

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	Experimental Design for Time-Series RNA-Seq Analysis of Gene Expression and Alternative Splicing. <i>Methods in Molecular Biology</i> , 2022, 2398, 173-188.	0.4	2
2	<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
3	A high-resolution single-molecule sequencing-based Arabidopsis transcriptome using novel methods of Iso-seq analysis. <i>Genome Biology</i> , 2022, 23, .	3.8	35
4	3D RNA-seq: a powerful and flexible tool for rapid and accurate differential expression and alternative splicing analysis of RNA-seq data for biologists. <i>RNA Biology</i> , 2021, 18, 1574-1587.	1.5	58
5	Nonsense-Mediated RNA Decay Factor UPF1 Is Critical for Posttranscriptional and Translational Gene Regulation in Arabidopsis. <i>Plant Cell</i> , 2020, 32, 2725-2741.	3.1	42
6	Illuminating the dark side of the human transcriptome with long read transcript sequencing. <i>BMC Genomics</i> , 2020, 21, 751.	1.2	97
7	Cold-Dependent Expression and Alternative Splicing of Arabidopsis Long Non-coding RNAs. <i>Frontiers in Plant Science</i> , 2019, 10, 235.	1.7	70
8	Alternative Splicing of Circadian Clock Genes Correlates With Temperature in Field-Grown Sugarcane. <i>Frontiers in Plant Science</i> , 2019, 10, 1614.	1.7	20
9	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
10	High-Resolution RT-PCR Analysis of Alternative Barley Transcripts. <i>Methods in Molecular Biology</i> , 2019, 1900, 269-281.	0.4	11
11	Light Regulates Plant Alternative Splicing through the Control of Transcriptional Elongation. <i>Molecular Cell</i> , 2019, 73, 1066-1074.e3.	4.5	102
12	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
13	Rapid and Dynamic Alternative Splicing Impacts the Arabidopsis Cold Response Transcriptome. <i>Plant Cell</i> , 2018, 30, 1424-1444.	3.1	294
14	A high quality Arabidopsis transcriptome for accurate transcript-level analysis of alternative splicing. <i>Nucleic Acids Research</i> , 2017, 45, 5061-5073.	6.5	262
15	TSIS: an R package to infer alternative splicing isoform switches for time-series data. <i>Bioinformatics</i> , 2017, 33, 3308-3310.	1.8	58
16	Evaluation and improvement of the regulatory inference for large co-expression networks with limited sample size. <i>BMC Systems Biology</i> , 2017, 11, 62.	3.0	14
17	High-quality reference transcript datasets hold the key to transcript-specific RNA-seq analysis in plants. <i>New Phytologist</i> , 2017, 213, 525-530.	3.5	35
18	Alternative Splicing of Barley Clock Genes in Response to Low Temperature. <i>PLoS ONE</i> , 2016, 11, e0168028.	1.1	39

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19	Exome sequencing of geographically diverse barley landraces and wild relatives gives insights into environmental adaptation. <i>Nature Genetics</i> , 2016, 48, 1024-1030.	9.4	259
20	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
21	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
22	Evolutionary Relationships Among Barley and Arabidopsis Core Circadian Clock and Clock-Associated Genes. <i>Journal of Molecular Evolution</i> , 2015, 80, 108-119.	0.8	59
23	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
24	Alternative splicing of mini-exons in the Arabidopsis leaf rust receptor-like kinase LRK10 genes affects subcellular localisation. <i>Plant Cell Reports</i> , 2015, 34, 495-505.	2.8	12
25	Lost in Translation: Pitfalls in Deciphering Plant Alternative Splicing Transcripts. <i>Plant Cell</i> , 2015, 27, 2083-2087.	3.1	53
26	A Chloroplast Retrograde Signal Regulates Nuclear Alternative Splicing. <i>Science</i> , 2014, 344, 427-430.	6.0	186
27	Arabidopsis 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
28	Long Noncoding RNA Modulates Alternative Splicing Regulators in Arabidopsis. <i>Developmental Cell</i> , 2014, 30, 166-176.	3.1	311
29	Alternative Splicing at the Intersection of Biological Timing, Development, and Stress Responses. <i>Plant Cell</i> , 2013, 25, 3640-3656.	3.1	590
30	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
31	Plant SILAC: Stable-Isotope Labelling with Amino Acids of Arabidopsis Seedlings for Quantitative Proteomics. <i>PLoS ONE</i> , 2013, 8, e72207.	1.1	39
32	Thermoplasticity in the plant circadian clock. <i>Plant Signaling and Behavior</i> , 2012, 7, 1219-1223.	1.2	41
33	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
34	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
35	Alternative Splicing Mediates Responses of the <i>Arabidopsis</i> Circadian Clock to Temperature Changes. <i>Plant Cell</i> , 2012, 24, 961-981.	3.1	325
36	A physical, genetic and functional sequence assembly of the barley genome. <i>Nature</i> , 2012, 491, 711-716.	13.7	1,416

