Miftahudin Miftahudin

List of Publications by Year in descending order

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33 papers 2,062 citations

430874 18 h-index 454955 30 g-index

33 all docs

33 docs citations

times ranked

33

1741 citing authors

#	Article	IF	CITATIONS
1	A Chromosome Bin Map of $16,000$ Expressed Sequence Tag Loci and Distribution of Genes Among the Three Genomes of Polyploid Wheat. Genetics, 2004, $168,701-712$.	2.9	369
2	Comparative DNA Sequence Analysis of Wheat and Rice Genomes. Genome Research, 2003, 13, 1818-1827.	5 . 5	369
3	The Organization and Rate of Evolution of Wheat Genomes Are Correlated With Recombination Rates Along Chromosome Arms. Genome Research, 2003, 13, 753-763.	5 . 5	298
4	Synteny perturbations between wheat homoeologous chromosomes caused by locus duplications and deletions correlate with recombination rates. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 10836-10841.	7.1	159
5	Analysis of Expressed Sequence Tag Loci on Wheat Chromosome Group 4. Genetics, 2004, 168, 651-663.	2.9	90
6	Development of an Expressed Sequence Tag (EST) Resource for Wheat (Triticum aestivum L.). Genetics, 2004, 168, 585-593.	2.9	87
7	Group 3 Chromosome Bin Maps of Wheat and Their Relationship to Rice Chromosome 1. Genetics, 2004, 168, 639-650.	2.9	81
8	Chromosome Bin Map of Expressed Sequence Tags in Homoeologous Group 1 of Hexaploid Wheat and Homoeology With Rice and Arabidopsis. Genetics, 2004, 168, 609-623.	2.9	78
9	A 2600-Locus Chromosome Bin Map of Wheat Homoeologous Group 2 Reveals Interstitial Gene-Rich Islands and Colinearity With Rice. Genetics, 2004, 168, 625-637.	2.9	78
10	AFLP markers tightly linked to the aluminum-tolerance gene Alt3 in rye (Secale cereale L.). Theoretical and Applied Genetics, 2002, 104, 626-631.	3.6	69
11	A Chromosome Bin Map of 2148 Expressed Sequence Tag Loci of Wheat Homoeologous Group 7. Genetics, 2004, 168, 687-699.	2.9	68
12	A 2500-Locus Bin Map of Wheat Homoeologous Group 5 Provides Insights on Gene Distribution and Colinearity With Rice. Genetics, 2004, 168, 665-676.	2.9	67
13	Deletion Mapping of Homoeologous Group 6-Specific Wheat Expressed Sequence Tags. Genetics, 2004, 168, 677-686.	2.9	43
14	Targeting the aluminum tolerance gene Alt3 region in rye, using rice/rye micro-colinearity. Theoretical and Applied Genetics, 2005, 110, 906-913.	3.6	33
15	Development of PCR-based codominant markers flanking the <i>Alt3</i> gene in rye. Genome, 2004, 47, 231-238.	2.0	21
16	Amplified fragment length polymorphism-based genetic diversity among cultivated and weedy rye (Secale cereale L.) accessions. Genetic Resources and Crop Evolution, 2012, 59, 1743-1752.	1.6	20
17	Oxidative Stress and Photosynthesis Reduction of Cultivated (Glycine max L.) and Wild Soybean (G.) Tj ETQq1 1	0.784314 0.4	FrgBT Overloo
18	Identification of chemical compounds in agarwood-producing species Aquilaria malaccensis and Gyrinops versteegii. Journal of Forestry Research, 2020, 31, 1371-1380.	3.6	19

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19	Structural and functional analyses of the wheat genomes based on expressed sequence tags (ESTs) related to abiotic stresses. Genome, 2006, 49, 1324-1340.	2.0	17
20	Iron toxicity-induced physiological and metabolite profile variations among tolerant and sensitive rice varieties. Plant Signaling and Behavior, 2019, 14, 1682829.	2.4	14
21	Uptake and Distribution of Aluminum in Root Apices of Two Rice Varieties under Aluminum Stress. HAYATI Journal of Biosciences, 2007, 14, 110-114.	0.4	11
22	Rye (Secale cereale L.) and Wheat (Triticum aestivum L.) Simple Sequence Repeat Variation within Secale spp. (Poaceae). HAYATI Journal of Biosciences, 2013, 20, 163-170.	0.4	8
23	Cellular and Ultrastructure Alteration of Plant Roots in Response to Metal Stress., 2018,,.		7
24	OsGERLP: A novel aluminum tolerance rice gene isolated from a local cultivar in Indonesia. Plant Physiology and Biochemistry, 2021, 162, 86-99.	5.8	7
25	Vegetative morphophysiological responses of four rice cultivars to drought stress. Biodiversitas, 2020, 21, .	0.6	6
26	Overexpression of B11 Gene in Transgenic Rice Increased Tolerance to Aluminum Stress. HAYATI Journal of Biosciences, 2017, 24, 96-104.	0.4	5
27	Correlation among Snpb 11 markers, root growth, and physiological characters of upland rice under aluminum stress. Biodiversitas, 2019, 20, .	0.6	5
28	Genome-wide SNP discovery, linkage mapping, and analysis of QTL for morpho-physiological traits in rice during vegetative stage under drought stress. Physiology and Molecular Biology of Plants, 2021, 27, 2635-2650.	3.1	5
29	Transgene Insertion Stability and Aluminum Tolerance Candidate Gene Expression in T3 Generation of Transgenic Tobacco. International Journal of Agriculture and Biology, 2016, 18, 607-614.	0.4	4
30	Construction of RNA Interference Vector to Silence Aluminum Tolerance Gene Candidate in Rice cv Hawara Bunar. HAYATI Journal of Biosciences, 2016, 23, 79-84.	0.4	2
31	The expression of OsPLA2-III and OsPPO genes in rice (Oryza sativa L.) under Fe toxicity stress. Journal of Tropical Life Science, 2021, 11, 209-216.	0.3	1
32	Genomic Improvement of Rice for Drought, Aluminum, and Iron Toxicity Stress Tolerance. , 2021 , , 1 -69.		1
33	Endurance Test of Three Paddy Genotypes to Different Iron Toxicity Level. Journal of Agronomy, 2014, 13, 110-116.	0.4	0