

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 Selection in Plant Breeding: Methods, Models, and Perspectives. Trends in Plant Science, 2017, 22, 961-975.	4.3	1,004
2	Hybrid breeding in autogamous cereals. Theoretical and Applied Genetics, 2012, 125, 1087-1096.	1.8	243
3	Accuracy of genomic selection in European maize elite breeding populations. Theoretical and Applied Genetics, 2012, 124, 769-776.	1.8	241
4	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
5	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
6	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
7	Hybrid wheat: quantitative genetic parameters and consequences for the design of breeding programs. Theoretical and Applied Genetics, 2013, 126, 2791-2801.	1.8	127
8	Association mapping for quality traits in soft winter wheat. Theoretical and Applied Genetics, 2011, 122, 961-970.	1.8	120
9	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
10	Development of an integrated intraspecific map of chickpea (<i>Cicer arietinum</i> L.) using two recombinant inbred line populations. Theoretical and Applied Genetics, 2007, 115, 209-216.	1.8	99
11	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
12	Comparison of biometrical models for joint linkage association mapping. Heredity, 2012, 108, 332-340.	1.2	81
13	Molecular mapping of wilt resistance genes in chickpea. Molecular Breeding, 2009, 24, 177-183.	1.0	74
14	Genomic prediction of sunflower hybrid performance. Plant Breeding, 2013, 132, 107-114.	1.0	71
15	Dissecting the genetic architecture of frost tolerance in Central European winter wheat. Journal of Experimental Botany, 2013, 64, 4453-4460.	2.4	69
16	Genomic Prediction Enhanced Sparse Testing for Multi-environment Trials. G3: Genes, Genomes, Genetics, 2020, 10, 2725-2739.	0.8	68
17	Relatedness severely impacts accuracy of marker-assisted selection for disease resistance in hybrid wheat. Heredity, 2014, 112, 552-561.	1.2	67
18	Genetic architecture of resistance to <i>Septoria tritici</i> blotch in European wheat. BMC Genomics, 2013, 14, 858.	1.2	62

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19	Impact of selective genotyping in the training population on accuracy and bias of genomic selection. <i>Theoretical and Applied Genetics</i> , 2012, 125, 707-713.	1.8	61
20	Quantitative Trait Loci Mapping and Molecular Breeding for Developing Stress Resilient Maize for Sub-Saharan Africa. <i>Crop Science</i> , 2015, 55, 1449-1459.	0.8	61
21	Empirical Comparison of Tropical Maize Hybrids Selected Through Genomic and Phenotypic Selections. <i>Frontiers in Plant Science</i> , 2019, 10, 1502.	1.7	54
22	Genetic architecture of maize chlorotic mottle virus and maize lethal necrosis through GWAS, linkage analysis and genomic prediction in tropical maize germplasm. <i>Theoretical and Applied Genetics</i> , 2019, 132, 2381-2399.	1.8	53
23	Maize lethal necrosis (MLN): Efforts toward containing the spread and impact of a devastating transboundary disease in sub-Saharan Africa. <i>Virus Research</i> , 2020, 282, 197943.	1.1	53
24	Relevance of Specific versus General Combining Ability in Winter Wheat. <i>Crop Science</i> , 2012, 52, 2494-2500.	0.8	51
25	Applications of genotyping-by-sequencing (GBS) in maize genetics and breeding. <i>Scientific Reports</i> , 2020, 10, 16308.	1.6	49
26	Genetic analysis of tropical maize inbred lines for resistance to maize lethal necrosis disease. <i>Euphytica</i> , 2017, 213, 224.	0.6	48
27	Predicting Hybrid Performances for Quality Traits through Genomic-Assisted Approaches in Central European Wheat. <i>PLoS ONE</i> , 2016, 11, e0158635.	1.1	48
28	Association mapping in an elite maize breeding population. <i>Theoretical and Applied Genetics</i> , 2011, 123, 847-858.	1.8	47
29	Multiple-line cross QTL mapping for biomass yield and plant height in triticale (Triticosecale) Tj ETQq1 1 0.784314 rgBT / Overlock 10	1.8	46
30	Hybrid Breeding in Durum Wheat: Heterosis and Combining Ability. <i>Crop Science</i> , 2010, 50, 2224-2230.	0.8	41
31	Genetic dynamics underlying phenotypic development of biomass yield in triticale. <i>BMC Genomics</i> , 2014, 15, 458.	1.2	41
32	Mapping of QTLs governing agronomic and yield traits in chickpea. <i>Journal of Applied Genetics</i> , 2011, 52, 9-21.	1.0	37
33	Maximizing efficiency of genomic selection in CIMMYT's tropical maize breeding program. <i>Theoretical and Applied Genetics</i> , 2021, 134, 279-294.	1.8	36
34	Hybrid rye performance under natural drought stress in Europe. <i>Theoretical and Applied Genetics</i> , 2013, 126, 475-482.	1.8	35
35	Genetic architecture is more complex for resistance to <i>Septoria tritici</i> blotch than to <i>Fusarium</i> head blight in Central European winter wheat. <i>BMC Genomics</i> , 2015, 16, 430.	1.2	34
36	Genome-Wide Analyses and Prediction of Resistance to MLN in Large Tropical Maize Germplasm. <i>Genes</i> , 2020, 11, 16.	1.0	34