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37	Mutation of <i>Arabidopsis</i> SPLICEOSOMAL TIMEKEEPER LOCUS1 Causes Circadian Clock Defects. <i>Plant Cell</i> , 2012, 24, 4066-4082.	3.1	112
38	Nucleoli: Composition, Function, and Dynamics. <i>Plant Physiology</i> , 2012, 158, 44-51.	2.3	109
39	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
40	Alternative splicing in plants – coming of age. <i>Trends in Plant Science</i> , 2012, 17, 616-623.	4.3	464
41	Regulation of plant gene expression by alternative splicing. <i>Biochemical Society Transactions</i> , 2010, 38, 667-671.	1.6	27
42	A methyl transferase links the circadian clock to the regulation of alternative splicing. <i>Nature</i> , 2010, 468, 112-116.	13.7	286
43	Plant U13 orthologues and orphan snoRNAs identified by RNomics of RNA from <i>Arabidopsis</i> nucleoli. <i>Nucleic Acids Research</i> , 2010, 38, 3054-3067.	6.5	39
44	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
45	Localization of eIF4A-III in the nucleolus and splicing speckles is an indicator of plant stress. <i>Plant Signaling and Behavior</i> , 2009, 4, 1148-1151.	1.2	15
46	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
47	Filtering of deep sequencing data reveals the existence of abundant Dicer-dependent small RNAs derived from tRNAs. <i>Rna</i> , 2009, 15, 2147-2160.	1.6	525
48	Monitoring changes in alternative precursor messenger RNA splicing in multiple gene transcripts. <i>Plant Journal</i> , 2008, 53, 1035-1048.	2.8	113
49	A Plant Virus Movement Protein Forms Ringlike Complexes with the Major Nucleolar Protein, Fibrillarin, In Vitro. <i>Journal of Molecular Biology</i> , 2008, 376, 932-937.	2.0	51
50	Intronic noncoding RNAs and splicing. <i>Trends in Plant Science</i> , 2008, 13, 335-342.	4.3	129
51	Alternative splicing in plants. <i>Biochemical Society Transactions</i> , 2008, 36, 508-510.	1.6	32
52	Interaction of a plant virus-encoded protein with the major nucleolar protein fibrillarin is required for systemic virus infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 11115-11120.	3.3	162
53	Cajal bodies and the nucleolus are required for a plant virus systemic infection. <i>EMBO Journal</i> , 2007, 26, 2169-2179.	3.5	138
54	Proteomic Analysis of the <i>Arabidopsis</i> Nucleolus Suggests Novel Nucleolar Functions. <i>Molecular Biology of the Cell</i> , 2005, 16, 260-269.	0.9	352

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55	Determinants of Plant U12-Dependent Intron Splicing Efficiency. <i>Plant Cell</i> , 2004, 16, 1340-1352.	3.1	54
56	Plant nuclear bodies. <i>Current Opinion in Plant Biology</i> , 2004, 7, 614-620.	3.5	118
57	Dual functionality of a plant U-rich intronic sequence element. <i>Plant Journal</i> , 2004, 37, 82-91.	2.8	30
58	Plant snoRNAs: functional evolution and new modes of gene expression. <i>Trends in Plant Science</i> , 2003, 8, 42-49.	4.3	126
59	Plant snoRNA database. <i>Nucleic Acids Research</i> , 2003, 31, 432-435.	6.5	82
60	Cloning and characterization of two subunits of Arabidopsis thaliana nuclear cap-binding complex. <i>Gene</i> , 2002, 283, 171-183.	1.0	48
61	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
62	Differential expression of potato U1A spliceosomal protein genes: a rapid method for expression profiling of multigene families. <i>Plant Molecular Biology</i> , 2001, 45, 449-460.	2.0	5
63	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
64	Interactions between introns via exon definition in plant pre-mRNA splicing. <i>Plant Journal</i> , 1999, 18, 293-302.	2.8	15
65	Splicing-independent processing of plant box C/D and box H/ACA small nucleolar RNAs. <i>Plant Molecular Biology</i> , 1999, 39, 1091-1100.	2.0	32
66	U14snoRNAs of the fern, <i>Asplenium nidus</i> , contain large sequence insertions compared with those of higher plants. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 1998, 1397, 325-330.	2.4	1
67	Processing of vertebrate box C/D small nucleolar RNAs in plant cells. <i>FEBS Journal</i> , 1998, 253, 154-160.	0.2	4
68	Characterization of exon skipping mutants of the COP1 gene from Arabidopsis. <i>Plant Journal</i> , 1998, 15, 125-131.	2.8	32
69	Small Nucleolar RNAs and Pre-rRNA Processing in Plants. <i>Plant Cell</i> , 1998, 10, 649-657.	3.1	58
70	Expression of intron modified NPT II genes in monocotyledonous and dicotyledonous plant cells. <i>Molecular Breeding</i> , 1997, 3, 15-28.	1.0	21
71	Mutation of putative branchpoint consensus sequences in plant introns reduces splicing efficiency. <i>Plant Journal</i> , 1996, 9, 369-380.	2.8	66
72	Arabidopsis intron mutations and pre-mRNA splicing. <i>Plant Journal</i> , 1996, 10, 771-780.	2.8	116

