

# Michael Janitz

## List of Publications by Year in descending order

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76  
papers

2,270  
citations

186265

28  
h-index

243625

44  
g-index

80  
all docs

80  
docs citations

80  
times ranked

3766  
citing authors

#	ARTICLE	IF	CITATIONS
1	RNA polyadenylation patterns in the human transcriptome. <i>Gene</i> , 2022, 816, 146133.	2.2	4
2	Proteomics and Transcriptomics of the Hippocampus and Cortex in SUDEP and High-Risk SUDEP Patients. <i>Neurology</i> , 2021, 96, e2639-e2652.	1.1	24
3	Coding and non-coding transcriptome of mesial temporal lobe epilepsy: Critical role of small non-coding RNAs. <i>Neurobiology of Disease</i> , 2020, 134, 104612.	4.4	33
4	Neural circular transcriptomes across mammalian species. <i>Genomics</i> , 2020, 112, 1162-1166.	2.9	15
5	Cell type-specific circular RNA expression in human glial cells. <i>Genomics</i> , 2020, 112, 5265-5274.	2.9	15
6	Analysis of the Circular Transcriptome in the Synaptosomes of Aged Mice. <i>Neuroscience</i> , 2020, 449, 202-213.	2.3	6
7	Cell Adhesion Molecules and Protein Synthesis Regulation in Neurons. <i>Frontiers in Molecular Neuroscience</i> , 2020, 13, 592126.	2.9	16
8	Identification of Specific Circular RNA Expression Patterns and MicroRNA Interaction Networks in Mesial Temporal Lobe Epilepsy. <i>Frontiers in Genetics</i> , 2020, 11, 564301.	2.3	11
9	Early transcriptome changes in response to chemical long-term potentiation induced via activation of synaptic NMDA receptors in mouse hippocampal neurons. <i>Genomics</i> , 2019, 111, 1676-1686.	2.9	10
10	Changes in circular RNA expression patterns during human foetal brain development. <i>Genomics</i> , 2019, 111, 753-758.	2.9	50
11	Circular RNAs in Human Health and Disease. , 2019, , 119-132.		0
12	Tropomyosin isoforms have specific effects on the transcriptome of undifferentiated and differentiated B35 neuroblastoma cells. <i>FEBS Open Bio</i> , 2018, 8, 570-583.	2.3	4
13	Region-specific expression of circular RNAs in the mouse brain. <i>Neuroscience Letters</i> , 2018, 666, 44-47.	2.1	16
14	Multiple System Atrophy: Many Lessons from the Transcriptome. <i>Neuroscientist</i> , 2018, 24, 294-307.	3.5	7
15	Microexons: novel regulators of the transcriptome. <i>Journal of Human Transcriptome</i> , 2018, 2, 1-6.	1.0	9
16	Analysis of the circular RNA transcriptome in endometrial cancer. <i>Oncotarget</i> , 2018, 9, 5786-5796.	1.8	58
17	RNA sequencing reveals pronounced changes in the noncoding transcriptome of aging synaptosomes. <i>Neurobiology of Aging</i> , 2017, 56, 67-77.	3.1	17
18	Transcriptome landscape of long intergenic non-coding RNAs in endometrial cancer. <i>Gynecologic Oncology</i> , 2017, 147, 654-662.	1.4	55

