Tim R Mercer

List of Publications by Year
in descending order

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Version: 2024-02-01

80	23,514	57631	62479
papers	citations	44 h-index	80 g-index

93	93	93	38047
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Emerging technologies and their impact on regulatory science. Experimental Biology and Medicine, 2022, 247, 1-75.	1.1	22
2	The splicing effect of variants at branchpoint elements in cancer genes. Genetics in Medicine, 2022, 24, 398-409.	1.1	9
3	Using synthetic chromosome controls to evaluate the sequencing of difficult regions within the human genome. Genome Biology, 2022, 23, 19.	3.8	4
4	A clinical laboratoryâ€“developed LSC17 stemness score assay for rapid risk assessment of patients with acute myeloid leukemia. Blood Advances, 2022, 6, 1064-1073.	2.5	11
5	The potential of long noncoding RNA therapies. Trends in Pharmacological Sciences, 2022, 43, 269-280.	4.0	28
6	ADRAM is an experience-dependent long noncoding RNA that drives fear extinction through a direct interaction with the chaperone protein 14-3-3. Cell Reports, 2022, 38, 110546.	2.9	19
7	Towards accurate and reliable resolution of structural variants for clinical diagnosis. Genome Biology, 2022, 23, 68.	3.8	34
8	Ultra-deep sequencing data from a liquid biopsy proficiency study demonstrating analytic validity. Scientific Data, 2022, 9, 170.	2.4	4
9	Evaluating the analytical validity of circulating tumor DNA sequencing assays for precision oncology. Nature Biotechnology, 2021, 39, 1115-1128.	9.4	126
10	Cross-oncopanel study reveals high sensitivity and accuracy with overall analytical performance depending on genomic regions. Genome Biology, 2021, 22, 109.	3.8	20
11	Testing at scale during the COVID-19 pandemic. Nature Reviews Genetics, 2021, 22, 415-426.	7.7	261
12	Long-read cDNA sequencing identifies functional pseudogenes in the human transcriptome. Genome Biology, 2021, 22, 146.	3.8	26
13	Toward best practice in cancer mutation detection with whole-genome and whole-exome sequencing. Nature Biotechnology, 2021, 39, 1141-1150.	9.4	66
14	Establishing community reference samples, data and call sets for benchmarking cancer mutation detection using whole-genome sequencing. Nature Biotechnology, 2021, 39, 1151-1160.	9.4	39
15	Chimeric synthetic reference standards enable cross-validation of positive and negative controls in SARS-CoV-2 molecular tests. Scientific Reports, 2021, 11, 2636.	1.6	2
16	The Sequencing Quality Control 2 study: establishing community standards for sequencing in precision medicine. Genome Biology, 2021, 22, 306.	3.8	7
17	Advancing NGS quality control to enable measurement of actionable mutations in circulating tumor DNA. Cell Reports Methods, 2021, 1, 100106.	1.4	9
18	Reporting guidelines for human microbiome research: the STORMS checklist. Nature Medicine, 2021, 27, 1885-1892.	15.2	170

