

Akio Miyao

List of Publications by Year in descending order

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104
papers

14,948
citations

34105

52
h-index

30087

103
g-index

106
all docs

106
docs citations

106
times ranked

13279
citing authors

#	ARTICLE	IF	CITATIONS
1	The map-based sequence of the rice genome. <i>Nature</i> , 2005, 436, 793-800.	27.8	3,365
2	An Overview of Gibberellin Metabolism Enzyme Genes and Their Related Mutants in Rice. <i>Plant Physiology</i> , 2004, 134, 1642-1653.	4.8	643
3	A 300 kilobase interval genetic map of rice including 883 expressed sequences. <i>Nature Genetics</i> , 1994, 8, 365-372.	21.4	578
4	Target Site Specificity of the <i>Tos17</i> Retrotransposon Shows a Preference for Insertion within Genes and against Insertion in Retrotransposon-Rich Regions of the Genome. <i>Plant Cell</i> , 2003, 15, 1771-1780.	6.6	493
5	Function, Intracellular Localization and the Importance in Salt Tolerance of a Vacuolar Na ⁺ /H ⁺ Antiporter from Rice. <i>Plant and Cell Physiology</i> , 2004, 45, 146-159.	3.1	397
6	Three Distinct Rice Cellulose Synthase Catalytic Subunit Genes Required for Cellulose Synthesis in the Secondary Wall. <i>Plant Physiology</i> , 2003, 133, 73-83.	4.8	392
7	Function and Characterization of Starch Synthase I Using Mutants in Rice. <i>Plant Physiology</i> , 2006, 140, 1070-1084.	4.8	339
8	Characterization of SSIIIa-Deficient Mutants of Rice: The Function of SSIIIa and Pleiotropic Effects by SSIIIa Deficiency in the Rice Endosperm. <i>Plant Physiology</i> , 2007, 144, 2009-2023.	4.8	335
9	Rice OsHKT2;1 transporter mediates large Na ⁺ influx component into K ⁺ -starved roots for growth. <i>EMBO Journal</i> , 2007, 26, 3003-3014.	7.8	333
10	A Germ Cell-Specific Gene of the <i>ARGONAUTE</i> Family Is Essential for the Progression of Premeiotic Mitosis and Meiosis during Sporogenesis in Rice. <i>Plant Cell</i> , 2007, 19, 2583-2594.	6.6	324
11	Functional Diversification of the Two C-Class MADS Box Genes OSMADS3 and OSMADS58 in <i>Oryza sativa</i> . <i>Plant Cell</i> , 2005, 18, 15-28.	6.6	322
12	Nonredundant Regulation of Rice Arbuscular Mycorrhizal Symbiosis by Two Members of the <i>PHOSPHATE TRANSPORTER1</i> Gene Family. <i>Plant Cell</i> , 2012, 24, 4236-4251.	6.6	306
13	Loss-of-Function Mutations of the Rice <i>GAMYB</i> Gene Impair β -Amylase Expression in Aleurone and Flower Development. <i>Plant Cell</i> , 2004, 16, 33-44.	6.6	296
14	The <i>MSP1</i> Gene Is Necessary to Restrict the Number of Cells Entering into Male and Female Sporogenesis and to Initiate Anther Wall Formation in Rice. <i>Plant Cell</i> , 2003, 15, 1728-1739.	6.6	291
15	Distinct and Cooperative Functions of Phytochromes A, B, and C in the Control of Deetiolation and Flowering in Rice. <i>Plant Cell</i> , 2005, 17, 3311-3325.	6.6	287
16	Characterization of a Rice Chlorophyll-Deficient Mutant Using the T-DNA Gene-Trap System. <i>Plant and Cell Physiology</i> , 2003, 44, 463-472.	3.1	277
17	Molecular cloning of <i>Sdr4</i> , a regulator involved in seed dormancy and domestication of rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 5792-5797.	7.1	272
18	A rice calcium-dependent protein kinase OsCPK12 oppositely modulates salt stress tolerance and blast disease resistance. <i>Plant Journal</i> , 2012, 69, 26-36.	5.7	269

