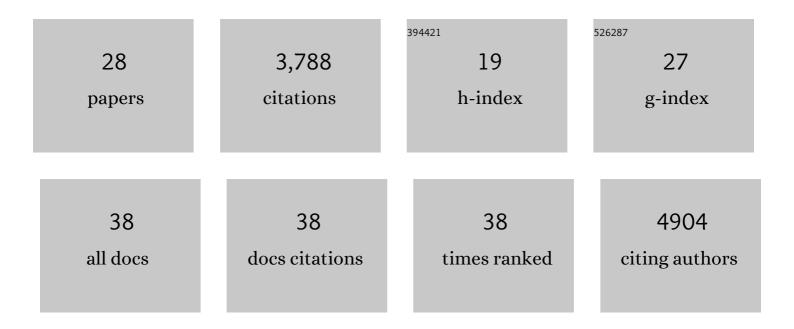
Gordon G Simpson

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/834808/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Two zinc finger proteins with functions in m6A writing interact with HAKAI. Nature Communications, 2022, 13, 1127.	12.8	32
2	Chromosome evolution and the genetic basis of agronomically important traits in greater yam. Nature Communications, 2022, 13, 2001.	12.8	35
3	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
4	Widespread premature transcription termination of Arabidopsis thaliana NLR genes by the spen protein FPA. ELife, 2021, 10, .	6.0	36
5	Nanopore direct RNA sequencing maps the complexity of Arabidopsis mRNA processing and m6A modification. ELife, 2020, 9, .	6.0	312
6	Relative Abundance of Transcripts (RATs): Identifying differential isoform abundance from RNA-seq. F1000Research, 2019, 8, 213.	1.6	20
7	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
8	How many biological replicates are needed in an RNA-seq experiment and which differential expression tool should you use?. Rna, 2016, 22, 839-851.	3.5	622
9	Crystal Structure of the SPOC Domain of the Arabidopsis Flowering Regulator FPA. PLoS ONE, 2016, 11, e0160694.	2.5	18
10	Enter exitrons. Genome Biology, 2015, 16, 136.	8.8	15
11	The Arabidopsis epitranscriptome. Current Opinion in Plant Biology, 2015, 27, 17-21.	7.1	39
12	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
13	Transcription Termination and Chimeric RNA Formation Controlled by Arabidopsis thaliana FPA. PLoS Genetics, 2013, 9, e1003867.	3.5	67
14	The RNA-binding protein FPA regulates flg22-triggered defense responses and transcription factor activity by alternative polyadenylation. Scientific Reports, 2013, 3, 2866.	3.3	58
15	Direct sequencing of Arabidopsis thaliana RNA reveals patterns of cleavage and polyadenylation. Nature Structural and Molecular Biology, 2012, 19, 845-852.	8.2	142
16	The Spen Family Protein FPA Controls Alternative Cleavage and Polyadenylation of RNA. Developmental Cell, 2010, 18, 203-213.	7.0	207
17	Arabidopsis RNA immunoprecipitation. Plant Journal, 2009, 59, 163-168.	5.7	75
10	NO flowering Dis Foreus 2005 27 220 241	0.5	

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#	Article	IF	CITATIONS
19	The autonomous pathway: epigenetic and post-transcriptional gene regulation in the control of Arabidopsis flowering time. Current Opinion in Plant Biology, 2004, 7, 570-574.	7.1	250
20	Autoregulation of FCA pre-mRNA processing controls Arabidopsis flowering time. EMBO Journal, 2003, 22, 3142-3152.	7.8	252
21	Evolution of flowering in response to day length: Flipping theCONSTANS switch. BioEssays, 2003, 25, 829-832.	2.5	61
22	FY Is an RNA $3\hat{a}\in^2$ End-Processing Factor that Interacts with FCA to Control the Arabidopsis Floral Transition. Cell, 2003, 113, 777-787.	28.9	399
23	Arabidopsis, the Rosetta Stone of Flowering Time?. Science, 2002, 296, 285-289.	12.6	954
24	Detection of antisense transcripts in transgenic plants by RT-PCR. Plant Journal, 1993, 4, 883-885.	5.7	3
25	Detection of a plant protein analogous to the yeast spliceosomal protein, PRP8. FEBS Letters, 1993, 318, 4-6.	2.8	13
26	Splicing of plant pre-mRNAs. Proceedings of the Royal Society of Edinburgh Section B Biological Sciences, 1992, 99, 31-50.	0.2	2
27	Evolutionary conservation of the spliceosaomal protein, U2 B― Nucleic Acids Research, 1991, 19, 5213-5217.	14.5	34
28	Detection and mitigation of spurious antisense expression with RoSA. F1000Research, 0, 8, 819.	1.6	13