Natesan Senthil

List of Publications by Year in descending order

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394421 330143 1,625 72 19 37 citations h-index g-index papers 73 73 73 2177 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Evolution of the Grain Dispersal System in Barley. Cell, 2015, 162, 527-539.	28.9	265
2	Nanocurcumin: A Promising Candidate for Therapeutic Applications. Frontiers in Pharmacology, 2020, 11, 487.	3.5	213
3	Transcriptome analysis of salinity responsiveness in contrasting genotypes of finger millet (Eleusine) Tj ETQq1 1	0.784314 3.9	rgBJ /Overloc
4	Novel Genetic Resources in the Genus Vigna Unveiled from Gene Bank Accessions. PLoS ONE, 2016, 11, e0147568.	2.5	74
5	High-density AFLP map of nonbrittle rachis 1 (btr1) and 2 (btr2) genes in barley (Hordeum vulgare L.). Theoretical and Applied Genetics, 2004, 109, 986-995.	3.6	71
6	Assessment of Genetic Diversity among Finger Millet (Eleusine coracana (L.) Gaertn.) Accessions using Molecular Markers. Genetic Resources and Crop Evolution, 2007, 54, 399-404.	1.6	53
7	Mungbean yellow mosaic virus (MYMV): a threat to green gram (<i>Vigna radiata</i>) production in Asia. International Journal of Pest Management, 2014, 60, 314-324.	1.8	53
8	Transcriptome profiling and comparative analysis of Panax ginseng adventitious roots. Journal of Ginseng Research, 2014, 38, 278-288.	5.7	53
9	Phenotype variations affect genetic association studies of degenerative disc disease: conclusions of analysis of genetic association of 58 single nucleotide polymorphisms with highly specific phenotypes for disc degeneration in 332 subjects. Spine Journal, 2013, 13, 1309-1320.	1.3	38
10	Marker-Assisted Selection to Pyramid the Opaque-2 (O2) and \hat{l}^2 -Carotene (crtRB1) Genes in Maize. Frontiers in Genetics, 2019, 10, 859.	2.3	35
11	Genomeâ€Wide Association Mapping for Leaf Tip Necrosis and Pseudoâ€black Chaff in Relation to Durable Rust Resistance in Wheat. Plant Genome, 2015, 8, eplantgenome2015.01.0002.	2.8	34
12	Transcriptome analysis reveals in vitro cultured Withania somnifera leaf and root tissues as a promising source for targeted withanolide biosynthesis. BMC Genomics, 2015, 16, 14.	2.8	34
13	Detection of QTLs associated with mungbean yellow mosaic virus (MYMV) resistance using the interspecific cross of Vigna radiata × Vigna umbellata. Journal of Applied Genetics, 2019, 60, 255-268.	1.9	31
14	Genetic susceptibility of lumbar degenerative disc disease in young Indian adults. European Spine Journal, 2015, 24, 1969-1975.	2.2	29
15	Screening of mungbean (<i>Vigna radiata</i>) germplasm for resistance to <i>Mungbean yellow mosaic virus</i> using agroinoculation. Canadian Journal of Plant Pathology, 2013, 35, 424-430.	1.4	27
16	Domesticating Vigna Stipulacea: A Potential Legume Crop With Broad Resistance to Biotic Stresses. Frontiers in Plant Science, 2019, 10, 1607.	3.6	27
17	Marker assisted selection of low phytic acid trait in maize (<i>Zea mays</i> L.). Hereditas, 2014, 151, 20-27.	1.4	24
18	Molecular Studies on the Transmission of Indian Cassava Mosaic Virus (ICMV) and Sri Lankan Cassava Mosaic Virus (SLCMV) in Cassava by Bemisia tabaci and Cloning of ICMV and SLCMV Replicase Gene from Cassava. Molecular Biotechnology, 2013, 53, 150-158.	2.4	23

