

# Gordon G Simpson

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/834808/publications.pdf>

Version: 2024-02-01

28  
papers

3,788  
citations

394421

19  
h-index

526287

27  
g-index

38  
all docs

38  
docs citations

38  
times ranked

4904  
citing authors

#	ARTICLE	IF	CITATIONS
1	Arabidopsis, the Rosetta Stone of Flowering Time?. <i>Science</i> , 2002, 296, 285-289.	12.6	954
2	How many biological replicates are needed in an RNA-seq experiment and which differential expression tool should you use?. <i>Rna</i> , 2016, 22, 839-851.	3.5	622
3	FY Is an RNA 3' End-Processing Factor that Interacts with FCA to Control the Arabidopsis Floral Transition. <i>Cell</i> , 2003, 113, 777-787.	28.9	399
4	Nanopore direct RNA sequencing maps the complexity of Arabidopsis mRNA processing and m6A modification. <i>ELife</i> , 2020, 9, .	6.0	312
5	Autoregulation of FCA pre-mRNA processing controls Arabidopsis flowering time. <i>EMBO Journal</i> , 2003, 22, 3142-3152.	7.8	252
6	The autonomous pathway: epigenetic and post-transcriptional gene regulation in the control of Arabidopsis flowering time. <i>Current Opinion in Plant Biology</i> , 2004, 7, 570-574.	7.1	250
7	The Spen Family Protein FPA Controls Alternative Cleavage and Polyadenylation of RNA. <i>Developmental Cell</i> , 2010, 18, 203-213.	7.0	207
8	Direct sequencing of Arabidopsis thaliana RNA reveals patterns of cleavage and polyadenylation. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 845-852.	8.2	142
9	Arabidopsis RNA immunoprecipitation. <i>Plant Journal</i> , 2009, 59, 163-168.	5.7	75
10	Transcription Termination and Chimeric RNA Formation Controlled by Arabidopsis thaliana FPA. <i>PLoS Genetics</i> , 2013, 9, e1003867.	3.5	67
11	Evolution of flowering in response to day length: Flipping theCONSTANS switch. <i>BioEssays</i> , 2003, 25, 829-832.	2.5	61
12	The RNA-binding protein FPA regulates flg22-triggered defense responses and transcription factor activity by alternative polyadenylation. <i>Scientific Reports</i> , 2013, 3, 2866.	3.3	58
13	The Arabidopsis epitranscriptome. <i>Current Opinion in Plant Biology</i> , 2015, 27, 17-21.	7.1	39
14	NO flowering. <i>BioEssays</i> , 2005, 27, 239-241.	2.5	36
15	Widespread premature transcription termination of Arabidopsis thaliana NLR genes by the spen protein FPA. <i>ELife</i> , 2021, 10, .	6.0	36
16	Chromosome evolution and the genetic basis of agronomically important traits in greater yam. <i>Nature Communications</i> , 2022, 13, 2001.	12.8	35
17	Evolutionary conservation of the spliceosomal protein, U2. <i>Nucleic Acids Research</i> , 1991, 19, 5213-5217.	14.5	34
18	Two zinc finger proteins with functions in m6A writing interact with HAKAI. <i>Nature Communications</i> , 2022, 13, 1127.	12.8	32

#	ARTICLE	IF	CITATIONS
19	Improved Annotation of 3' Untranslated Regions and Complex Loci by Combination of Strand-Specific Direct RNA Sequencing, RNA-Seq and ESTs. PLoS ONE, 2014, 9, e94270.	2.5	27
20	Relative Abundance of Transcripts (RATs): Identifying differential isoform abundance from RNA-seq. F1000Research, 2019, 8, 213.	1.6	20
21	Crystal Structure of the SPOC Domain of the Arabidopsis Flowering Regulator FPA. PLoS ONE, 2016, 11, e0160694.	2.5	18
22	2passtools: two-pass alignment using machine-learning-filtered splice junctions increases the accuracy of intron detection in long-read RNA sequencing. Genome Biology, 2021, 22, 72.	8.8	16
23	Enter exitrans. Genome Biology, 2015, 16, 136.	8.8	15
24	Detection of a plant protein analogous to the yeast spliceosomal protein, PRP8. FEBS Letters, 1993, 318, 4-6.	2.8	13
25	Detection and mitigation of spurious antisense expression with RoSA. F1000Research, 0, 8, 819.	1.6	13
26	How well do RNA-Seq differential gene expression tools perform in a complex eukaryote? A case study in <i>Arabidopsis thaliana</i> . Bioinformatics, 2019, 35, 3372-3377.	4.1	9
27	Detection of antisense transcripts in transgenic plants by RT-PCR. Plant Journal, 1993, 4, 883-885.	5.7	3
28	Splicing of plant pre-mRNAs. Proceedings of the Royal Society of Edinburgh Section B Biological Sciences, 1992, 99, 31-50.	0.2	2