

# Michael Janitz

## 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.

77  
papers

1,773  
citations

25  
h-index

40  
g-index

80  
ext. papers

2,075  
ext. citations

4.5  
avg, IF

4.82  
L-index

#	Paper	IF	Citations
77	RNA polyadenylation patterns in the human transcriptome.. <i>Gene</i> , <b>2022</b> , 816, 146133	3.8	0
76	Proteomics and Transcriptomics of the Hippocampus and Cortex in SUDEP and High-Risk SUDEP Patients. <i>Neurology</i> , <b>2021</b> , 96, e2639-e2652	6.5	9
75	Cell type-specific circular RNA expression in human glial cells. <i>Genomics</i> , <b>2020</b> , 112, 5265-5274	4.3	6
74	Analysis of the Circular Transcriptome in the Synaptosomes of Aged Mice. <i>Neuroscience</i> , <b>2020</b> , 449, 202-213	3.1	3
73	Cell Adhesion Molecules and Protein Synthesis Regulation in Neurons. <i>Frontiers in Molecular Neuroscience</i> , <b>2020</b> , 13, 592126	6.1	4
72	Identification of Specific Circular RNA Expression Patterns and MicroRNA Interaction Networks in Mesial Temporal Lobe Epilepsy. <i>Frontiers in Genetics</i> , <b>2020</b> , 11, 564301	4.5	6
71	Coding and non-coding transcriptome of mesial temporal lobe epilepsy: Critical role of small non-coding RNAs. <i>Neurobiology of Disease</i> , <b>2020</b> , 134, 104612	7.5	15
70	Neural circular transcriptomes across mammalian species. <i>Genomics</i> , <b>2020</b> , 112, 1162-1166	4.3	9
69	Circular RNAs in Human Health and Disease <b>2019</b> , 119-132		
68	Early transcriptome changes in response to chemical long-term potentiation induced via activation of synaptic NMDA receptors in mouse hippocampal neurons. <i>Genomics</i> , <b>2019</b> , 111, 1676-1686	4.3	1
67	Changes in circular RNA expression patterns during human foetal brain development. <i>Genomics</i> , <b>2019</b> , 111, 753-758	4.3	33
66	Tropomyosin isoforms have specific effects on the transcriptome of undifferentiated and differentiated B35 neuroblastoma cells. <i>FEBS Open Bio</i> , <b>2018</b> , 8, 570-583	2.7	0
65	Region-specific expression of circular RNAs in the mouse brain. <i>Neuroscience Letters</i> , <b>2018</b> , 666, 44-47	3.3	9
64	Analysis of the circular RNA transcriptome in endometrial cancer. <i>Oncotarget</i> , <b>2018</b> , 9, 5786-5796	3.3	44
63	Multiple System Atrophy: Many Lessons from the Transcriptome. <i>Neuroscientist</i> , <b>2018</b> , 24, 294-307	7.6	5
62	Microexons: novel regulators of the transcriptome <b>2018</b> , 2, 1-6		8
61	RNA sequencing reveals pronounced changes in the noncoding transcriptome of aging synaptosomes. <i>Neurobiology of Aging</i> , <b>2017</b> , 56, 67-77	5.6	13