#	Article	IF	Citations
19	Transcriptomes of Indian barnyard millet and barnyardgrass reveal putative genes involved in drought adaptation and micronutrient accumulation. Acta Physiologiae Plantarum, 2019, 41, 1.	2.1	22
20	Prevalence, Patterns, and Genetic Association Analysis of Modic Vertebral Endplate Changes. Asian Spine Journal, 2017, 11, 594-600.	2.0	22
21	Molecular studies on mungbean (<i>Vigna radiata</i> (L.) Wilczek) and ricebean (<i>Vigna) Tj ETQq1 1 0.784314</i>	1.3	erlock 10 T
21	development of species-specific SCAR marker for ricebean. Archives of Phytopathology and Plant Protection. 2013. 46. 503-517.	1.0	21
22	Comparative Root Protein Profiles of Korean Ginseng (<i>Panax ginseng</i>) and Indian Ginseng (<i>Withania somnifera</i>). The American Journal of Chinese Medicine, 2012, 40, 203-218.	3.8	20
23	Genetic diversity in the barnyard millet (Echinochola frumentacea) germplasms revealed by morphological traits and simple sequence repeat markers. Current Plant Biology, 2018, 14, 71-78.	4.7	20
24	BrassicaTED - a public database for utilization of miniature transposable elements in Brassica species. BMC Research Notes, 2014, 7, 379.	1.4	18
25	Search for Vigna species conferring resistance to Mungbean yellow mosaic virus in mungbean. Plant Genetic Resources: Characterisation and Utilisation, 2015, 13, 162-167.	0.8	17
26	Screening of IR50Â×ÂRathu Heenati F7 RILs and Identification of SSR Markers Linked to Brown Planthopper (Nilaparvata lugens StÃ¥l) Resistance in Rice (Oryza sativa L.). Molecular Biotechnology, 2010, 46, 63-71.	2.4	16
27	Enhancing \hat{I}^2 -Carotene Concentration in Parental Lines of CO6 Maize Hybrid Through Marker-Assisted Backcross Breeding (MABB). Frontiers in Nutrition, 2020, 7, 134.	3.7	16
28	Inter-subspecific maps of non-brittle rachis genes btr1/btr2 using occidental, oriental and wild barley lines. Euphytica, 2005, 145, 215-220.	1.2	15
29	COMPARATIVE STUDIES ON THE IRON AND ZINC CONTENTS ESTIMATION USING ATOMIC ABSORPTION SPECTROPHOTOMETER AND GRAIN STAINING TECHNIQUES (PRUSSIAN BLUE AND DTZ) IN MAIZE GERMPLASMS. Journal of Plant Nutrition, 2013, 36, 329-342.	1.9	15
30	Incorporation of <i>opaque-2</i> into â€~UMI 1200', an elite maize inbred line, through marker-assisted backcross breeding. Biotechnology and Biotechnological Equipment, 2019, 33, 144-153.	1.3	15
31	Evaluation of Morphological and Molecular Diversity among South Asian Germplasms of Cucumis sativus and Cucumis melo., 2012, 2012, 1-11.		14
32	Fingerprinting of Rice Hybrids and their Parental Lines using Microsatellite Markers and their Utilization in Genetic Purity Assessment of Hybrid Rice. Research Journal of Seed Science, 2009, 2, 40-47.	0.3	14
33	Screening and identification of random amplified polymorphic DNA (RAPD) markers linked to mungbean yellow mosaic virus (MYMV) resistance in mungbean (Vigna radiata(L.) Wilczek). Archives of Phytopathology and Plant Protection, 2012, 45, 712-716.	1.3	13
34	Markerâ€assisted introgression of lpa2 locus responsible for lowâ€phytic acid trait into an elite tropical maize inbred (<i><scp>Z</scp>ea mays</i> L.). Plant Breeding, 2014, 133, 566-578.	1.9	12
35	How Reliable Are the Reported Genetic Associations in Disc Degeneration?. Spine, 2016, 41, 1649-1660.	2.0	12
36	The complete chloroplast genome sequence of Indian barnyard millet, <i>Echinochloa frumentacea</i> (Poaceae). Mitochondrial DNA Part B: Resources, 2016, 1, 79-80.	0.4	12

