John W S Brown

List of Publications by Year
in descending order

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99 papers	11,026 citations	50170 46 h-index	32761 100 g-index
112 all docs	112 docs citations	112 times ranked	10576 citing authors

#	Article	IF	Citations
1	A physical, genetic and functional sequence assembly of the barley genome. Nature, 2012, 491, 711-716.	13.7	1,416
2	Transcriptome survey reveals increased complexity of the alternative splicing landscape in Arabidopsis. Genome Research, 2012, 22, 1184-1195.	2.4	750
3	Alternative Splicing at the Intersection of Biological Timing, Development, and Stress Responses. Plant Cell, 2013, 25, 3640-3656.	3.1	590
4	Filtering of deep sequencing data reveals the existence of abundant Dicer-dependent small RNAs derived from tRNAs. Rna, 2009, 15, 2147-2160.	1.6	525
5	Alternative splicing in plants â€“ coming of age. Trends in Plant Science, 2012, 17, 616-623.	4.3	464
6	Alternative splicing and nonsense-mediated decay modulate expression of important regulatory genes in Arabidopsis. Nucleic Acids Research, 2012, 40, 2454-2469.	6.5	439
7	A catalogue of splice junction and putative branch point sequences from plant introns. Nucleic Acids Research, 1986, 14, 9549-9559.	6.5	396
8	Proteomic Analysis of the Arabidopsis Nucleolus Suggests Novel Nucleolar Functions. Molecular Biology of the Cell, 2005, 16, 260-269.	0.9	352
9	Alternative Splicing Mediates Responses of the Arabidopsis Circadian Clock to Temperature Changes. Plant Cell, 2012, 24, 961-981.	3.1	325
10	Long Noncoding RNA Modulates Alternative Splicing Regulators in Arabidopsis. Developmental Cell, 2014, 30, 166-176.	3.1	311
11	Rapid and Dynamic Alternative Splicing Impacts the Arabidopsis Cold Response Transcriptome. Plant Cell, 2018, 30, 1424-1444.	3.1	294
12	A methyl transferase links the circadian clock to the regulation of alternative splicing. Nature, 2010, 468, 112-116.	13.7	286
13	A high quality Arabidopsis transcriptome for accurate transcript-level analysis of alternative splicing. Nucleic Acids Research, 2017, 45, 5061-5073.	6.5	262
14	Exome sequencing of geographically diverse barley landraces and wild relatives gives insights into environmental adaptation. Nature Genetics, 2016, 48, 1024-1030.	9.4	259
15	Molecular analysis of resveratrol synthase. cDNA, genomic clones and relationship with chalcone synthase. FEBS Journal, 1988, 172, 161-169.	0.2	198
16	A Chloroplast Retrograde Signal Regulates Nuclear Alternative Splicing. Science, 2014, 344, 427-430.	6.0	186
17	Interaction of a plant virus-encoded protein with the major nucleolar protein fibrillarin is required for systemic virus infection. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 11115-11120.	3.3	162
18	Cajal bodies and the nucleolus are required for a plant virus systemic infection. EMBO Journal, 2007, 26, 2169-2179.	3.5	138

