

# Jason M Johnson

## List of Publications by Year in descending order

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Version: 2024-02-01

28  
papers

11,839  
citations

218677

26  
h-index

501196

28  
g-index

28  
all docs

28  
docs citations

28  
times ranked

18885  
citing authors

#	ARTICLE	IF	CITATIONS
1	Microarray analysis shows that some microRNAs downregulate large numbers of target mRNAs. <i>Nature</i> , 2005, 433, 769-773.	27.8	4,435
2	Genome-Wide Survey of Human Alternative Pre-mRNA Splicing with Exon Junction Microarrays. <i>Science</i> , 2003, 302, 2141-2144.	12.6	1,297
3	Mapping the Genetic Architecture of Gene Expression in Human Liver. <i>PLoS Biology</i> , 2008, 6, e107.	5.6	872
4	Position-specific chemical modification of siRNAs reduces "off-target" transcript silencing. <i>Rna</i> , 2006, 12, 1197-1205.	3.5	686
5	Plasma MicroRNAs as Sensitive and Specific Biomarkers of Tissue Injury. <i>Clinical Chemistry</i> , 2009, 55, 1977-1983.	3.2	599
6	A quantitative atlas of polyadenylation in five mammals. <i>Genome Research</i> , 2012, 22, 1173-1183.	5.5	557
7	Transcripts Targeted by the MicroRNA-16 Family Cooperatively Regulate Cell Cycle Progression. <i>Molecular and Cellular Biology</i> , 2007, 27, 2240-2252.	2.3	516
8	A postnatal switch of CELF and MBNL proteins reprograms alternative splicing in the developing heart. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 20333-20338.	7.1	433
9	Regulation of RNA splicing by the methylation-dependent transcriptional repressor methyl-CpG binding protein 2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 17551-17558.	7.1	413
10	Simple, quantitative primer-extension PCR assay for direct monitoring of microRNAs and short-interfering RNAs. <i>Rna</i> , 2005, 11, 1737-1744.	3.5	397
11	Expression of 24,426 human alternative splicing events and predicted cis regulation in 48 tissues and cell lines. <i>Nature Genetics</i> , 2008, 40, 1416-1425.	21.4	272
12	Digital transcriptome profiling using selective hexamer priming for cDNA synthesis. <i>Nature Methods</i> , 2009, 6, 647-649.	19.0	160
13	Global Survey of Genomic Imprinting by Transcriptome Sequencing. <i>Current Biology</i> , 2008, 18, 1735-1741.	3.9	154
14	Global regulation of alternative splicing during myogenic differentiation. <i>Nucleic Acids Research</i> , 2010, 38, 7651-7664.	14.5	135
15	Definition, conservation and epigenetics of housekeeping and tissue-enriched genes. <i>BMC Genomics</i> , 2009, 10, 269.	2.8	134
16	Digital Genome-Wide ncRNA Expression, Including SnoRNAs, across 11 Human Tissues Using PolyA-Neutral Amplification. <i>PLoS ONE</i> , 2010, 5, e11779.	2.5	108
17	Expression of Alternatively Spliced Sodium Channel $\alpha$ -Subunit Genes. <i>Journal of Biological Chemistry</i> , 2004, 279, 46234-46241.	3.4	104
18	Pathway and gene-set activation measurement from mRNA expression data: the tissue distribution of human pathways. <i>Genome Biology</i> , 2006, 7, R93.	9.6	93

#	ARTICLE	IF	CITATIONS
19	A comprehensive transcript index of the human genome generated using microarrays and computational approaches. <i>Genome Biology</i> , 2004, 5, R73.	9.6	92
20	Optimization of oligonucleotide arrays and RNA amplification protocols for analysis of transcript structure and alternative splicing. <i>Genome Biology</i> , 2003, 4, R66.	9.6	70
21	PDE4B5, a Novel, Super-Short, Brain-Specific cAMP Phosphodiesterase-4 Variant Whose Isoform-Specifying N-Terminal Region Is Identical to That of cAMP Phosphodiesterase-4D6 (PDE4D6). <i>Journal of Pharmacology and Experimental Therapeutics</i> , 2007, 322, 600-609.	2.5	65
22	Evolutionarily conserved and diverged alternative splicing events show different expression and functional profiles. <i>Nucleic Acids Research</i> , 2005, 33, 5659-5666.	14.5	62
23	Characteristics of mismatch repair deficiency in sarcomas. <i>Modern Pathology</i> , 2019, 32, 977-987.	5.5	49
24	DNA copy number, including telomeres and mitochondria, assayed using next-generation sequencing. <i>BMC Genomics</i> , 2010, 11, 244.	2.8	45
25	ACC2 Is Expressed at High Levels Human White Adipose and Has an Isoform with a Novel N-Terminus. <i>PLoS ONE</i> , 2009, 4, e4369.	2.5	32
26	Genetic validation of whole-transcriptome sequencing for mapping expression affected by cis-regulatory variation. <i>BMC Genomics</i> , 2010, 11, 473.	2.8	29
27	Exon and junction microarrays detect widespread mouse strain- and sex-bias expression differences. <i>BMC Genomics</i> , 2008, 9, 273.	2.8	19
28	Clinical Pan-Cancer Assessment of Mismatch Repair Deficiency Using Tumor-Only, Targeted Next-Generation Sequencing. <i>JCO Precision Oncology</i> , 2020, 4, 1084-1097.	3.0	11