

Raman Sundaram

List of Publications by Year in descending order

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92
papers

2,645
citations

186265

28
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214800

47
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94
all docs

94
docs citations

94
times ranked

2234
citing authors

#	ARTICLE	IF	CITATIONS
1	Microstructure, matrix interactions, and molecular structure are the key determinants of inherent glycemic potential in pearl millet (<i>Pennisetum glaucum</i>). <i>Food Hydrocolloids</i> , 2022, 127, 107481.	10.7	12
2	Improvement of bacterial blight resistance of the popular variety, Nellore Mahsuri (NLR34449) through marker-assisted breeding. <i>Journal of Genetics</i> , 2022, 101, 1.	0.7	2
3	Marker assisted pedigree breeding based improvement of the Indian mega variety of rice MTU1010 for resistance against bacterial blight and blast and tolerance to low soil phosphorus. <i>PLoS ONE</i> , 2022, 17, e0260535.	2.5	2
4	Whole genome sequencing data of native isolates of <i>Bacillus</i> and <i>Trichoderma</i> having potential biocontrol and plant growth promotion activities in rice. <i>Data in Brief</i> , 2022, 41, 107923.	1.0	5
5	Multiparent-Derived, Marker-Assisted Introgression Lines of the Elite Indian Rice Cultivar, "Krishna Hamsa"™ Show Resistance against Bacterial Blight and Blast and Tolerance to Drought. <i>Plants</i> , 2022, 11, 622.	3.5	5
6	Stacking of Pup1 QTL for low soil phosphorus tolerance and bacterial blight resistance genes in the background of APMS6B, the maintainer line of rice hybrid DRRH-3. <i>Euphytica</i> , 2022, 218, 1.	1.2	1
7	Climate-Based Modeling and Prediction of Rice Gall Midge Populations Using Count Time Series and Machine Learning Approaches. <i>Agronomy</i> , 2022, 12, 22.	3.0	9
8	Improvement of bacterial blight resistance of the popular variety, Nellore Mahsuri (NLR34449) through marker-assisted breeding.. <i>Journal of Genetics</i> , 2022, 101, .	0.7	0
9	Assessment of heterotic potential and combining ability of novel iso-cytoplasmic restorer lines derived from an elite rice hybrid, KRH-2, for the development of superior rice hybrids. <i>Euphytica</i> , 2022, 218, .	1.2	0
10	Characterization and Prediction of Water Stress Using Time Series and Artificial Intelligence Models. <i>Sustainability</i> , 2022, 14, 6690.	3.2	4
11	Morphological and molecular screening of rice germplasm lines for low soil P tolerance. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2021, 30, 275-286.	1.7	4
12	PAP90, a novel rice protein plays a critical role in regulation of D1 protein stability of PSII. <i>Journal of Advanced Research</i> , 2021, 30, 197-211.	9.5	6
13	Molecular Approaches for Insect Pest Management in Rice. , 2021, , 379-423.		3
14	Novel major QTLs associated with low soil phosphorus tolerance identified from the Indian rice landrace, Wazuhophek. <i>PLoS ONE</i> , 2021, 16, e0254526.	2.5	11
15	Artificial-Intelligence-Based Time-Series Intervention Models to Assess the Impact of the COVID-19 Pandemic on Tomato Supply and Prices in Hyderabad, India. <i>Agronomy</i> , 2021, 11, 1878.	3.0	9
16	Nested Association Mapping (NAM) Populations: Present Status and Future Prospects in the Genomics Era. <i>Critical Reviews in Plant Sciences</i> , 2021, 40, 49-67.	5.7	6
17	Identification and molecular characterization of high-yielding, blast-resistant lines derived from <i>Oryza rufipogon</i> Griff. in the background of "Samba Mahsuri"™ rice. <i>Genetic Resources and Crop Evolution</i> , 2021, 68, 1905-1921.	1.6	7
18	Development of coreset of aromatic rice (<i>Oryza sativa</i> L. Indica) based on molecular and morphological diversity. <i>Genetic Resources and Crop Evolution</i> , 2021, 68, 441-450.	1.6	4

