

Michael Janitz

List of Publications by Citations

Source: <https://exaly.com/author-pdf/4730925/michael-janitz-publications-by-citations.pdf>

Version: 2024-04-23

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.

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	Whole transcriptome sequencing reveals gene expression and splicing differences in brain regions affected by Alzheimer's disease. <i>PLoS ONE</i> , 2011 , 6, e16266	3.7	213
76	The emerging role of circular RNAs in transcriptome regulation. <i>Genomics</i> , 2017 , 109, 401-407	4.3	112
75	Alternative splicing of mRNA in the molecular pathology of neurodegenerative diseases. <i>Neurobiology of Aging</i> , 2012 , 33, 1012.e11-24	5.6	76
74	Autoregulation of Th1-mediated inflammation by twist1. <i>Journal of Experimental Medicine</i> , 2008 , 205, 1889-901	16.6	75
73	Characterization of circular RNAs landscape in multiple system atrophy brain. <i>Journal of Neurochemistry</i> , 2016 , 139, 485-496	6	62
72	Strand-Specific RNA-Seq Provides Greater Resolution of Transcriptome Profiling. <i>Current Genomics</i> , 2013 , 14, 173-81	2.6	62
71	Conservation and tissue-specific transcription patterns of long noncoding RNAs 2015 , 1, 2-9		56
70	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, 90-5	3.3	55
69	Transcriptome profiling in neurodegenerative disease. <i>Journal of Neuroscience Methods</i> , 2010 , 193, 189-202	3.0	50
68	Understanding the pathogenesis of Alzheimer's disease: will RNA-Seq realize the promise of transcriptomics?. <i>Journal of Neurochemistry</i> , 2011 , 116, 937-46	6	49
67	High-throughput gene silencing using cell arrays. <i>Oncogene</i> , 2004 , 23, 8353-8	9.2	44
66	Analysis of the circular RNA transcriptome in endometrial cancer. <i>Oncotarget</i> , 2018 , 9, 5786-5796	3.3	44
65	Functional genomics using high-throughput RNA interference. <i>Drug Discovery Today</i> , 2005 , 10, 205-12	8.8	43
64	The distribution of variation in regulatory gene segments, as present in MHC class II promoters. <i>Genome Research</i> , 1998 , 8, 124-34	9.7	40
63	Transcriptome landscape of long intergenic non-coding RNAs in endometrial cancer. <i>Gynecologic Oncology</i> , 2017 , 147, 654-662	4.9	36
62	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	3.7	35
61	The emerging role of long non-coding RNAs in endometrial cancer. <i>Cancer Genetics</i> , 2016 , 209, 445-455	2.3	33

60	Changes in circular RNA expression patterns during human foetal brain development. <i>Genomics</i> , 2019 , 111, 753-758	4.3	33
59	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, 165-75	3.8	31
58	Analysis of mRNA for class I HLA on human gametogenic cells. <i>Molecular Reproduction and Development</i> , 1994 , 38, 231-7	2.6	31
57	Cell array-based intracellular localization screening reveals novel functional features of human chromosome 21 proteins. <i>BMC Genomics</i> , 2006 , 7, 155	4.5	30
56	Follistatin antagonizes transforming growth factor-beta3-induced epithelial-mesenchymal transition in vitro: implications for murine palatal development supported by microarray analysis. <i>Differentiation</i> , 2008 , 76, 404-16	3.5	28
55	Long noncoding RNAs in TDP-43 and FUS/TLS-related frontotemporal lobar degeneration (FTLD). <i>Neurobiology of Disease</i> , 2015 , 82, 445-454	7.5	27
54	Polymorphic MHC class II promoters exhibit distinct expression pattern in various antigen-presenting cell lines. <i>Tissue Antigens</i> , 1997 , 49, 99-106		27
53	The role of RNA structure in posttranscriptional regulation of gene expression. <i>Journal of Genetics and Genomics</i> , 2012 , 39, 535-43	4	26
52	Transcriptome analysis of grey and white matter cortical tissue in multiple system atrophy. <i>Neurogenetics</i> , 2015 , 16, 107-22	3	25
51	Mouse protein arrays from a TH1 cell cDNA library for antibody screening and serum profiling. <i>Genomics</i> , 2005 , 85, 285-96	4.3	25
50	High-throughput mammalian two-hybrid screening for protein-protein interactions using transfected cell arrays. <i>BMC Genomics</i> , 2008 , 9, 68	4.5	24
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> , 2015 , 8, 2	4.5	23
48	A second generation radiation hybrid map to aid the assembly of the bovine genome sequence. <i>BMC Genomics</i> , 2006 , 7, 283	4.5	23
47	Strand-specific RNA-sequencing analysis of multiple system atrophy brain transcriptome. <i>Neuroscience</i> , 2016 , 322, 234-50	3.9	19
46	Functional analysis and identification of cis-regulatory elements of human chromosome 21 gene promoters. <i>Nucleic Acids Research</i> , 2010 , 38, 6112-23	20.1	18
45	Long intervening non-coding RNA 00320 is human brain-specific and highly expressed in the cortical white matter. <i>Neurogenetics</i> , 2015 , 16, 201-13	3	16
44	Three alternatively spliced variants of the gene coding for the human bone morphogenetic protein-1. <i>Journal of Molecular Medicine</i> , 1998 , 76, 141-6	5.5	15
43	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	7.5	15