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37	Functional characterization and substrate specificity analysis of Δ6-desaturase from marine microalga Isochrysis sp Biotechnology Letters, 2018, 40, 577-584.	2.2	12
38	QTL mapping in Vigna radiata $\tilde{A}-$ Vigna umbellata population uncovers major genomic regions associated with bruchid resistance. Molecular Breeding, 2019, 39, 1.	2.1	12
39	Delineation of Genotype $\tilde{A}-$ Environment Interaction for Identification of Stable Genotypes to Grain Yield in Mungbean. Frontiers in Agronomy, 2020, 2, .	3.3	12
40	Heterologous Production of Polyunsaturated Fatty Acids in E. coli Using î"5-Desaturase Gene from Microalga Isochrysis Sp Applied Biochemistry and Biotechnology, 2021, 193, 869-883.	2.9	9
41	Interaction of water activity and temperature on growth, gene expression, and aflatoxin B1 production in Aspergillus flavus on Indian senna (Cassia angustifolia Vahl.). International Journal of Food Microbiology, 2022, 361, 109457.	4.7	9
42	Levels of Plant Resistance in Chillies Capsicum spp against Whitefly, Bemisia tabaci. International Journal of Current Microbiology and Applied Sciences, 2018, 7, 1419-1441.	0.1	7
43	Biochemical Changes Due to Seed Priming in Maize Hybrid COH(M) 5. Research Journal of Seed Science, 2012, 5, 71-83.	0.3	7
44	Development of \hat{l}^2 -carotene, lysine, and tryptophan-rich maize (Zea mays) inbreds through marker-assisted gene pyramiding. Scientific Reports, 2022, 12, .	3.3	7
45	Marker aided introgression of opaque 2 (o2) allele improving lysine and tryptophan in maize (Zea mays) Tj ETQq1	1 ₃ 0,78431	.4 rgBT /C∨
46	Improvement of a Yairipok Chujak Maize Landrace from North Eastern Himalayan Region for \hat{l}^2 -Carotene Content through Molecular Marker-Assisted Backcross Breeding. Genes, 2021, 12, 762.	2.4	6
47	Dynamic Transcriptome Profiling of Mungbean Genotypes Unveil the Genes Respond to the Infection of Mungbean Yellow Mosaic Virus. Pathogens, 2022, 11, 190.	2.8	6
48	Assessment ofcrtRB1Polymorphism Associated with IncreasedÎ2-Carotene Content in Maize (Zea maysL.) Seeds. Food Biotechnology, 2014, 28, 41-49.	1.5	5
49	A new taxonomic treatment for some wild relatives of mungbean (Vigna radiata (L.) Wilcz.) based on their molecular phylogenetic relationships and morphological variations. Genetic Resources and Crop Evolution, 2018, 65, 1109-1121.	1.6	5
50	Characterization of potential probiotic bacteria from †panchamirthamâ€; A Southern Indian ethinic fermented fruit mix. LWT - Food Science and Technology, 2019, 116, 108540.	5.2	5
51	Population structure and association mapping studies for yield-related traits in Maize (Zea mays L.). Current Plant Biology, 2019, 18, 100103.	4.7	5
52	QTL mapping for sorghum downy mildew disease resistance in maize (Zea mays L.) in recombinant inbred line population of UMI79 X UMI936 (w). Current Plant Biology, 2019, 20, 100124.	4.7	4
53	A web accessible resource for investigating cassava phenomics and genomics information: BIOGEN BASE. Bioinformation, 2011, 6, 391-392.	0.5	4
54	Introgression of QTLs determining sorghum downy mildew (SDM) resistance into elite maize line UMI 79 through marker-assisted backcross breeding (MABC). Australasian Plant Pathology, 2020, 49, 159-165.	1.0	3