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19	Mapping novel QTLs for yield related traits from a popular rice hybrid KRH-2 derived doubled haploid (DH) population. <i>3 Biotech</i> , 2021, 11, 513.	2.2	4
20	Genes for NUE in rice: a way forward for molecular breeding and genome editing. <i>Plant Physiology Reports</i> , 2021, 26, 587-599.	1.5	8
21	Genetic, Epigenetic, Genomic and Microbial Approaches to Enhance Salt Tolerance of Plants: A Comprehensive Review. <i>Biology</i> , 2021, 10, 1255.	2.8	10
22	Two-Stage Spatiotemporal Time Series Modelling Approach for Rice Yield Prediction & Advanced Agroecosystem Management. <i>Agronomy</i> , 2021, 11, 2502.	3.0	7
23	Evaluation of genetic diversity of parental lines for development of heterotic groups in hybrid rice (<i>Oryza sativa</i> L.). <i>Journal of Plant Biochemistry and Biotechnology</i> , 2020, 29, 236-252.	1.7	13
24	Marker assisted improvement of low soil phosphorus tolerance in the bacterial blight resistant, fine-grain type rice variety, Improved Samba Mahsuri. <i>Scientific Reports</i> , 2020, 10, 21143.	3.3	8
25	Deployment of Genetic and Genomic Tools Toward Gaining a Better Understanding of Rice- <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> Interactions for Development of Durable Bacterial Blight Resistant Rice. <i>Frontiers in Plant Science</i> , 2020, 11, 1152.	3.6	41
26	Marker Assisted Gene Pyramiding (MAGP) for bacterial blight and blast resistance into mega rice variety "Tellahamsa". <i>PLoS ONE</i> , 2020, 15, e0234088.	2.5	43
27	Assessment of genetic purity of bulked seed of rice CMS lines using capillary electrophoresis. <i>Electrophoresis</i> , 2020, 41, 1749-1751.	2.4	1
28	Marker assisted introgression of a major bacterial blight resistance gene, Xa38 into a rice maintainer line, APMS 6B. <i>Indian Phytopathology</i> , 2019, 72, 35-41.	1.2	2
29	Expression profiling of immature florets of IR58025A, a wild-abortive cytoplasmic male sterile line of rice and its cognate, isonuclear maintainer line, IR58025B. <i>3 Biotech</i> , 2019, 9, 278.	2.2	1
30	Phenotypic and molecular characterization of rice germplasm lines and identification of novel source for low soil phosphorus tolerance in rice. <i>Euphytica</i> , 2019, 215, 1.	1.2	16
31	Pectin induced transcriptome of a <i>Rhizoctonia solani</i> strain causing sheath blight disease in rice reveals insights on key genes and RNAi machinery for development of pathogen derived resistance. <i>Plant Molecular Biology</i> , 2019, 100, 59-71.	3.9	32
32	Improvement of blast resistance of the popular high-yielding, medium slender-grain type, bacterial blight resistant rice variety, Improved Samba Mahsuri by marker-assisted breeding. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2018, 27, 463-472.	1.7	12
33	Marker-assisted pyramiding of two major, broad-spectrum bacterial blight resistance genes, Xa21 and Xa33 into an elite maintainer line of rice, DRR17B. <i>PLoS ONE</i> , 2018, 13, e0201271.	2.5	21
34	Breeding lines of the Indian mega-rice variety, MTU 1010, possessing protein kinase OsPSTOL (Pup1), show better root system architecture and higher yield in soils with low phosphorus. <i>Molecular Breeding</i> , 2018, 38, 1.	2.1	13
35	Prediction of heterosis in rice based on divergence of morphological and molecular markers. <i>Journal of Genetics</i> , 2018, 97, 1263-1279.	0.7	10
36	Proteomic and transcriptomic approaches to identify resistance and susceptibility related proteins in contrasting rice genotypes infected with fungal pathogen <i>Rhizoctonia solani</i> . <i>Plant Physiology and Biochemistry</i> , 2018, 130, 258-266.	5.8	22