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19	Intronic noncoding RNAs and splicing. Trends in Plant Science, 2008, 13, 335-342.	4.3	129
20	Plant snoRNAs: functional evolution and new modes of gene expression. Trends in Plant Science, 2003, 8, 42-49.	4.3	126
21	An hnRNP-like RNA-binding protein affects alternative splicing by in vivo interaction with transcripts in Arabidopsis thaliana. Nucleic Acids Research, 2012, 40, 11240-11255.	6.5	124
22	Arabidopsis consensus intron sequences. Plant Molecular Biology, 1996, 32, 531-535.	2.0	119
23	Plant nuclear bodies. Current Opinion in Plant Biology, 2004, 7, 614-620.	3.5	118
24	Arabidopsis intron mutations and pre-mRNA splicing. Plant Journal, 1996, 10, 771-780.	2.8	116
25	Monitoring changes in alternative precursor messenger RNA splicing in multiple gene transcripts. Plant Journal, 2008, 53, 1035-1048.	2.8	113
26	Mutation of Arabidopsis SPLICEOSOMAL TIMEKEEPER LOCUS1 Causes Circadian Clock Defects. Plant Cell, 2012, 24, 4066-4082.	3.1	112
27	Nucleoli: Composition, Function, and Dynamics. Plant Physiology, 2012, 158, 44-51.	2.3	109
28	Light Regulates Plant Alternative Splicing through the Control of Transcriptional Elongation. Molecular Cell, 2019, 73, 1066-1074.e3.	4.5	102
29	Involvement of the nuclear cap-binding protein complex in alternative splicing in Arabidopsis thaliana. Nucleic Acids Research, 2010, 38, 265-278.	6.5	99
30	The spliceosome assembly factor GEMIN2 attenuates the effects of temperature on alternative splicing and circadian rhythms. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 9382-9387.	3.3	97
31	Illuminating the dark side of the human transcriptome with long read transcript sequencing. BMC Genomics, 2020, 21, 751.	1.2	97
32	Aberrant mRNA Transcripts and the Nonsense-Mediated Decay Proteins UPF2 and UPF3 Are Enriched in theArabidopsisNucleolus Â. Plant Cell, 2009, 21, 2045-2057.	3.1	93
33	Plant snoRNA database. Nucleic Acids Research, 2003, 31, 432-435.	6.5	82
34	The Arabidopsis SR45 Splicing Factor, a Negative Regulator of Sugar Signaling, Modulates SNF1-Related Protein Kinase 1 Stability. Plant Cell, 2016, 28, 1910-1925.	3.1	71
35	Cold-Dependent Expression and Alternative Splicing of Arabidopsis Long Non-coding RNAs. Frontiers in Plant Science, 2019, 10, 235.	1.7	70
36	Mutation of putative branchpoint consensus sequences in plant introns reduces splicing efficiency. Plant Journal, 1996, 9, 369-380.	2.8	66

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37	Evolutionary Relationships Among Barley and Arabidopsis Core Circadian Clock and Clock-Associated Genes. Journal of Molecular Evolution, 2015, 80, 108-119.	0.8	59
38	Small Nucleolar RNAs and Pre-rRNA Processing in Plants. Plant Cell, 1998, 10, 649-657.	3.1	58
39	TSIS: an R package to infer alternative splicing isoform switches for time-series data. Bioinformatics, 2017, 33, 3308-3310.	1.8	58
40	3D RNA-seq: a powerful and flexible tool for rapid and accurate differential expression and alternative splicing analysis of RNA-seq data for biologists. RNA Biology, 2021, 18, 1574-1587.	1.5	58
41	CONTROL OF ENDOSPERM PROTEINS IN TRITICUM AESTIVUM (var. CHINESE SPRING) AND AEGILOPS UMBELLULATA BY HOMOEOLOGOUS GROUP 1 CHROMOSOMES. Genetics, 1979, 93, 189-200.	1.2	55
42	Determinants of Plant U12-Dependent Intron Splicing Efficiency. Plant Cell, 2004, 16, 1340-1352.	3.1	54
43	Lost in Translation: Pitfalls in Deciphering Plant Alternative Splicing Transcripts. Plant Cell, 2015, 27, 2083-2087.	3.1	53
44	A Plant Virus Movement Protein Forms Ringlike Complexes with the Major Nucleolar Protein, Fibrillarin, In Vitro. Journal of Molecular Biology, 2008, 376, 932-937.	2.0	51
45	At RTD â€“ a comprehensive reference transcript dataset resource forÂaccurate quantification of transcriptâ€specific expression in Arabidopsis thaliana. New Phytologist, 2015, 208, 96-101.	3.5	50
46	BaRTv1.0: an improved barley reference transcript dataset to determine accurate changes in the barley transcriptome using RNA-seq. BMC Genomics, 2019, 20, 968.	1.2	50
47	Cloning and characterization of two subunits of Arabidopsis thaliana nuclear cap-binding complex. Gene, 2002, 283, 171-183.	1.0	48
48	The malate synthase gene of cucumber. Plant Molecular Biology, 1989, 13, 673-684.	2.0	47
49	Molecular characterisation of plant U14 small nucleolar RNA genes: closely linked genes are transcribed as polycistronic U14 transcripts. Nucleic Acids Research, 1994, 22, 5196-5203.	6.5	46
50	Phaseolin mRNA is translated to yield glycosylated polypeptides in Xenopus oocytes. Nature, 1981, 294, 175-176.	13.7	44
51	Nonsense-Mediated RNA Decay Factor UPF1 Is Critical for Posttranscriptional and Translational Gene Regulation in Arabidopsis. Plant Cell, 2020, 32, 2725-2741.	3.1	42
52	Thermoplasticity in the plant circadian clock. Plant Signaling and Behavior, 2012, 7, 1219-1223.	1.2	41
53	Maize U2 snRNAs: gene sequence and expression. Nucleic Acids Research, 1989, 17, 8991-9001.	6.5	40
54	Plant U13 orthologues and orphan snoRNAs identified by RNomics of RNA from Arabidopsis nucleoli. Nucleic Acids Research, 2010, 38, 3054-3067.	6.5	39