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19	The emerging role of circular RNAs in transcriptome regulation. <i>Genomics</i> , 2017, 109, 401-407.	2.9	155
20	Non-coding transcriptome in brain aging. <i>Aging</i> , 2017, 9, 1943-1944.	3.1	5
21	LINC00507 Is Specifically Expressed in the Primate Cortex and Has Age-Dependent Expression Patterns. <i>Journal of Molecular Neuroscience</i> , 2016, 59, 431-439.	2.3	14
22	Characterization of circular <scp>RNA</scp>s landscape in multiple system atrophy brain. <i>Journal of Neurochemistry</i> , 2016, 139, 485-496.	3.9	79
23	The emerging role of long non-coding RNAs in endometrial cancer. <i>Cancer Genetics</i> , 2016, 209, 445-455.	0.4	39
24	Transcriptional regulation of long-term potentiation. <i>Neurogenetics</i> , 2016, 17, 201-210.	1.4	13
25	Strand-specific RNA-sequencing analysis of multiple system atrophy brain transcriptome. <i>Neuroscience</i> , 2016, 322, 234-250.	2.3	24
26	The Antisense Transcriptome and the Human Brain. <i>Journal of Molecular Neuroscience</i> , 2016, 58, 1-15.	2.3	12
27	RNA-Sequencing to Elucidate Early Patterns of Dysregulation Underlying the Onset of Alzheimerâ€™s Disease. <i>Methods in Molecular Biology</i> , 2016, 1303, 327-347.	0.9	5
28	Transcriptome analysis of grey and white matter cortical tissue in multiple system atrophy. <i>Neurogenetics</i> , 2015, 16, 107-122.	1.4	33
29	Long intervening non-coding RNA 00320 is human brain-specific and highly expressed in the cortical white matter. <i>Neurogenetics</i> , 2015, 16, 201-213.	1.4	18
30	High expression of long intervening non-coding RNA OLMALINC in the human cortical white matter is associated with regulation of oligodendrocyte maturation. <i>Molecular Brain</i> , 2015, 8, 2.	2.6	25
31	Long noncoding RNAs in TDP-43 and FUS/TLS-related frontotemporal lobar degeneration (FTLD). <i>Neurobiology of Disease</i> , 2015, 82, 445-454.	4.4	33
32	Conservation and tissue-specific transcription patterns of long noncoding RNAs. <i>Journal of Human Transcriptome</i> , 2015, 1, 2-9.	1.0	79
33	The role of transcriptional control in multiple system atrophy. <i>Neurobiology of Aging</i> , 2015, 36, 394-400.	3.1	10
34	The alternative splicing of the apolipoprotein E gene is unperturbed in the brains of Alzheimerâ€™s disease patients. <i>Molecular Biology Reports</i> , 2014, 41, 6365-6376.	2.3	13
35	Pathway Analysis of the Human Brain Transcriptome in Disease. <i>Journal of Molecular Neuroscience</i> , 2013, 51, 28-36.	2.3	17
36	RNA-Seq analysis of the parietal cortex in Alzheimer's disease reveals alternatively spliced isoforms related to lipid metabolism. <i>Neuroscience Letters</i> , 2013, 536, 90-95.	2.1	77

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37	Sequencing of hippocampal and cerebellar transcriptomes provides new insights into the complexity of gene regulation in the human brain. <i>Neuroscience Letters</i> , 2013, 541, 263-268.	2.1	8
38	Unique Transcriptome Patterns of the White and Grey Matter Corroborate Structural and Functional Heterogeneity in the Human Frontal Lobe. <i>PLoS ONE</i> , 2013, 8, e78480.	2.5	40
39	Strand-Specific RNA-Seq Provides Greater Resolution of Transcriptome Profiling. <i>Current Genomics</i> , 2013, 14, 173-181.	1.6	77
40	Alternative splicing of mRNA in the molecular pathology of neurodegenerative diseases. <i>Neurobiology of Aging</i> , 2012, 33, 1012.e11-1012.e24.	3.1	88
41	The Role of RNA Structure in Posttranscriptional Regulation of Gene Expression. <i>Journal of Genetics and Genomics</i> , 2012, 39, 535-543.	3.9	34
42	Single-Cell and Regional Gene Expression Analysis in Alzheimer's Disease. <i>Cellular and Molecular Neurobiology</i> , 2012, 32, 477-489.	3.3	2
43	Assessing Epigenetic Information. , 2011, , 173-181.		5
44	Understanding the pathogenesis of Alzheimer's disease: will RNA-Seq realize the promise of transcriptomics?. <i>Journal of Neurochemistry</i> , 2011, 116, 937-946.	3.9	65
45	Whole Transcriptome Sequencing Reveals Gene Expression and Splicing Differences in Brain Regions Affected by Alzheimer's Disease. <i>PLoS ONE</i> , 2011, 6, e16266.	2.5	266
46	Apoptosis screening of human chromosome 21 proteins reveals novel cell death regulators. <i>Molecular Biology Reports</i> , 2010, 37, 3381-3387.	2.3	10
47	Transcriptome profiling in neurodegenerative disease. <i>Journal of Neuroscience Methods</i> , 2010, 193, 189-202.	2.5	57
48	Functional analysis and identification of cis-regulatory elements of human chromosome 21 gene promoters. <i>Nucleic Acids Research</i> , 2010, 38, 6112-6123.	14.5	19
49	Screening of human gene promoter activities using transfected-cell arrays. <i>Gene</i> , 2010, 450, 48-54.	2.2	8
50	Comparative analysis of an experimental subcellular protein localization assay and in silico prediction methods. <i>Journal of Molecular Histology</i> , 2009, 40, 343-352.	2.2	3
51	Follistatin antagonizes transforming growth factor- $\beta$ -induced epithelial-mesenchymal transition in vitro: implications for murine palatal development supported by microarray analysis. <i>Differentiation</i> , 2008, 76, 404-416.	1.9	32
52	High-throughput mammalian two-hybrid screening for protein-protein interactions using transfected cell arrays. <i>BMC Genomics</i> , 2008, 9, 68.	2.8	25
53	Autoregulation of Th1-mediated inflammation by <i>twist1</i> . <i>Journal of Experimental Medicine</i> , 2008, 205, 1889-1901.	8.5	96
54	Oligonucleotide Fingerprinting of Arrayed Genomic DNA Sequences Using LNA-Modified Hybridization Probes. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2007, 10, 269-276.	1.1	3

