

Masanori Yamasaki

List of Publications by Year in descending order

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Version: 2024-02-01

55
papers

6,838
citations

361045

20
h-index

223531

46
g-index

58
all docs

58
docs citations

58
times ranked

8023
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 1 | Genetic Background Negates Improvements in Rice Flour Characteristics and Food Processing Properties Caused by a Mutant Allele of the PDIL1-1 Seed Storage Protein Gene. <i>Rice</i> , 2022, 15, 13. | 1.7 | 5 |
| 2 | Identification of a unique allele in the quantitative trait locus for crown root number in <i>japonica</i> rice from Japan using genome-wide association studies. <i>Breeding Science</i> , 2022, 72, 222-231. | 0.9 | 4 |
| 3 | Development of an Aus-Derived Nested Association Mapping (Aus-NAM) Population in Rice. <i>Plants</i> , 2021, 10, 1255. | 1.6 | 23 |
| 4 | Coupling day length data and genomic prediction tools for predicting time-related traits under complex scenarios. <i>Scientific Reports</i> , 2020, 10, 13382. | 1.6 | 9 |
| 5 | Genetic and epistatic effects for grain quality and yield of three grain-size QTLs identified in brewing rice (<i>Oryza sativa</i> L.). <i>Molecular Breeding</i> , 2020, 40, 1. | 1.0 | 6 |
| 6 | Landraces of temperate japonica rice have superior alleles for improving culm strength associated with lodging resistance. <i>Scientific Reports</i> , 2020, 10, 19855. | 1.6 | 11 |
| 7 | Predicting Rice Heading Date Using an Integrated Approach Combining a Machine Learning Method and a Crop Growth Model. <i>Frontiers in Genetics</i> , 2020, 11, 599510. | 1.1 | 10 |
| 8 | Choosing the optimal population for a genome-wide association study: A simulation of whole-genome sequences from rice. <i>Plant Genome</i> , 2020, 13, e20005. | 1.6 | 9 |
| 9 | Predicting biomass of rice with intermediate traits: Modeling method combining crop growth models and genomic prediction models. <i>PLoS ONE</i> , 2020, 15, e0233951. | 1.1 | 14 |
| 10 | Title is missing!. , 2020, 15, e0233951. | | 0 |
| 11 | Title is missing!. , 2020, 15, e0233951. | | 0 |
| 12 | Title is missing!. , 2020, 15, e0233951. | | 0 |
| 13 | Title is missing!. , 2020, 15, e0233951. | | 0 |
| 14 | Title is missing!. , 2020, 15, e0233951. | | 0 |
| 15 | Title is missing!. , 2020, 15, e0233951. | | 0 |
| 16 | Title is missing!. , 2020, 15, e0233951. | | 0 |
| 17 | QTL analysis of resistance to bacterial wilt caused by <i>Ralstonia solanacearum</i> in potato. <i>Breeding Science</i> , 2019, 69, 592-600. | 0.9 | 20 |
| 18 | Validation of a quantitative trait locus for the white-core expression rate of grain on chromosome 6 in a brewing rice cultivar and development of DNA markers for marker-assisted selection. <i>Breeding Science</i> , 2019, 69, 401-409. | 0.9 | 6 |

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|----|---|-----|-----------|
| 19 | Whole genome sequencing data of <i>Oryza sativa</i> L. cv. Takanari. <i>Data in Brief</i> , 2019, 27, 104546. | 0.5 | 0 |
| 20 | Genetic and phenotypic assessment of sugar beet (<i>Beta vulgaris</i> L. subsp.) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 707 T Science, 2019, 69, 255-265. | 0.9 | 6 |
| 21 | A novel Rice QTL qOPW11 Associated with Panicle Weight Affects Panicle and Plant Architecture. <i>Rice</i> , 2018, 11, 53. | 1.7 | 14 |
| 22 | Description of grain weight distribution leading to genomic selection for grain-filling characteristics in rice. <i>PLoS ONE</i> , 2018, 13, e0207627. | 1.1 | 25 |
| 23 | Identification of QTLs for rice grain size using a novel set of chromosomal segment substitution lines derived from Yamadanishiki in the genetic background of Koshihikari. <i>Breeding Science</i> , 2018, 68, 210-218. | 0.9 | 19 |
| 24 | Ethylene-gibberellin signaling underlies adaptation of rice to periodic flooding. <i>Science</i> , 2018, 361, 181-186. | 6.0 | 188 |
| 25 | Differences in glucose yield of residues from among varieties of rice, wheat, and sorghum after dilute acid pretreatment. <i>Bioscience, Biotechnology and Biochemistry</i> , 2017, 81, 1650-1656. | 0.6 | 2 |
| 26 | Genetic dissection of grain traits in Yamadanishiki, an excellent sake-brewing rice cultivar. <i>Theoretical and Applied Genetics</i> , 2017, 130, 2567-2585. | 1.8 | 13 |
| 27 | Genetic Tracing of <i>Jatropha curcas</i> L. from Its Mesoamerican Origin to the World. <i>Frontiers in Plant Science</i> , 2017, 8, 1539. | 1.7 | 19 |
| 28 | Genome-wide association study using whole-genome sequencing rapidly identifies new genes influencing agronomic traits in rice. <i>Nature Genetics</i> , 2016, 48, 927-934. | 9.4 | 600 |
| 29 | Natural variation in the glucose content of dilute sulfuric acidâ€“pretreated rice straw liquid hydrolysates: implications for bioethanol production. <i>Bioscience, Biotechnology and Biochemistry</i> , 2016, 80, 863-869. | 0.6 | 4 |
| 30 | Uncovering a Nuisance Influence of a Phenological Trait of Plants Using a Nonlinear Structural Equation: Application to Days to Heading and Culm Length in Asian Cultivated Rice (<i>Oryza Sativa</i> L.). <i>PLoS ONE</i> , 2016, 11, e0148609. | 1.1 | 8 |
| 31 | Island-Model Genomic Selection for Long-Term Genetic Improvement of Autogamous Crops. <i>PLoS ONE</i> , 2016, 11, e0153945. | 1.1 | 17 |
| 32 | Rare allele of a previously unidentified histone H4 acetyltransferase enhances grain weight, yield, and plant biomass in rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 76-81. | 3.3 | 236 |
| 33 | Exploring the areas of applicability of whole-genome prediction methods for Asian rice (<i>Oryza sativa</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 707 T | 1.8 | 72 |
| 34 | Natural Variation in the Flag Leaf Morphology of Rice Due to a Mutation of the <i>NARROW LEAF 1</i> Gene in <i>Oryza sativa</i> L.. <i>Genetics</i> , 2015, 201, 795-808. | 1.2 | 20 |
| 35 | Changes in Lignin and Polysaccharide Components in 13 Cultivars of Rice Straw following Dilute Acid Pretreatment as Studied by Solution-State 2D 1H-13C NMR. <i>PLoS ONE</i> , 2015, 10, e0128417. | 1.1 | 26 |
| 36 | Glucose content in the liquid hydrolysate after dilute acid pretreatment is affected by the starch content in rice straw. <i>Bioresource Technology</i> , 2013, 149, 520-524. | 4.8 | 16 |

