

# 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	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
2	Comparison of the root, leaf and internode transcriptomes in sugarcane ( <i>Saccharum</i> spp. hybrids). <i>Current Research in Biotechnology</i> , 2022, 4, 167-178.	1.9	2
3	Transcriptome of Sugarcane, a Highly Complex Polyploid. , 2021, , 614-626.		0
4	Iso-Seq Long Read Transcriptome Sequencing. , 2021, , 486-500.		2
5	Oxidative stress response and programmed cell death guided by NAC013 modulate pithiness in radish taproots. <i>Plant Journal</i> , 2021, , .	2.8	2
6	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
7	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
8	Variation in sugarcane biomass composition and enzymatic saccharification of leaves, internodes and roots. <i>Biotechnology for Biofuels</i> , 2020, 13, 201.	6.2	11
9	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
10	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
11	The Impact of cDNA Normalization on Long-Read Sequencing of a Complex Transcriptome. <i>Frontiers in Genetics</i> , 2019, 10, 654.	1.1	8
12	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
13	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
14	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
15	The Challenge of Analyzing the Sugarcane Genome. <i>Frontiers in Plant Science</i> , 2018, 9, 616.	1.7	80
16	High-Throughput Profiling of the Fiber and Sugar Composition of Sugarcane Biomass. <i>Bioenergy Research</i> , 2017, 10, 400-416.	2.2	42
17	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
18	Association of variation in the sugarcane transcriptome with sugar content. <i>BMC Genomics</i> , 2017, 18, 909.	1.2	41

#	ARTICLE	IF	CITATIONS
19	Association of gene expression with biomass content and composition in sugarcane. PLoS ONE, 2017, 12, e0183417.	1.1	26
20	Next generation sequencing of total DNA from sugarcane provides no evidence for chloroplast heteroplasmy. New Negatives in Plant Science, 2015, 1-2, 33-45.	0.9	23
21	Potential for Genetic Improvement of Sugarcane as a Source of Biomass for Biofuels. Frontiers in Bioengineering and Biotechnology, 2015, 3, 182.	2.0	109
22	Modifying plants for biofuel and biomaterial production. Plant Biotechnology Journal, 2014, 12, 1246-1258.	4.1	82