

MaizeGDB update: new tools, data and interface for the

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Synthesis and Functions of Jasmonates in Maize. <i>Plants</i> , 2016, 5, 41.	1.6	92
2	High Quality Maize Centromere 10 Sequence Reveals Evidence of Frequent Recombination Events. <i>Frontiers in Plant Science</i> , 2016, 7, 308.	1.7	28
3	The earliest maize from San Marcos Tehuacán is a partial domesticate with genomic evidence of inbreeding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 14151-14156.	3.3	93
4	Genome-wide Association for Plant Height and Flowering Time across 15 Tropical Maize Populations under Managed Drought Stress and Well-watered Conditions in Sub-Saharan Africa. <i>Crop Science</i> , 2016, 56, 2365-2378.	0.8	88
5	Quantitative imaging for development of companion diagnostics to drugs targeting HGF/MET. <i>Journal of Pathology: Clinical Research</i> , 2016, 2, 210-222.	1.3	16
6	Gain-of-function in Arabidopsis (GAINA) for identifying functional genes in <i>Hevea brasiliensis</i> . <i>SpringerPlus</i> , 2016, 5, 1853.	1.2	3
7	NABIC: A New Access Portal to Search, Visualize, and Share Agricultural Genomics Data. <i>Evolutionary Bioinformatics</i> , 2016, 12, EBO.S34493.	0.6	10
8	The quality of metabolic pathway resources depends on initial enzymatic function assignments: a case for maize. <i>BMC Systems Biology</i> , 2016, 10, 129.	3.0	15
9	Distant eQTLs and Non-coding Sequences Play Critical Roles in Regulating Gene Expression and Quantitative Trait Variation in Maize. <i>Molecular Plant</i> , 2017, 10, 414-426.	3.9	137
10	Aberrant splicing in maize <i>rough endosperm3</i> reveals a conserved role for U12 splicing in eukaryotic multicellular development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E2195-E2204.	3.3	38
11	Gibberellin in plant height control: old player, new story. <i>Plant Cell Reports</i> , 2017, 36, 391-398.	2.8	126
12	Naming CRISPR alleles: endonuclease-mediated mutation nomenclature across species. <i>Mammalian Genome</i> , 2017, 28, 367-376.	1.0	7
13	Water-deficit-induced changes in transcription factor expression in maize seedlings. <i>Plant, Cell and Environment</i> , 2017, 40, 686-701.	2.8	18
14	Genomic Analysis of the DNA Replication Timing Program during Mitotic S Phase in Maize (<i>Zea mays</i>). <i>Plant Cell</i> , 2017, 29, 1073-1084.	3.1	28
15	Review of combinations of experimental and computational techniques to identify and understand genes involved in innate immunity and effector-triggered defence. <i>Methods</i> , 2017, 131, 120-127.	1.9	17
16	Towards CRISPR/Cas crops – bringing together genomics and genome editing. <i>New Phytologist</i> , 2017, 216, 682-698.	3.5	235
17	Surveying the Maize community for their diversity and pedigree visualization needs to prioritize tool development and curation. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	1.4	4
18	PCPPI: a comprehensive database for the prediction of Penicillium crop protein-protein interactions. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	1.4	10

