John W S Brown

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/8607662/publications.pdf

Version: 2024-02-01

99 papers	11,026 citations	50276 46 h-index	32842 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. Methods in Molecular Biology, 2022, 2398, 173-188.	0.9	2
2	<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.	5.7	17
3	A high-resolution single-molecule sequencing-based Arabidopsis transcriptome using novel methods of Iso-seq analysis. Genome Biology, 2022, 23, .	8.8	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. RNA Biology, 2021, 18, 1574-1587.	3.1	58
5	Nonsense-Mediated RNA Decay Factor UPF1 Is Critical for Posttranscriptional and Translational Gene Regulation in Arabidopsis. Plant Cell, 2020, 32, 2725-2741.	6.6	42
6	Illuminating the dark side of the human transcriptome with long read transcript sequencing. BMC Genomics, 2020, 21, 751.	2.8	97
7	Cold-Dependent Expression and Alternative Splicing of Arabidopsis Long Non-coding RNAs. Frontiers in Plant Science, 2019, 10, 235.	3.6	70
8	Alternative Splicing of Circadian Clock Genes Correlates With Temperature in Field-Grown Sugarcane. Frontiers in Plant Science, 2019, 10, 1614.	3.6	20
9	BaRTv1.0: an improved barley reference transcript dataset to determine accurate changes in the barley transcriptome using RNA-seq. BMC Genomics, 2019, 20, 968.	2.8	50
10	High-Resolution RT-PCR Analysis of Alternative Barley Transcripts. Methods in Molecular Biology, 2019, 1900, 269-281.	0.9	11
11	Light Regulates Plant Alternative Splicing through the Control of Transcriptional Elongation. Molecular Cell, 2019, 73, 1066-1074.e3.	9.7	102
12	How does temperature affect splicing events? Isoform switching of splicing factors regulates splicing of <i>LATE ELONGATED HYPOCOTYL</i> (<i>LHY</i>). Plant, Cell and Environment, 2018, 41, 1539-1550.	5.7	25
13	Rapid and Dynamic Alternative Splicing Impacts the Arabidopsis Cold Response Transcriptome. Plant Cell, 2018, 30, 1424-1444.	6.6	294
14	A high quality Arabidopsis transcriptome for accurate transcript-level analysis of alternative splicing. Nucleic Acids Research, 2017, 45, 5061-5073.	14.5	262
15	TSIS: an R package to infer alternative splicing isoform switches for time-series data. Bioinformatics, 2017, 33, 3308-3310.	4.1	58
16	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
17	Highâ€quality reference transcript datasets hold the key to transcriptâ€specific RNAâ€sequencing analysis in plants. New Phytologist, 2017, 213, 525-530.	7.3	35
18	Alternative Splicing of Barley Clock Genes in Response to Low Temperature. PLoS ONE, 2016, 11, e0168028.	2.5	39

#	ARTICLE	IF	CITATIONS
19	Exome sequencing of geographically diverse barley landraces and wild relatives gives insights into environmental adaptation. Nature Genetics, 2016, 48, 1024-1030.	21.4	259
20	The Arabidopsis SR45 Splicing Factor, a Negative Regulator of Sugar Signaling, Modulates SNF1-Related Protein Kinase 1 Stability. Plant Cell, 2016, 28, 1910-1925.	6.6	71
21	At RTD â€“ a comprehensive reference transcript dataset resource forÂaccurate quantification of transcriptâ€specific expression in Arabidopsis thaliana. New Phytologist, 2015, 208, 96-101.	7.3	50
22	Evolutionary Relationships Among Barley and Arabidopsis Core Circadian Clock and Clock-Associated Genes. Journal of Molecular Evolution, 2015, 80, 108-119.	1.8	59
23	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.	7.1	97
24	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.	5.6	12
25	Lost in Translation: Pitfalls in Deciphering Plant Alternative Splicing Transcripts. Plant Cell, 2015, 27, 2083-2087.	6.6	53
26	A Chloroplast Retrograde Signal Regulates Nuclear Alternative Splicing. Science, 2014, 344, 427-430.	12.6	186
27	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.	7.3	15
28	Long Noncoding RNA Modulates Alternative Splicing Regulators in Arabidopsis. Developmental Cell, 2014, 30, 166-176.	7.0	311
29	Alternative Splicing at the Intersection of Biological Timing, Development, and Stress Responses. Plant Cell, 2013, 25, 3640-3656.	6.6	590
30	Small changes in ambient temperature affect alternative splicing in<i>Arabidopsis thaliana</i>. Plant Signaling and Behavior, 2013, 8, e24638.	2.4	34
31	Plant SILAC: Stable-Isotope Labelling with Amino Acids of Arabidopsis Seedlings for Quantitative Proteomics. PLoS ONE, 2013, 8, e72207.	2.5	39
32	Thermoplasticity in the plant circadian clock. Plant Signaling and Behavior, 2012, 7, 1219-1223.	2.4	41
33	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.	14.5	124
34	Transcriptome survey reveals increased complexity of the alternative splicing landscape in <i>Arabidopsis</i>. Genome Research, 2012, 22, 1184-1195.	5.5	750
35	Alternative Splicing Mediates Responses of the <i>Arabidopsis</i> Circadian Clock to Temperature Changes. Plant Cell, 2012, 24, 961-981.	6.6	325
36	A physical, genetic and functional sequence assembly of the barley genome. Nature, 2012, 491, 711-716.	27.8	1,416

