

# Michael Sammeth

## List of Publications by Citations

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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	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , <b>2012</b> , 489, 57-74	50.4	11449
54	The Genotype-Tissue Expression (GTEx) project. <i>Nature Genetics</i> , <b>2013</b> , 45, 580-5	36.3	4179
53	Landscape of transcription in human cells. <i>Nature</i> , <b>2012</b> , 489, 101-8	50.4	3544
52	Human genomics. The Genotype-Tissue Expression (GTEx) pilot analysis: multitissue gene regulation in humans. <i>Science</i> , <b>2015</b> , 348, 648-60	33.3	3242
51	Genetic effects on gene expression across human tissues. <i>Nature</i> , <b>2017</b> , 550, 204-213	50.4	2086
50	Transcriptome and genome sequencing uncovers functional variation in humans. <i>Nature</i> , <b>2013</b> , 501, 506-514	51.4	1323
49	A user's guide to the encyclopedia of DNA elements (ENCODE). <i>PLoS Biology</i> , <b>2011</b> , 9, e1001046	9.7	1060
48	Human genomics. The human transcriptome across tissues and individuals. <i>Science</i> , <b>2015</b> , 348, 660-5	33.3	833
47	A Novel Approach to High-Quality Postmortem Tissue Procurement: The GTEx Project. <i>Biopreservation and Biobanking</i> , <b>2015</b> , 13, 311-9	2.1	432
46	Landscape of X chromosome inactivation across human tissues. <i>Nature</i> , <b>2017</b> , 550, 244-248	50.4	417
45	The GEM mapper: fast, accurate and versatile alignment by filtration. <i>Nature Methods</i> , <b>2012</b> , 9, 1185-8	21.6	382
44	Exploring the phenotypic consequences of tissue specific gene expression variation inferred from GWAS summary statistics. <i>Nature Communications</i> , <b>2018</b> , 9, 1825	17.4	367
43	Improving genetic diagnosis in Mendelian disease with transcriptome sequencing. <i>Science Translational Medicine</i> , <b>2017</b> , 9,	17.5	338
42	Nucleosome positioning as a determinant of exon recognition. <i>Nature Structural and Molecular Biology</i> , <b>2009</b> , 16, 996-1001	17.6	337
41	The human pancreatic islet transcriptome: expression of candidate genes for type 1 diabetes and the impact of pro-inflammatory cytokines. <i>PLoS Genetics</i> , <b>2012</b> , 8, e1002552	6	313
40	Dynamic landscape and regulation of RNA editing in mammals. <i>Nature</i> , <b>2017</b> , 550, 249-254	50.4	286
39	ASTALAVISTA: dynamic and flexible analysis of alternative splicing events in custom gene datasets. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, W297-9	20.1	216

38	Modelling and simulating generic RNA-Seq experiments with the flux simulator. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, 10073-83	20.1	200
37	Reproducibility of high-throughput mRNA and small RNA sequencing across laboratories. <i>Nature Biotechnology</i> , <b>2013</b> , 31, 1015-22	44.5	187
36	RNA sequencing identifies dysregulation of the human pancreatic islet transcriptome by the saturated fatty acid palmitate. <i>Diabetes</i> , <b>2014</b> , 63, 1978-93	0.9	174
35	Based Upon Repeat Pattern (BURP): an algorithm to characterize the long-term evolution of <i>Staphylococcus aureus</i> populations based on <i>spa</i> polymorphisms. <i>BMC Microbiology</i> , <b>2007</b> , 7, 98	4.5	172
34	Human genomics. Effect of predicted protein-truncating genetic variants on the human transcriptome. <i>Science</i> , <b>2015</b> , 348, 666-9	33.3	170
33	A general definition and nomenclature for alternative splicing events. <i>PLoS Computational Biology</i> , <b>2008</b> , 4, e1000147	5	165
32	The impact of rare variation on gene expression across tissues. <i>Nature</i> , <b>2017</b> , 550, 239-243	50.4	146
31	Synchronized age-related gene expression changes across multiple tissues in human and the link to complex diseases. <i>Scientific Reports</i> , <b>2015</b> , 5, 15145	4.9	128
30	RIDOM: comprehensive and public sequence database for identification of <i>Mycobacterium</i> species. <i>BMC Infectious Diseases</i> , <b>2003</b> , 3, 26	4	121
29	Bioinformatics approaches for genomics and post genomics applications of next-generation sequencing. <i>Briefings in Bioinformatics</i> , <b>2010</b> , 11, 181-97	13.4	120
28	The effects of death and post-mortem cold ischemia on human tissue transcriptomes. <i>Nature Communications</i> , <b>2018</b> , 9, 490	17.4	108
27	Sharing and Specificity of Co-expression Networks across 35 Human Tissues. <i>PLoS Computational Biology</i> , <b>2015</b> , 11, e1004220	5	104
26	Co-expression networks reveal the tissue-specific regulation of transcription and splicing. <i>Genome Research</i> , <b>2017</b> , 27, 1843-1858	9.7	98
25	Evaluating characteristics of de novo assembly software on 454 transcriptome data: a simulation approach. <i>PLoS ONE</i> , <b>2012</b> , 7, e31410	3.7	68
24	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> , <b>2014</b> , 10, e1004496	6	55
23	Nova1 is a master regulator of alternative splicing in pancreatic beta cells. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, 11818-30	20.1	53
22	Estimation of alternative splicing variability in human populations. <i>Genome Research</i> , <b>2012</b> , 22, 528-38	9.7	49
21	Identifying -mediators for -eQTLs across many human tissues using genomic mediation analysis. <i>Genome Research</i> , <b>2017</b> , 27, 1859-1871	9.7	38

