

Michael Sammeth

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

55
papers

33,185
citations

35
h-index

58
g-index

58
ext. papers

42,460
ext. citations

15.4
avg, IF

8.19
L-index

#	Paper	IF	Citations
55	Analysis of ovarian transcriptomes reveals thousands of novel genes in the insect vector <i>Rhodnius prolixus</i> . <i>Scientific Reports</i> , 2021 , 11, 1918	4.9	4
54	Echocardiographic Measurements in a Preclinical Model of Chronic Chagasic Cardiomyopathy in Dogs: Validation and Reproducibility. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019 , 9, 332	5.9	9
53	Characterization of HPV integration, viral gene expression and E6E7 alternative transcripts by RNA-Seq: A descriptive study in invasive cervical cancer. <i>Genomics</i> , 2019 , 111, 1853-1861	4.3	15
52	Landscape of the spliced leader trans-splicing mechanism in <i>Schistosoma mansoni</i> . <i>Scientific Reports</i> , 2018 , 8, 3877	4.9	11
51	The effects of death and post-mortem cold ischemia on human tissue transcriptomes. <i>Nature Communications</i> , 2018 , 9, 490	17.4	108
50	Comparative Genomics in <i>Drosophila</i> . <i>Methods in Molecular Biology</i> , 2018 , 1704, 433-450	1.4	1
49	Comparative Genomics in <i>Homo sapiens</i> . <i>Methods in Molecular Biology</i> , 2018 , 1704, 451-472	1.4	2
48	Exploring the phenotypic consequences of tissue specific gene expression variation inferred from GWAS summary statistics. <i>Nature Communications</i> , 2018 , 9, 1825	17.4	367
47	Transcriptomic and functional analyses of the piRNA pathway in the Chagas disease vector <i>Rhodnius prolixus</i> . <i>PLoS Neglected Tropical Diseases</i> , 2018 , 12, e0006760	4.8	16
46	An automated method for detecting alternatively spliced protein domains. <i>Bioinformatics</i> , 2018 , 34, 3809-3816		
45	Improving genetic diagnosis in Mendelian disease with transcriptome sequencing. <i>Science Translational Medicine</i> , 2017 , 9,	17.5	338
44	Dynamic landscape and regulation of RNA editing in mammals. <i>Nature</i> , 2017 , 550, 249-254	50.4	286
43	Landscape of X chromosome inactivation across human tissues. <i>Nature</i> , 2017 , 550, 244-248	50.4	417
42	The impact of rare variation on gene expression across tissues. <i>Nature</i> , 2017 , 550, 239-243	50.4	146
41	Genetic effects on gene expression across human tissues. <i>Nature</i> , 2017 , 550, 204-213	50.4	2086
40	Identifying β -mediators for β -eQTLs across many human tissues using genomic mediation analysis. <i>Genome Research</i> , 2017 , 27, 1859-1871	9.7	38
39	Co-expression networks reveal the tissue-specific regulation of transcription and splicing. <i>Genome Research</i> , 2017 , 27, 1843-1858	9.7	98

