

William Barbazuk

List of Publications by Year in descending order

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Version: 2024-02-01

64
papers

10,806
citations

134610

34
h-index

156644

58
g-index

68
all docs

68
docs citations

68
times ranked

15028
citing authors

#	ARTICLE	IF	CITATIONS
1	Spiny mouse (<i>Acomys</i>): an emerging research organism for regenerative medicine with applications beyond the skin. <i>Npj Regenerative Medicine</i> , 2021, 6, 1.	2.5	48
2	Biological features between miRNAs and their targets are unveiled from deep learning models. <i>Scientific Reports</i> , 2021, 11, 23825.	1.6	0
3	Jasmonate induced alternative splicing responses in <i>Arabidopsis</i> . <i>Plant Direct</i> , 2020, 4, e00245.	0.8	11
4	The Genetic Regulation of Alternative Splicing in <i>Populus deltoides</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 590.	1.7	5
5	Targeted amplicon sequencing of 40 nuclear genes supports a single introduction and rapid radiation of Hawaiian <i>Metrosideros</i> (Myrtaceae). <i>Plant Systematics and Evolution</i> , 2019, 305, 961-974.	0.3	15
6	Deep expression analysis reveals distinct cold-response strategies in rubber tree (<i>Hevea brasiliensis</i>). <i>BMC Genomics</i> , 2019, 20, 455.	1.2	19
7	Comparative transcriptomic analysis of dermal wound healing reveals de novo skeletal muscle regeneration in <i>Acomys cahirinus</i> . <i>PLoS ONE</i> , 2019, 14, e0216228.	1.1	27
8	Spaceflight-induced alternative splicing during seedling development in <i>Arabidopsis thaliana</i> . <i>Npj Microgravity</i> , 2019, 5, 9.	1.9	31
9	RNA Binding Motif Protein 48 Is Required for U12 Splicing and Maize Endosperm Differentiation. <i>Plant Cell</i> , 2019, 31, 715-733.	3.1	27
10	The avocado genome informs deep angiosperm phylogeny, highlights introgressive hybridization, and reveals pathogen-influenced gene space adaptation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 17081-17089.	3.3	134
11	The C-Fern (<i>Ceratopteris richardii</i>) genome: insights into plant genome evolution with the first partial homosporous fern genome assembly. <i>Scientific Reports</i> , 2019, 9, 18181.	1.6	79
12	Computational analysis of alternative splicing in plant genomes. <i>Gene</i> , 2019, 685, 186-195.	1.0	9
13	A Robust Methodology for Assessing Differential Homeolog Contributions to the Transcriptomes of Allopolyploids. <i>Genetics</i> , 2018, 210, 883-894.	1.2	21
14	The maize W22 genome provides a foundation for functional genomics and transposon biology. <i>Nature Genetics</i> , 2018, 50, 1282-1288.	9.4	183
15	Aberrant splicing in maize <i>rough endosperm3</i> reveals a conserved role for U12 splicing in eukaryotic multicellular development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E2195-E2204.	3.3	38
16	Detecting alternatively spliced transcript isoforms from single-molecule long-read sequences without a reference genome. <i>Molecular Ecology Resources</i> , 2017, 17, 1243-1256.	2.2	126
17	Evolutionarily Conserved Alternative Splicing Across Monocots. <i>Genetics</i> , 2017, 207, 465-480.	1.2	47
18	Population genomics of the eastern cottonwood (<i>Populus deltoides</i>). <i>Ecology and Evolution</i> , 2017, 7, 9426-9440.	0.8	55