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37	Improved versions of rice maintainer line, APMS 6B, possessing two resistance genes, Xa21 and Xa38, exhibit high level of resistance to bacterial blight disease. <i>Molecular Breeding</i> , 2018, 38, 1.	2.1	9
38	Incorporation of the novel bacterial blight resistance gene Xa38 into the genetic background of elite rice variety Improved Samba Mahsuri. <i>PLoS ONE</i> , 2018, 13, e0198260.	2.5	36
39	Introgression of durable blast resistance gene Pi-54 into <i>indica</i> rice cv. samba mahsuri, through Marker Assisted Backcross Breeding. <i>Electronic Journal of Plant Breeding</i> , 2018, 9, 705.	0.1	7
40	Prediction of heterosis in rice based on divergence of morphological and molecular markers. <i>Journal of Genetics</i> , 2018, 97, 1263-1279.	0.7	3
41	Marker-assisted pyramiding of bacterial blight and gall midge resistance genes into RPHR-1005, the restorer line of the popular rice hybrid DRRH-3. <i>Molecular Breeding</i> , 2017, 37, 1.	2.1	24
42	Development of Gene-Pyramid Lines of the Elite Restorer Line, RPHR-1005 Possessing Durable Bacterial Blight and Blast Resistance. <i>Frontiers in Plant Science</i> , 2016, 7, 1195.	3.6	21
43	Marker-assisted improvement of the elite restorer line of rice, RPHR-1005 for resistance against bacterial blight and blast diseases. <i>Journal of Genetics</i> , 2016, 95, 895-903.	0.7	13
44	Marker assisted introgression of blast (Pi-2 and Pi-54) genes in to the genetic background of elite, bacterial blight resistant indica rice variety, Improved Samba Mahsuri. <i>Euphytica</i> , 2016, 212, 331-342.	1.2	19
45	Development and validation of candidate gene-specific markers for the major fertility restorer genes, Rf4 and Rf3 in rice. <i>Molecular Breeding</i> , 2016, 36, 1.	2.1	12
46	Comparative analysis of sequences of mitochondrial genomes of wild abortive male sterile (WA-CMS) and male fertile lines of rice, development of functional markers for WA-CMS trait and their use in assessment of genetic purity of seeds of WA-CMS lines. <i>Molecular Breeding</i> , 2016, 36, 1.	2.1	4
47	Marker-assisted introgression of the major bacterial blight resistance gene, Xa21 and blast resistance gene, Pi54 into RPHR-1005, the restorer line of the popular rice hybrid, DRRH3. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2016, 25, 400-409.	1.7	11
48	Identification and validation of novel alleles of rice blast resistant gene Pi54, and analysis of their nucleotide diversity in landraces and wild <i>Oryza</i> species. <i>Euphytica</i> , 2016, 209, 725-737.	1.2	7
49	Nucleotide Diversity Analysis of Three Major Bacterial Blight Resistance Genes in Rice. <i>PLoS ONE</i> , 2015, 10, e0120186.	2.5	13
50	Pathogenic and Genetic Variation among the Isolates of <i>Rhizoctonia solani</i> (<i>AG</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.0	22
51	Marker-assisted introgression of bacterial blight and blast resistance into DRR17B, an elite, fine-grain type maintainer line of rice. <i>Molecular Breeding</i> , 2015, 35, 1.	2.1	44
52	Identification of cis-elements and evaluation of upstream regulatory region of a rice anther-specific gene, OSIPP3, conferring pollen-specific expression in <i>Oryza sativa</i> (L.) ssp. indica. <i>Plant Reproduction</i> , 2015, 28, 133-142.	2.2	15
53	Constitutive expression and silencing of a novel seed specific calcium dependent protein kinase gene in rice reveals its role in grain filling. <i>Journal of Plant Physiology</i> , 2015, 174, 41-48.	3.5	22
54	Assessment of Genetic Diversity of Elite Indian Rice Varieties Using Agro-Morphological Traits and SSR Markers. <i>American Journal of Experimental Agriculture</i> , 2015, 6, 384-401.	0.2	1

