Tim R Mercer

List of Publications by Year
in descending order

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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	Integrative analysis of 111 reference human epigenomes. Nature, 2015, 518, 317-330.	13.7	5,653
2	Long non-coding RNAs: insights into functions. Nature Reviews Genetics, 2009, 10, 155-159.	7.7	5,105
3	Structure and function of long noncoding RNAs in epigenetic regulation. Nature Structural and Molecular Biology, 2013, 20, 300-307.	3.6	1,325
4	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
5	Nonâ€coding RNAs: regulators of disease. Journal of Pathology, 2010, 220, 126-139.	2.1	906
6	The Human Mitochondrial Transcriptome. Cell, 2011, 146, 645-658.	13.5	716
7	Long noncoding RNAs in mouse embryonic stem cell pluripotency and differentiation. Genome Research, 2008, 18, 1433-1445.	2.4	698
8	The Eukaryotic Genome as an RNA Machine. Science, 2008, 319, 1787-1789.	6.0	579
9	Differentiating Protein-Coding and Noncoding RNA: Challenges and Ambiguities. PLoS Computational Biology, 2008, 4, e1000176.	1.5	493
10	Targeted RNA sequencing reveals the deep complexity of the human transcriptome. Nature Biotechnology, 2012, 30, 99-104.	9.4	437
11	Long noncoding RNAs in neuronal-glial fate specification and oligodendrocyte lineage maturation. BMC Neuroscience, 2010, 11, 14.	0.8	381
12	RNA regulation of epigenetic processes. BioEssays, 2009, 31, 51-59.	1.2	333
13	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
14	Testing at scale during the COVID-19 pandemic. Nature Reviews Genetics, 2021, 22, 415-426.	7.7	261
15	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
16	NRED: a database of long noncoding RNA expression. Nucleic Acids Research, 2009, 37, D122-D126.	6.5	252
17	Long noncoding RNAs are generated from the mitochondrial genome and regulated by nuclear-encoded proteins. Rna, 2011, 17, 2085-2093.	1.6	251
18	RNA processing in human mitochondria. Cell Cycle, 2011, 10, 2904-2916.	1.3	226

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19	Genome-wide discovery of human splicing branchpoints. Genome Research, 2015, 25, 290-303.	2.4	222
20	Genome-Wide Identification of Long Noncoding RNAs in CD8+ T Cells. Journal of Immunology, 2009, 182, 7738-7748.	0.4	221
21	RNAs as extracellular signaling molecules. Journal of Molecular Endocrinology, 2008, 40, 151-159.	1.1	195
22	Reference standards for next-generation sequencing. Nature Reviews Genetics, 2017, 18, 473-484.	7.7	194
23	Expression of distinct RNAs from 3â€² untranslated regions. Nucleic Acids Research, 2011, 39, 2393-2403.	6.5	185
24	The Dimensions, Dynamics, and Relevance of the Mammalian Noncoding Transcriptome. Trends in Genetics, 2017, 33, 464-478.	2.9	181
25	Targeted sequencing for gene discovery and quantification using RNA CaptureSeq. Nature Protocols, 2014, 9, 989-1009.	5.5	171
26	Reporting guidelines for human microbiome research: the STORMS checklist. Nature Medicine, 2021, 27, 1885-1892.	15.2	170
27	Quantitative gene profiling of long noncoding RNAs with targeted RNA sequencing. Nature Methods, 2015, 12, 339-342.	9.0	155
28	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
29	Pervasive transcription of the eukaryotic genome: functional indices and conceptual implications. Briefings in Functional Genomics & Proteomics, 2009, 8, 407-423.	3.8	140
30	Evaluating the analytical validity of circulating tumor DNA sequencing assays for precision oncology. Nature Biotechnology, 2021, 39, 1115-1128.	9.4	126
31	Spliced synthetic genes as internal controls in RNA sequencing experiments. Nature Methods, 2016, 13, 792-798.	9.0	123
32	Diagnosis of fusion genes using targeted RNA sequencing. Nature Communications, 2019, 10, 1388.	5.8	122
33	Noncoding RNAs in Long-Term Memory Formation. Neuroscientist, 2008, 14, 434-445.	2.6	116
34	DNase Iâ€“hypersensitive exons colocalize with promoters and distal regulatory elements. Nature Genetics, 2013, 45, 852-859.	9.4	112
35	Universal Alternative Splicing of Noncoding Exons. Cell Systems, 2018, 6, 245-255.e5.	2.9	110
36	The human mitochondrial transcriptome and the RNAâ€binding proteins that regulate its expression. Wiley Interdisciplinary Reviews RNA, 2012, 3, 675-695.	3.2	88

