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List of Publications by Year in descending order

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Version: 2024-02-01

45
papers

3,726
citations

236925

25
h-index

265206

42
g-index

50
all docs

50
docs citations

50
times ranked

6867
citing authors

#	ARTICLE	IF	CITATIONS
1	Integrated Genome Browser App Store. <i>Bioinformatics</i> , 2022, , .	4.1	0
2	BioViz Connect: Web Application Linking CyVerse Cloud Resources to Genomic Visualization in the Integrated Genome Browser. <i>Frontiers in Bioinformatics</i> , 2022, 2, .	2.1	0
3	AINTEGUMENTA and AINTEGUMENTA-LIKE6 directly regulate floral homeotic, growth, and vascular development genes in young <i>Arabidopsis</i> flowers. <i>Journal of Experimental Botany</i> , 2021, 72, 5478-5493.	4.8	21
4	Anno genominis XX: 20 years of <i>Arabidopsis</i> genomics. <i>Plant Cell</i> , 2021, 33, 832-845.	6.6	11
5	The <i>Arabidopsis</i> transcription factor AINTEGUMENTA orchestrates patterning genes and auxin signaling in the establishment of floral growth and form. <i>Plant Journal</i> , 2020, 103, 752-768.	5.7	42
6	An <i>scRNA-Seq</i> Browser™ for visualizing and exploring <i>scRNA</i> sequencing data. <i>Plant Journal</i> , 2019, 100, 641-654.	5.7	41
7	Many rice genes are differentially spliced between roots and shoots but cytokinin has minimal effect on splicing. <i>Plant Direct</i> , 2019, 3, e00136.	1.9	2
8	<i>Arabidopsis</i> bioinformatics resources: The current state, challenges, and priorities for the future. <i>Plant Direct</i> , 2019, 3, e00109.	1.9	14
9	Coordination of Chloroplast Development through the Action of the GNC and GLK Transcription Factor Families. <i>Plant Physiology</i> , 2018, 178, 130-147.	4.8	85
10	Cell-specific cis-natural antisense transcripts (cis-NATs) in the sperm and the pollen vegetative cells of <i>Arabidopsis thaliana</i> . <i>F1000Research</i> , 2018, 7, 93.	1.6	2
11	Genome-wide characterization of differential transcript usage in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2017, 92, 1218-1231.	5.7	31
12	Salt tolerance response revealed by RNA-Seq in a diploid halophytic wild relative of sweet potato. <i>Scientific Reports</i> , 2017, 7, 9624.	3.3	22
13	Cytokinin induces genome-wide binding of the type-B response regulator ARR10 to regulate growth and development in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E5995-E6004.	7.1	154
14	RNA-Seq Links the Transcription Factors AINTEGUMENTA and AINTEGUMENTA-LIKE6 to Cell Wall Remodeling and Plant Defense Pathways. <i>Plant Physiology</i> , 2016, 171, 2069-2084.	4.8	57
15	Characterization of the cytokinin-responsive transcriptome in rice. <i>BMC Plant Biology</i> , 2016, 16, 260.	3.6	38
16	ProtAnnot: an App for Integrated Genome Browser to display how alternative splicing and transcription affect proteins. <i>Bioinformatics</i> , 2016, 32, 2499-2501.	4.1	12
17	Integrated genome browser: visual analytics platform for genomics. <i>Bioinformatics</i> , 2016, 32, 2089-2095.	4.1	347
18	Analysis of pollen-specific alternative splicing in <i>Arabidopsis thaliana</i> via semi-quantitative PCR. <i>PeerJ</i> , 2015, 3, e919.	2.0	11