42	RNA sequencing reveals pronounced changes in the noncoding transcriptome of aging synaptosomes. <i>Neurobiology of Aging</i> , 2017 , 56, 67-77	5.6	13
41	LINC00507 Is Specifically Expressed in the Primate Cortex and Has Age-Dependent Expression Patterns. <i>Journal of Molecular Neuroscience</i> , 2016 , 59, 431-9	3.3	13
40	2008 ,		13
39	Pathway analysis of the human brain transcriptome in disease. <i>Journal of Molecular Neuroscience</i> , 2013 , 51, 28-36	3.3	11
38	Region-specific expression of circular RNAs in the mouse brain. <i>Neuroscience Letters</i> , 2018 , 666, 44-47	3.3	9
37	The Antisense Transcriptome and the Human Brain. <i>Journal of Molecular Neuroscience</i> , 2016 , 58, 1-15	3.3	9
36	The alternative splicing of the apolipoprotein E gene is unperturbed in the brains of Alzheimer's disease patients. <i>Molecular Biology Reports</i> , 2014 , 41, 6365-76	2.8	9
35	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, 1821-9	2.2	9
34	High-throughput subcellular protein localization using cell arrays. <i>Biochemical Society Transactions</i> , 2005 , 33, 1407-8	5.1	9
33	Analysis of the sequence polymorphism within class II transactivator gene promoters. <i>Experimental and Clinical Immunogenetics</i> , 2001 , 18, 199-205		9
32	Proteomics and Transcriptomics of the Hippocampus and Cortex in SUDEP and High-Risk SUDEP Patients. <i>Neurology</i> , 2021 , 96, e2639-e2652	6.5	9
31	Neural circular transcriptomes across mammalian species. <i>Genomics</i> , 2020 , 112, 1162-1166	4.3	9
30	Role of transcriptional control in multiple system atrophy. <i>Neurobiology of Aging</i> , 2015 , 36, 394-400	5.6	8
29	Screening of human gene promoter activities using transfected-cell arrays. <i>Gene</i> , 2010 , 450, 48-54	3.8	8
28	Apoptosis screening of human chromosome 21 proteins reveals novel cell death regulators. <i>Molecular Biology Reports</i> , 2010 , 37, 3381-7	2.8	8
27	Expression of the H2-Ea gene is modulated by a polymorphic transcriptional enhancer. <i>Immunogenetics</i> , 1998 , 48, 266-72	3.2	8
26	Analysis of mRNA expression for interleukin-1 genes on human testicular cells. <i>Immunology Letters</i> , 1995 , 48, 139-43	4.1	8
25	Microexons: novel regulators of the transcriptome 2018 , 2, 1-6		8

24	Transcriptional regulation of long-term potentiation. <i>Neurogenetics</i> , 2016 , 17, 201-210	3	7
23	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, 263-8	3.3	7
22	Assigning functions to genes--the main challenge of the post-genomics era. <i>Reviews of Physiology, Biochemistry and Pharmacology</i> , 2007 , 159, 115-29	2.9	7
21	High-throughput RNA interference in functional genomics. <i>Handbook of Experimental Pharmacology</i> , 2006 , 97-104	3.2	7
20	Cell type-specific circular RNA expression in human glial cells. <i>Genomics</i> , 2020 , 112, 5265-5274	4.3	6
19	Identification of Specific Circular RNA Expression Patterns and MicroRNA Interaction Networks in Mesial Temporal Lobe Epilepsy. <i>Frontiers in Genetics</i> , 2020 , 11, 564301	4.5	6
18	RNA-Sequencing to Elucidate Early Patterns of Dysregulation Underlying the Onset of Alzheimer's Disease. <i>Methods in Molecular Biology</i> , 2016 , 1303, 327-47	1.4	5
17	In situ localization of HLA class I mRNA in human testis. <i>Experimental and Clinical Immunogenetics</i> , 1993 , 10, 202-7		5
16	Multiple System Atrophy: Many Lessons from the Transcriptome. <i>Neuroscientist</i> , 2018 , 24, 294-307	7.6	5
15	Cell Adhesion Molecules and Protein Synthesis Regulation in Neurons. <i>Frontiers in Molecular Neuroscience</i> , 2020 , 13, 592126	6.1	4
14	Comparative analysis of an experimental subcellular protein localization assay and in silico prediction methods. <i>Journal of Molecular Histology</i> , 2009 , 40, 343-52	3.3	3
13	Liquid-based hybridization assay with real-time detection in miniaturized array platforms. <i>New Biotechnology</i> , 2006 , 23, 35-40		3
12	Analysis of the Circular Transcriptome in the Synaptosomes of Aged Mice. <i>Neuroscience</i> , 2020 , 449, 202-213	3.1	3
11	Moving Towards Third-Generation Sequencing Technologies 2012 , 323-336		2
10	Single-cell and regional gene expression analysis in Alzheimer's disease. <i>Cellular and Molecular Neurobiology</i> , 2012 , 32, 477-89	4.6	2
9	Assessing Epigenetic Information 2011 , 173-181		2
8	Enhancer activity in the 5' untranslated region of the H2-Eb gene. <i>Immunogenetics</i> , 1997 , 45, 432-5	3.2	2
7	Oligonucleotide fingerprinting of arrayed genomic DNA sequences using LNA-modified hybridization probes. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2007 , 10, 269-76	1.3	2

6	LNA-modified oligodeoxynucleotide hybridization with DNA microarrays printed on nanoporous membrane slides. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2006 , 9, 591-7	1.3	1
5	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	4.3	1
4	Tropomyosin isoforms have specific effects on the transcriptome of undifferentiated and differentiated B35 neuroblastoma cells. <i>FEBS Open Bio</i> , 2018 , 8, 570-583	2.7	0
3	RNA polyadenylation patterns in the human transcriptome.. <i>Gene</i> , 2022 , 816, 146133	3.8	0
2	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, 253-7		
1	Circular RNAs in Human Health and Disease 2019 , 119-132		