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55	Assigning functions to genes—the main challenge of the post-genomics era. , 2007, 159, 115-129.		7
56	High-Throughput RNA Interference in Functional Genomics. , 2006, , 97-104.		9
57	Liquid-based hybridization assay with real-time detection in miniaturized array platforms. <i>New Biotechnology</i> , 2006, 23, 35-40.	2.7	3
58	Cell array-based intracellular localization screening reveals novel functional features of human chromosome 21 proteins. <i>BMC Genomics</i> , 2006, 7, 155.	2.8	31
59	A second generation radiation hybrid map to aid the assembly of the bovine genome sequence. <i>BMC Genomics</i> , 2006, 7, 283.	2.8	26
60	LNA-Modified Oligodeoxynucleotide Hybridization with DNA Microarrays Printed on Nanoporous Membrane Slides. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2006, 9, 591-597.	1.1	1
61	High-throughput subcellular protein localization using cell arrays. <i>Biochemical Society Transactions</i> , 2005, 33, 1407.	3.4	9
62	Functional genomics using high-throughput RNA interference. <i>Drug Discovery Today</i> , 2005, 10, 205-212.	6.4	44
63	Mouse protein arrays from a TH1 cell cDNA library for antibody screening and serum profiling. <i>Genomics</i> , 2005, 85, 285-296.	2.9	31
64	High-throughput gene silencing using cell arrays. <i>Oncogene</i> , 2004, 23, 8353-8358.	5.9	50
65	Establishment of T cell-specific and natural killer cell-specific unigene sets: towards high-throughput genomics of leukaemia. <i>International Journal of Immunogenetics</i> , 2004, 31, 253-257.	1.2	0
66	Multiplexed hybridizations of positively charge-tagged peptide nucleic acids detected by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2004, 18, 1821-1829.	1.5	10
67	Honeybee ( <i>Apis mellifera</i> L.) mrjp gene family: computational analysis of putative promoters and genomic structure of mrjp1, the gene coding for the most abundant protein of larval food. <i>Gene</i> , 2003, 303, 165-175.	2.2	32
68	Analysis of the Sequence Polymorphism within Class II Transactivator Gene Promoters. <i>Experimental and Clinical Immunogenetics</i> , 2001, 18, 199-205.	1.2	10
69	Expression of the H2-Ea gene is modulated by a polymorphic transcriptional enhancer. <i>Immunogenetics</i> , 1998, 48, 266-272.	2.4	10
70	Three alternatively spliced variants of the gene coding for the human bone morphogenetic protein-1. <i>Journal of Molecular Medicine</i> , 1998, 76, 141-146.	3.9	20
71	The Distribution of Variation in Regulatory Gene Segments, as Present in MHC Class II Promoters. <i>Genome Research</i> , 1998, 8, 124-134.	5.5	43
72	Polymorphic MHC class II promoters exhibit distinct expression pattern in various antigen-presenting cell lines. <i>Tissue Antigens</i> , 1997, 49, 99-106.	1.0	30

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73	Enhancer activity in the 5' untranslated region of the H2-Eb gene. Immunogenetics, 1997, 45, 432-435.	2.4	2
74	Analysis of mRNA expression for interleukin-1 genes on human testicular cells. Immunology Letters, 1995, 48, 139-143.	2.5	8
75	Analysis of mRNA for class I HLA on human gametogenic cells. Molecular Reproduction and Development, 1994, 38, 231-237.	2.0	31
76	In situ localization of HLA class I mRNA in human testis. Experimental and Clinical Immunogenetics, 1993, 10, 202-7.	1.2	5