Ismail Rabbi

List of Publications by Year
in descending order

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46 papers	2,125 citations	331259 21 h-index	276539 41 g-index
53 all docs	53 docs citations	53 times ranked	2230 citing authors

#	Article	IF	Citations
1	Genome-wide association analysis reveals new insights into the genetic architecture of defensive, agro-morphological and quality-related traits in cassava. Plant Molecular Biology, 2022, 109, 195-213.	2.0	33
2	Selection for resistance to cassava mosaic disease in African cassava germplasm using single nucleotide polymorphism markers. South African Journal of Science, 2022, 118, .	0.3	3
3	Lowâ€cost, handheld nearâ€infrared spectroscopy for root dry matter content prediction in cassava. The Plant Phenome Journal, 2022, 5, .	1.0	6
4	Breedbase: a digital ecosystem for modern plant breeding. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	17
5	Largeâ€scale genomeâ€wide association study, using historical data, identifies conserved genetic architecture of cyanogenic glucoside content in cassava (<i>Manihot esculenta</i> Crantz) root. Plant Journal, 2021, 105, 754-770.	2.8	26
6	Understanding cassava varietal preferences through pairwise ranking of <i>gariâ€eba</i> and <i>fufu</i> prepared by local farmerâ€“processors. International Journal of Food Science and Technology, 2021, 56, 1258-1277.	1.3	31
7	Conversion and Validation of Uniplex SNP Markers for Selection of Resistance to Cassava Mosaic Disease in Cassava Breeding Programs. Agronomy, 2021, 11, 420.	1.3	10
8	Portable Spectroscopy Calibration with Inexpensive and Simple Sampling Reference Alternatives for Dry Matter and Total Carotenoid Contents in Cassava Roots. Applied Sciences (Switzerland), 2021, 11, 1714.	1.3	4
9	Identifying New Resistance to Cassava Mosaic Disease and Validating Markers for the CMD2 Locus. Agriculture (Switzerland), 2021, 11, 829.	1.4	8
10	Genetic Diversity and Population Structure of Cowpea [Vigna unguiculata (L.) Walp.] Germplasm Collected from Togo Based on DArT Markers. Genes, 2021, 12, 1451.	1.0	16
11	Genomic mating in outbred species: predicting cross usefulness with additive and total genetic covariance matrices. Genetics, 2021, 219, .	1.2	13
12	Genome-Wide Association Study of Root Mealiness and Other Texture-Associated Traits in Cassava. Frontiers in Plant Science, 2021, 12, 770434.	1.7	5
13	Genetic characterization of cassava (Manihot esculenta Crantz) genotypes using agro-morphological and single nucleotide polymorphism markers. Physiology and Molecular Biology of Plants, 2020, 26, 317-330.	1.4	14
14	Improving root characterisation for genomic prediction in cassava. Scientific Reports, 2020, 10, 8003.	1.6	15
15	The Cassava Sourceâ€“Sink project: opportunities and challenges for crop improvement by metabolic engineering. Plant Journal, 2020, 103, 1655-1665.	2.8	33
16	Gene Expression and Metabolite Profiling of Thirteen Nigerian Cassava Landraces to Elucidate Starch and Carotenoid Composition. Agronomy, 2020, 10, 424.	1.3	7
17	Genomic prediction and quantitative trait locus discovery in a cassava training population constructed from multiple breeding stages. Crop Science, 2020, 60, 896-913.	0.8	9
18	Identification of additional /novel QTL associated with resistance to cassava green mite in a biparental mapping population. PLoS ONE, 2020, 15, e0231008.	1.1	10

