

# Stephen M Mount

## List of Publications by Year in descending order

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44  
papers

20,968  
citations

186265  
28  
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254184  
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all docs

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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.	5.7	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.	7.7	31
3	Expanding the scope of plant genome engineering with Cas12a orthologs and highly multiplexable editing systems. <i>Nature Communications</i> , 2021, 12, 1944.	12.8	79
4	An Atlas of Genomic Resources for Studying Rosaceae Fruits and Ornamentals. <i>Frontiers in Plant Science</i> , 2021, 12, 644881.	3.6	5
5	Yanagi: Fast and interpretable segment-based alternative splicing and gene expression analysis. <i>BMC Bioinformatics</i> , 2019, 20, 421.	2.6	3
6	Assessing predictions of the impact of variants on splicing in CAG15. <i>Human Mutation</i> , 2019, 40, 1215-1224.	2.5	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.	0.8	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.	4.8	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.	2.8	64
10	A Genealogical Look at Shared Ancestry on the X Chromosome. <i>Genetics</i> , 2016, 204, 57-75.	2.9	10
11	Insights from GWAS: emerging landscape of mechanisms underlying complex trait disease. <i>BMC Genomics</i> , 2015, 16, S4.	2.8	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.	2.1	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.	2.6	18
14	Sailfish enables alignment-free isoform quantification from RNA-seq reads using lightweight algorithms. <i>Nature Biotechnology</i> , 2014, 32, 462-464.	17.5	594
15	Two Alternatively Spliced Isoforms of the Arabidopsis SR45 Protein Have Distinct Roles during Normal Plant Development. <i>Plant Physiology</i> , 2009, 150, 1450-1458.	4.8	135
16	The draft genome of the transgenic tropical fruit tree papaya ( <i>Carica papaya</i> Linnaeus). <i>Nature</i> , 2008, 452, 991-996.	27.8	964
17	SplicePort—An interactive splice-site analysis tool. <i>Nucleic Acids Research</i> , 2007, 35, W285-W291.	14.5	190
18	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007, 450, 203-218.	27.8	1,886

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19	Comprehensive analysis of alternative splicing in rice and comparative analyses with Arabidopsis. BMC Genomics, 2006, 7, 327.	2.8	375
20	Spliceosomal small nuclear RNA genes in 11 insect genomes. Rna, 2006, 13, 5-14.	3.5	33
21	The Drosophila U1-70K Protein Is Required for Viability, but Its Arginine-Rich Domain Is Dispensable. Genetics, 2004, 168, 2059-2065.	2.9	25
22	Sex-lethalsplicing autoregulation in vivo: interactions between SEX-LETHAL, the U1 snRNP and U2AF underlie male exon skipping. Development (Cambridge), 2003, 130, 463-471.	2.5	44
23	Improving the Arabidopsis genome annotation using maximal transcript alignment assemblies. Nucleic Acids Research, 2003, 31, 5654-5666.	14.5	1,597
24	Evidence for a Plastid Origin of Plant Ethylene Receptor Genes. Plant Physiology, 2002, 130, 10-14.	4.8	60
25	The Draft Genome of <i>Ciona intestinalis</i> : Insights into Chordate and Vertebrate Origins. Science, 2002, 298, 2157-2167.	12.6	1,539
26	Expanding the definition of informational suppression. Trends in Genetics, 2000, 16, 157.	6.7	7
27	The Genome Sequence of <i>Drosophila melanogaster</i> . Science, 2000, 287, 2185-2195.	12.6	5,566
28	Pre-Messenger RNA Processing Factors in the Drosophila Genome. Journal of Cell Biology, 2000, 150, F37-F44.	5.2	83
29	Genomic Sequence, Splicing, and Gene Annotation. American Journal of Human Genetics, 2000, 67, 788-792.	6.2	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.. Rna, 1999, 5, 1133-1134.	3.5	1
31	Genetic depletion reveals an essential role for an SR protein splicing factor in vertebrate cells. BioEssays, 1997, 19, 189-192.	2.5	10
32	Ribosomal RNA: Small nucleolar RNAs make their mark. Current Biology, 1996, 6, 1413-1415.	3.9	20
33	Localization of Sequences Required for Size-specific Splicing of a SmallDrosophilaIntronin Vitro. Journal of Molecular Biology, 1995, 253, 426-437.	4.2	20
34	Nested genes take flight. Current Biology, 1993, 3, 372-374.	3.9	11
35	Splicing signals inDrosophila: intron size, information content, and consensus sequences. Nucleic Acids Research, 1992, 20, 4255-4262.	14.5	419
36	Sequence of a cDNA from theDrosophila melanogaster whitegene. Nucleic Acids Research, 1990, 18, 1633-1633.	14.5	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.	14.5	63
38	Sequence similarity. Nature, 1987, 325, 487-487.	27.8	50
39	The U1 small nuclear RNA-protein complex selectively binds a 5' splice site in vitro. Cell, 1983, 33, 509-518.	28.9	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.	28.9	192
41	Splicing of messenger RNA precursors is inhibited by antisera to small nuclear ribonucleoprotein. Cell, 1983, 35, 101-107.	28.9	359
42	A catalogue of splice junction sequences. Nucleic Acids Research, 1982, 10, 459-472.	14.5	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.	14.5	203
44	Are snRNPs involved in splicing?. Nature, 1980, 283, 220-224.	27.8	1,264