Manje Gowda

List of Publications by Year
in descending order

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77 papers	4,448 citations	126708 33 h-index	114278 63 g-index
78 all docs	78 docs citations	78 times ranked	3485 citing authors

#	Article	IF	Citations
1	Genomic Analysis of Resistance to Fall Armyworm (Spodoptera frugiperda) in CIMMYT Maize Lines. Genes, 2022, 13, 251.	1.0	13
2	Relationship between Grain Yield and Quality Traits under Optimum and Low-Nitrogen Stress Environments in Tropical Maize. Agronomy, 2022, 12, 438.	1.3	6
3	Identification of Genomic Regions Associated with Agronomic and Disease Resistance Traits in a Large Set of Multiple DH Populations. Genes, 2022, 13, 351.	1.0	3
4	Host plant resistance for fall armyworm management in maize: relevance, status and prospects in Africa and Asia. Theoretical and Applied Genetics, 2022, 135, 3897-3916.	1.8	29
5	Maximizing efficiency of genomic selection in CIMMYTâ€™s tropical maize breeding program. Theoretical and Applied Genetics, 2021, 134, 279-294.	1.8	36
6	Genetic dissection of Striga hermonthica (Del.) Benth. resistance via genome-wide association and genomic prediction in tropical maize germplasm. Theoretical and Applied Genetics, 2021, 134, 941-958.	1.8	19
7	Beat the stress: breeding for climate resilience in maize for the tropical rainfed environments. Theoretical and Applied Genetics, 2021, 134, 1729-1752.	1.8	92
8	Brief Overview of Maize Lethal Necrosis and the Molecular Basis of Variability in Concentrations of the Causal Viruses in Co-infected Maize Plant. , 2021, , 13-39.		0
9	Introgression of Maize Lethal Necrosis Resistance Quantitative Trait Loci Into Susceptible Maize Populations and Validation of the Resistance Under Field Conditions in Naivasha, Kenya. Frontiers in Plant Science, 2021, 12, 649308.	1.7	9
10	Scalable Sparse Testing Genomic Selection Strategy for Early Yield Testing Stage. Frontiers in Plant Science, 2021, 12, 658978.	1.7	15
11	Application of Genomic Selection at the Early Stage of Breeding Pipeline in Tropical Maize. Frontiers in Plant Science, 2021, 12, 685488.	1.7	18
12	Multi-generation genomic prediction of maize yield using parametric and non-parametric sparse selection indices. Heredity, 2021, 127, 423-432.	1.2	4
13	Evidence of a plant genetic basis for maize roots impacting soil organic matter mineralization. Soil Biology and Biochemistry, 2021, 161, 108402.	4.2	5
14	Discovery and Validation of a Recessively Inherited Major-Effect QTL Conferring Resistance to Maize Lethal Necrosis (MLN) Disease. Frontiers in Genetics, 2021, 12, 767883.	1.1	10
15	Performance and yield stability of maize hybrids in stress-prone environments in eastern Africa. Crop Journal, 2020, 8, 107-118.	2.3	26
16	Genetic Analysis of QTL for Resistance to Maize Lethal Necrosis in Multiple Mapping Populations. Genes, 2020, 11, 32.	1.0	19
17	Genetic dissection of maternal influence on in vivo haploid induction in maize. Crop Journal, 2020, 8, 287-298.	2.3	5
18	Genome-Wide Analyses and Prediction of Resistance to MLN in Large Tropical Maize Germplasm. Genes, 2020, 11, 16.	1.0	34