60	Transcriptome landscape of long intergenic non-coding RNAs in endometrial cancer. <i>Gynecologic Oncology</i> , <b>2017</b> , 147, 654-662	4.9	36
59	The emerging role of circular RNAs in transcriptome regulation. <i>Genomics</i> , <b>2017</b> , 109, 401-407	4.3	112
58	RNA-Sequencing to Elucidate Early Patterns of Dysregulation Underlying the Onset of Alzheimer's Disease. <i>Methods in Molecular Biology</i> , <b>2016</b> , 1303, 327-47	1.4	5
57	Characterization of circular RNAs landscape in multiple system atrophy brain. <i>Journal of Neurochemistry</i> , <b>2016</b> , 139, 485-496	6	62
56	The emerging role of long non-coding RNAs in endometrial cancer. <i>Cancer Genetics</i> , <b>2016</b> , 209, 445-455	2.3	33
55	Transcriptional regulation of long-term potentiation. <i>Neurogenetics</i> , <b>2016</b> , 17, 201-210	3	7
54	Strand-specific RNA-sequencing analysis of multiple system atrophy brain transcriptome. <i>Neuroscience</i> , <b>2016</b> , 322, 234-50	3.9	19
53	The Antisense Transcriptome and the Human Brain. <i>Journal of Molecular Neuroscience</i> , <b>2016</b> , 58, 1-15	3.3	9
52	LINC00507 Is Specifically Expressed in the Primate Cortex and Has Age-Dependent Expression Patterns. <i>Journal of Molecular Neuroscience</i> , <b>2016</b> , 59, 431-9	3.3	13
51	Transcriptome analysis of grey and white matter cortical tissue in multiple system atrophy. <i>Neurogenetics</i> , <b>2015</b> , 16, 107-22	3	25
50	Long intervening non-coding RNA 00320 is human brain-specific and highly expressed in the cortical white matter. <i>Neurogenetics</i> , <b>2015</b> , 16, 201-13	3	16
49	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> , <b>2015</b> , 8, 2	4.5	23
48	Long noncoding RNAs in TDP-43 and FUS/TLS-related frontotemporal lobar degeneration (FTLD). <i>Neurobiology of Disease</i> , <b>2015</b> , 82, 445-454	7.5	27
47	Conservation and tissue-specific transcription patterns of long noncoding RNAs <b>2015</b> , 1, 2-9		56
46	Role of transcriptional control in multiple system atrophy. <i>Neurobiology of Aging</i> , <b>2015</b> , 36, 394-400	5.6	8
45	The alternative splicing of the apolipoprotein E gene is unperturbed in the brains of Alzheimer's disease patients. <i>Molecular Biology Reports</i> , <b>2014</b> , 41, 6365-76	2.8	9
44	Pathway analysis of the human brain transcriptome in disease. <i>Journal of Molecular Neuroscience</i> , <b>2013</b> , 51, 28-36	3.3	11
43	RNA-Seq analysis of the parietal cortex in Alzheimer's disease reveals alternatively spliced isoforms related to lipid metabolism. <i>Neuroscience Letters</i> , <b>2013</b> , 536, 90-5	3.3	55

42	Sequencing of hippocampal and cerebellar transcriptomes provides new insights into the complexity of gene regulation in the human brain. <i>Neuroscience Letters</i> , <b>2013</b> , 541, 263-8	3.3	7
41	Unique transcriptome patterns of the white and grey matter corroborate structural and functional heterogeneity in the human frontal lobe. <i>PLoS ONE</i> , <b>2013</b> , 8, e78480	3.7	35
40	Strand-Specific RNA-Seq Provides Greater Resolution of Transcriptome Profiling. <i>Current Genomics</i> , <b>2013</b> , 14, 173-81	2.6	62
39	Alternative splicing of mRNA in the molecular pathology of neurodegenerative diseases. <i>Neurobiology of Aging</i> , <b>2012</b> , 33, 1012.e11-24	5.6	76
38	The role of RNA structure in posttranscriptional regulation of gene expression. <i>Journal of Genetics and Genomics</i> , <b>2012</b> , 39, 535-43	4	26
37	Moving Towards Third-Generation Sequencing Technologies <b>2012</b> , 323-336		2
36	Single-cell and regional gene expression analysis in Alzheimer's disease. <i>Cellular and Molecular Neurobiology</i> , <b>2012</b> , 32, 477-89	4.6	2
35	Assessing Epigenetic Information <b>2011</b> , 173-181		2
34	Understanding the pathogenesis of Alzheimer's disease: will RNA-Seq realize the promise of transcriptomics?. <i>Journal of Neurochemistry</i> , <b>2011</b> , 116, 937-46	6	49
33	Whole transcriptome sequencing reveals gene expression and splicing differences in brain regions affected by Alzheimer's disease. <i>PLoS ONE</i> , <b>2011</b> , 6, e16266	3.7	213
32	Functional analysis and identification of cis-regulatory elements of human chromosome 21 gene promoters. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, 6112-23	20.1	18
31	Screening of human gene promoter activities using transfected-cell arrays. <i>Gene</i> , <b>2010</b> , 450, 48-54	3.8	8
30	Apoptosis screening of human chromosome 21 proteins reveals novel cell death regulators. <i>Molecular Biology Reports</i> , <b>2010</b> , 37, 3381-7	2.8	8
29	Transcriptome profiling in neurodegenerative disease. <i>Journal of Neuroscience Methods</i> , <b>2010</b> , 193, 189-202	3.0	50
28	Comparative analysis of an experimental subcellular protein localization assay and in silico prediction methods. <i>Journal of Molecular Histology</i> , <b>2009</b> , 40, 343-52	3.3	3
27	Follistatin antagonizes transforming growth factor-beta3-induced epithelial-mesenchymal transition in vitro: implications for murine palatal development supported by microarray analysis. <i>Differentiation</i> , <b>2008</b> , 76, 404-16	3.5	28
26	High-throughput mammalian two-hybrid screening for protein-protein interactions using transfected cell arrays. <i>BMC Genomics</i> , <b>2008</b> , 9, 68	4.5	24
25	Autoregulation of Th1-mediated inflammation by twist1. <i>Journal of Experimental Medicine</i> , <b>2008</b> , 205, 1889-901	16.6	75