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19	Evolution of the 3R-MYB Gene Family in Plants. <i>Genome Biology and Evolution</i> , 2017, 9, 1013-1029.	1.1	50
20	Genome Sequences of Mycobacteriophages Findley, Hurricane, and TBond007. <i>Genome Announcements</i> , 2017, 5, .	0.8	0
21	Cellular events during scar-free skin regeneration in the spiny mouse, <i>Acomys</i> . <i>Wound Repair and Regeneration</i> , 2016, 24, 75-88.	1.5	78
22	Genome-Wide Identification of Evolutionarily Conserved Alternative Splicing Events in Flowering Plants. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 33.	2.0	138
23	A Comparative Analysis of Gene Expression Profiles during Skin Regeneration in <i>Mus</i> and <i>Acomys</i> . <i>PLoS ONE</i> , 2015, 10, e0142931.	1.1	70
24	MarkerMiner 1.0: A new application for phylogenetic marker development using angiosperm transcriptomes. <i>Applications in Plant Sciences</i> , 2015, 3, 1400115.	0.8	156
25	Primers for low-copy nuclear genes in <i>Metrosideros</i> and cross-amplification in Myrtaceae. <i>Applications in Plant Sciences</i> , 2014, 2, 1400049.	0.8	10
26	Adaptive expansion of the maize maternally expressed gene (Meg) family involves changes in expression patterns and protein secondary structures of its members. <i>BMC Plant Biology</i> , 2014, 14, 204.	1.6	16
27	Potential use of low-copy nuclear genes in DNA barcoding: a comparison with plastid genes in two Hawaiian plant radiations. <i>BMC Evolutionary Biology</i> , 2013, 13, 35.	3.2	36
28	Assembly and Validation of the Genome of the Nonmodel Basal Angiosperm <i>Amborella</i> . <i>Science</i> , 2013, 342, 1516-1517.	6.0	89
29	Validation of reference transcripts in strawberry (<i>Fragaria</i> spp.). <i>Molecular Genetics and Genomics</i> , 2013, 288, 671-681.	1.0	34
30	Primers for Low-Copy Nuclear Genes in the Hawaiian Endemic <i>Clermontia</i> (Campanulaceae) and Cross-Amplification in Lobelioideae. <i>Applications in Plant Sciences</i> , 2013, 1, 1200450.	0.8	3
31	A genome-enabled, high-throughput, and multiplexed fingerprinting platform for strawberry (<i>Fragaria</i>) Tj ETQq1 1 0,784314 rgBT /Over P7	1.0	1
32	The potential of genomics in plant systematics. <i>Taxon</i> , 2013, 62, 886-898.	0.4	67
33	Inside Arbuscular Mycorrhizal Roots - Molecular Probes to Understand the Symbiosis. <i>Plant Genome</i> , 2013, 6, plantgenome2012.06.0007.	1.6	19
34	The Early Stages of Polyploidy: Rapid and Repeated Evolution in <i>Tragopogon</i> . , 2012, , 271-292.		36
35	Exploring Diversification and Genome Size Evolution in Extant Gymnosperms through Phylogenetic Synthesis. <i>Journal of Botany</i> , 2012, 2012, 1-6.	1.2	40
36	Rapid, Repeated, and Clustered Loss of Duplicate Genes in Allopolyploid Plant Populations of Independent Origin. <i>Current Biology</i> , 2012, 22, 248-252.	1.8	159

