

# Stephen M Mount

## List of Publications by Year in descending order

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44  
papers

20,968  
citations

185998

28  
h-index

253896

43  
g-index

49  
all docs

49  
docs citations

49  
times ranked

20123  
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparative transcriptomic analysis of apple and peach fruits: insights into fruit type specification. <i>Plant Journal</i> , 2022, 109, 1614-1629.	2.8	4
2	Expanding plant genome-editing scope by an engineered iSpyMacCas9 system that targets A-rich PAM sequences. <i>Plant Communications</i> , 2021, 2, 100101.	3.6	31
3	Expanding the scope of plant genome engineering with Cas12a orthologs and highly multiplexable editing systems. <i>Nature Communications</i> , 2021, 12, 1944.	5.8	79
4	An Atlas of Genomic Resources for Studying Rosaceae Fruits and Ornamentals. <i>Frontiers in Plant Science</i> , 2021, 12, 644881.	1.7	5
5	Yanagi: Fast and interpretable segment-based alternative splicing and gene expression analysis. <i>BMC Bioinformatics</i> , 2019, 20, 421.	1.2	3
6	Assessing predictions of the impact of variants on splicing in CAG15. <i>Human Mutation</i> , 2019, 40, 1215-1224.	1.1	18
7	The Splicing Factor <i>RNA-Binding Fox Protein 1</i> Mediates the Cellular Immune Response in <i>Drosophila melanogaster</i> . <i>Journal of Immunology</i> , 2018, 201, 1154-1164.	0.4	11
8	Consensus Coexpression Network Analysis Identifies Key Regulators of Flower and Fruit Development in Wild Strawberry. <i>Plant Physiology</i> , 2018, 178, 202-216.	2.3	57
9	Transcriptome analyses reveal SR45 to be a neutral splicing regulator and a suppressor of innate immunity in <i>Arabidopsis thaliana</i> . <i>BMC Genomics</i> , 2017, 18, 772.	1.2	64
10	A Genealogical Look at Shared Ancestry on the X Chromosome. <i>Genetics</i> , 2016, 204, 57-75.	1.2	10
11	Insights from GWAS: emerging landscape of mechanisms underlying complex trait disease. <i>BMC Genomics</i> , 2015, 16, S4.	1.2	16
12	Recognizing the 35th anniversary of the proposal that snRNPs are involved in splicing. <i>Molecular Biology of the Cell</i> , 2015, 26, 3557-3560.	0.9	0
13	Evaluation of BLAST-based edge-weighting metrics used for homology inference with the Markov Clustering algorithm. <i>BMC Bioinformatics</i> , 2015, 16, 218.	1.2	18
14	Sailfish enables alignment-free isoform quantification from RNA-seq reads using lightweight algorithms. <i>Nature Biotechnology</i> , 2014, 32, 462-464.	9.4	594
15	Two Alternatively Spliced Isoforms of the <i>Arabidopsis</i> SR45 Protein Have Distinct Roles during Normal Plant Development. <i>Plant Physiology</i> , 2009, 150, 1450-1458.	2.3	135
16	The draft genome of the transgenic tropical fruit tree papaya ( <i>Carica papaya</i> Linnaeus). <i>Nature</i> , 2008, 452, 991-996.	13.7	964
17	SplicePort—An interactive splice-site analysis tool. <i>Nucleic Acids Research</i> , 2007, 35, W285-W291.	6.5	190
18	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007, 450, 203-218.	13.7	1,886

