

Michael Sammeth

List of Publications by Year in descending order

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Version: 2024-02-01

54
papers

47,355
citations

101384

36
h-index

174990

52
g-index

58
all docs

58
docs citations

58
times ranked

73773
citing authors

#	ARTICLE	IF	CITATIONS
1	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012, 489, 57-74.	13.7	15,516
2	The Genotype-Tissue Expression (GTEx) project. <i>Nature Genetics</i> , 2013, 45, 580-585.	9.4	6,815
3	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. <i>Science</i> , 2015, 348, 648-660.	6.0	4,659
4	Landscape of transcription in human cells. <i>Nature</i> , 2012, 489, 101-108.	13.7	4,484
5	Genetic effects on gene expression across human tissues. <i>Nature</i> , 2017, 550, 204-213.	13.7	3,500
6	Transcriptome and genome sequencing uncovers functional variation in humans. <i>Nature</i> , 2013, 501, 506-511.	13.7	1,857
7	A User's Guide to the Encyclopedia of DNA Elements (ENCODE). <i>PLoS Biology</i> , 2011, 9, e1001046.	2.6	1,257
8	The human transcriptome across tissues and individuals. <i>Science</i> , 2015, 348, 660-665.	6.0	1,127
9	Landscape of X chromosome inactivation across human tissues. <i>Nature</i> , 2017, 550, 244-248.	13.7	764
10	Exploring the phenotypic consequences of tissue specific gene expression variation inferred from GWAS summary statistics. <i>Nature Communications</i> , 2018, 9, 1825.	5.8	748
11	A Novel Approach to High-Quality Postmortem Tissue Procurement: The GTEx Project. <i>Biopreservation and Biobanking</i> , 2015, 13, 311-319.	0.5	674
12	Improving genetic diagnosis in Mendelian disease with transcriptome sequencing. <i>Science Translational Medicine</i> , 2017, 9, .	5.8	516
13	The GEM mapper: fast, accurate and versatile alignment by filtration. <i>Nature Methods</i> , 2012, 9, 1185-1188.	9.0	500
14	Dynamic landscape and regulation of RNA editing in mammals. <i>Nature</i> , 2017, 550, 249-254.	13.7	495
15	Nucleosome positioning as a determinant of exon recognition. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 996-1001.	3.6	406
16	The Human Pancreatic Islet Transcriptome: Expression of Candidate Genes for Type 1 Diabetes and the Impact of Pro-Inflammatory Cytokines. <i>PLoS Genetics</i> , 2012, 8, e1002552.	1.5	398
17	ASTALAVISTA: dynamic and flexible analysis of alternative splicing events in custom gene datasets. <i>Nucleic Acids Research</i> , 2007, 35, W297-W299.	6.5	325
18	Modelling and simulating generic RNA-Seq experiments with the flux simulator. <i>Nucleic Acids Research</i> , 2012, 40, 10073-10083.	6.5	264