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55	Alternative Splicing of Barley Clock Genes in Response to Low Temperature. PLoS ONE, 2016, 11, e0168028.	1.1	39
56	Plant SILAC: Stable-Isotope Labelling with Amino Acids of Arabidopsis Seedlings for Quantitative Proteomics. PLoS ONE, 2013, 8, e72207.	1.1	39
57	Mutational analysis of a plant branchpoint and polypyrimidine tract required for constitutive splicing of a mini-exon. Rna, 2002, 8, 47-56.	1.6	36
58	Highâ€quality reference transcript datasets hold the key to transcriptâ€specific RNAâ€sequencing analysis in plants. New Phytologist, 2017, 213, 525-530.	3.5	35
59	A high-resolution single-molecule sequencing-based Arabidopsis transcriptome using novel methods of Iso-seq analysis. Genome Biology, 2022, 23, .	3.8	35
60	Evolutionary conservation of the spliceosaomal protein, U2 Bâ€. Nucleic Acids Research, 1991, 19, 5213-5217.	6.5	34
61	Small changes in ambient temperature affect alternative splicing inArabidopsis thaliana. Plant Signaling and Behavior, 2013, 8, e24638.	1.2	34
62	Characterization of exon skipping mutants of the COP1 gene from Arabidopsis. Plant Journal, 1998, 15, 125-131.	2.8	32
63	Splicing-independent processing of plant box C/D and box H/ACA small nucleolar RNAs. Plant Molecular Biology, 1999, 39, 1091-1100.	2.0	32
64	Alternative splicing in plants. Biochemical Society Transactions, 2008, 36, 508-510.	1.6	32
65	Requirements for mini-exon inclusion in potato invertase mRNAs provides evidence for exon-scanning interactions in plants. Rna, 2000, 6, 422-433.	1.6	31
66	Dual functionality of a plant U-rich intronic sequence element. Plant Journal, 2004, 37, 82-91.	2.8	30
67	Genetic control of bean seed protein. Critical Reviews in Plant Sciences, 1988, 7, 93-116.	2.7	28
68	Sequence and expression of potato U2 snRNA genes. Nucleic Acids Research, 1991, 19, 249-256.	6.5	28
69	Regulation of plant gene expression by alternative splicing. Biochemical Society Transactions, 2010, 38, 667-671.	1.6	27
70	Efficient splicing of an AU-rich antisense intron sequence. Plant Molecular Biology, 1993, 21, 205-211.	2.0	25
71	How does temperature affect splicing events? Isoform switching of splicing factors regulates splicing of LATE ELONGATED HYPOCOTYL (LHY). Plant, Cell and Environment, 2018, 41, 1539-1550.	2.8	25
72	Microheterogeneity of Globulin-1 Storage Protein from French Bean with Isoelectrofocusing. Plant Physiology, 1980, 66, 838-840.	2.3	21

