

# Craig G Simpson

## List of Publications by Year in descending order

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47  
papers

4,074  
citations

201385

27  
h-index

233125

45  
g-index

53  
all docs

53  
docs citations

53  
times ranked

4643  
citing authors

#	ARTICLE	IF	CITATIONS
1	<scp>BaRTv2</scp>: a highly resolved barley reference transcriptome for accurate transcript-specific RNA-seq quantification. <i>Plant Journal</i> , 2022, 111, 1183-1202.	2.8	17
2	EORNA, a barley gene and transcript abundance database. <i>Scientific Data</i> , 2021, 8, 90.	2.4	20
3	Nonsense-Mediated RNA Decay Factor LUPF1 Is Critical for Posttranscriptional and Translational Gene Regulation in Arabidopsis. <i>Plant Cell</i> , 2020, 32, 2725-2741.	3.1	42
4	Editorial: Alternative Splicing Regulation in Plants. <i>Frontiers in Plant Science</i> , 2020, 11, 913.	1.7	6
5	The Effect of Drought on Transcriptome and Hormonal Profiles in Barley Genotypes With Contrasting Drought Tolerance. <i>Frontiers in Plant Science</i> , 2020, 11, 618491.	1.7	33
6	BaRTv1.0: an improved barley reference transcript dataset to determine accurate changes in the barley transcriptome using RNA-seq. <i>BMC Genomics</i> , 2019, 20, 968.	1.2	50
7	High-Resolution RT-PCR Analysis of Alternative Barley Transcripts. <i>Methods in Molecular Biology</i> , 2019, 1900, 269-281.	0.4	11
8	Light Regulates Plant Alternative Splicing through the Control of Transcriptional Elongation. <i>Molecular Cell</i> , 2019, 73, 1066-1074.e3.	4.5	102
9	How does temperature affect splicing events? Isoform switching of splicing factors regulates splicing of <i>LATE ELONGATED HYPOCOTYL</i> ( <i>LHY</i> ). <i>Plant, Cell and Environment</i> , 2018, 41, 1539-1550.	2.8	25
10	QTL Mapping and Marker Assisted Breeding in <i>Rubus</i> spp., 2018, , 121-144.		6
11	Enhancement of Glen Moy x Latham raspberry linkage map using CbS to further understand control of developmental processes leading to fruit ripening. <i>BMC Genetics</i> , 2018, 19, 59.	2.7	31
12	The Expressed Portion of the Barley Genome. <i>Compendium of Plant Genomes</i> , 2018, , 89-107.	0.3	0
13	Developmental Transitions to Fruiting in Red Raspberry. <i>Compendium of Plant Genomes</i> , 2018, , 199-212.	0.3	15
14	Mapping and expression of genes associated with raspberry fruit ripening and softening. <i>Theoretical and Applied Genetics</i> , 2017, 130, 557-572.	1.8	29
15	Alternative Splicing of Barley Clock Genes in Response to Low Temperature. <i>PLoS ONE</i> , 2016, 11, e0168028.	1.1	39
16	The Arabidopsis SR45 Splicing Factor, a Negative Regulator of Sugar Signaling, Modulates SNF1-Related Protein Kinase 1 Stability. <i>Plant Cell</i> , 2016, 28, 1910-1925.	3.1	71
17	Monitoring Alternative Splicing Changes in Arabidopsis Circadian Clock Genes. <i>Methods in Molecular Biology</i> , 2016, 1398, 119-132.	0.4	11
18	At RTD – a comprehensive reference transcript dataset resource for accurate quantification of transcript-specific expression in <i>Arabidopsis thaliana</i> . <i>New Phytologist</i> , 2015, 208, 96-101.	3.5	50