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19	Effect of predicted protein-truncating genetic variants on the human transcriptome. <i>Science</i> , 2015, 348, 666-669.	6.0	252
20	Reproducibility of high-throughput mRNA and small RNA sequencing across laboratories. <i>Nature Biotechnology</i> , 2013, 31, 1015-1022.	9.4	251
21	A General Definition and Nomenclature for Alternative Splicing Events. <i>PLoS Computational Biology</i> , 2008, 4, e1000147.	1.5	232
22	The impact of rare variation on gene expression across tissues. <i>Nature</i> , 2017, 550, 239-243.	13.7	229
23	RNA Sequencing Identifies Dysregulation of the Human Pancreatic Islet Transcriptome by the Saturated Fatty Acid Palmitate. <i>Diabetes</i> , 2014, 63, 1978-1993.	0.3	226
24	Based Upon Repeat Pattern (BURP): an algorithm to characterize the long-term evolution of <i>Staphylococcus aureus</i> populations based on spa polymorphisms. <i>BMC Microbiology</i> , 2007, 7, 98.	1.3	203
25	The effects of death and post-mortem cold ischemia on human tissue transcriptomes. <i>Nature Communications</i> , 2018, 9, 490.	5.8	198
26	Synchronized age-related gene expression changes across multiple tissues in human and the link to complex diseases. <i>Scientific Reports</i> , 2015, 5, 15145.	1.6	180
27	Sharing and Specificity of Co-expression Networks across 35 Human Tissues. <i>PLoS Computational Biology</i> , 2015, 11, e1004220.	1.5	158
28	RIDOM: Comprehensive and public sequence database for identification of <i>Mycobacterium</i> species. <i>BMC Infectious Diseases</i> , 2003, 3, 26.	1.3	141
29	Bioinformatics approaches for genomics and post genomics applications of next-generation sequencing. <i>Briefings in Bioinformatics</i> , 2010, 11, 181-197.	3.2	141
30	Co-expression networks reveal the tissue-specific regulation of transcription and splicing. <i>Genome Research</i> , 2017, 27, 1843-1858.	2.4	139
31	Gene Expansion Shapes Genome Architecture in the Human Pathogen <i>Lichtheimia corymbifera</i> : An Evolutionary Genomics Analysis in the Ancient Terrestrial Mucorales (Mucoromycotina). <i>PLoS Genetics</i> , 2014, 10, e1004496.	1.5	80
32	Evaluating Characteristics of De Novo Assembly Software on 454 Transcriptome Data: A Simulation Approach. <i>PLoS ONE</i> , 2012, 7, e31410.	1.1	72
33	Identifying <i>cis</i> -mediators for <i>trans</i> -eQTLs across many human tissues using genomic mediation analysis. <i>Genome Research</i> , 2017, 27, 1859-1871.	2.4	72
34	Noxa1 is a master regulator of alternative splicing in pancreatic beta cells. <i>Nucleic Acids Research</i> , 2014, 42, 11818-11830.	6.5	71
35	Estimation of alternative splicing variability in human populations. <i>Genome Research</i> , 2012, 22, 528-538.	2.4	59
36	Complete Alternative Splicing Events Are Bubbles in Splicing Graphs. <i>Journal of Computational Biology</i> , 2009, 16, 1117-1140.	0.8	46

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37	Exact Transcriptome Reconstruction from Short Sequence Reads. Lecture Notes in Computer Science, 2008, , 50-63.	1.0	40
38	Characterization of HPV integration, viral gene expression and E6E7 alternative transcripts by RNA-Seq: A descriptive study in invasive cervical cancer. Genomics, 2019, 111, 1853-1861.	1.3	34
39	Sequence variation between 462 human individuals fine-tunes functional sites of RNA processing. Scientific Reports, 2016, 6, 32406.	1.6	28
40	Transcriptomic and functional analyses of the piRNA pathway in the Chagas disease vector Rhodnius prolixus. PLoS Neglected Tropical Diseases, 2018, 12, e0006760.	1.3	28
41	Comparing Tandem Repeats with Duplications and Excisions of Variable Degree. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2006, 3, 395-407.	1.9	22
42	Analysis of Alternative Splicing Events in Custom Gene Datasets by AStalavista. Methods in Molecular Biology, 2015, 1269, 379-392.	0.4	21
43	Landscape of the spliced leader trans-splicing mechanism in Schistosoma mansoni. Scientific Reports, 2018, 8, 3877.	1.6	20
44	Analysis of ovarian transcriptomes reveals thousands of novel genes in the insect vector Rhodnius prolixus. Scientific Reports, 2021, 11, 1918.	1.6	18
45	Divide-and-conquer multiple alignment with segment-based constraints. Bioinformatics, 2003, 19, ii189-ii195.	1.8	17
46	QAlign: quality-based multiple alignments with dynamic phylogenetic analysis. Bioinformatics, 2003, 19, 1592-1593.	1.8	16
47	Global multiple sequence alignment with repeats. Proteins: Structure, Function and Bioinformatics, 2006, 64, 263-274.	1.5	16
48	Echocardiographic Measurements in a Preclinical Model of Chronic Chagasic Cardiomyopathy in Dogs: Validation and Reproducibility. Frontiers in Cellular and Infection Microbiology, 2019, 9, 332.	1.8	12
49	Alignment of Tandem Repeats with Excision, Duplication, Substitution and Indels (EDSI). Lecture Notes in Computer Science, 2005, , 276-290.	1.0	7
50	Comparative Genomics in Homo sapiens. Methods in Molecular Biology, 2018, 1704, 451-472.	0.4	7
51	Panta rhei (QAlign2): an open graphical environment for sequence analysis. Bioinformatics, 2006, 22, 889-890.	1.8	6
52	Bubbles: Alternative Splicing Events of Arbitrary Dimension in Splicing Graphs. , 2008, , 372-395.		6
53	Comparative Genomics in Drosophila. Methods in Molecular Biology, 2018, 1704, 433-450.	0.4	1
54	An automated method for detecting alternatively spliced protein domains. Bioinformatics, 2018, 34, 3809-3816.	1.8	0