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37	Lymphoma Driver Mutations in the Pathogenic Evolution of an Iconic Human Autoantibody. Cell, 2020, 180, 878-894.e19.	13.5	82
38	A 60-GHz 144-Element Phased-Array Transceiver for Backhaul Application. IEEE Journal of Solid-State Circuits, 2018, 53, 3640-3659.	3.5	81
39	Synthetic microbe communities provide internal reference standards for metagenome sequencing and analysis. Nature Communications, 2018, 9, 3096.	5.8	81
40	Understanding the regulatory and transcriptional complexity of the genome through structure. Genome Research, 2013, 23, 1081-1088.	2.4	77
41	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
42	Regulated post-transcriptional RNA cleavage diversifies the eukaryotic transcriptome. Genome Research, 2010, 20, 1639-1650.	2.4	76
43	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
44	Toward best practice in cancer mutation detection with whole-genome and whole-exome sequencing. Nature Biotechnology, 2021, 39, 1141-1150.	9.4	66
45	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
46	Machine learning annotation of human branchpoints. Bioinformatics, 2018, 34, 920-927.	1.8	52
47	Intergenic disease-associated regions are abundant in novel transcripts. Genome Biology, 2017, 18, 241.	3.8	45
48	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
49	Representing genetic variation with synthetic DNA standards. Nature Methods, 2016, 13, 784-791.	9.0	37
50	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
51	Mapping of Mitochondrial RNA-Protein Interactions by Digital RNase Footprinting. Cell Reports, 2013, 5, 839-848.	2.9	36
52	Towards accurate and reliable resolution of structural variants for clinical diagnosis. Genome Biology, 2022, 23, 68.	3.8	34
53	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
54	Improved definition of the mouse transcriptome via targeted RNA sequencing. Genome Research, 2016, 26, 705-716.	2.4	33

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55	Phosphoproteomic Profiling Reveals ALK and MET as Novel Actionable Targets across Synovial Sarcoma Subtypes. Cancer Research, 2017, 77, 4279-4292.	0.4	31
56	Targeted, High-Resolution RNA Sequencing of Non-coding Genomic Regions Associated With Neuropsychiatric Functions. Frontiers in Genetics, 2019, 10, 309.	1.1	28
57	TMPRSS2â€ERG fusions linked to prostate cancer racial health disparities: A focus on Africa. Prostate, 2019, 79, 1191-1196.	1.2	28
58	The potential of long noncoding RNA therapies. Trends in Pharmacological Sciences, 2022, 43, 269-280.	4.0	28
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	Long-read cDNA sequencing identifies functional pseudogenes in the human transcriptome. Genome Biology, 2021, 22, 146.	3.8	26
61	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
62	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
63	Use of synthetic DNA spike-in controls (sequins) for human genome sequencing. Nature Protocols, 2019, 14, 2119-2151.	5.5	22
64	Emerging technologies and their impact on regulatory science. Experimental Biology and Medicine, 2022, 247, 1-75.	1.1	22
65	Re-annotation of the Saccharopolyspora erythraea genome using a systems biology approach. BMC Genomics, 2013, 14, 699.	1.2	21
66	Cross-oncopanel study reveals high sensitivity and accuracy with overall analytical performance depending on genomic regions. Genome Biology, 2021, 22, 109.	3.8	20
67	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
68	ANAQUIN: a software toolkit for the analysis of spike-in controls for next generation sequencing. Bioinformatics, 2017, 33, 1723-1724.	1.8	17
69	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
70	Chiral DNA sequences as commutable controls for clinical genomics. Nature Communications, 2019, 10, 1342.	5.8	11
71	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
72	Advancing NGS quality control to enable measurement of actionable mutations in circulating tumor DNA. Cell Reports Methods, 2021, 1, 100106.	1.4	9

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73	The splicing effect of variants at branchpoint elements in cancer genes. Genetics in Medicine, 2022, 24, 398-409.	1.1	9
74	A universal and independent synthetic DNA ladder for the quantitative measurement of genomic features. Nature Communications, 2020, 11, 3609.	5.8	7
75	The Sequencing Quality Control 2 study: establishing community standards for sequencing in precision medicine. Genome Biology, 2021, 22, 306.	3.8	7
76	Using synthetic chromosome controls to evaluate the sequencing of difficult regions within the human genome. Genome Biology, 2022, 23, 19.	3.8	4
77	Ultra-deep sequencing data from a liquid biopsy proficiency study demonstrating analytic validity. Scientific Data, 2022, 9, 170.	2.4	4
78	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
79	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
80	Advancing Quality-Control for NGS Measurement of Actionable Mutations in Circulating Tumor DNA. SSRN Electronic Journal, 0, , .	0.4	0