

Anil Kumar Nalini Chandran

List of Publications by Year in descending order

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Version: 2024-02-01

25
papers

577
citations

567281

15
h-index

642732

23
g-index

26
all docs

26
docs citations

26
times ranked

794
citing authors

#	ARTICLE	IF	CITATIONS
1	Emerging concepts of potassium homeostasis in plants. <i>Journal of Experimental Botany</i> , 2020, 71, 608-619.	4.8	81
2	<i>Loose Plant Architecture1</i> (<i>LPA1</i>) determines lamina joint bending by suppressing auxin signalling that interacts with C-22-hydroxylated and 6-deoxo brassinosteroids in rice. <i>Journal of Experimental Botany</i> , 2016, 67, 1883-1895.	4.8	51
3	Transcriptome analysis of rice-seedling roots under soil "salt stress using RNA-Seq method. <i>Plant Biotechnology Reports</i> , 2019, 13, 567-578.	1.5	37
4	Rice RHC Encoding a Putative Cellulase is Essential for Normal Root Hair Elongation. <i>Journal of Plant Biology</i> , 2019, 62, 82-91.	2.1	35
5	Resources for systems biology in rice. <i>Journal of Plant Biology</i> , 2014, 57, 80-92.	2.1	34
6	Molecular insights into the function of ankyrin proteins in plants. <i>Journal of Plant Biology</i> , 2015, 58, 271-284.	2.1	34
7	Genome-wide transcriptome analysis of expression in rice seedling roots in response to supplemental nitrogen. <i>Journal of Plant Physiology</i> , 2016, 200, 62-75.	3.5	33
8	Genome-wide identification and analysis of rice genes preferentially expressed in pollen at an early developmental stage. <i>Plant Molecular Biology</i> , 2016, 92, 71-88.	3.9	32
9	Genome-wide identification and analysis of Japonica and Indica cultivar-preferred transcripts in rice using 983 Affymetrix array data. <i>Rice</i> , 2013, 6, 19.	4.0	28
10	CAFRI Rice: CRISPR applicable functional redundancy inspector to accelerate functional genomics in rice. <i>Plant Journal</i> , 2020, 104, 532-545.	5.7	26
11	Infrastructures of systems biology that facilitate functional genomic study in rice. <i>Rice</i> , 2019, 12, 15.	4.0	21
12	Updated Rice Kinase Database RKD 2.0: enabling transcriptome and functional analysis of rice kinase genes. <i>Rice</i> , 2016, 9, 40.	4.0	20
13	Comparative Expression Analysis of Rice and Arabidopsis Peroxiredoxin Genes Suggests Conserved or Diversified Roles Between the Two Species and Leads to the Identification of Tandemly Duplicated Rice Peroxiredoxin Genes Differentially Expressed in Seeds. <i>Rice</i> , 2017, 10, 30.	4.0	20
14	Development of functional modules based on co-expression patterns for cell-wall biosynthesis related genes in rice. <i>Journal of Plant Biology</i> , 2016, 59, 1-15.	2.1	18
15	Functional classification of rice flanking sequence tagged genes using MapMan terms and global understanding on metabolic and regulatory pathways affected by dxr mutant having defects in light response. <i>Rice</i> , 2016, 9, 17.	4.0	17
16	Comparative Transcriptome Analysis Reveals Gene Regulatory Mechanism of UDT1 on Anther Development. <i>Journal of Plant Biology</i> , 2020, 63, 289-296.	2.1	16
17	Genome-Wide Transcriptome Analysis of Rice Seedlings after Seed Dressing with <i>Paenibacillus yonginensis</i> DCY84T and Silicon. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5883.	4.1	15
18	Rice Male Gamete Expression Database (RMEDB): A Web Resource for Functional Genomic Studies of Rice Male Organ Development. <i>Journal of Plant Biology</i> , 2020, 63, 421-430.	2.1	14

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19	Rice CaM-binding transcription factor (OsCBT) mediates defense signaling via transcriptional reprogramming. <i>Plant Biotechnology Reports</i> , 2020, 14, 309-321.	1.5	13
20	A web-based tool for the prediction of rice transcription factor function. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	7
21	Global Analysis of Cereal microProteins Suggests Diverse Roles in Crop Development and Environmental Adaptation. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3709-3717.	1.8	7
22	Integrated omics analysis of root-preferred genes across diverse rice varieties including Japonica and indica cultivars. <i>Journal of Plant Physiology</i> , 2018, 220, 11-23.	3.5	6
23	Genome-wide identification and analysis of rice genes to elucidate morphological agronomic traits. <i>Journal of Plant Biology</i> , 2016, 59, 639-647.	2.1	5
24	Meta-expression analysis of unannotated genes in rice and approaches for network construction to suggest the probable roles. <i>Plant Molecular Biology</i> , 2018, 96, 17-34.	3.9	4
25	Construction and application of functional gene modules to regulatory pathways in rice. <i>Journal of Plant Biology</i> , 2017, 60, 358-379.	2.1	2