#	Article	IF	Citations
19	Diallelic Analysis of Tropical Maize Germplasm Response to Spontaneous Chromosomal Doubling. Plants, 2020, 9, 1224.	1.6	0
20	Applications of genotyping-by-sequencing (GBS) in maize genetics and breeding. Scientific Reports, 2020, 10, 16308.	1.6	49
21	Genetic Dissection of Resistance to Gray Leaf Spot by Combining Genome-Wide Association, Linkage Mapping, and Genomic Prediction in Tropical Maize Germplasm. Frontiers in Plant Science, 2020, 11, 572027.	1.7	20
22	Efficiency of indirect selection for grain yield in maize (Zea mays L.) under low nitrogen conditions through secondary traits under low nitrogen and grain yield under optimum conditions. Euphytica, 2020, 216, 1.	0.6	12
23	Combination of Linkage Mapping, GWAS, and GP to Dissect the Genetic Basis of Common Rust Resistance in Tropical Maize Germplasm. International Journal of Molecular Sciences, 2020, 21, 6518.	1.8	16
24	Maize lethal necrosis (MLN): Efforts toward containing the spread and impact of a devastating transboundary disease in sub-Saharan Africa. Virus Research, 2020, 282, 197943.	1.1	53
25	Genetic Dissection of Nitrogen Use Efficiency in Tropical Maize Through Genome-Wide Association and Genomic Prediction. Frontiers in Plant Science, 2020, 11, 474.	1.7	33
26	Genomic Prediction Enhanced Sparse Testing for Multi-environment Trials. G3: Genes, Genomes, Genetics, 2020, 10, 2725-2739.	0.8	68
27	Genetic Dissection of Grain Yield and Agronomic Traits in Maize under Optimum and Low-Nitrogen Stressed Environments. International Journal of Molecular Sciences, 2020, 21, 543.	1.8	18
28	Improving the Efficiency of Colchicine-Based Chromosomal Doubling of Maize Haploids. Plants, 2020, 9, 459.	1.6	10
29	Hybrid Breeding for MLN Resistance: Heterosis, Combining Ability, and Hybrid Prediction. Plants, 2020, 9, 468.	1.6	10
30	Strategies for Effective Use of Genomic Information in Crop Breeding Programs Serving Africa and South Asia. Frontiers in Plant Science, 2020, 11, 353.	1.7	33
31	Increasing Genetic Gains in Maize in Stress-Prone Environments of the Tropics. , 2020, , 97-132.		6
32	Genome-wide association study to identify genomic regions influencing spontaneous fertility in maize haploids. Euphytica, 2019, 215, 138.	0.6	29
33	Comparison of Weighted and Unweighted Stageâ€Wise Analysis for Genomeâ€Wide Association Studies and Genomic Selection. Crop Science, 2019, 59, 2572-2584.	0.8	9
34	Maize lethal necrosis and the molecular basis of variability in concentrations of the causal viruses in co-infected maize plant. Journal of General and Molecular Virology, 2019, 9, 1-19.	1.7	10
35	Molecular diversity and selective sweeps in maize inbred lines adapted to African highlands. Scientific Reports, 2019, 9, 13490.	1.6	14
36	Genetic architecture of maize chlorotic mottle virus and maize lethal necrosis through GWAS, linkage analysis and genomic prediction in tropical maize germplasm. Theoretical and Applied Genetics, 2019, 132, 2381-2399.	1.8	53

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37	Empirical Comparison of Tropical Maize Hybrids Selected Through Genomic and Phenotypic Selections. Frontiers in Plant Science, 2019, 10, 1502.	1.7	54
38	Discovery and validation of genomic regions associated with resistance to maize lethal necrosis in four biparental populations. Molecular Breeding, 2018, 38, 66.	1.0	29
39	Genome-Wide Association Mapping and Genomic Prediction Analyses Reveal the Genetic Architecture of Grain Yield and Flowering Time Under Drought and Heat Stress Conditions in Maize. Frontiers in Plant Science, 2018, 9, 1919.	1.7	102
40	Genomic Selection in Plant Breeding: Methods, Models, and Perspectives. Trends in Plant Science, 2017, 22, 961-975.	4.3	1,004
41	Genetic analysis of tropical maize inbred lines for resistance to maize lethal necrosis disease. Euphytica, 2017, 213, 224.	0.6	48
42	High accuracy of predicting hybrid performance of Fusarium head blight resistance by mid-parent values in wheat. Theoretical and Applied Genetics, 2017, 130, 461-470.	1.8	24
43	Predicting Hybrid Performances for Quality Traits through Genomic-Assisted Approaches in Central European Wheat. PLoS ONE, 2016, 11, e0158635.	1.1	48
44	Quantitative Trait Loci Mapping and Molecular Breeding for Developing Stress Resilient Maize for Subâ€Saharan Africa. Crop Science, 2015, 55, 1449-1459.	0.8	61
45	Genetic architecture is more complex for resistance to Septoria tritici blotch than to Fusarium head blight in Central European winter wheat. BMC Genomics, 2015, 16, 430.	1.2	34
46	Genome-based establishment of a high-yielding heterotic pattern for hybrid wheat breeding. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 15624-15629.	3.3	178
47	Genome-wide association and genomic prediction of resistance to maize lethal necrosis disease in tropical maize germplasm. Theoretical and Applied Genetics, 2015, 128, 1957-1968.	1.8	145
48	Genetic Architecture of Winter Hardiness and Frost Tolerance in Triticale. PLoS ONE, 2014, 9, e99848.	1.1	18
49	Adult Plant Development in Triticale (Ã— Triticosecale Wittmack) Is Controlled by Dynamic Genetic Patterns of Regulation. G3: Genes, Genomes, Genetics, 2014, 4, 1585-1591.	0.8	26
50	Relatedness severely impacts accuracy of marker-assisted selection for disease resistance in hybrid wheat. Heredity, 2014, 112, 552-561.	1.2	67
51	Bridging the gap between marker-assisted and genomic selection of heading time and plant height in hybrid wheat. Heredity, 2014, 112, 638-645.	1.2	142
52	Multiple-line cross QTL mapping for biomass yield and plant height in triticale (Ã— Triticosecale) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 14	1.8	46
53	Genotypic correlations and QTL correspondence between line per se and testcross performance in sugar beet (Beta vulgaris L.) for the three agronomic traits beet yield, potassium content, and sodium content. Molecular Breeding, 2014, 34, 205-215.	1.0	5
54	Genetic dynamics underlying phenotypic development of biomass yield in triticale. BMC Genomics, 2014, 15, 458.	1.2	41

