Matthew N McCall

List of Publications by Year
in descending order

36	1,549	516681	377849
papers	citations	16	34
		h-index	g-index

50	50	50	3577
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Autoregressive modeling and diagnostics for qPCR amplification. Bioinformatics, 2021, 36, 5386-5391.	4.1	0
2	Spatial Proteomic Approach to Characterize Skeletal Muscle Myofibers. Journal of Proteome Research, 2021, 20, 888-894.	3.7	7
3	Airway Gene Expression Correlates of Respiratory Syncytial Virus Disease Severity and Microbiome Composition in Infants. Journal of Infectious Diseases, 2021, 223, 1639-1649.	4.0	17
4	The effect of tissue composition on gene co-expression. Briefings in Bioinformatics, 2021, 22, 127-139.	6.5	25
5	Airway gene-expression classifiers for respiratory syncytial virus (RSV) disease severity in infants. BMC Medical Genomics, 2021, 14, 57.	1.5	5
6	Single cell RNA-seq analysis of the flexor digitorum brevis mouse myofibers. Skeletal Muscle, 2021, 11, 13.	4.2	6
7	The role of P2Y12 in the kinetics of microglial self-renewal and maturation in the adult visual cortex in vivo. ELife, 2021, 10, .	6.0	19
8	The effect of air pollution on the transcriptomics of the immune response to respiratory infection. Scientific Reports, 2021, 11, 19436.	3.3	7
9	Tissue, age, sex, and disease patterns of matrisome expression in GTEx transcriptome data. Scientific Reports, 2021, 11, 21549.	3.3	4
10	Gene network modeling via TopNet reveals functional dependencies between diverse tumor-critical mediator genes. Cell Reports, 2021, 37, 110136.	6.4	1
11	A systems genomics approach uncovers molecular associates of RSV severity. PLoS Computational Biology, 2021, 17, e1009617.	3.2	3
12	Multiple imputation and direct estimation for qPCR data with non-detects. BMC Bioinformatics, 2020, 21, 545.	2.6	3
13	Consistent RNA sequencing contamination in GTEx and other data sets. Nature Communications, 2020, 11, 1933.	12.8	43
14	Cardioprotection by the mitochondrial unfolded protein response requires ATF5. American Journal of Physiology - Heart and Circulatory Physiology, 2019, 317, H472-H478.	3.2	90
15	Identification of the novel *Ido1* imprinted locus and its potential epigenetic role in pregnancy loss. Human Molecular Genetics, 2019, 28, 662-674.	2.9	11
16	Aims, Study Design, and Enrollment Results From the Assessing Predictors of Infant Respiratory Syncytial Virus Effects and Severity Study. JMIR Research Protocols, 2019, 8, e12907.	1.0	9
17	Big Strides in Cellular MicroRNA Expression. Trends in Genetics, 2018, 34, 165-167.	6.7	32
18	xMD-miRNA-seq to generate near in vivo miRNA expression estimates in colon epithelial cells. Scientific Reports, 2018, 8, 9783.	3.3	10

#	Article	IF	Citations
19	Systematic exploration of cell morphological phenotypes associated with a transcriptomic query. Nucleic Acids Research, 2018, 46, e116-e116.	14.5	42
20	<i>Kras</i> and <i>Tp53</i> Mutations Cause Cholangiocyte- and Hepatocyte-Derived Cholangiocarcinoma. Cancer Research, 2018, 78, 4445-4451.	0.9	79
21	Toward the human cellular microRNAome. Genome Research, 2017, 27, 1769-1781.	5.5	142
22	Complex Sources of Variation in Tissue Expression Data: Analysis of the GTEx Lung Transcriptome. American Journal of Human Genetics, 2016, 99, 624-635.	6.2	65
23	A benchmark for microRNA quantification algorithms using the OpenArray platform. BMC Bioinformatics, 2016, 17, 138.	2.6	6
24	A microRNA biomarker of hepatocellular carcinoma recurrence following liver transplantation accounting for within-patient heterogeneity. BMC Medical Genomics, 2016, 9, 18.	1.5	16
25	On non-detects in qPCR data. Bioinformatics, 2014, 30, 2310-2316.	4.1	157
26	Lessons from miR-143/145: the importance of cell-type localization of miRNAs. Nucleic Acids Research, 2014, 42, 7528-7538.	14.5	185
27	The Gene Expression Barcode 3.0: improved data processing and mining tools. Nucleic Acids Research, 2014, 42, D938-D943.	14.5	69
28	A Critical Evaluation of microRNA Biomarkers in Non-Neoplastic Disease. PLoS ONE, 2014, 9, e89565.	2.5	135
29	Estimation of Gene Regulatory Networks. Postdoc Journal, 2013, 1, 60-69.	0.4	2
30	fRMA ST: frozen robust multiarray analysis for Affymetrix Exon and Gene ST arrays. Bioinformatics, 2012, 28, 3153-3154.	4.1	39
31	Affymetrix GeneChip microarray preprocessing for multivariate analyses. Briefings in Bioinformatics, 2012, 13, 536-546.	6.5	17
32	Thawing Frozen Robust Multi-array Analysis (fRMA). BMC Bioinformatics, 2011, 12, 369.	2.6	38
33	MicroRNA profiling of diverse endothelial cell types. BMC Medical Genomics, 2011, 4, 78.	1.5	88
34	The Gene Expression Barcode: leveraging public data repositories to begin cataloging the human and murine transcriptomes. Nucleic Acids Research, 2011, 39, D1011-D1015.	14.5	156
35	Fitting Boolean Networks from Steady State Perturbation Data. Statistical Applications in Genetics and Molecular Biology, 2011, 10, .	0.6	10
36	miRcomp-Shiny: Interactive assessment of qPCR-based microRNA quantification and quality control algorithms. F1000Research, 0, 6, 2046.	1.6	1