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37	SNP Discovery by Transcriptome Pyrosequencing. <i>Methods in Molecular Biology</i> , 2011, 729, 225-246.	0.4	18
38	Transcriptomic Shock Generates Evolutionary Novelty in a Newly Formed, Natural Allopolyploid Plant. <i>Current Biology</i> , 2011, 21, 551-556.	1.8	192
39	Silencing of Soybean Seed Storage Proteins Results in a Rebalanced Protein Composition Preserving Seed Protein Content without Major Collateral Changes in the Metabolome and Transcriptome. <i>Plant Physiology</i> , 2011, 156, 330-345.	2.3	135
40	Changes in protein abundance during powdery mildew infection of leaf tissues of Cabernet Sauvignon grapevine (<i>Vitis vinifera</i> L.). <i>Proteomics</i> , 2010, 10, 2057-2064.	1.3	69
41	Repeat subtraction-mediated sequence capture from a complex genome. <i>Plant Journal</i> , 2010, 62, 898-909.	2.8	89
42	Characterization of duplicate gene evolution in the recent natural allopolyploid <i>Tragopogon miscellus</i> by next-generation sequencing and Sequenom iPLEX MassARRAY genotyping. <i>Molecular Ecology</i> , 2010, 19, 132-146.	2.0	167
43	A Transcript Accounting from Diverse Tissues of a Cultivated Strawberry. <i>Plant Genome</i> , 2010, 3, .	1.6	22
44	High-Throughput Genetic Mapping of Mutants via Quantitative Single Nucleotide Polymorphism Typing. <i>Genetics</i> , 2010, 184, 19-26.	1.2	66
45	A conserved alternative splicing event in plants reveals an ancient exonization of 5S rRNA that regulates TFIIIA. <i>RNA Biology</i> , 2010, 7, 397-402.	1.5	13
46	Maize Inbreds Exhibit High Levels of Copy Number Variation (CNV) and Presence/Absence Variation (PAV) in Genome Content. <i>PLoS Genetics</i> , 2009, 5, e1000734.	1.5	484
47	Alternative splicing of anciently exonized 5S rRNA regulates plant transcription factor TFIIIA. <i>Genome Research</i> , 2009, 19, 913-921.	2.4	34
48	The B73 Maize Genome: Complexity, Diversity, and Dynamics. <i>Science</i> , 2009, 326, 1112-1115.	6.0	3,612
49	Sequencing Genes and Gene Islands by Gene Enrichment. , 2009, , 673-689.		1
50	Molecular Markers. <i>Biotechnology in Agriculture and Forestry</i> , 2009, , 231-240.	0.2	0
51	Novel and nodulation-regulated microRNAs in soybean roots. <i>BMC Genomics</i> , 2008, 9, 160.	1.2	283
52	The <i>Physcomitrella</i> Genome Reveals Evolutionary Insights into the Conquest of Land by Plants. <i>Science</i> , 2008, 319, 64-69.	6.0	1,712
53	Genome-wide analyses of alternative splicing in plants: Opportunities and challenges. <i>Genome Research</i> , 2008, 18, 1381-1392.	2.4	348
54	Natural Variation for Alleles Under Epigenetic Control by the Maize Chromomethylase <i>Zmet2</i> . <i>Genetics</i> , 2007, 177, 749-760.	1.2	31

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55	SNP discovery via 454 transcriptome sequencing. <i>Plant Journal</i> , 2007, 51, 910-918.	2.8	361
56	The TIGR Maize Database. <i>Nucleic Acids Research</i> , 2006, 34, D771-D776.	6.5	35
57	Uneven chromosome contraction and expansion in the maize genome. <i>Genome Research</i> , 2006, 16, 1241-1251.	2.4	105
58	Gene discovery and annotation using LCM-454 transcriptome sequencing. <i>Genome Research</i> , 2006, 17, 69-73.	2.4	321
59	Extension of Lander-Waterman theory for sequencing filtered DNA libraries. <i>BMC Bioinformatics</i> , 2005, 6, 245.	1.2	20
60	Reduced representation sequencing: A success in maize and a promise for other plant genomes. <i>BioEssays</i> , 2005, 27, 839-848.	1.2	41
61	Utility of Different Gene Enrichment Approaches Toward Identifying and Sequencing the Maize Gene Space. <i>Plant Physiology</i> , 2004, 136, 3023-3033.	2.3	41
62	Sequence and Comparative Analysis of the Maize NB Mitochondrial Genome. <i>Plant Physiology</i> , 2004, 136, 3486-3503.	2.3	279
63	An Integrated Physical and Genetic Map of the Rice Genome. <i>Plant Cell</i> , 2002, 14, 537-545.	3.1	422
64	Phylotranscriptomics Illuminates the Placement of Whole Genome Duplications and Gene Retention in Ferns. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	10