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19	MGIS: managing banana (<i>Musa</i> spp.) genetic resources information and high-throughput genotyping data. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	1.4	41
20	Plant Reactome: a resource for plant pathways and comparative analysis. Nucleic Acids Research, 2017, 45, D1029-D1039.	6.5	95
21	Unraveling gene function in agricultural species using gene co-expression networks. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2017, 1860, 53-63.	0.9	47
22	The art of curation at a biological database: Principles and application. Current Plant Biology, 2017, 11-12, 2-11.	2.3	30
23	Investigation of Antimicrobial Peptide Genes Associated with Fungus and Insect Resistance in Maize. International Journal of Molecular Sciences, 2017, 18, 1938.	1.8	26
24	Maize network analysis revealed gene modules involved in development, nutrients utilization, metabolism, and stress response. BMC Plant Biology, 2017, 17, 131.	1.6	24
25	Genome-wide identification and characterization of the RIO atypical kinase family in plants. Genes and Genomics, 2018, 40, 669-683.	0.5	6
26	Diverse Chromosomal Locations of Quantitative Trait Loci for Tolerance to <i>Maize chlorotic mottle virus</i> in Five Maize Populations. Phytopathology, 2018, 108, 748-758.	1.1	26
27	Maize leaf PPK regulatory protein isoform-2 is specific to bundle sheath chloroplasts and paradoxically lacks a Pi-dependent PPK activation activity. Journal of Experimental Botany, 2018, 69, 1171-1181.	2.4	6
28	Computational characterization of substrate and product specificities, and functionality of S-adenosylmethionine binding pocket in histone lysine methyltransferases from Arabidopsis, rice and maize. Proteins: Structure, Function and Bioinformatics, 2018, 86, 21-34.	1.5	8
29	Cell-Type Transcriptomes of the Multicellular Green Alga <i>Volvox carteri</i> Yield Insights into the Evolutionary Origins of Germ and Somatic Differentiation Programs. G3: Genes, Genomes, Genetics, 2018, 8, 531-550.	0.8	29
30	PhytoTypeDB: a database of plant protein inter-cultivar variability and function. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	1
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33	Integrating Coexpression Networks with GWAS to Prioritize Causal Genes in Maize. Plant Cell, 2018, 30, 2922-2942.	3.1	137
34	<i>De novo</i> Short Read Assembly and Functional Annotation of <i>Eleocharis vivipara</i> , a C ₃ /C ₄ Interconvertible Sedge Plant. Environmental Control in Biology, 2018, 56, 81-87.	0.3	2
35	SNPversity: a web-based tool for visualizing diversity. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	9
36	Camoco: A Net for the Sea of Candidate Genes. Plant Cell, 2018, 30, 2889-2889.	3.1	2

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37	PlaD: A Transcriptomics Database for Plant Defense Responses to Pathogens, Providing New Insights into Plant Immune System. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 283-293.	3.0	19
38	AgBioData consortium recommendations for sustainable genomics and genetics databases for agriculture. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	1.4	52
39	Opaque-2 Regulates a Complex Gene Network Associated with Cell Differentiation and Storage Functions of Maize Endosperm. <i>Plant Cell</i> , 2018, 30, 2425-2446.	3.1	83
40	A Comparative Assessment of Human and Chimpanzee iPSC-derived Cardiomyocytes with Primary Heart Tissues. <i>Scientific Reports</i> , 2018, 8, 15312.	1.6	57
41	Maize GO Annotationâ€™Methods, Evaluation, and Review (maizeâ€™GAMER). <i>Plant Direct</i> , 2018, 2, e00052.	0.8	97
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46	The Quantitative Genetic Control of Root Architecture in Maize. <i>Plant and Cell Physiology</i> , 2018, 59, 1919-1930.	1.5	46
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50	MaizeDIG: Maize Database of Images and Genomes. <i>Frontiers in Plant Science</i> , 2019, 10, 1050.	1.7	9
51	Integrated Genome-Scale Analysis Identifies Novel Genes and Networks Underlying Senescence in Maize. <i>Plant Cell</i> , 2019, 31, 1968-1989.	3.1	63
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63	Identification of quantitative trait loci contributing resistance to aflatoxin accumulation in maize inbred Mp715. Molecular Breeding, 2019, 39, 1.	1.0	9
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69	Recruitment of specific flavonoid ring hydroxylases for two independent biosynthesis pathways of flavone-derived metabolites in grasses. New Phytologist, 2019, 223, 204-219.	3.5	38
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74	Classifying cold stress responses of inbred maize seedlings using <sc>RGB</sc> imaging. <i>Plant Direct</i> , 2019, 3, e00104.	0.8	34
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84	Characterization of natural genetic variation identifies multiple genes involved in salt tolerance in maize. <i>Functional and Integrative Genomics</i> , 2020, 20, 261-275.	1.4	17
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86	Global Profiling of Alternative Splicing in Callus Induction of Immature Maize Embryo. <i>In Vitro Cellular and Developmental Biology - Plant</i> , 2020, 56, 159-168.	0.9	3
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111	Prediction and Activity of a Cationic Î±-Helix Antimicrobial Peptide ZM-804 from Maize. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2643.	1.8	9
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147	Effect of aneuploidy of a non-essential chromosome on gene expression in maize. <i>Plant Journal</i> , 2022, 110, 193-211.	2.8	8
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161	Exploring the relationship between pattern-triggered immunity and quantitative resistance to <i>Xanthomonas vasicola</i> pv. <i>vasculorum</i> in maize. <i>Phytopathology</i> , 0, , .	1.1	1