20	Exact Transcriptome Reconstruction from Short Sequence Reads. <i>Lecture Notes in Computer Science</i> , <b>2008</b> , 50-63	0.9	34
19	Complete alternative splicing events are bubbles in splicing graphs. <i>Journal of Computational Biology</i> , <b>2009</b> , 16, 1117-40	1.7	27
18	Sequence variation between 462 human individuals fine-tunes functional sites of RNA processing. <i>Scientific Reports</i> , <b>2016</b> , 6, 32406	4.9	21
17	Transcriptomic and functional analyses of the piRNA pathway in the Chagas disease vector <i>Rhodnius prolixus</i> . <i>PLoS Neglected Tropical Diseases</i> , <b>2018</b> , 12, e0006760	4.8	16
16	Comparing tandem repeats with duplications and excisions of variable degree. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2006</b> , 3, 395-407	3	15
15	Characterization of HPV integration, viral gene expression and E6E7 alternative transcripts by RNA-Seq: A descriptive study in invasive cervical cancer. <i>Genomics</i> , <b>2019</b> , 111, 1853-1861	4.3	15
14	Analysis of alternative splicing events in custom gene datasets by AStalavista. <i>Methods in Molecular Biology</i> , <b>2015</b> , 1269, 379-92	1.4	14
13	QAlign: quality-based multiple alignments with dynamic phylogenetic analysis. <i>Bioinformatics</i> , <b>2003</b> , 19, 1592-3	7.2	14
12	Global multiple-sequence alignment with repeats. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2006</b> , 64, 263-74	4.2	13
11	Landscape of the spliced leader trans-splicing mechanism in <i>Schistosoma mansoni</i> . <i>Scientific Reports</i> , <b>2018</b> , 8, 3877	4.9	11
10	Divide-and-conquer multiple alignment with segment-based constraints. <i>Bioinformatics</i> , <b>2003</b> , 19 Suppl 2, ii189-95	7.2	11
9	Echocardiographic Measurements in a Preclinical Model of Chronic Chagasic Cardiomyopathy in Dogs: Validation and Reproducibility. <i>Frontiers in Cellular and Infection Microbiology</i> , <b>2019</b> , 9, 332	5.9	9
8	Panta rhei (QAlign2): an open graphical environment for sequence analysis. <i>Bioinformatics</i> , <b>2006</b> , 22, 889-90	7.2	6
7	Alignment of Tandem Repeats with Excision, Duplication, Substitution and Indels (EDSI). <i>Lecture Notes in Computer Science</i> , <b>2005</b> , 276-290	0.9	6
6	Bubbles: Alternative Splicing Events of Arbitrary Dimension in Splicing Graphs <b>2008</b> , 372-395		5
5	Analysis of ovarian transcriptomes reveals thousands of novel genes in the insect vector <i>Rhodnius prolixus</i> . <i>Scientific Reports</i> , <b>2021</b> , 11, 1918	4.9	4
4	Comparative Genomics in <i>Homo sapiens</i> . <i>Methods in Molecular Biology</i> , <b>2018</b> , 1704, 451-472	1.4	2
3	Comparative Genomics in <i>Drosophila</i> . <i>Methods in Molecular Biology</i> , <b>2018</b> , 1704, 433-450	1.4	1

- 2 Analysis of RNA Transcripts by High-Throughput RNA Sequencing **2012**, 544-554 1
- 1 An automated method for detecting alternatively spliced protein domains. *Bioinformatics*, **2018**, 34, 3809-3816