNA complement. <i>Nucleic Acids Research</i> , 2020 , 48, D132-D141	20.1	105
70	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
69	Non-invasive prostate cancer detection by measuring miRNA variants (isomiRs) in urine extracellular vesicles. <i>Oncotarget</i> , 2016 , 7, 22566-78	3.3	85
68	Surface analysis of <i>Dicrocoelium dendriticum</i> . The molecular characterization of exosomes reveals the presence of miRNAs. <i>Journal of Proteomics</i> , 2014 , 105, 232-41	3.9	83
67	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
66	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
65	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
64	sRNAbench and sRNAtoolbox 2019: intuitive fast small RNA profiling and differential expression. <i>Nucleic Acids Research</i> , 2019 , 47, W530-W535	20.1	71
63	IsoFinder: computational prediction of isochores in genome sequences. <i>Nucleic Acids Research</i> , 2004 , 32, W287-92	20.1	64
62	A systems level analysis reveals transcriptomic and proteomic complexity in <i>Ixodes ricinus</i> midgut and salivary glands during early attachment and feeding. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 2725-35	7.6	61

61	Level statistics of words: finding keywords in literary texts and symbolic sequences. <i>Physical Review E</i> , 2009 , 79, 035102	2.4	55
60	Isochore chromosome maps of the human genome. <i>Gene</i> , 2002 , 300, 117-27	3.8	48
59	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
58	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
57	Identifying characteristic scales in the human genome. <i>Physical Review E</i> , 2007 , 75, 032903	2.4	39
56	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
55	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
54	Prediction of CpG-island function: CpG clustering vs. sliding-window methods. <i>BMC Genomics</i> , 2010 , 11, 327	4.5	35
53	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
52	sRNAbench: profiling of small RNAs and its sequence variants in single or multi-species high-throughput experiments 2014 , 1,		30
51	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
50	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
49	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
48	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
47	Annotation-Modules: a tool for finding significant combinations of multisource annotations for gene lists. <i>Bioinformatics</i> , 2008 , 24, 1386-93	7.2	25
46	MethylExtract: High-Quality methylation maps and SNV calling from whole genome bisulfite sequencing data. <i>F1000Research</i> , 2013 , 2, 217	3.6	25
45	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
44	Unification of miRNA and isomiR research: the mirGFF3 format and the mirtop API. <i>Bioinformatics</i> , 2020 , 36, 698-703	7.2	23

43	MethylExtract: High-Quality methylation maps and SNV calling from whole genome bisulfite sequencing data. <i>F1000Research</i> , 2013 , 2, 217	3.6	20
42	Clustering of DNA words and biological function: a proof of principle. <i>Journal of Theoretical Biology</i> , 2012 , 297, 127-36	2.3	19
41	Segmentation of time series with long-range fractal correlations. <i>European Physical Journal B</i> , 2012 , 85, 1	1.2	19
40	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
39	NGSmethDB: an updated genome resource for high quality, single-cytosine resolution methylomes. <i>Nucleic Acids Research</i> , 2014 , 42, D53-9	20.1	18
38	High-level organization of isochores into gigantic superstructures in the human genome. <i>Physical Review E</i> , 2011 , 83, 031908	2.4	18
37	Discovery of novel microRNAs in rat kidney using next generation sequencing and microarray validation. <i>PLoS ONE</i> , 2012 , 7, e34394	3.7	17
36	Identification and characterisation of a previously unknown drought tolerance-associated microRNA in barley. <i>Plant Journal</i> , 2018 , 95, 138-149	6.9	16
35	Exosome-Mediated Pathogen Transmission by Arthropod Vectors. <i>Trends in Parasitology</i> , 2018 , 34, 549-552	5.2	16
34	Noncoding RNAs in Parasite-Vector-Host Interactions. <i>Trends in Parasitology</i> , 2019 , 35, 715-724	6.4	13
33	WordCluster: detecting clusters of DNA words and genomic elements. <i>Algorithms for Molecular Biology</i> , 2011 , 6, 2	1.8	13
32	NGSmethDB 2017: enhanced methylomes and differential methylation. <i>Nucleic Acids Research</i> , 2017 , 45, D97-D103	20.1	11
31	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
30	Whole transcriptome analysis of a reversible neurodegenerative process in <i>Drosophila</i> reveals potential neuroprotective genes. <i>BMC Genomics</i> , 2012 , 13, 483	4.5	10
29	Bioinformatics for High Throughput Sequencing 2012 ,		9
28	MirGeneDB 2.1: toward a complete sampling of all major animal phyla. <i>Nucleic Acids Research</i> , 2021 ,	20.1	9
27	Viral Ubiquitin Ligase Stimulates Selective Host MicroRNA Expression by Targeting ZEB Transcriptional Repressors. <i>Viruses</i> , 2017 , 9,	6.2	7
26	Phylogenetic distribution of large-scale genome patchiness. <i>BMC Evolutionary Biology</i> , 2008 , 8, 107	3	7

25	MirGeneDB 2.0: The metazoan microRNA complement		7
24	mirnaQC: a webserver for comparative quality control of miRNA-seq data. <i>Nucleic Acids Research</i> , 2020 , 48, W262-W267	20.1	6
23	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
22	DNA clustering and genome complexity. <i>Computational Biology and Chemistry</i> , 2014 , 53 Pt A, 71-8	3.6	6
21	ContDist: a tool for the analysis of quantitative gene and promoter properties. <i>BMC Bioinformatics</i> , 2009 , 10, 7	3.6	6
20	liqDB: a small-RNAseq knowledge discovery database for liquid biopsy studies. <i>Nucleic Acids Research</i> , 2019 , 47, D113-D120	20.1	6
19	On the Need of Interpretability for Biomedical Applications: Using Fuzzy Models for Lung Cancer Prediction with Liquid Biopsy 2019 ,		5
18	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
17	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
16	CpGislandEVO: a database and genome browser for comparative evolutionary genomics of CpG islands. <i>BioMed Research International</i> , 2013 , 2013, 709042	3	4
15	DNA Methylation Profiling from High-Throughput Sequencing Data		3
14	The limits of human microRNA annotation have been met.. <i>Rna</i> , 2022 ,	5.8	3
13	sRNAtoolboxVM: Small RNA Analysis in a Virtual Machine. <i>Methods in Molecular Biology</i> , 2017 , 1580, 149-174	17.4	2
12	Herpes simplex virus 1 miRNA sequence variations in latently infected human trigeminal ganglia. <i>Virus Research</i> , 2018 , 256, 90-95	6.4	2
11	Algorithms and methods for correlating experimental results with annotation databases. <i>Methods in Molecular Biology</i> , 2010 , 593, 315-40	1.4	2
10	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
9	Transcriptional Dynamics and Candidate Genes Involved in Pod Maturation of Common Bean (L.). <i>Plants</i> , 2020 , 9,	4.5	1
8	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

7	Intersubband transitions in coupled wells with disorder. <i>Physica E: Low-Dimensional Systems and Nanostructures</i> , 2000 , 6, 606-610	3	1
6	Error Correction in Methylation Profiling From NGS Bisulfite Protocols 2017 , 167-183		1
5	Emerging roles of non-coding RNAs in vector-borne infections. <i>Journal of Cell Science</i> , 2020 , 134,	5.3	1
4	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
3	MicroRNA Expression Profiling and Discovery 2012 , 191-208		
2	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	
1	In Silico Analysis of Micro-RNA Sequencing Data. <i>Methods in Molecular Biology</i> , 2021 , 2284, 231-251	1.4	