#	ARTICLE	IF	CITATIONS
37	Mutation of <i>Arabidopsis SPLICEOSOMAL TIMEKEEPER LOCUS1</i> Causes Circadian Clock Defects. Plant Cell, 2012, 24, 4066-4082.	6.6	112
38	Nucleoli: Composition, Function, and Dynamics. Plant Physiology, 2012, 158, 44-51.	4.8	109
39	Alternative splicing and nonsense-mediated decay modulate expression of important regulatory genes in Arabidopsis. Nucleic Acids Research, 2012, 40, 2454-2469.	14.5	439
40	Alternative splicing in plants â€“ coming of age. Trends in Plant Science, 2012, 17, 616-623.	8.8	464
41	Regulation of plant gene expression by alternative splicing. Biochemical Society Transactions, 2010, 38, 667-671.	3.4	27
42	A methyl transferase links the circadian clock to the regulation of alternative splicing. Nature, 2010, 468, 112-116.	27.8	286
43	Plant U13 orthologues and orphan snoRNAs identified by RNomics of RNA from Arabidopsis nucleoli. Nucleic Acids Research, 2010, 38, 3054-3067.	14.5	39
44	Involvement of the nuclear cap-binding protein complex in alternative splicing in Arabidopsis thaliana. Nucleic Acids Research, 2010, 38, 265-278.	14.5	99
45	Localization of eIF4A-III in the nucleolus and splicing speckles is an indicator of plant stress. Plant Signaling and Behavior, 2009, 4, 1148-1151.	2.4	15
46	Aberrant mRNA Transcripts and the Nonsense-Mediated Decay Proteins UPF2 and UPF3 Are Enriched in the<i>Arabidopsis</i>Nucleolus Â. Plant Cell, 2009, 21, 2045-2057.	6.6	93
47	Filtering of deep sequencing data reveals the existence of abundant Dicer-dependent small RNAs derived from tRNAs. Rna, 2009, 15, 2147-2160.	3.5	525
48	Monitoring changes in alternative precursor messenger RNA splicing in multiple gene transcripts. Plant Journal, 2008, 53, 1035-1048.	5.7	113
49	A Plant Virus Movement Protein Forms Ringlike Complexes with the Major Nucleolar Protein, Fibrillarin, In Vitro. Journal of Molecular Biology, 2008, 376, 932-937.	4.2	51
50	Intronic noncoding RNAs and splicing. Trends in Plant Science, 2008, 13, 335-342.	8.8	129
51	Alternative splicing in plants. Biochemical Society Transactions, 2008, 36, 508-510.	3.4	32
52	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.	7.1	162
53	Cajal bodies and the nucleolus are required for a plant virus systemic infection. EMBO Journal, 2007, 26, 2169-2179.	7.8	138
54	Proteomic Analysis of the Arabidopsis Nucleolus Suggests Novel Nucleolar Functions. Molecular Biology of the Cell, 2005, 16, 260-269.	2.1	352

#	ARTICLE	IF	CITATIONS
55	Determinants of Plant U12-Dependent Intron Splicing Efficiency. Plant Cell, 2004, 16, 1340-1352.	6.6	54
56	Plant nuclear bodies. Current Opinion in Plant Biology, 2004, 7, 614-620.	7.1	118
57	Dual functionality of a plant U-rich intronic sequence element. Plant Journal, 2004, 37, 82-91.	5.7	30
58	Plant snoRNAs: functional evolution and new modes of gene expression. Trends in Plant Science, 2003, 8, 42-49.	8.8	126
59	Plant snoRNA database. Nucleic Acids Research, 2003, 31, 432-435.	14.5	82
60	Cloning and characterization of two subunits of Arabidopsis thaliana nuclear cap-binding complex. Gene, 2002, 283, 171-183.	2.2	48
61	Mutational analysis of a plant branchpoint and polypyrimidine tract required for constitutive splicing of a mini-exon. Rna, 2002, 8, 47-56.	3.5	36
62	Differential expression of potato U1A spliceosomal protein genes: a rapid method for expression profiling of multigene families. Plant Molecular Biology, 2001, 45, 449-460.	3.9	5
63	Requirements for mini-exon inclusion in potato invertase mRNAs provides evidence for exon-scanning interactions in plants. Rna, 2000, 6, 422-433.	3.5	31
64	Interactions between introns via exon definition in plant pre-mRNA splicing. Plant Journal, 1999, 18, 293-302.	5.7	15
65	Splicing-independent processing of plant box C/D and box H/ACA small nucleolar RNAs. Plant Molecular Biology, 1999, 39, 1091-1100.	3.9	32
66	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
67	Processing of vertebrate box C/D small nucleolar RNAs in plant cells. FEBS Journal, 1998, 253, 154-160.	0.2	4
68	Characterization of exon skipping mutants of the COP1 gene from Arabidopsis. Plant Journal, 1998, 15, 125-131.	5.7	32
69	Small Nucleolar RNAs and Pre-rRNA Processing in Plants. Plant Cell, 1998, 10, 649-657.	6.6	58
70	Expression of intron modified NPT II genes in monocotyledonous and dicotyledonous plant cells. Molecular Breeding, 1997, 3, 15-28.	2.1	21
71	Mutation of putative branchpoint consensus sequences in plant introns reduces splicing efficiency. Plant Journal, 1996, 9, 369-380.	5.7	66
72	Arabidopsis intron mutations and pre-mRNA splicing. Plant Journal, 1996, 10, 771-780.	5.7	116