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|----|---|-----|-----------|
| 37 | OsLG1 regulates a closed panicle trait in domesticated rice. <i>Nature Genetics</i> , 2013, 45, 462-465. | 9.4 | 181 |
| 38 | Development of INDEL markers to discriminate all genome types rapidly in the genus <i>Oryza</i> . <i>Breeding Science</i> , 2013, 63, 246-254. | 0.9 | 42 |
| 39 | Population structure in Japanese rice population. <i>Breeding Science</i> , 2013, 63, 49-57. | 0.9 | 31 |
| 40 | Diversity and population structure of black soybean landraces originating from Tanba and neighboring regions. <i>Breeding Science</i> , 2012, 61, 593-601. | 0.9 | 11 |
| 41 | Variation in Biomass Properties among Rice Diverse Cultivars. <i>Bioscience, Biotechnology and Biochemistry</i> , 2011, 75, 1603-1605. | 0.6 | 18 |
| 42 | Artificial selection for a green revolution gene during <i>japonica</i> rice domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 11034-11039. | 3.3 | 179 |
| 43 | Allelic interaction at seed-shattering loci in the genetic backgrounds of wild and cultivated rice species. <i>Genes and Genetic Systems</i> , 2010, 85, 265-271. | 0.2 | 37 |
| 44 | Biological control for rice blast disease by employing detachment action with gelatinolytic bacteria. <i>Biological Control</i> , 2010, 55, 85-91. | 1.4 | 25 |
| 45 | Population structure of wild wheat genome progenitor <i>Aegilops tauschii</i> Coss.: implications for intraspecific lineage diversification and evolution of common wheat. <i>Molecular Ecology</i> , 2010, 19, 999-1013. | 2.0 | 115 |
| 46 | DNAAlignEditor: DNA alignment editor tool. <i>BMC Bioinformatics</i> , 2008, 9, 154. | 1.2 | 11 |
| 47 | Empirical Analysis of Selection Screens for Domestication and Improvement Loci in Maize by Extended DNA Sequencing. <i>Plant Genome</i> , 2008, 1, . | 1.6 | 5 |
| 48 | Genomic Screening for Artificial Selection during Domestication and Improvement in Maize. <i>Annals of Botany</i> , 2007, 100, 967-973. | 1.4 | 70 |
| 49 | A unified mixed-model method for association mapping that accounts for multiple levels of relatedness. <i>Nature Genetics</i> , 2006, 38, 203-208. | 9.4 | 3,622 |
| 50 | A Large-Scale Screen for Artificial Selection in Maize Identifies Candidate Agronomic Loci for Domestication and Crop Improvement. <i>Plant Cell</i> , 2005, 17, 2859-2872. | 3.1 | 234 |
| 51 | The Effects of Artificial Selection on the Maize Genome. <i>Science</i> , 2005, 308, 1310-1314. | 6.0 | 742 |
| 52 | Title is missing!. <i>Molecular Breeding</i> , 2003, 12, 133-143. | 1.0 | 55 |
| 53 | Mapping of Quantitative Trait Loci of Ovicidal Response to Brown Planthopper (<i>Nilaparvata lugens</i>) Tj ETQq1 1 0.784314 rgBT /Overlock | 0.9 | 23 |
| 54 | Quantitative Trait Locus Mapping of Ovicidal Response in Rice (<i>Oryza sativa</i> L.) against Whitebacked Planthopper (<i>Sogatella furcifera</i> Horváth). <i>Crop Science</i> , 1999, 39, 1178-1183. | 0.8 | 33 |

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|----|--|-----|-----------|
| 55 | A novel index to evaluate resource allocation pattern in panicles in Japanese rice cultivars. Plant Production Science, 0, , 1-16. | 0.9 | 0 |