

Hiroshi Mizuno

List of Publications by Year in descending order

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36
papers

1,589
citations

430754

18
h-index

395590

33
g-index

36
all docs

36
docs citations

36
times ranked

2413
citing authors

#	ARTICLE	IF	CITATIONS
1	The genome sequence and structure of rice chromosome 1. <i>Nature</i> , 2002, 420, 312-316.	13.7	519
2	Physical maps and recombination frequency of six rice chromosomes. <i>Plant Journal</i> , 2003, 36, 720-730.	2.8	126
3	The sorghum SWEET gene family: stem sucrose accumulation as revealed through transcriptome profiling. <i>Biotechnology for Biofuels</i> , 2016, 9, 127.	6.2	99
4	Sorghum Dw1, an agronomically important gene for lodging resistance, encodes a novel protein involved in cell proliferation. <i>Scientific Reports</i> , 2016, 6, 28366.	1.6	81
5	Simultaneous Transcriptome Analysis of Sorghum and <i>Bipolaris sorghicola</i> by Using RNA-seq in Combination with De Novo Transcriptome Assembly. <i>PLoS ONE</i> , 2013, 8, e62460.	1.1	79
6	Massive parallel sequencing of mRNA in identification of unannotated salinity stress-inducible transcripts in rice (<i>Oryza sativa</i> L.). <i>BMC Genomics</i> , 2010, 11, 683.	1.2	76
7	Independent Domestication of Asian Rice Followed by Gene Flow from japonica to indica. <i>Molecular Biology and Evolution</i> , 2012, 29, 1471-1479.	3.5	70
8	Retrogenes in Rice (<i>Oryza sativa</i> L. ssp. japonica) Exhibit Correlated Expression with Their Source Genes. <i>Genome Biology and Evolution</i> , 2011, 3, 1357-1368.	1.1	62
9	Sequencing and characterization of telomere and subtelomere regions on rice chromosomes 1S, 2S, 2L, 6L, 7S, 7L and 8S. <i>Plant Journal</i> , 2006, 46, 206-217.	2.8	60
10	Gibberellin deficiency pleiotropically induces culm bending in sorghum: an insight into sorghum semi-dwarf breeding. <i>Scientific Reports</i> , 2014, 4, 5287.	1.6	54
11	mRNA-Seq Reveals a Comprehensive Transcriptome Profile of Rice under Phosphate Stress. <i>Rice</i> , 2011, 4, 50-65.	1.7	45
12	Global transcriptome analysis reveals distinct expression among duplicated genes during sorghum- <i>Bipolaris sorghicola</i> interaction. <i>BMC Plant Biology</i> , 2012, 12, 121.	1.6	42
13	The Sorghum Gene for Leaf Color Changes upon Wounding (<i>Slc1</i>) Encodes a Flavanone 4-Reductase in the 3-Deoxyanthocyanidin Biosynthesis Pathway. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1439-1447.	0.8	36
14	Root lodging is a physical stress that changes gene expression from sucrose accumulation to degradation in sorghum. <i>BMC Plant Biology</i> , 2018, 18, 2.	1.6	27
15	Comparative analysis of complete orthologous centromeres from two subspecies of rice reveals rapid variation of centromere organization and structure. <i>Plant Journal</i> , 2009, 60, 805-819.	2.8	22
16	Expression level of a flavonoid 3- β -hydroxylase gene determines pathogen-induced color variation in sorghum. <i>BMC Research Notes</i> , 2014, 7, 761.	0.6	22
17	Evolutionary dynamics and impacts of chromosome regions carrying R-gene clusters in rice. <i>Scientific Reports</i> , 2020, 10, 872.	1.6	22
18	Identification and Mapping of Expressed Genes, Simple Sequence Repeats and Transposable Elements in Centromeric Regions of Rice Chromosomes. <i>DNA Research</i> , 2006, 13, 267-274.	1.5	18

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19	Expression of Flavone Synthase II and Flavonoid 3- ² -Hydroxylase Is Associated with Color Variation in Tan-Colored Injured Leaves of Sorghum. <i>Frontiers in Plant Science</i> , 2016, 7, 1718.	1.7	18
20	Chromosome-Specific Distribution of Nucleotide Substitutions in Telomeric Repeats of Rice (<i>Oryza</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	3.5	17
21	Asymmetric Distribution of Gene Expression in the Centromeric Region of Rice Chromosome 5. <i>Frontiers in Plant Science</i> , 2011, 2, 16.	1.7	15
22	A ^{BAC} physical map of <i>aus</i> rice cultivar ^K asalath TM , and the map-based genomic sequence of ^K asalath TM chromosome 1. <i>Plant Journal</i> , 2013, 76, 699-708.	2.8	13
23	Characterization of chromosome ends on the basis of the structure of TrsA subtelomeric repeats in rice (<i>Oryza sativa</i> L.). <i>Molecular Genetics and Genomics</i> , 2008, 280, 19-24.	1.0	12
24	Genomic inversion caused by gamma irradiation contributes to downregulation of a WBC11 homolog in bloomless sorghum. <i>Theoretical and Applied Genetics</i> , 2013, 126, 1513-1520.	1.8	12
25	Ethical acceptability of research on human-animal chimeric embryos: summary of opinions by the Japanese Expert Panel on Bioethics. <i>Life Sciences, Society and Policy</i> , 2015, 11, 15.	3.1	11
26	Comparative Analysis of Rice Genome Sequence to Understand the Molecular Basis of Genome Evolution. <i>Rice</i> , 2008, 1, 119-126.	1.7	6
27	Composition and Structure of Rice Centromeres and Telomeres. , 2018, , 37-52.		6
28	Classification of genotypes of leaf phenotype (<i>P</i> / <i>tan</i>) and seed phenotype (<i>Y1</i>) and Tj ETQq0 0 0 rgBT /Overlock 10	1.0	4
29	Characterization of Chromosomal Ends on the Basis of Chromosome-Specific Telomere Variants and Subtelomeric Repeats in Rice (<i>Oryza sativa</i> L.). , 2014, , 187-194.		4
30	Ethical Issues for Clinical Studies That use Human Embryonic Stem Cells: The 2014 Revisions to the Japanese Guidelines. <i>Stem Cell Reviews and Reports</i> , 2015, 11, 676-680.	5.6	3
31	The Rice Genome Sequence as an Indispensable Tool for Crop Improvement. <i>Biotechnology in Agriculture and Forestry</i> , 2008, , 3-12.	0.2	2
32	Molecular mapping and identification of candidate gene conferring organophosphate-sensitive reaction in sorghum (<i>Sorghum bicolor</i>). <i>Plant Breeding</i> , 2020, 139, 600-607.	1.0	2
33	DNA marker analysis of flowering time, semi-dwarf, fertility restorer, and brown midrib genes in sorghum (<i>Sorghum bicolor</i> [L.] Moench). <i>Grassland Science</i> , 2022, 68, 101-113.	0.6	2
34	Recommended Ethical Safeguards on Fertilization of Human Germ Cells Derived from Pluripotent Stem Cells Solely for Research Purposes. <i>Stem Cell Reviews and Reports</i> , 2016, 12, 377-384.	5.6	1
35	Fine mapping of <i>Rf5</i> region for a sorghum fertility restorer gene and microsynteny analysis across grass species. <i>Breeding Science</i> , 2022, 72, 141-149.	0.9	1
36	Characterization of 2159 Unmapped Full-length cDNA Sequences of <i>Oryza sativa</i> L. ssp. <i>japonica</i> ^{Nipponbare} TM . <i>Plant Molecular Biology Reporter</i> , 2010, 28, 357-362.	1.0	0