#	ARTICLE	IF	CITATIONS
73	Arabidopsis consensus intron sequences. Plant Molecular Biology, 1996, 32, 531-535.	3.9	119
74	Genomic organisation of plant U14 snoRNA genes. Biochemical Society Transactions, 1995, 23, 314S-314S.	3.4	1
75	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.	14.5	46
76	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.	5.7	4
77	Detection of antisense transcripts in transgenic plants by RT-PCR. Plant Journal, 1993, 4, 883-885.	5.7	3
78	Efficient splicing of an AU-rich antisense intron sequence. Plant Molecular Biology, 1993, 21, 205-211.	3.9	25
79	Differential expression of U5snRNA gene variants in maize (Zea mays) protoplasts. Plant Molecular Biology, 1993, 21, 133-143.	3.9	16
80	Detection of a plant protein analogous to the yeast spliceosomal protein, PRP8. FEBS Letters, 1993, 318, 4-6.	2.8	13
81	Splicing of plant pre-mRNAs. Proceedings of the Royal Society of Edinburgh Section B Biological Sciences, 1992, 99, 31-50.	0.2	2
82	The effects of ribozymes on gene expression in plants. Biochemical Society Transactions, 1992, 20, 344S-344S.	3.4	1
83	Characterization and expression of U1snRNA genes from potato. Plant Molecular Biology, 1992, 19, 959-971.	3.9	14
84	Rapid analysis of plant gene expression by a novel reverse transcriptaseâ€PCR method. Plant Journal, 1992, 2, 835-836.	5.7	21
85	Sequence variation and linkage of potato U2snRNA-encoding genes established by PCR. Gene, 1991, 107, 197-204.	2.2	13
86	Evolutionary conservation of the spliceosaomal protein, U2 Bâ€• Nucleic Acids Research, 1991, 19, 5213-5217.	14.5	34
87	Sequence and expression of potato U2 snRNA genes. Nucleic Acids Research, 1991, 19, 249-256.	14.5	28
88	Plant UsnRNA genes. Molecular Biology Reports, 1990, 14, 147-147.	2.3	1
89	A functional splice site in the 5' untranslated region of a zein gene. Nucleic Acids Research, 1990, 18, 111-117.	14.5	16
90	Maize U2 snRNAs: gene sequence and expression. Nucleic Acids Research, 1989, 17, 8991-9001.	14.5	40

#	ARTICLE	IF	CITATIONS
91	The malate synthase gene of cucumber. Plant Molecular Biology, 1989, 13, 673-684.	3.9	47
92	Analysis of distal flanking regions of maize 19-kDa zein genes. Gene, 1989, 80, 249-258.	2.2	18
93	Molecular analysis of resveratrol synthase. cDNA, genomic clones and relationship with chalcone synthase. FEBS Journal, 1988, 172, 161-169.	0.2	198
94	Genetic control of bean seed protein. Critical Reviews in Plant Sciences, 1988, 7, 93-116.	5.7	28
95	A catalogue of splice junction and putative branch point sequences from plant introns. Nucleic Acids Research, 1986, 14, 9549-9559.	14.5	396
96	Bean lectins. III. Evidence for greater complexity in the structural model of Phaseolus vulgaris lectin. Plant Science Letters, 1983, 31, 193-203.	1.8	19
97	Phaseolin mRNA is translated to yield glycosylated polypeptides in Xenopus oocytes. Nature, 1981, 294, 175-176.	27.8	44
98	Microheterogeneity of Globulin-1 Storage Protein from French Bean with Isoelectrofocusing. Plant Physiology, 1980, 66, 838-840.	4.8	21
99	CONTROL OF ENDOSPERM PROTEINS IN TRITICUM AESTIVUM (var. CHINESE SPRING) AND AEGILOPS UMBELLULATA BY HOMOEOLOGOUS GROUP 1 CHROMOSOMES. Genetics, 1979, 93, 189-200.	2.9	55