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19	Arbuscular Mycorrhizaâ€“Specific Signaling in Rice Transcends the Common Symbiosis Signaling Pathway. <i>Plant Cell</i> , 2008, 20, 2989-3005.	6.6	235
20	Ethylene Promotes Submergence-Induced Expression of OsABA8ox1, a Gene that Encodes ABA 8'-Hydroxylase in Rice. <i>Plant and Cell Physiology</i> , 2006, 48, 287-298.	3.1	223
21	Curated genome annotation of <i>Oryza sativa</i> ssp. japonica and comparative genome analysis with <i>Arabidopsis thaliana</i> . <i>Genome Research</i> , 2007, 17, 175-183.	5.5	218
22	Screening of the Rice Viviparous Mutants Generated by Endogenous Retrotransposon Tos17 Insertion. Tagging of a Zeaxanthin Epoxidase Gene and a Novel OsTATC Gene. <i>Plant Physiology</i> , 2001, 125, 1248-1257.	4.8	211
23	A rice fungal MAMPâ€“responsive MAPK cascade regulates metabolic flow to antimicrobial metabolite synthesis. <i>Plant Journal</i> , 2010, 63, 599-612.	5.7	208
24	<i>MOSAIC FLORAL ORGANS1</i> , an <i>AGL6</i> -Like MADS Box Gene, Regulates Floral Organ Identity and Meristem Fate in Rice. <i>Plant Cell</i> , 2009, 21, 3008-3025.	6.6	195
25	Isolation and Characterization of Rice Phytochrome A Mutants. <i>Plant Cell</i> , 2001, 13, 521-534.	6.6	179
26	OsATG7 is required for autophagy-dependent lipid metabolism in rice postmeiotic anther development. <i>Autophagy</i> , 2014, 10, 878-888.	9.1	176
27	PANICLE PHYTOMER2 (PAP2), encoding a SEPALLATA subfamily MADS-box protein, positively controls spikelet meristem identity in rice. <i>Plant and Cell Physiology</i> , 2010, 51, 47-57.	3.1	174
28	Characterization of pullulanase (PUL)-deficient mutants of rice (<i>Oryza sativa</i> L.) and the function of PUL on starch biosynthesis in the developing rice endosperm. <i>Journal of Experimental Botany</i> , 2009, 60, 1009-1023.	4.8	158
29	The Novel Gene <i>HOMOLOGOUS PAIRING ABERRATION IN RICE MEIOSIS1</i> of Rice Encodes a Putative Coiled-Coil Protein Required for Homologous Chromosome Pairing in Meiosis. <i>Plant Cell</i> , 2004, 16, 1008-1020.	6.6	151
30	An ATP-binding cassette subfamily G full transporter is essential for the retention of leaf water in both wild barley and rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 12354-12359.	7.1	134
31	A large-scale collection of phenotypic data describing an insertional mutant population to facilitate functional analysis of rice genes. <i>Plant Molecular Biology</i> , 2007, 63, 625-635.	3.9	131
32	Conservation of the E-function for Floral Organ Identity in Rice Revealed by the Analysis of Tissue Culture-induced Loss-of-Function Mutants of the OsMADS1 Gene. <i>Plant Molecular Biology</i> , 2005, 59, 125-135.	3.9	129
33	Identification of a putative voltage-gated Ca ²⁺ channel as a key regulator of elicitor-induced hypersensitive cell death and mitogen-activated protein kinase activation in rice. <i>Plant Journal</i> , 2005, 42, 798-809.	5.7	120
34	Molecular Spectrum of Somaclonal Variation in Regenerated Rice Revealed by Whole-Genome Sequencing. <i>Plant and Cell Physiology</i> , 2012, 53, 256-264.	3.1	114
35	Disruption of a gene for rice sucrose transporter, OsSUT1, impairs pollen function but pollen maturation is unaffected. <i>Journal of Experimental Botany</i> , 2010, 61, 3639-3646.	4.8	107
36	RICE SALT SENSITIVE3 Forms a Ternary Complex with JAZ and Class-C bHLH Factors and Regulates Jasmonate-Induced Gene Expression and Root Cell Elongation. <i>Plant Cell</i> , 2013, 25, 1709-1725.	6.6	107

