

Hiroshi Mizuno

List of Publications by Year in descending order

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Version: 2024-02-01

36
papers

1,589
citations

430754

18
h-index

395590

33
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36
all docs

36
docs citations

36
times ranked

2413
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 1 | 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 |
| 2 | 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 |
| 3 | Evolutionary dynamics and impacts of chromosome regions carrying R-gene clusters in rice. <i>Scientific Reports</i> , 2020, 10, 872. | 1.6 | 22 |
| 4 | 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 |
| 5 | Composition and Structure of Rice Centromeres and Telomeres. , 2018, , 37-52. | | 6 |
| 6 | 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 |
| 7 | Expression of Flavone Synthase II and Flavonoid 3-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 |
| 8 | Classification of genotypes of leaf phenotype (<i>P</i>) and seed phenotype (<i>Y1</i>) and <i>Tj</i> <i>ETQq0</i> <i>Q0</i> <i>rgBT</i> / <i>Overlock</i> 10 | 1.0 | 4 |
| 9 | The sorghum SWEET gene family: stem sucrose accumulation as revealed through transcriptome profiling. <i>Biotechnology for Biofuels</i> , 2016, 9, 127. | 6.2 | 99 |
| 10 | The Sorghum Gene for Leaf Color Changes upon Wounding (<i>P</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 |
| 11 | Sorghum <i>Dw1</i> , 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 |
| 12 | 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 |
| 13 | 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 |
| 14 | 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 |
| 15 | Expression level of a flavonoid 3-hydroxylase gene determines pathogen-induced color variation in sorghum. <i>BMC Research Notes</i> , 2014, 7, 761. | 0.6 | 22 |
| 16 | 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 |
| 17 | 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 |
| 18 | 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 |

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 19 | A BAC physical map of <i>aus</i> rice cultivar <i>Kasalath</i> TM , and the map-based genomic sequence of <i>Kasalath</i> TM chromosome 1. <i>Plant Journal</i> , 2013, 76, 699-708. | 2.8 | 13 |
| 20 | 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 |
| 21 | 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 |
| 22 | 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 |
| 23 | 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 |
| 24 | mRNA-Seq Reveals a Comprehensive Transcriptome Profile of Rice under Phosphate Stress. <i>Rice</i> , 2011, 4, 50-65. | 1.7 | 45 |
| 25 | 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 |
| 26 | Characterization of 2159 Unmapped Full-length cDNA Sequences of <i>Oryza sativa</i> L. ssp. japonica <i>Nipponbare</i> TM . <i>Plant Molecular Biology Reporter</i> , 2010, 28, 357-362. | 1.0 | 0 |
| 27 | 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 |
| 28 | 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 |
| 29 | Comparative Analysis of Rice Genome Sequence to Understand the Molecular Basis of Genome Evolution. <i>Rice</i> , 2008, 1, 119-126. | 1.7 | 6 |
| 30 | 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 |
| 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 | 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 |
| 33 | 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 |
| 34 | 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 |
| 35 | Physical maps and recombination frequency of six rice chromosomes. <i>Plant Journal</i> , 2003, 36, 720-730. | 2.8 | 126 |
| 36 | The genome sequence and structure of rice chromosome 1. <i>Nature</i> , 2002, 420, 312-316. | 13.7 | 519 |