

Nam V Hoang

List of Publications by Year in descending order

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Version: 2024-02-01

22
papers

821
citations

686830

13
h-index

752256

20
g-index

25
all docs

25
docs citations

25
times ranked

951
citing authors

#	ARTICLE	IF	CITATIONS
1	A survey of the complex transcriptome from the highly polyploid sugarcane genome using full-length isoform sequencing and de novo assembly from short read sequencing. <i>BMC Genomics</i> , 2017, 18, 395.	1.2	180
2	Potential for Genetic Improvement of Sugarcane as a Source of Biomass for Biofuels. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 182.	2.0	109
3	Transcriptome analysis highlights key differentially expressed genes involved in cellulose and lignin biosynthesis of sugarcane genotypes varying in fiber content. <i>Scientific Reports</i> , 2018, 8, 11612.	1.6	91
4	Modifying plants for biofuel and biomaterial production. <i>Plant Biotechnology Journal</i> , 2014, 12, 1246-1258.	4.1	82
5	The Challenge of Analyzing the Sugarcane Genome. <i>Frontiers in Plant Science</i> , 2018, 9, 616.	1.7	80
6	High-Throughput Profiling of the Fiber and Sugar Composition of Sugarcane Biomass. <i>Bioenergy Research</i> , 2017, 10, 400-416.	2.2	42
7	Association of variation in the sugarcane transcriptome with sugar content. <i>BMC Genomics</i> , 2017, 18, 909.	1.2	41
8	Analysis of the diversity and tissue specificity of sucrose synthase genes in the long read transcriptome of sugarcane. <i>BMC Plant Biology</i> , 2019, 19, 160.	1.6	36
9	Association of gene expression with biomass content and composition in sugarcane. <i>PLoS ONE</i> , 2017, 12, e0183417.	1.1	26
10	Next generation sequencing of total DNA from sugarcane provides no evidence for chloroplast heteroplasmy. <i>New Negatives in Plant Science</i> , 2015, 1-2, 33-45.	0.9	23
11	Root transcriptome analysis of <i>Saccharum spontaneum</i> uncovers key genes and pathways in response to low-temperature stress. <i>Environmental and Experimental Botany</i> , 2020, 171, 103935.	2.0	23
12	Identification of Conserved Gene-Regulatory Networks that Integrate Environmental Sensing and Growth in the Root Cambium. <i>Current Biology</i> , 2020, 30, 2887-2900.e7.	1.8	22
13	Gene Regulatory Network Guided Investigations and Engineering of Storage Root Development in Root Crops. <i>Frontiers in Plant Science</i> , 2020, 11, 762.	1.7	17
14	De novo assembly and characterizing of the culm-derived meta-transcriptome from the polyploid sugarcane genome based on coding transcripts. <i>Heliyon</i> , 2018, 4, e00583.	1.4	12
15	Variation in sugarcane biomass composition and enzymatic saccharification of leaves, internodes and roots. <i>Biotechnology for Biofuels</i> , 2020, 13, 201.	6.2	11
16	The Impact of cDNA Normalization on Long-Read Sequencing of a Complex Transcriptome. <i>Frontiers in Genetics</i> , 2019, 10, 654.	1.1	8
17	Deep sequencing of suppression subtractive library identifies differentially expressed transcripts of <i>Saccharum spontaneum</i> exposed to salinity stress. <i>Physiologia Plantarum</i> , 2022, 174, e13645.	2.6	4
18	An Optimized Protocol of Laser Capture Microdissection for Tissue-Specific RNA Profiling in a Radish Tap Root. <i>STAR Protocols</i> , 2020, 1, 100110.	0.5	3

#	ARTICLE	IF	CITATIONS
19	Iso-Seq Long Read Transcriptome Sequencing. , 2021, , 486-500.		2
20	Oxidative stress response and programmed cell death guided by NAC013 modulate pithiness in radish taproots. Plant Journal, 2021, , .	2.8	2
21	Comparison of the root, leaf and internode transcriptomes in sugarcane (Saccharum spp. hybrids). Current Research in Biotechnology, 2022, 4, 167-178.	1.9	2
22	Transcriptome of Sugarcane, a Highly Complex Polyploid. , 2021, , 614-626.		0