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55	Molecular Mapping of Non-Brittle Rachis Genes btr1 and btr2 using STS Markers in Barley. Japan Agricultural Research Quarterly, 2006, 40, 239-242.	0.4	3
56	Proteomic Analysis of Cassava Mosaic Virus (CMV) Responsive Proteins in Cassava Leaf. International Journal of Current Microbiology and Applied Sciences, 2019, 8, 2988-3005.	0.1	3
57	Characterization of Little millet (Panicum sumatrense) varieties using Morphological descriptors and SSR based DNA fingerprinting. Journal of Phytology, 0, , 29-34.	0.3	3
58	The Hunt for Mungbean (Vigna radiata (L.) Wilczek) Genotypes and Breeding Lines Resistance to South Indian Bruchid Strain. Agriculture (Switzerland), 2022, 12, 1050.	3.1	3
59	Proteomic analysis of compatible and incompatible interactions of wheat with Puccinia triticina. Physiological and Molecular Plant Pathology, 2016, 96, 36-46.	2.5	2
60	Characterization of crtRB1 Gene Polymorphism and \hat{I}^2 -Carotene Content in Maize Landraces Originated From North Eastern Himalayan Region (NEHR) of India. Frontiers in Sustainable Food Systems, 2020, 4, .	3.9	2
61	Genetics and molecular markers for anthocyanin pigmentation in barnyard millet (<code>Echinochloa</code>) Tj <code>ETQq1 1 0.7</code>	84314 rgBT 1.9	Overlock 1
62	DNA fingerprinting of foxtail millet (Setaria italica L.) variety ATL 1 using SSR and RAPD markers along with morphological descriptors. Tropical Plant Research, 2020, 7, 587-593.	0.4	2
63	Distinctive Physio-Biochemical Properties and Transcriptional Changes Unfold the Mungbean Cultivars Differing by Their Response to Drought Stress at Flowering Stage. Horticulturae, 2022, 8, 424.	2.8	2
64	Starch content and cassava mosaic disease genetic diversity with relation to yield in south Indian cassava (Manihot esculenta Crantz) germplasm. Journal of Crop Science and Biotechnology, 2011, 14, 179-189.	1.5	1
65	Interactive Effect of Environmental Factors on Biological Responses of Storage Pulse Beetle. Madras Agricultural Journal, 2017, 104, 368.	0.0	1
66	Varietal identification and fingerprinting of Pearl Millet (Pennisetum glaucum L.) varieties and hybrid using morphological descriptors and SSR markers. Current Botany, 0, , 105-109.	0.0	0
67	Structural Insights and Characterization of a Novel Transmembrane Binding Site for Potential Allosteric Modulation of the Muâ€opioid Receptor. FASEB Journal, 2021, 35, .	0.5	0
68	Allosteric modulation of cannabinoid receptors through transmembrane binding sites as a potential therapeutic intervention for pain and inflammation. FASEB Journal, 2021, 35, .	0.5	0
69	Development of Genome-wide Simple Sequence Repeat Markers from Whole-genome Sequence of Mungbean (Vigna radiata). Legume Research, 2021, , .	0.1	0
70	MAGICdb – Mango Genetic stocks Identification and Characterisation database. Bioinformation, 2013, 9, 838-839.	0.5	0
71	Estimates of genetic variability among the backcross populations involving UMI1200 and UMI1230 maize inbreds. Electronic Journal of Plant Breeding, 2018, 9, 1577.	0.1	0
72	In vitro Evaluation of Antimicrobial Activity of Lactic Acid Bacteria Isolated From Fermented Fruit Mix - Indian Traditional Fermented Foods, Against Selected Food Borne Pathogens. International Journal of Current Microbiology and Applied Sciences, 2019, 8, 3122-3126.	0.1	0