24	<b>2008,</b>			13
23	Oligonucleotide fingerprinting of arrayed genomic DNA sequences using LNA-modified hybridization probes. <i>Combinatorial Chemistry and High Throughput Screening</i> , <b>2007</b> , 10, 269-76	1.3		2
22	Assigning functions to genes--the main challenge of the post-genomics era. <i>Reviews of Physiology, Biochemistry and Pharmacology</i> , <b>2007</b> , 159, 115-29	2.9		7
21	Cell array-based intracellular localization screening reveals novel functional features of human chromosome 21 proteins. <i>BMC Genomics</i> , <b>2006</b> , 7, 155	4.5		30
20	A second generation radiation hybrid map to aid the assembly of the bovine genome sequence. <i>BMC Genomics</i> , <b>2006</b> , 7, 283	4.5		23
19	LNA-modified oligodeoxynucleotide hybridization with DNA microarrays printed on nanoporous membrane slides. <i>Combinatorial Chemistry and High Throughput Screening</i> , <b>2006</b> , 9, 591-7	1.3		1
18	High-throughput RNA interference in functional genomics. <i>Handbook of Experimental Pharmacology</i> , <b>2006</b> , 97-104	3.2		7
17	Liquid-based hybridization assay with real-time detection in miniaturized array platforms. <i>New Biotechnology</i> , <b>2006</b> , 23, 35-40			3
16	Mouse protein arrays from a TH1 cell cDNA library for antibody screening and serum profiling. <i>Genomics</i> , <b>2005</b> , 85, 285-96	4.3		25
15	High-throughput subcellular protein localization using cell arrays. <i>Biochemical Society Transactions</i> , <b>2005</b> , 33, 1407-8	5.1		9
14	Functional genomics using high-throughput RNA interference. <i>Drug Discovery Today</i> , <b>2005</b> , 10, 205-12	8.8		43
13	High-throughput gene silencing using cell arrays. <i>Oncogene</i> , <b>2004</b> , 23, 8353-8	9.2		44
12	Establishment of T cell-specific and natural killer cell-specific unigene sets: towards high-throughput genomics of leukaemia. <i>International Journal of Immunogenetics</i> , <b>2004</b> , 31, 253-7			
11	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> , <b>2004</b> , 18, 1821-9	2.2		9
10	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> , <b>2003</b> , 303, 165-75	3.8		31
9	Analysis of the sequence polymorphism within class II transactivator gene promoters. <i>Experimental and Clinical Immunogenetics</i> , <b>2001</b> , 18, 199-205			9
8	Expression of the H2-Ea gene is modulated by a polymorphic transcriptional enhancer. <i>Immunogenetics</i> , <b>1998</b> , 48, 266-72	3.2		8
7	Three alternatively spliced variants of the gene coding for the human bone morphogenetic protein-1. <i>Journal of Molecular Medicine</i> , <b>1998</b> , 76, 141-6	5.5		15

6	The distribution of variation in regulatory gene segments, as present in MHC class II promoters. <i>Genome Research</i> , <b>1998</b> , 8, 124-34	9.7	40
5	Polymorphic MHC class II promoters exhibit distinct expression pattern in various antigen-presenting cell lines. <i>Tissue Antigens</i> , <b>1997</b> , 49, 99-106		27
4	Enhancer activity in the 5' untranslated region of the H2-Eb gene. <i>Immunogenetics</i> , <b>1997</b> , 45, 432-5	3.2	2
3	Analysis of mRNA expression for interleukin-1 genes on human testicular cells. <i>Immunology Letters</i> , <b>1995</b> , 48, 139-43	4.1	8
2	Analysis of mRNA for class I HLA on human gametogenic cells. <i>Molecular Reproduction and Development</i> , <b>1994</b> , 38, 231-7	2.6	31
1	In situ localization of HLA class I mRNA in human testis. <i>Experimental and Clinical Immunogenetics</i> , <b>1993</b> , 10, 202-7		5