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19	The spliceosome assembly factor GEMIN2 attenuates the effects of temperature on alternative splicing and circadian rhythms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 9382-9387.	3.3	97
20	Lost in Translation: Pitfalls in Deciphering Plant Alternative Splicing Transcripts. <i>Plant Cell</i> , 2015, 27, 2083-2087.	3.1	53
21	The SERRATE protein is involved in alternative splicing in <i>Arabidopsis thaliana</i> . <i>Nucleic Acids Research</i> , 2014, 42, 1224-1244.	6.5	94
22	A Chloroplast Retrograde Signal Regulates Nuclear Alternative Splicing. <i>Science</i> , 2014, 344, 427-430.	6.0	186
23	<i>Arabidopsis</i> PTB 1 and PTB 2 proteins negatively regulate splicing of a mini-exon splicing reporter and affect alternative splicing of endogenous genes differentially. <i>New Phytologist</i> , 2014, 203, 424-436.	3.5	15
24	Long Noncoding RNA Modulates Alternative Splicing Regulators in <i>Arabidopsis</i> . <i>Developmental Cell</i> , 2014, 30, 166-176.	3.1	311
25	Small changes in ambient temperature affect alternative splicing in <i>Arabidopsis thaliana</i> . <i>Plant Signaling and Behavior</i> , 2013, 8, e24638.	1.2	34
26	An hnRNP-like RNA-binding protein affects alternative splicing by in vivo interaction with transcripts in <i>Arabidopsis thaliana</i> . <i>Nucleic Acids Research</i> , 2012, 40, 11240-11255.	6.5	124
27	Transcriptome survey reveals increased complexity of the alternative splicing landscape in <i>Arabidopsis</i> . <i>Genome Research</i> , 2012, 22, 1184-1195.	2.4	750
28	Mutation of <i>Arabidopsis</i> SPLICEOSOMAL TIMEKEEPER LOCUS1 Causes Circadian Clock Defects. <i>Plant Cell</i> , 2012, 24, 4066-4082.	3.1	112
29	Alternative splicing and nonsense-mediated decay modulate expression of important regulatory genes in <i>Arabidopsis</i> . <i>Nucleic Acids Research</i> , 2012, 40, 2454-2469.	6.5	439
30	INTERMEDIUM-C, a modifier of lateral spikelet fertility in barley, is an ortholog of the maize domestication gene TEOSINTE BRANCHED 1. <i>Nature Genetics</i> , 2011, 43, 169-172.	9.4	302
31	A methyl transferase links the circadian clock to the regulation of alternative splicing. <i>Nature</i> , 2010, 468, 112-116.	13.7	286
32	Involvement of the nuclear cap-binding protein complex in alternative splicing in <i>Arabidopsis thaliana</i> . <i>Nucleic Acids Research</i> , 2010, 38, 265-278.	6.5	99
33	Aberrant mRNA Transcripts and the Nonsense-Mediated Decay Proteins UPF2 and UPF3 Are Enriched in the <i>Arabidopsis</i> Nucleolus. <i>Plant Cell</i> , 2009, 21, 2045-2057.	3.1	93
34	Monitoring changes in alternative precursor messenger RNA splicing in multiple gene transcripts. <i>Plant Journal</i> , 2008, 53, 1035-1048.	2.8	113
35	Alternative splicing in plants. <i>Biochemical Society Transactions</i> , 2008, 36, 508-510.	1.6	32
36	Dual functionality of a plant U-rich intronic sequence element. <i>Plant Journal</i> , 2004, 37, 82-91.	2.8	30

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37	Mutational analysis of a plant branchpoint and polypyrimidine tract required for constitutive splicing of a mini-exon. <i>Rna</i> , 2002, 8, 47-56.	1.6	36
38	Requirements for mini-exon inclusion in potato invertase mRNAs provides evidence for exon-scanning interactions in plants. <i>Rna</i> , 2000, 6, 422-433.	1.6	31
39	Interactions between introns via exon definition in plant pre-mRNA splicing. <i>Plant Journal</i> , 1999, 18, 293-302.	2.8	15
40	Processing of vertebrate box C/D small nucleolar RNAs in plant cells. <i>FEBS Journal</i> , 1998, 253, 154-160.	0.2	4
41	Characterization of exon skipping mutants of the COP1 gene from <i>Arabidopsis</i> . <i>Plant Journal</i> , 1998, 15, 125-131.	2.8	32
42	Mutation of putative branchpoint consensus sequences in plant introns reduces splicing efficiency. <i>Plant Journal</i> , 1996, 9, 369-380.	2.8	66
43	<i>Arabidopsis</i> consensus intron sequences. <i>Plant Molecular Biology</i> , 1996, 32, 531-535.	2.0	119
44	Complementary deletions in expressed potato U2snRNA gene variants support the hypothesis that stem-loop IIb is dispensable for splicing. <i>Plant Journal</i> , 1994, 6, 921-925.	2.8	4
45	Detection of antisense transcripts in transgenic plants by RT-PCR. <i>Plant Journal</i> , 1993, 4, 883-885.	2.8	3
46	Splicing of plant pre-mRNAs. <i>Proceedings of the Royal Society of Edinburgh Section B Biological Sciences</i> , 1992, 99, 31-50.	0.2	2
47	Rapid analysis of plant gene expression by a novel reverse transcriptase-PCR method. <i>Plant Journal</i> , 1992, 2, 835-836.	2.8	21