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73	Rapid analysis of plant gene expression by a novel reverse transcriptaseâ€PCR method. Plant Journal, 1992, 2, 835-836.	2.8	21
74	Expression of intron modified NPT II genes in monocotyledonous and dicotyledonous plant cells. Molecular Breeding, 1997, 3, 15-28.	1.0	21
75	Alternative Splicing of Circadian Clock Genes Correlates With Temperature in Field-Grown Sugarcane. Frontiers in Plant Science, 2019, 10, 1614.	1.7	20
76	Bean lectins. III. Evidence for greater complexity in the structural model of Phaseolus vulgaris lectin. Plant Science Letters, 1983, 31, 193-203.	1.9	19
77	Analysis of distal flanking regions of maize 19-kDa zein genes. Gene, 1989, 80, 249-258.	1.0	18
78	<scp>BaRTv2</scp>: a highly resolved barley reference transcriptome for accurate transcriptâ€specific <scp>RNA</scp>â€seq quantification. Plant Journal, 2022, 111, 1183-1202.	2.8	17
79	A functional splice site in the 5' untranslated region of a zein gene. Nucleic Acids Research, 1990, 18, 111-117.	6.5	16
80	Differential expression of U5snRNA gene variants in maize (Zea mays) protoplasts. Plant Molecular Biology, 1993, 21, 133-143.	2.0	16
81	Interactions between introns via exon definition in plant pre-mRNA splicing. Plant Journal, 1999, 18, 293-302.	2.8	15
82	Localization of eIF4A-III in the nucleolus and splicing speckles is an indicator of plant stress. Plant Signaling and Behavior, 2009, 4, 1148-1151.	1.2	15
83	Arabidopsis PTB 1 and PTB 2 proteins negatively regulate splicing of a miniâ€exon splicing reporter and affect alternative splicing of endogenous genes differentially. New Phytologist, 2014, 203, 424-436.	3.5	15
84	Characterization and expression of U1snRNA genes from potato. Plant Molecular Biology, 1992, 19, 959-971.	2.0	14
85	Evaluation and improvement of the regulatory inference for large co-expression networks with limited sample size. BMC Systems Biology, 2017, 11, 62.	3.0	14
86	Sequence variation and linkage of potato U2snRNA-encoding genes established by PCR. Gene, 1991, 107, 197-204.	1.0	13
87	Detection of a plant protein analogous to the yeast spliceosomal protein, PRP8. FEBS Letters, 1993, 318, 4-6.	1.3	13
88	Alternative splicing of mini-exons in the Arabidopsis leaf rust receptor-like kinase LRK10 genes affects subcellular localisation. Plant Cell Reports, 2015, 34, 495-505.	2.8	12
89	High-Resolution RT-PCR Analysis of Alternative Barley Transcripts. Methods in Molecular Biology, 2019, 1900, 269-281.	0.4	11
90	Differential expression of potato U1A spliceosomal protein genes: a rapid method for expression profiling of multigene families. Plant Molecular Biology, 2001, 45, 449-460.	2.0	5

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91	Complementary deletions in expressed potato U2snRNA gene variants support the hypothesis that stem-loop IIb is dispensable for splicing. Plant Journal, 1994, 6, 921-925.	2.8	4
92	Processing of vertebrate box C/D small nucleolar RNAs in plant cells. FEBS Journal, 1998, 253, 154-160.	0.2	4
93	Detection of antisense transcripts in transgenic plants by RT-PCR. Plant Journal, 1993, 4, 883-885.	2.8	3
94	Splicing of plant pre-mRNAs. Proceedings of the Royal Society of Edinburgh Section B Biological Sciences, 1992, 99, 31-50.	0.2	2
95	Experimental Design for Time-Series RNA-Seq Analysis of Gene Expression and Alternative Splicing. Methods in Molecular Biology, 2022, 2398, 173-188.	0.4	2
96	Plant UsnRNA genes. Molecular Biology Reports, 1990, 14, 147-147.	1.0	1
97	The effects of ribozymes on gene expression in plants. Biochemical Society Transactions, 1992, 20, 344S-344S.	1.6	1
98	Genomic organisation of plant U14 snoRNA genes. Biochemical Society Transactions, 1995, 23, 314S-314S.	1.6	1
99	U14snoRNAs of the fern, Asplenium nidus, contain large sequence insertions compared with those of higher plants. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 1998, 1397, 325-330.	2.4	1