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55	Stress-inducible expression of AtDREB1A transcription factor greatly improves drought stress tolerance in transgenic indica rice. <i>Transgenic Research</i> , 2014, 23, 421-439.	2.4	106
56	A putative candidate for the recessive gall midge resistance gene gm3 in rice identified and validated. <i>Theoretical and Applied Genetics</i> , 2014, 127, 113-124.	3.6	34
57	Update on Bacterial Blight of Rice: Fourth International Conference on Bacterial Blight. <i>Rice</i> , 2014, 7, 12.	4.0	41
58	Nucleotide diversity of Pita, a major blast resistance gene and identification of its minimal promoter. <i>Gene</i> , 2014, 546, 250-256.	2.2	12
59	Marker-assisted introgression of bacterial blight and blast resistance into IR 58025B, an elite maintainer line of rice. <i>Plant Breeding</i> , 2013, 132, 586-594.	1.9	40
60	Improvement of two traditional Basmati rice varieties for bacterial blight resistance and plant stature through morphological and marker-assisted selection. <i>Molecular Breeding</i> , 2013, 31, 239-246.	2.1	39
61	Analysis of nucleotide diversity among alleles of the major bacterial blight resistance gene Xa27 in cultivars of rice (<i>Oryza sativa</i>) and its wild relatives. <i>Planta</i> , 2013, 238, 293-305.	3.2	18
62	Arabidopsis and <i>Brachypodium distachyon</i> Transgenic Plants Expressing <i>Aspergillus nidulans</i> Acetyltransferases Have Decreased Degree of Polysaccharide Acetylation and Increased Resistance to Pathogens. <i>Plant Physiology</i> , 2013, 162, 9-23.	4.8	104
63	Identification and Fine-Mapping of Xa33, a Novel Gene for Resistance to <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> . <i>Phytopathology</i> , 2012, 102, 222-228.	2.2	80
64	Mapping and marker-assisted breeding of a gene allelic to the major Asian rice gall midge resistance gene Gm8. <i>Euphytica</i> , 2012, 187, 393-400.	1.2	21
65	Fine mapping of Rf3 and Rf4 fertility restorer loci of WA-CMS of rice (<i>Oryza sativa</i> L.) and validation of the developed marker system for identification of restorer lines. <i>Euphytica</i> , 2012, 187, 421-435.	1.2	56
66	Different isoforms of starch-synthesizing enzymes controlling amylose and amylopectin content in rice (<i>Oryza sativa</i> L.). <i>Biotechnology Advances</i> , 2012, 30, 1697-1706.	11.7	60
67	Isolation and characterization of <i>Ustilaginoidea virens</i> and survey of false smut disease of rice in India. <i>Phytoparasitica</i> , 2012, 40, 171-176.	1.2	118
68	Marker-assisted improvement of a stable restorer line, KMR and its derived hybrid KRH2 for bacterial blight resistance and grain quality. <i>Plant Breeding</i> , 2011, 130, 608-616.	1.9	31
69	Suitability of non-lethal marker and marker-free systems for development of transgenic crop plants: Present status and future prospects. <i>Biotechnology Advances</i> , 2011, 29, 703-714.	11.7	36
70	Development and validation of functional marker targeting an InDel in the major rice blast disease resistance gene Pi54 (Pik h). <i>Molecular Breeding</i> , 2011, 27, 129-135.	2.1	71
71	Indel polymorphism in sugar translocation and transport genes associated with grain filling of rice (<i>Oryza sativa</i> L.). <i>Molecular Breeding</i> , 2011, 28, 683-691.	2.1	21
72	Determination of genetic relationships among elite thermosensitive genic male sterile lines (TGMS) of rice (<i>Oryza sativa</i> L.) employing morphological and simple sequence repeat (SSR) markers. <i>Journal of Genetics</i> , 2011, 90, 11-19.	0.7	9