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19	A universal and independent synthetic DNA ladder for the quantitative measurement of genomic features. Nature Communications, 2020, 11, 3609.	5.8	7
20	Lymphoma Driver Mutations in the Pathogenic Evolution of an Iconic Human Autoantibody. Cell, 2020, 180, 878-894.e19.	13.5	82
21	Use of synthetic DNA spike-in controls (sequins) for human genome sequencing. Nature Protocols, 2019, 14, 2119-2151.	5.5	22
22	Crizotinib and Surgery for Long-Term Disease Control in Children and Adolescents With ALK-Positive Inflammatory Myofibroblastic Tumors. JCO Precision Oncology, 2019, 3, 1-11.	1.5	25
23	Targeted, High-Resolution RNA Sequencing of Non-coding Genomic Regions Associated With Neuropsychiatric Functions. Frontiers in Genetics, 2019, 10, 309.	1.1	28
24	TMPRSS2â€ERG fusions linked to prostate cancer racial health disparities: A focus on Africa. Prostate, 2019, 79, 1191-1196.	1.2	28
25	Natural and Regenerated Saltmarshes Exhibit Similar Soil and Belowground Organic Carbon Stocks, Root Production and Soil Respiration. Ecosystems, 2019, 22, 1803-1822.	1.6	25
26	Diagnosis of fusion genes using targeted RNA sequencing. Nature Communications, 2019, 10, 1388.	5.8	122
27	Chiral DNA sequences as commutable controls for clinical genomics. Nature Communications, 2019, 10, 1342.	5.8	11
28	Universal Alternative Splicing of Noncoding Exons. Cell Systems, 2018, 6, 245-255.e5.	2.9	110
29	Machine learning annotation of human branchpoints. Bioinformatics, 2018, 34, 920-927.	1.8	52
30	A 60-GHz 144-Element Phased-Array Transceiver for Backhaul Application. IEEE Journal of Solid-State Circuits, 2018, 53, 3640-3659.	3.5	81
31	Synthetic microbe communities provide internal reference standards for metagenome sequencing and analysis. Nature Communications, 2018, 9, 3096.	5.8	81
32	Reference standards for next-generation sequencing. Nature Reviews Genetics, 2017, 18, 473-484.	7.7	194
33	The Dimensions, Dynamics, and Relevance of the Mammalian Noncoding Transcriptome. Trends in Genetics, 2017, 33, 464-478.	2.9	181
34	Phosphoproteomic Profiling Reveals ALK and MET as Novel Actionable Targets across Synovial Sarcoma Subtypes. Cancer Research, 2017, 77, 4279-4292.	0.4	31
35	ANAQUIN: a software toolkit for the analysis of spike-in controls for next generation sequencing. Bioinformatics, 2017, 33, 1723-1724.	1.8	17
36	Long Noncoding RNAs CUPID1 and CUPID2 Mediate Breast Cancer Risk at 11q13 by Modulating the Response to DNA Damage. American Journal of Human Genetics, 2017, 101, 255-266.	2.6	77

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37	Intergenic disease-associated regions are abundant in novel transcripts. Genome Biology, 2017, 18, 241.	3.8	45
38	Improved definition of the mouse transcriptome via targeted RNA sequencing. Genome Research, 2016, 26, 705-716.	2.4	33
39	Representing genetic variation with synthetic DNA standards. Nature Methods, 2016, 13, 784-791.	9.0	37
40	Spliced synthetic genes as internal controls in RNA sequencing experiments. Nature Methods, 2016, 13, 792-798.	9.0	123
41	Genome-wide discovery of human splicing branchpoints. Genome Research, 2015, 25, 290-303.	2.4	222
42	Integrative analysis of 111 reference human epigenomes. Nature, 2015, 518, 317-330.	13.7	5,653
43	Quantitative gene profiling of long noncoding RNAs with targeted RNA sequencing. Nature Methods, 2015, 12, 339-342.	9.0	155
44	Extracellular Vesicles from Neural Stem Cells Transfer IFN-Î³ via Ifngr1 to Activate Stat1 Signaling in Target Cells. Molecular Cell, 2014, 56, 609.	4.5	3
45	Targeted sequencing for gene discovery and quantification using RNA CaptureSeq. Nature Protocols, 2014, 9, 989-1009.	5.5	171
46	Extracellular Vesicles from Neural Stem Cells Transfer IFN-Î³ via Ifngr1 to Activate Stat1 Signaling in Target Cells. Molecular Cell, 2014, 56, 193-204.	4.5	258
47	Saccharopolyspora erythraeaâ€™sgenome is organised in high-order transcriptional regions mediated by targeted degradation at the metabolic switch. BMC Genomics, 2013, 14, 15.	1.2	33
48	Understanding the regulatory and transcriptional complexity of the genome through structure. Genome Research, 2013, 23, 1081-1088.	2.4	77
49	Mapping of Mitochondrial RNA-Protein Interactions by Digital RNase Footprinting. Cell Reports, 2013, 5, 839-848.	2.9	36
50	DNase Iâ€“hypersensitive exons colocalize with promoters and distal regulatory elements. Nature Genetics, 2013, 45, 852-859.	9.4	112
51	Structure and function of long noncoding RNAs in epigenetic regulation. Nature Structural and Molecular Biology, 2013, 20, 300-307.	3.6	1,325
52	Re-annotation of the Saccharopolyspora erythraea genome using a systems biology approach. BMC Genomics, 2013, 14, 699.	1.2	21
53	The human mitochondrial transcriptome and the RNAâ€binding proteins that regulate its expression. Wiley Interdisciplinary Reviews RNA, 2012, 3, 675-695.	3.2	88
54	Targeted RNA sequencing reveals the deep complexity of the human transcriptome. Nature Biotechnology, 2012, 30, 99-104.	9.4	437