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55	Multiple-line cross quantitative trait locus mapping in sugar beet (Beta vulgaris L.). Molecular Breeding, 2013, 31, 279-287.	1.0	3
56	Hybrid wheat: quantitative genetic parameters and consequences for the design of breeding programs. Theoretical and Applied Genetics, 2013, 126, 2791-2801.	1.8	127
57	Genetic architecture of resistance to Septoria tritici blotch in European wheat. BMC Genomics, 2013, 14, 858.	1.2	62
58	Genomic prediction of sunflower hybrid performance. Plant Breeding, 2013, 132, 107-114.	1.0	71
59	Hybrid rye performance under natural drought stress in Europe. Theoretical and Applied Genetics, 2013, 126, 475-482.	1.8	35
60	Choice of shrinkage parameter and prediction of genomic breeding values in elite maize breeding populations. Plant Breeding, 2013, 132, 99-106.	1.0	20
61	Dissecting the genetic architecture of frost tolerance in Central European winter wheat. Journal of Experimental Botany, 2013, 64, 4453-4460.	2.4	69
62	Best linear unbiased prediction of triticale hybrid performance. Euphytica, 2013, 191, 223-230.	0.6	33
63	Relevance of Specific versus General Combining Ability in Winter Wheat. Crop Science, 2012, 52, 2494-2500.	0.8	51
64	Impact of selective genotyping in the training population on accuracy and bias of genomic selection. Theoretical and Applied Genetics, 2012, 125, 707-713.	1.8	61
65	Hybrid breeding in autogamous cereals. Theoretical and Applied Genetics, 2012, 125, 1087-1096.	1.8	243
66	Comparison of biometrical models for joint linkage association mapping. Heredity, 2012, 108, 332-340.	1.2	81
67	Accuracy of genomic selection in European maize elite breeding populations. Theoretical and Applied Genetics, 2012, 124, 769-776.	1.8	241
68	Morpho-agronomic and simple sequence repeat-based diversity in colored rice (Oryza sativa L.) germplasm from peninsular India. Genetic Resources and Crop Evolution, 2012, 59, 179-189.	0.8	15
69	Potential for simultaneous improvement of grain and biomass yield in Central European winter triticale germplasm. Field Crops Research, 2011, 121, 153-157.	2.3	33
70	Association mapping for quality traits in soft winter wheat. Theoretical and Applied Genetics, 2011, 122, 961-970.	1.8	120
71	Association mapping in an elite maize breeding population. Theoretical and Applied Genetics, 2011, 123, 847-858.	1.8	47
72	Mapping of QTLs governing agronomic and yield traits in chickpea. Journal of Applied Genetics, 2011, 52, 9-21.	1.0	37

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73	Genetic basis of agronomically important traits in sugar beet (Beta vulgaris L.) investigated with joint linkage association mapping. Theoretical and Applied Genetics, 2010, 121, 1489-1499.	1.8	25
74	Hybrid Breeding in Durum Wheat: Heterosis and Combining Ability. Crop Science, 2010, 50, 2224-2230.	0.8	41
75	Molecular mapping of wilt resistance genes in chickpea. Molecular Breeding, 2009, 24, 177-183.	1.0	74
76	Development of an integrated intraspecific map of chickpea (Cicer arietinum L.) using two recombinant inbred line populations. Theoretical and Applied Genetics, 2007, 115, 209-216.	1.8	99
77	Comparison of non-overlapping maize populations of unequal sizes for resistance to maize lethal necrosis. Journal of Crop Improvement, 0, , 1-20.	0.9	0