

Krishan Mohan Rai

List of Publications by Year in descending order

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Version: 2024-02-01

36
papers

1,038
citations

516710

16
h-index

434195

31
g-index

38
all docs

38
docs citations

38
times ranked

1533
citing authors

#	ARTICLE	IF	CITATIONS
1	CRISPR DNA- and RNP-Mediated Genome Editing via <i>Nicotiana benthamiana</i> Protoplast Transformation and Regeneration. <i>Methods in Molecular Biology</i> , 2022, 2464, 65-82.	0.9	2
2	Epigenetic features drastically impact CRISPR-Cas9 efficacy in plants. <i>Plant Physiology</i> , 2022, 190, 1153-1164.	4.8	25
3	Long noncoding RNAs and their implication in novel trait development in soybean. , 2021, , 133-150.		1
4	Long noncoding RNAs™ involvement in comprehensive development of <i>Gossypium</i> species. , 2021, , 243-255.		0
5	De novo transcriptome analysis of white teak (<i>Gmelina arborea</i> Roxb) wood reveals critical genes involved in xylem development and secondary metabolism. <i>BMC Genomics</i> , 2021, 22, 494.	2.8	1
6	Study of <i>Triticum aestivum</i> Resistome in Response to Wheat dwarf India Virus Infection. <i>Life</i> , 2021, 11, 955.	2.4	2
7	TRANSPARENT TESTA 2 allele confers major reduction in pennycress (<i>Thlaspi arvense</i> L.) seed dormancy. <i>Industrial Crops and Products</i> , 2021, 174, 114216.	5.2	5
8	Research Advances in Plant Genomics. <i>Life</i> , 2021, 11, 1313.	2.4	0
9	Efficiency, Specificity and Temperature Sensitivity of Cas9 and Cas12a RNPs for DNA-free Genome Editing in Plants. <i>Frontiers in Genome Editing</i> , 2021, 3, 760820.	5.2	12
10	Epigenetic regulation of gene expression improves Fusarium head blight resistance in durum wheat. <i>Scientific Reports</i> , 2020, 10, 17610.	3.3	18
11	Unravelling Cotton Nonexpressor of Pathogenesis-Related 1(NPR1)-Like Genes Family: Evolutionary Analysis and Putative Role in Fiber Development and Defense Pathway. <i>Plants</i> , 2020, 9, 999.	3.5	9
12	Distinct defensive activity of phenolics and phenylpropanoid pathway genes in different cotton varieties toward chewing pests. <i>Plant Signaling and Behavior</i> , 2020, 15, 1747689.	2.4	23
13	Mutation in a PHD-finger protein MS4 causes male sterility in soybean. <i>BMC Plant Biology</i> , 2019, 19, 378.	3.6	19
14	Genome Engineering Tools in Plant Synthetic Biology. , 2019, , 47-73.		12
15	Inhibition of Heat Shock proteins HSP90 and HSP70 induce oxidative stress, suppressing cotton fiber development. <i>Scientific Reports</i> , 2018, 8, 3620.	3.3	64
16	Plant Biosynthetic Engineering Through Transcription Regulation: An Insight into Molecular Mechanisms During Environmental Stress. <i>Energy, Environment, and Sustainability</i> , 2018, , 51-72.	1.0	10
17	Genome-wide identification and characterization of LRR-RLKs reveal functional conservation of the SIF subfamily in cotton (<i>Gossypium hirsutum</i>). <i>BMC Plant Biology</i> , 2018, 18, 185.	3.6	28
18	Role of Gh<sc>HDA</sc>5 in H3K9 deacetylation and fiber initiation in <i>Gossypium hirsutum</i>. <i>Plant Journal</i> , 2018, 95, 1069-1083.	5.7	35

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19	Genetics and Physiology of the Nuclearly Inherited Yellow Foliar Mutants in Soybean. <i>Frontiers in Plant Science</i> , 2018, 9, 471.	3.6	10
20	Identification, Characterization, and Expression Analysis of Cell Wall Related Genes in Sorghum bicolor (L.) Moench, a Food, Fodder, and Biofuel Crop. <i>Frontiers in Plant Science</i> , 2016, 7, 1287.	3.6	58
21	Genome-wide identification of multifunctional laccase gene family in cotton (<i>Gossypium</i> spp.); expression and biochemical analysis during fiber development. <i>Scientific Reports</i> , 2016, 6, 34309.	3.3	45
22	Transcriptome sequencing of a thalloid bryophyte; <i>Dumortiera hirsuta</i> (Sw) Nees: assembly, annotation and marker discovery. <i>Scientific Reports</i> , 2015, 5, 15350.	3.3	21
23	Engineering Plant Biomass Lignin Content and Composition for Biofuels and Bioproducts. <i>Energies</i> , 2015, 8, 7654-7676.	3.1	154
24	Spt-Ada-Gcn5-Acetyltransferase (SAGA) Complex in Plants: Genome Wide Identification, Evolutionary Conservation and Functional Determination. <i>PLoS ONE</i> , 2015, 10, e0134709.	2.5	32
25	Genomic-derived microsatellite markers for diversity analysis in <i>Jatropha curcas</i> . <i>Trees - Structure and Function</i> , 2015, 29, 849-858.	1.9	5
26	Development of a 63K SNP Array for Cotton and High-Density Mapping of Intraspecific and Interspecific Populations of <i>Gossypium</i> spp.. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1187-1209.	1.8	226
27	Genome wide comprehensive analysis and web resource development on cell wall degrading enzymes from phyto-parasitic nematodes. <i>BMC Plant Biology</i> , 2015, 15, 187.	3.6	26
28	Distinct Role of Core Promoter Architecture in Regulation of Light-Mediated Responses in Plant Genes. <i>Molecular Plant</i> , 2014, 7, 626-641.	8.3	41
29	Microsatellite polymorphism in <i>Jatropha curcas</i> L. – A biodiesel plant. <i>Industrial Crops and Products</i> , 2013, 49, 136-142.	5.2	8
30	Large-scale resource development in <i>Gossypium hirsutum</i> L. by 454 sequencing of genic-enriched libraries from six diverse genotypes. <i>Plant Biotechnology Journal</i> , 2013, 11, 953-963.	8.3	23
31	Genome wide expression profiling of two accession of <i>G. herbaceum</i> L. in response to drought. <i>BMC Genomics</i> , 2012, 13, 94.	2.8	47
32	Development and characterization of genomic and expressed SSRs for levant cotton (<i>Gossypium</i>) Tj ETQq0 0 0 rgBT /Overlock_10 Tf 50	3.6	35
33	Enhanced Expression of Rabies Virus Surface G-Protein in <i>Escherichia coli</i> using SUMO Fusion. <i>Protein Journal</i> , 2012, 31, 68-74.	1.6	13
34	Analysis of Histones and Histone Variants in Plants. <i>Methods in Molecular Biology</i> , 2012, 833, 225-236.	0.9	6
35	Analysis of Chromatin Structure in Plant Cells. <i>Methods in Molecular Biology</i> , 2012, 833, 201-223.	0.9	0
36	Analysis of genetic diversity, population structure and linkage disequilibrium in elite cotton (<i>Gossypium</i> L.) germplasm in India. <i>Crop and Pasture Science</i> , 2011, 62, 859.	1.5	21