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73	Arabidopsis consensus intron sequences. <i>Plant Molecular Biology</i> , 1996, 32, 531-535.	2.0	119
74	Genomic organisation of plant U14 snoRNA genes. <i>Biochemical Society Transactions</i> , 1995, 23, 314S-314S.	1.6	1
75	Molecular characterisation of plant U14 small nucleolar RNA genes: closely linked genes are transcribed as polycistronic U14 transcripts. <i>Nucleic Acids Research</i> , 1994, 22, 5196-5203.	6.5	46
76	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
77	Detection of antisense transcripts in transgenic plants by RT-PCR. <i>Plant Journal</i> , 1993, 4, 883-885.	2.8	3
78	Efficient splicing of an AU-rich antisense intron sequence. <i>Plant Molecular Biology</i> , 1993, 21, 205-211.	2.0	25
79	Differential expression of U5snRNA gene variants in maize (<i>Zea mays</i>) protoplasts. <i>Plant Molecular Biology</i> , 1993, 21, 133-143.	2.0	16
80	Detection of a plant protein analogous to the yeast spliceosomal protein, PRP8. <i>FEBS Letters</i> , 1993, 318, 4-6.	1.3	13
81	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
82	The effects of ribozymes on gene expression in plants. <i>Biochemical Society Transactions</i> , 1992, 20, 344S-344S.	1.6	1
83	Characterization and expression of U1snRNA genes from potato. <i>Plant Molecular Biology</i> , 1992, 19, 959-971.	2.0	14
84	Rapid analysis of plant gene expression by a novel reverse transcriptase-PCR method. <i>Plant Journal</i> , 1992, 2, 835-836.	2.8	21
85	Sequence variation and linkage of potato U2snRNA-encoding genes established by PCR. <i>Gene</i> , 1991, 107, 197-204.	1.0	13
86	Evolutionary conservation of the spliceosomal protein, U2. <i>Nucleic Acids Research</i> , 1991, 19, 5213-5217.	6.5	34
87	Sequence and expression of potato U2 snRNA genes. <i>Nucleic Acids Research</i> , 1991, 19, 249-256.	6.5	28
88	Plant UsnRNA genes. <i>Molecular Biology Reports</i> , 1990, 14, 147-147.	1.0	1
89	A functional splice site in the 5' untranslated region of a zein gene. <i>Nucleic Acids Research</i> , 1990, 18, 111-117.	6.5	16
90	Maize U2 snRNAs: gene sequence and expression. <i>Nucleic Acids Research</i> , 1989, 17, 8991-9001.	6.5	40

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91	The malate synthase gene of cucumber. <i>Plant Molecular Biology</i> , 1989, 13, 673-684.	2.0	47
92	Analysis of distal flanking regions of maize 19-kDa zein genes. <i>Gene</i> , 1989, 80, 249-258.	1.0	18
93	Molecular analysis of resveratrol synthase. cDNA, genomic clones and relationship with chalcone synthase. <i>FEBS Journal</i> , 1988, 172, 161-169.	0.2	198
94	Genetic control of bean seed protein. <i>Critical Reviews in Plant Sciences</i> , 1988, 7, 93-116.	2.7	28
95	A catalogue of splice junction and putative branch point sequences from plant introns. <i>Nucleic Acids Research</i> , 1986, 14, 9549-9559.	6.5	396
96	Bean lectins. III. Evidence for greater complexity in the structural model of <i>Phaseolus vulgaris</i> lectin. <i>Plant Science Letters</i> , 1983, 31, 193-203.	1.9	19
97	Phaseolin mRNA is translated to yield glycosylated polypeptides in <i>Xenopus</i> oocytes. <i>Nature</i> , 1981, 294, 175-176.	13.7	44
98	Microheterogeneity of Globulin-1 Storage Protein from French Bean with Isoelectrofocusing. <i>Plant Physiology</i> , 1980, 66, 838-840.	2.3	21
99	CONTROL OF ENDOSPERM PROTEINS IN <i>TRITICUM AESTIVUM</i> (var. CHINESE SPRING) AND <i>AEGILOPS UMBELLULATA</i> BY HOMOELOGOUS GROUP 1 CHROMOSOMES. <i>Genetics</i> , 1979, 93, 189-200.	1.2	55