38	Sequence variation between 462 human individuals fine-tunes functional sites of RNA processing. <i>Scientific Reports</i> , 2016 , 6, 32406	4.9	21
37	Sharing and Specificity of Co-expression Networks across 35 Human Tissues. <i>PLoS Computational Biology</i> , 2015 , 11, e1004220	5	104
36	Human genomics. The human transcriptome across tissues and individuals. <i>Science</i> , 2015 , 348, 660-5	33.3	833
35	Human genomics. The Genotype-Tissue Expression (GTEx) pilot analysis: multitissue gene regulation in humans. <i>Science</i> , 2015 , 348, 648-60	33.3	3242
34	Human genomics. Effect of predicted protein-truncating genetic variants on the human transcriptome. <i>Science</i> , 2015 , 348, 666-9	33.3	170
33	A Novel Approach to High-Quality Postmortem Tissue Procurement: The GTEx Project. <i>Biopreservation and Biobanking</i> , 2015 , 13, 311-9	2.1	432
32	Synchronized age-related gene expression changes across multiple tissues in human and the link to complex diseases. <i>Scientific Reports</i> , 2015 , 5, 15145	4.9	128
31	Analysis of alternative splicing events in custom gene datasets by AStalavista. <i>Methods in Molecular Biology</i> , 2015 , 1269, 379-92	1.4	14
30	RNA sequencing identifies dysregulation of the human pancreatic islet transcriptome by the saturated fatty acid palmitate. <i>Diabetes</i> , 2014 , 63, 1978-93	0.9	174
29	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	6	55
28	Nova1 is a master regulator of alternative splicing in pancreatic beta cells. <i>Nucleic Acids Research</i> , 2014 , 42, 11818-30	20.1	53
27	Reproducibility of high-throughput mRNA and small RNA sequencing across laboratories. <i>Nature Biotechnology</i> , 2013 , 31, 1015-22	44.5	187
26	Transcriptome and genome sequencing uncovers functional variation in humans. <i>Nature</i> , 2013 , 501, 506-514	31.4	1323
25	The Genotype-Tissue Expression (GTEx) project. <i>Nature Genetics</i> , 2013 , 45, 580-5	36.3	4179
24	Analysis of RNA Transcripts by High-Throughput RNA Sequencing 2012 , 544-554		1
23	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012 , 489, 57-74	50.4	11449
22	The GEM mapper: fast, accurate and versatile alignment by filtration. <i>Nature Methods</i> , 2012 , 9, 1185-8	21.6	382
21	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	6	313

20	Landscape of transcription in human cells. <i>Nature</i> , 2012 , 489, 101-8	50.4	3544
19	Evaluating characteristics of de novo assembly software on 454 transcriptome data: a simulation approach. <i>PLoS ONE</i> , 2012 , 7, e31410	3.7	68
18	Estimation of alternative splicing variability in human populations. <i>Genome Research</i> , 2012 , 22, 528-38	9.7	49
17	Modelling and simulating generic RNA-Seq experiments with the flux simulator. <i>Nucleic Acids Research</i> , 2012 , 40, 10073-83	20.1	200
16	A user's guide to the encyclopedia of DNA elements (ENCODE). <i>PLoS Biology</i> , 2011 , 9, e1001046	9.7	1060
15	Bioinformatics approaches for genomics and post genomics applications of next-generation sequencing. <i>Briefings in Bioinformatics</i> , 2010 , 11, 181-97	13.4	120
14	Nucleosome positioning as a determinant of exon recognition. <i>Nature Structural and Molecular Biology</i> , 2009 , 16, 996-1001	17.6	337
13	Complete alternative splicing events are bubbles in splicing graphs. <i>Journal of Computational Biology</i> , 2009 , 16, 1117-40	1.7	27
12	A general definition and nomenclature for alternative splicing events. <i>PLoS Computational Biology</i> , 2008 , 4, e1000147	5	165
11	Bubbles: Alternative Splicing Events of Arbitrary Dimension in Splicing Graphs 2008 , 372-395		5
10	Exact Transcriptome Reconstruction from Short Sequence Reads. <i>Lecture Notes in Computer Science</i> , 2008 , 50-63	0.9	34
9	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	4.5	172
8	ASTALAVISTA: dynamic and flexible analysis of alternative splicing events in custom gene datasets. <i>Nucleic Acids Research</i> , 2007 , 35, W297-9	20.1	216
7	Panta rhei (QAlign2): an open graphical environment for sequence analysis. <i>Bioinformatics</i> , 2006 , 22, 889-90	7.2	6
6	Comparing tandem repeats with duplications and excisions of variable degree. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2006 , 3, 395-407	3	15
5	Global multiple-sequence alignment with repeats. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 64, 263-74	4.2	13
4	Alignment of Tandem Repeats with Excision, Duplication, Substitution and Indels (EDSI). <i>Lecture Notes in Computer Science</i> , 2005 , 276-290	0.9	6
3	Divide-and-conquer multiple alignment with segment-based constraints. <i>Bioinformatics</i> , 2003 , 19 Suppl 2, ii189-95	7.2	11

2	RIDOM: comprehensive and public sequence database for identification of Mycobacterium species. <i>BMC Infectious Diseases</i> , 2003 , 3, 26	4	121
1	QAlign: quality-based multiple alignments with dynamic phylogenetic analysis. <i>Bioinformatics</i> , 2003 , 19, 1592-3	7.2	14