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73	Inheritance of bacterial blight resistance in the rice cultivar Ajaya and high-resolution mapping of a major QTL associated with resistance. <i>Genetical Research</i> , 2011, 93, 397-408.	0.9	8
74	Development and validation of a PCR-based functional marker system for the major wide-compatible gene locus S5 in rice. <i>Molecular Breeding</i> , 2010, 26, 719-727.	2.1	21
75	Development of a PCR-based SNP marker system for effective selection of kernel length and kernel elongation in rice. <i>Molecular Breeding</i> , 2010, 26, 735-740.	2.1	43
76	Allele mining in crops: Prospects and potentials. <i>Biotechnology Advances</i> , 2010, 28, 451-461.	11.7	123
77	Prediction of heterosis for grain yield in rice using "key"™ informative EST-SSR markers. <i>Plant Breeding</i> , 2010, 129, 108-111.	1.9	24
78	Genetic and molecular basis of fragrance in rice. <i>Biotechnology Advances</i> , 2009, 27, 468-473.	11.7	96
79	Development of a simple functional marker for fragrance in rice and its validation in Indian Basmati and non-Basmati fragrant rice varieties. <i>Molecular Breeding</i> , 2009, 24, 185-190.	2.1	48
80	Validation of molecular markers linked to fertility restorer gene(s) for WA-CMS lines of rice. <i>Euphytica</i> , 2009, 167, 217-227.	1.2	41
81	Development and validation of class I SSR markers targeting (GATA) n repeat motifs in rice. <i>Euphytica</i> , 2009, 169, 263-271.	1.2	7
82	Introduction of bacterial blight resistance into Triguna, a high yielding, mid-early duration rice variety. <i>Biotechnology Journal</i> , 2009, 4, 400-407.	3.5	103
83	Marker assisted introgression of bacterial blight resistance in Samba Mahsuri, an elite indica rice variety. <i>Euphytica</i> , 2008, 160, 411-422.	1.2	264
84	Identification of informative SSR markers capable of distinguishing hybrid rice parental lines and their utilization in seed purity assessment. <i>Euphytica</i> , 2008, 163, 215-224.	1.2	87
85	In silico analysis of microsatellites in organellar genomes of major cereals for understanding their phylogenetic relationships. <i>In Silico Biology</i> , 2008, 8, 87-104.	0.9	18
86	A Mitochondrial Repeat Specific Marker for Distinguishing Wild Abortive Type Cytoplasmic Male Sterile Rice Lines from their Cognate Isogenic Maintainer Lines. <i>Crop Science</i> , 2007, 47, 207-211.	1.8	24
87	Flanking SSR markers for allelism test for the Asian rice gall midge (<i>Orseolia oryzae</i>) resistance genes. <i>Euphytica</i> , 2007, 157, 267-279.	1.2	11
88	Identification of simple sequence repeat markers for utilizing wide-compatibility genes in inter-subspecific hybrids in rice (<i>Oryza sativa</i> L.). <i>Theoretical and Applied Genetics</i> , 2006, 113, 509-517.	3.6	25
89	Identification of flanking SSR markers for a major rice gall midge resistance gene Gm1 and their validation. <i>Theoretical and Applied Genetics</i> , 2004, 109, 1468-1473.	3.6	49
90	A Sequence Specific PCR Marker for Distinguishing Rice Lines on the Basis of Wild Abortive Cytoplasm from Their Cognate Maintainer Lines. <i>Crop Science</i> , 2004, 44, 920-924.	1.8	20

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91	A Sequence Specific PCR Marker for Distinguishing Rice Lines on the Basis of Wild Abortive Cytoplasm from Their Cognate Maintainer Lines. <i>Crop Science</i> , 2004, 44, 920.	1.8	16
92	Assessment of purity of rice hybrids using microsatellite and STS markers. <i>Crop Science</i> , 2002, 42, 1369-1373.	1.8	82