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37	Potential for simultaneous improvement of grain and biomass yield in Central European winter triticale germplasm. <i>Field Crops Research</i> , 2011, 121, 153-157.	2.3	33
38	Best linear unbiased prediction of triticale hybrid performance. <i>Euphytica</i> , 2013, 191, 223-230.	0.6	33
39	Genetic Dissection of Nitrogen Use Efficiency in Tropical Maize Through Genome-Wide Association and Genomic Prediction. <i>Frontiers in Plant Science</i> , 2020, 11, 474.	1.7	33
40	Strategies for Effective Use of Genomic Information in Crop Breeding Programs Serving Africa and South Asia. <i>Frontiers in Plant Science</i> , 2020, 11, 353.	1.7	33
41	Discovery and validation of genomic regions associated with resistance to maize lethal necrosis in four biparental populations. <i>Molecular Breeding</i> , 2018, 38, 66.	1.0	29
42	Genome-wide association study to identify genomic regions influencing spontaneous fertility in maize haploids. <i>Euphytica</i> , 2019, 215, 138.	0.6	29
43	Host plant resistance for fall armyworm management in maize: relevance, status and prospects in Africa and Asia. <i>Theoretical and Applied Genetics</i> , 2022, 135, 3897-3916.	1.8	29
44	Adult Plant Development in Triticale (<i>Triticosecale</i> Wittmack) Is Controlled by Dynamic Genetic Patterns of Regulation. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1585-1591.	0.8	26
45	Performance and yield stability of maize hybrids in stress-prone environments in eastern Africa. <i>Crop Journal</i> , 2020, 8, 107-118.	2.3	26
46	Genetic basis of agronomically important traits in sugar beet (<i>Beta vulgaris</i> L.) investigated with joint linkage association mapping. <i>Theoretical and Applied Genetics</i> , 2010, 121, 1489-1499.	1.8	25
47	High accuracy of predicting hybrid performance of Fusarium head blight resistance by mid-parent values in wheat. <i>Theoretical and Applied Genetics</i> , 2017, 130, 461-470.	1.8	24
48	Choice of shrinkage parameter and prediction of genomic breeding values in elite maize breeding populations. <i>Plant Breeding</i> , 2013, 132, 99-106.	1.0	20
49	Genetic Dissection of Resistance to Gray Leaf Spot by Combining Genome-Wide Association, Linkage Mapping, and Genomic Prediction in Tropical Maize Germplasm. <i>Frontiers in Plant Science</i> , 2020, 11, 572027.	1.7	20
50	Genetic Analysis of QTL for Resistance to Maize Lethal Necrosis in Multiple Mapping Populations. <i>Genes</i> , 2020, 11, 32.	1.0	19
51	Genetic dissection of <i>Striga hermonthica</i> (Del.) Benth. resistance via genome-wide association and genomic prediction in tropical maize germplasm. <i>Theoretical and Applied Genetics</i> , 2021, 134, 941-958.	1.8	19
52	Genetic Architecture of Winter Hardiness and Frost Tolerance in Triticale. <i>PLoS ONE</i> , 2014, 9, e99848.	1.1	18
53	Genetic Dissection of Grain Yield and Agronomic Traits in Maize under Optimum and Low-Nitrogen Stressed Environments. <i>International Journal of Molecular Sciences</i> , 2020, 21, 543.	1.8	18
54	Application of Genomic Selection at the Early Stage of Breeding Pipeline in Tropical Maize. <i>Frontiers in Plant Science</i> , 2021, 12, 685488.	1.7	18