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19	Analysis and Visualization of RNA-Seq Expression Data Using RStudio, Bioconductor, and Integrated Genome Browser. <i>Methods in Molecular Biology</i> , 2015, 1284, 481-501.	0.9	69
20	RNA-Seq analysis and annotation of a draft blueberry genome assembly identifies candidate genes involved in fruit ripening, biosynthesis of bioactive compounds, and stage-specific alternative splicing. <i>GigaScience</i> , 2015, 4, 5.	6.4	138
21	COBRA-LIKE2, a Member of the Glycosylphosphatidylinositol-Anchored COBRA-LIKE Family, Plays a Role in Cellulose Deposition in Arabidopsis Seed Coat Mucilage Secretory Cells. <i>Plant Physiology</i> , 2015, 167, 711-724.	4.8	82
22	Comparisons of computational methods for differential alternative splicing detection using RNA-seq in plant systems. <i>BMC Bioinformatics</i> , 2014, 15, 364.	2.6	91
23	A Protocol for Visual Analysis of Alternative Splicing in RNA-Seq Data Using Integrated Genome Browser. <i>Methods in Molecular Biology</i> , 2014, 1158, 123-137.	0.9	5
24	Efficient Quantification of the Health-Relevant Anthocyanin and Phenolic Acid Profiles in Commercial Cultivars and Breeding Selections of Blueberries (<i>Vaccinium</i> spp.). <i>Journal of Agricultural and Food Chemistry</i> , 2013, 61, 4806-4815.	5.2	88
25	RNA-Seq of Arabidopsis Pollen Uncovers Novel Transcription and Alternative Splicing. <i>Plant Physiology</i> , 2013, 162, 1092-1109.	4.8	195
26	Identification of Cytokinin-Responsive Genes Using Microarray Meta-Analysis and RNA-Seq in Arabidopsis. <i>Plant Physiology</i> , 2013, 162, 272-294.	4.8	230
27	Mining <i>Arabidopsis thaliana</i> RNA-seq data with Integrated Genome Browser reveals stress-induced alternative splicing of the putative splicing regulator SR45a. <i>American Journal of Botany</i> , 2012, 99, 219-231.	1.7	50
28	A regulon conserved in monocot and dicot plants defines a functional module in antifungal plant immunity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 21896-21901.	7.1	110
29	Prevalence of alternative splicing choices in <i>Arabidopsis thaliana</i> . <i>BMC Plant Biology</i> , 2010, 10, 102.	3.6	34
30	Assembly of an Interactive Correlation Network for the Arabidopsis Genome Using a Novel Heuristic Clustering Algorithm. <i>Plant Physiology</i> , 2009, 152, 29-43.	4.8	174
31	The Integrated Genome Browser: free software for distribution and exploration of genome-scale datasets. <i>Bioinformatics</i> , 2009, 25, 2730-2731.	4.1	558
32	Consistency Analysis of Redundant Probe Sets on Affymetrix Three-Prime Expression Arrays and Applications to Differential mRNA Processing. <i>PLoS ONE</i> , 2009, 4, e4229.	2.5	20
33	Large-scale transposon mutagenesis of <i>Mycoplasma pulmonis</i> . <i>Molecular Microbiology</i> , 2008, 69, 67-76.	2.5	117
34	Commonality of functional annotation: a method for prioritization of candidate genes from genome-wide linkage studies. <i>Nucleic Acids Research</i> , 2008, 36, e26-e26.	14.5	24
35	Genome of <i>Mycoplasma arthritidis</i> . <i>Infection and Immunity</i> , 2008, 76, 4000-4008.	2.2	33
36	CressExpress: A Tool For Large-Scale Mining of Expression Data from Arabidopsis. <i>Plant Physiology</i> , 2008, 147, 1004-1016.	4.8	103

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37	GLOBAL CORRELATION ANALYSIS BETWEEN REDUNDANT PROBE SETS USING A LARGE COLLECTION OF ARABIDOPSIS ATH1 EXPRESSION PROFILING DATA. , 2006, , .		4
38	Transcriptional Coordination of the Metabolic Network in Arabidopsis. <i>Plant Physiology</i> , 2006, 142, 762-774.	4.8	178
39	Global correlation analysis between redundant probe sets using a large collection of Arabidopsis ath1 expression profiling data. <i>Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference</i> , 2006, , 223-6.	0.4	5
40	MARA: a novel approach for highly multiplexed locus-specific SNP genotyping using high-density DNA oligonucleotide arrays. <i>Nucleic Acids Research</i> , 2004, 32, e181-e181.	14.5	18
41	Exploring Alternative Transcript Structure in the Human Genome Using BLOCKS and InterPro. <i>Journal of Bioinformatics and Computational Biology</i> , 2003, 01, 289-306.	0.8	10
42	NetAffx: Affymetrix probesets and annotations. <i>Nucleic Acids Research</i> , 2003, 31, 82-86.	14.5	438
43	Visualizing the genome: techniques for presenting human genome data and annotations. <i>BMC Bioinformatics</i> , 2002, 3, 19.	2.6	30
44	Protein-based analysis of alternative splicing in the human genome. <i>Proceedings</i> , 2002, 1, 118-24.	0.1	3
45	BioViews: Java-Based Tools for Genomic Dataâ€™Visualization. <i>Genome Research</i> , 1998, 8, 291-305.	5.5	28