

Charles Joel McManus

List of Publications by Year in descending order

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Version: 2024-02-01

34
papers

2,359
citations

279798

23
h-index

395702

33
g-index

39
all docs

39
docs citations

39
times ranked

3566
citing authors

#	ARTICLE	IF	CITATIONS
1	Regulatory divergence in <i>Drosophila</i> revealed by mRNA-seq. <i>Genome Research</i> , 2010, 20, 816-825.	5.5	385
2	RNA structure and the mechanisms of alternative splicing. <i>Current Opinion in Genetics and Development</i> , 2011, 21, 373-379.	3.3	222
3	Ribosome profiling reveals post-transcriptional buffering of divergent gene expression in yeast. <i>Genome Research</i> , 2014, 24, 422-430.	5.5	195
4	Tempo and mode of regulatory evolution in <i>Drosophila</i> . <i>Genome Research</i> , 2014, 24, 797-808.	5.5	177
5	Mod-seq: high-throughput sequencing for chemical probing of RNA structure. <i>Rna</i> , 2014, 20, 713-720.	3.5	167
6	Structural analyses of NEAT1 lncRNAs suggest long-range RNA interactions that may contribute to paraspeckle architecture. <i>Nucleic Acids Research</i> , 2018, 46, 3742-3752.	14.5	125
7	U2 ^{â€} U6 RNA folding reveals a group II intron-like domain and a four-helix junction. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 1237-1242.	8.2	123
8	DNA copy number evolution in <i>Drosophila</i> cell lines. <i>Genome Biology</i> , 2014, 15, R70.	8.8	96
9	Conserved non-AUG uORFs revealed by a novel regression analysis of ribosome profiling data. <i>Genome Research</i> , 2018, 28, 214-222.	5.5	93
10	Global analysis of <i>trans</i> -splicing in <i>Drosophila</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 12975-12979.	7.1	92
11	Genome-wide analysis of the skeletogenic gene regulatory network of sea urchins. <i>Development (Cambridge)</i> , 2014, 141, 950-961.	2.5	82
12	Next-generation analysis of gene expression regulation â€ comparing the roles of synthesis and degradation. <i>Molecular BioSystems</i> , 2015, 11, 2680-2689.	2.9	82
13	Circuit diversification in a biofilm regulatory network. <i>PLoS Pathogens</i> , 2019, 15, e1007787.	4.7	79
14	Competing RNA secondary structures are required for mutually exclusive splicing of the <i>Dscam</i> exon 6 cluster. <i>Rna</i> , 2011, 17, 222-229.	3.5	54
15	Impacts of uORF codon identity and position on translation regulation. <i>Nucleic Acids Research</i> , 2019, 47, 9358-9367.	14.5	46
16	Genomic Imprinting Absent in <i>Drosophila melanogaster</i> Adult Females. <i>Cell Reports</i> , 2012, 2, 69-75.	6.4	44
17	Tales of diversity: Genomic and morphological characteristics of forty-six <i>Arthrobacter</i> phages. <i>PLoS ONE</i> , 2017, 12, e0180517.	2.5	38
18	Roles of <i>Candida albicans</i> Mig1 and Mig2 in glucose repression, pathogenicity traits, and SNF1 essentiality. <i>PLoS Genetics</i> , 2020, 16, e1008582.	3.5	38

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19	Molecular Mechanisms and Evolutionary Processes Contributing to Accelerated Divergence of Gene Expression on the <i>Drosophila</i> X Chromosome. <i>Molecular Biology and Evolution</i> , 2015, 32, 2605-2615.	8.9	35
20	Evolution of splicing regulatory networks in <i>Drosophila</i> . <i>Genome Research</i> , 2014, 24, 786-796.	5.5	34
21	Isoform-level ribosome occupancy estimation guided by transcript abundance with Ribomap. <i>Bioinformatics</i> , 2016, 32, 1880-1882.	4.1	31
22	A dynamic bulge in the U6 RNA internal stem-loop functions in spliceosome assembly and activation. <i>Rna</i> , 2007, 13, 2252-2265.	3.5	25
23	Identification of the binding site of Rlp7 on assembling 60S ribosomal subunits in <i>Saccharomyces cerevisiae</i> . <i>Rna</i> , 2013, 19, 1639-1647.	3.5	23
24	Accurate Recovery of Ribosome Positions Reveals Slow Translation of Wobble-Pairing Codons in Yeast. <i>Journal of Computational Biology</i> , 2017, 24, 486-500.	1.6	22
25	Mod-seq. <i>Methods in Enzymology</i> , 2015, 558, 125-152.	1.0	9
26	Exploring Ribosome Positioning on Translating Transcripts with Ribosome Profiling. <i>Methods in Molecular Biology</i> , 2016, 1358, 71-97.	0.9	9
27	Control of translation by eukaryotic mRNA transcript leaders—Insights from high-throughput assays and computational modeling. <i>Wiley Interdisciplinary Reviews RNA</i> , 2021, 12, e1623.	6.4	9
28	Quantitative mapping of mRNA 3' ends in <i>Pseudomonas aeruginosa</i> reveals a pervasive role for premature 3' end formation in response to azithromycin. <i>PLoS Genetics</i> , 2021, 17, e1009634.	3.5	7
29	Using the Ribodeblur pipeline to recover A-sites from yeast ribosome profiling data. <i>Methods</i> , 2018, 137, 67-70.	3.8	3
30	uORF-seq: A Machine Learning-Based Approach to the Identification of Upstream Open Reading Frames in Yeast. <i>Methods in Molecular Biology</i> , 2021, 2252, 313-329.	0.9	3
31	Accurate Recovery of Ribosome Positions Reveals Slow Translation of Wobble-Pairing Codons in Yeast. <i>Lecture Notes in Computer Science</i> , 2016, , 37-52.	1.3	3
32	High-Throughput Quantitation of Yeast uORF Regulatory Impacts Using FACS-uORF. <i>Methods in Molecular Biology</i> , 2022, 2404, 331-351.	0.9	2
33	Multiplexed Analysis of Human uORF Regulatory Functions During the ISR Using PoLib-Seq. <i>Methods in Molecular Biology</i> , 2022, 2428, 41-62.	0.9	1
34	Getting the Message Out. <i>Molecular Cell</i> , 2008, 31, 4-6.	9.7	0