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55	Transcriptional effects of a lupus-associated polymorphism in the 5â€² untranslated region (UTR) of human complement receptor 2 (CR2/CD21). Molecular Immunology, 2012, 52, 165-173.	1.0	12
56	The Human Mitochondrial Transcriptome. Cell, 2011, 146, 645-658.	13.5	716
57	Expression of distinct RNAs from 3â€² untranslated regions. Nucleic Acids Research, 2011, 39, 2393-2403.	6.5	185
58	SNORD-host RNA Zfas1 is a regulator of mammary development and a potential marker for breast cancer. Rna, 2011, 17, 878-891.	1.6	321
59	Refining transcriptional programs in kidney development by integration of deep RNA-sequencing and array-based spatial profiling. BMC Genomics, 2011, 12, 441.	1.2	27
60	RNA processing in human mitochondria. Cell Cycle, 2011, 10, 2904-2916.	1.3	226
61	Long noncoding RNAs are generated from the mitochondrial genome and regulated by nuclear-encoded proteins. Rna, 2011, 17, 2085-2093.	1.6	251
62	Global analysis of the mammalian RNA degradome reveals widespread miRNA-dependent and miRNA-independent endonucleolytic cleavage. Nucleic Acids Research, 2011, 39, 5658-5668.	6.5	76
63	Long noncoding RNAs in neuronal-glial fate specification and oligodendrocyte lineage maturation. BMC Neuroscience, 2010, 11, 14.	0.8	381
64	Nonâ€coding RNAs: regulators of disease. Journal of Pathology, 2010, 220, 126-139.	2.1	906
65	Nuclear-localized tiny RNAs are associated with transcription initiation and splice sites in metazoans. Nature Structural and Molecular Biology, 2010, 17, 1030-1034.	3.6	146
66	A variant of the KLK4 gene is expressed as a cis sense-antisense chimeric transcript in prostate cancer cells. Rna, 2010, 16, 1156-1166.	1.6	36
67	Regulated post-transcriptional RNA cleavage diversifies the eukaryotic transcriptome. Genome Research, 2010, 20, 1639-1650.	2.4	76
68	Genome-Wide Identification of Long Noncoding RNAs in CD8+ T Cells. Journal of Immunology, 2009, 182, 7738-7748.	0.4	221
69	NRED: a database of long noncoding RNA expression. Nucleic Acids Research, 2009, 37, D122-D126.	6.5	252
70	RNA regulation of epigenetic processes. BioEssays, 2009, 31, 51-59.	1.2	333
71	Long non-coding RNAs: insights into functions. Nature Reviews Genetics, 2009, 10, 155-159.	7.7	5,105
72	Pervasive transcription of the eukaryotic genome: functional indices and conceptual implications. Briefings in Functional Genomics & Proteomics, 2009, 8, 407-423.	3.8	140

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73	RNAs as extracellular signaling molecules. Journal of Molecular Endocrinology, 2008, 40, 151-159.	1.1	195
74	Noncoding RNAs in Long-Term Memory Formation. Neuroscientist, 2008, 14, 434-445.	2.6	116
75	The Eukaryotic Genome as an RNA Machine. Science, 2008, 319, 1787-1789.	6.0	579
76	Long noncoding RNAs in mouse embryonic stem cell pluripotency and differentiation. Genome Research, 2008, 18, 1433-1445.	2.4	698
77	Differentiating Protein-Coding and Noncoding RNA: Challenges and Ambiguities. PLoS Computational Biology, 2008, 4, e1000176.	1.5	493
78	Specific expression of long noncoding RNAs in the mouse brain. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 716-721.	3.3	1,081
79	Association of a common complement receptor 2 haplotype with increased risk of systemic lupus erythematosus. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 3961-3966.	3.3	62
80	Advancing Quality-Control for NGS Measurement of Actionable Mutations in Circulating Tumor DNA. SSRN Electronic Journal, 0, , .	0.4	0