#	ARTICLE	IF	CITATIONS
19	Technological Innovations for Improving Cassava Production in Sub-Saharan Africa. Frontiers in Genetics, 2020, 11, 623736.	1.1	30
20	Historical Introgressions from a Wild Relative of Modern Cassava Improved Important Traits and May Be Under Balancing Selection. Genetics, 2019, 213, 1237-1253.	1.2	27
21	Improving Genomic Prediction in Cassava Field Experiments by Accounting for Interplot Competition. G3: Genes, Genomes, Genetics, 2018, 8, 933-944.	0.8	4
22	Improving Genomic Prediction in Cassava Field Experiments Using Spatial Analysis. G3: Genes, Genomes, Genetics, 2018, 8, 53-62.	0.8	20
23	Regional Heritability Mapping Provides Insights into Dry Matter Content in African White and Yellow Cassava Populations. Plant Genome, 2018, 11, 170050.	1.6	10
24	Genetic diversity and population structure of a mini-core subset from the world cowpea (Vigna) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 54	1.6	63
25	Training Population Optimization for Prediction of Cassava Brown Streak Disease Resistance in West African Clones. G3: Genes, Genomes, Genetics, 2018, 8, 3903-3913.	0.8	23
26	Genomeâ€Wide Association Study of Resistance to Cassava Green Mite Pest and Related Traits in Cassava. Crop Science, 2018, 58, 1907-1918.	0.8	28
27	Genomics-Assisted Breeding in the CGIAR Research Program on Roots, Tubers and Bananas (RTB). Agriculture (Switzerland), 2018, 8, 89.	1.4	16
28	Cassava haplotype map highlights fixation of deleterious mutations during clonal propagation. Nature Genetics, 2017, 49, 959-963.	9.4	208
29	Candidate gene sequencing and validation of SNP markers linked to carotenoid content in cassava (Manihot esculenta Crantz). Molecular Breeding, 2017, 37, 1.	1.0	15
30	Accuracies of univariate and multivariate genomic prediction models in African cassava. Genetics Selection Evolution, 2017, 49, 88.	1.2	54
31	Genomeâ€Wide Association Mapping of Correlated Traits in Cassava: Dry Matter and Total Carotenoid Content. Plant Genome, 2017, 10, plantgenome2016.09.0094.	1.6	63
32	Genome sequencing of the staple food crop white Guinea yam enables the development of a molecular marker for sex determination. BMC Biology, 2017, 15, 86.	1.7	114
33	Prospects for Genomic Selection in Cassava Breeding. Plant Genome, 2017, 10, plantgenome2017.03.0015.	1.6	101
34	Marker-Based Estimates Reveal Significant Nonadditive Effects in Clonally Propagated Cassava (<i>Manihot esculenta</i>): Implications for the Prediction of Total Genetic Value and the Selection of Varieties. G3: Genes, Genomes, Genetics, 2016, 6, 3497-3506.	0.8	34
35	Genomeâ€Wide Association and Prediction Reveals Genetic Architecture of Cassava Mosaic Disease Resistance and Prospects for Rapid Genetic Improvement. Plant Genome, 2016, 9, plantgenome2015.11.0118.	1.6	120
36	Sequencing wild and cultivated cassava and related species reveals extensive interspecific hybridization and genetic diversity. Nature Biotechnology, 2016, 34, 562-570.	9.4	340

#	ARTICLE	IF	CITATIONS
37	Tracking crop varieties using genotyping-by-sequencing markers: a case study using cassava (Manihot) Tj ETQq1 1 0.784314 rgBT /Over	2.7	83
38	The Effects of Restrictionâ€Enzyme Choice on Properties of Genotypingâ€byâ€Sequencing Libraries: A Study in Cassava (<i>Manihot esculenta</i>). Crop Science, 2014, 54, 2603-2608.	0.8	51
39	solGS: a web-based tool for genomic selection. BMC Bioinformatics, 2014, 15, 398.	1.2	18
40	High-resolution mapping of resistance to cassava mosaic geminiviruses in cassava using genotyping-by-sequencing and its implications for breeding. Virus Research, 2014, 186, 87-96.	1.1	143
41	Genetic Mapping Using Genotypingâ€byâ€Sequencing in the Clonally Propagated Cassava. Crop Science, 2014, 54, 1384-1396.	0.8	50
42	Relatedness and Genotype Ã— Environment Interaction Affect Prediction Accuracies in Genomic Selection: A Study in Cassava. Crop Science, 2013, 53, 1312-1325.	0.8	102
43	An EST-derived SNP and SSR genetic linkage map of cassava (Manihot esculenta Crantz). Theoretical and Applied Genetics, 2012, 125, 329-342.	1.8	31
44	Molecular Markers and Their Application to Cassava Breeding: Past, Present and Future. Tropical Plant Biology, 2012, 5, 95-109.	1.0	34
45	Identification, validation and high-throughput genotyping of transcribed gene SNPs in cassava. Theoretical and Applied Genetics, 2012, 124, 685-695.	1.8	55
46	Perspectives on the Application of Next-generation Sequencing to the Improvement of Africaâ€™s Staple Food Crops. , 0, , .		1