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19	Comprehensive analysis of alternative splicing in rice and comparative analyses with Arabidopsis. <i>BMC Genomics</i> , 2006, 7, 327.	1.2	375
20	Spliceosomal small nuclear RNA genes in 11 insect genomes. <i>Rna</i> , 2006, 13, 5-14.	1.6	33
21	The Drosophila U1-70K Protein Is Required for Viability, but Its Arginine-Rich Domain Is Dispensable. <i>Genetics</i> , 2004, 168, 2059-2065.	1.2	25
22	Sex-lethalsplicing autoregulation in vivo: interactions between SEX-LETHAL, the U1 snRNP and U2AF underlie male exon skipping. <i>Development (Cambridge)</i> , 2003, 130, 463-471.	1.2	44
23	Improving the Arabidopsis genome annotation using maximal transcript alignment assemblies. <i>Nucleic Acids Research</i> , 2003, 31, 5654-5666.	6.5	1,597
24	Evidence for a Plastid Origin of Plant Ethylene Receptor Genes. <i>Plant Physiology</i> , 2002, 130, 10-14.	2.3	60
25	The Draft Genome of <i>Ciona intestinalis</i> : Insights into Chordate and Vertebrate Origins. <i>Science</i> , 2002, 298, 2157-2167.	6.0	1,539
26	Expanding the definition of informational suppression. <i>Trends in Genetics</i> , 2000, 16, 157.	2.9	7
27	The Genome Sequence of <i>Drosophila melanogaster</i> . <i>Science</i> , 2000, 287, 2185-2195.	6.0	5,566
28	Pre-Messenger RNA Processing Factors in the <i>Drosophila</i> Genome. <i>Journal of Cell Biology</i> , 2000, 150, F37-F44.	2.3	83
29	Genomic Sequence, Splicing, and Gene Annotation. <i>American Journal of Human Genetics</i> , 2000, 67, 788-792.	2.6	88
30	The RNA World, second edition, edited by Raymond F. Gesteland, Thomas R. Cech, and John F. Atkins. 1999. Cold Spring Harbor, New York: Cold Spring Harbor Laboratory Press. Hardcover, 709 pp. \$129.. <i>Rna</i> , 1999, 5, 1133-1134.	1.6	1
31	Genetic depletion reveals an essential role for an SR protein splicing factor in vertebrate cells. <i>BioEssays</i> , 1997, 19, 189-192.	1.2	10
32	Ribosomal RNA: Small nucleolar RNAs make their mark. <i>Current Biology</i> , 1996, 6, 1413-1415.	1.8	20
33	Localization of Sequences Required for Size-specific Splicing of a Small <i>Drosophila</i> Intron in Vitro. <i>Journal of Molecular Biology</i> , 1995, 253, 426-437.	2.0	20
34	Nested genes take flight. <i>Current Biology</i> , 1993, 3, 372-374.	1.8	11
35	Splicing signals in <i>Drosophila</i> : intron size, information content, and consensus sequences. <i>Nucleic Acids Research</i> , 1992, 20, 4255-4262.	6.5	419
36	Sequence of a cDNA from the <i>Drosophila melanogaster</i> white gene. <i>Nucleic Acids Research</i> , 1990, 18, 1633-1633.	6.5	70

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37	Drosophila melanogaster genes for U1 snRNA variants and their expression during development. Nucleic Acids Research, 1990, 18, 6971-6979.	6.5	63
38	Sequence similarity. Nature, 1987, 325, 487-487.	13.7	50
39	The U1 small nuclear RNA-protein complex selectively binds a 5' splice site in vitro. Cell, 1983, 33, 509-518.	13.5	609
40	Pseudogenes for human small nuclear RNA U3 appear to arise by integration of self-primed reverse transcripts of the RNA into new chromosomal sites. Cell, 1983, 32, 461-472.	13.5	192
41	Splicing of messenger RNA precursors is inhibited by antisera to small nuclear ribonucleoprotein. Cell, 1983, 35, 101-107.	13.5	359
42	A catalogue of splice junction sequences. Nucleic Acids Research, 1982, 10, 459-472.	6.5	4,153
43	Sequence of U1 RNA from Drosophila melanogaster: implications for U1 secondary structure and possible involvement in splicing. Nucleic Acids Research, 1981, 9, 6351-6368.	6.5	203
44	Are snRNPs involved in splicing?. Nature, 1980, 283, 220-224.	13.7	1,264