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55	Combination of Linkage Mapping, GWAS, and GP to Dissect the Genetic Basis of Common Rust Resistance in Tropical Maize Germplasm. <i>International Journal of Molecular Sciences</i> , 2020, 21, 6518.	1.8	16
56	Morpho-agronomic and simple sequence repeat-based diversity in colored rice (<i>Oryza sativa</i> L.) germplasm from peninsular India. <i>Genetic Resources and Crop Evolution</i> , 2012, 59, 179-189.	0.8	15
57	Scalable Sparse Testing Genomic Selection Strategy for Early Yield Testing Stage. <i>Frontiers in Plant Science</i> , 2021, 12, 658978.	1.7	15
58	Molecular diversity and selective sweeps in maize inbred lines adapted to African highlands. <i>Scientific Reports</i> , 2019, 9, 13490.	1.6	14
59	Genomic Analysis of Resistance to Fall Armyworm (<i>Spodoptera frugiperda</i>) in CIMMYT Maize Lines. <i>Genes</i> , 2022, 13, 251.	1.0	13
60	Efficiency of indirect selection for grain yield in maize (<i>Zea mays</i> L.) under low nitrogen conditions through secondary traits under low nitrogen and grain yield under optimum conditions. <i>Euphytica</i> , 2020, 216, 1.	0.6	12
61	Maize lethal necrosis and the molecular basis of variability in concentrations of the causal viruses in co-infected maize plant. <i>Journal of General and Molecular Virology</i> , 2019, 9, 1-19.	1.7	10
62	Improving the Efficiency of Colchicine-Based Chromosomal Doubling of Maize Haploids. <i>Plants</i> , 2020, 9, 459.	1.6	10
63	Hybrid Breeding for MLN Resistance: Heterosis, Combining Ability, and Hybrid Prediction. <i>Plants</i> , 2020, 9, 468.	1.6	10
64	Discovery and Validation of a Recessively Inherited Major-Effect QTL Conferring Resistance to Maize Lethal Necrosis (MLN) Disease. <i>Frontiers in Genetics</i> , 2021, 12, 767883.	1.1	10
65	Comparison of Weighted and Unweighted Stage-Wise Analysis for Genome-Wide Association Studies and Genomic Selection. <i>Crop Science</i> , 2019, 59, 2572-2584.	0.8	9
66	Introgression of Maize Lethal Necrosis Resistance Quantitative Trait Loci Into Susceptible Maize Populations and Validation of the Resistance Under Field Conditions in Naivasha, Kenya. <i>Frontiers in Plant Science</i> , 2021, 12, 649308.	1.7	9
67	Increasing Genetic Gains in Maize in Stress-Prone Environments of the Tropics. , 2020, , 97-132.		6
68	Relationship between Grain Yield and Quality Traits under Optimum and Low-Nitrogen Stress Environments in Tropical Maize. <i>Agronomy</i> , 2022, 12, 438.	1.3	6
69	Genotypic correlations and QTL correspondence between line per se and testcross performance in sugar beet (<i>Beta vulgaris</i> L.) for the three agronomic traits beet yield, potassium content, and sodium content. <i>Molecular Breeding</i> , 2014, 34, 205-215.	1.0	5
70	Genetic dissection of maternal influence on in vivo haploid induction in maize. <i>Crop Journal</i> , 2020, 8, 287-298.	2.3	5
71	Evidence of a plant genetic basis for maize roots impacting soil organic matter mineralization. <i>Soil Biology and Biochemistry</i> , 2021, 161, 108402.	4.2	5
72	Multi-generation genomic prediction of maize yield using parametric and non-parametric sparse selection indices. <i>Heredity</i> , 2021, 127, 423-432.	1.2	4

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73	Multiple-line cross quantitative trait locus mapping in sugar beet (<i>Beta vulgaris</i> L.). <i>Molecular Breeding</i> , 2013, 31, 279-287.	1.0	3
74	Identification of Genomic Regions Associated with Agronomic and Disease Resistance Traits in a Large Set of Multiple DH Populations. <i>Genes</i> , 2022, 13, 351.	1.0	3
75	Diallelic Analysis of Tropical Maize Germplasm Response to Spontaneous Chromosomal Doubling. <i>Plants</i> , 2020, 9, 1224.	1.6	0
76	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
77	Comparison of non-overlapping maize populations of unequal sizes for resistance to maize lethal necrosis. <i>Journal of Crop Improvement</i> , 0, , 1-20.	0.9	0