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37	Identification of Transcription Factors Involved in Rice Secondary Cell Wall Formation. <i>Plant and Cell Physiology</i> , 2013, 54, 1791-1802.	3.1	105
38	A genome-wide gain-of-function analysis of rice genes using the FOX-hunting system. <i>Plant Molecular Biology</i> , 2007, 65, 357-371.	3.9	103
39	Divergence of Evolutionary Ways Among Common sym Genes: CASTOR and CCaMK Show Functional Conservation Between Two Symbiosis Systems and Constitute the Root of a Common Signaling Pathway. <i>Plant and Cell Physiology</i> , 2008, 49, 1659-1671.	3.1	103
40	An insertional mutation in the rice PAIR2 gene, the ortholog of Arabidopsis ASY1, results in a defect in homologous chromosome pairing during meiosis. <i>Molecular Genetics and Genomics</i> , 2004, 271, 121-129.	2.1	96
41	Unique features of the rice blast resistance Pish locus revealed by large scale retrotransposon-tagging. <i>BMC Plant Biology</i> , 2010, 10, 175.	3.6	94
42	RSS1 regulates the cell cycle and maintains meristematic activity under stress conditions in rice. <i>Nature Communications</i> , 2011, 2, 278.	12.8	87
43	Disruption of a novel gene for a NAC domain protein in rice confers resistance to <i>Rice dwarf virus</i> . <i>Plant Journal</i> , 2009, 57, 615-625.	5.7	84
44	The NAC transcription factor RIM1 of rice is a new regulator of jasmonate signaling. <i>Plant Journal</i> , 2010, 61, 804-815.	5.7	82
45	Loss of cytosolic fructose-1,6-bisphosphatase limits photosynthetic sucrose synthesis and causes severe growth retardations in rice (<i>Oryza sativa</i>). <i>Plant, Cell and Environment</i> , 2008, 31, 1851-1863.	5.7	73
46	Identification of a Putative Voltage-Gated Ca ²⁺ -permeable Channel (OsTPC1) Involved in Ca ²⁺ Influx and Regulation of Growth and Development in Rice. <i>Plant and Cell Physiology</i> , 2004, 45, 693-702.	3.1	72
47	Reverse genetic approach to verify physiological roles of rice phytoalexins: characterization of a knockdown mutant of <i>OsCPS4</i> phytoalexin biosynthetic gene in rice. <i>Physiologia Plantarum</i> , 2014, 150, 55-62.	5.2	71
48	Sequence-tagged sites (STSs) as standard landmarks in the rice genome. <i>Theoretical and Applied Genetics</i> , 1994, 89, 728-734.	3.6	67
49	A Calmodulin-Binding Mitogen-Activated Protein Kinase Phosphatase is Induced by Wounding and Regulates the Activities of Stress-Related Mitogen-Activated Protein Kinases in Rice. <i>Plant and Cell Physiology</i> , 2007, 48, 332-344.	3.1	60
50	Rice Pti1a Negatively Regulates RAR1-Dependent Defense Responses. <i>Plant Cell</i> , 2007, 19, 2940-2951.	6.6	58
51	A Novel RNA-Recognition-Motif Protein Is Required for Premeiotic G1/S-Phase Transition in Rice (<i>Oryza</i>) Tj ETQq1 1 0.784314 rgBT /Over	3.5	56
52	Loss of function mutations in the rice chromomethylase <i>OsCMT3a</i> cause a burst of transposition. <i>Plant Journal</i> , 2015, 83, 1069-1081.	5.7	56
53	Determination of RAPD Markers in Rice and their Conversion into Sequence Tagged Sites (STSs) and STS-Specific Primers. <i>DNA Research</i> , 1994, 1, 139-148.	3.4	55
54	Disruption of a rice gene for β -glucan water dikinase, <i>OsGWD1</i> , leads to hyperaccumulation of starch in leaves but exhibits limited effects on growth. <i>Frontiers in Plant Science</i> , 2013, 4, 147.	3.6	55

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55	Cryptochrome and Phytochrome Cooperatively but Independently Reduce Active Gibberellin Content in Rice Seedlings under Light Irradiation. <i>Plant and Cell Physiology</i> , 2012, 53, 1570-1582.	3.1	48
56	Genetic Evidence for the Role of a Rice Vacuolar Invertase as a Molecular Sink Strength Determinant. <i>Rice</i> , 2018, 11, 6.	4.0	46
57	A loss-of-function mutation of rice DENSE PANICLE 1 causes semi-dwarfness and slightly increased number of spikelets. <i>Breeding Science</i> , 2011, 61, 17-25.	1.9	45
58	<i>COLLAPSED ABNORMAL POLLEN1</i> Gene Encoding the Arabinokinase-Like Protein Is Involved in Pollen Development in Rice. <i>Plant Physiology</i> , 2013, 162, 858-871.	4.8	45
59	A rice Serine/Threonine receptor-like kinase regulates arbuscular mycorrhizal symbiosis at the peri-arbuscular membrane. <i>Nature Communications</i> , 2018, 9, 4677.	12.8	45
60	Transposon Insertion Finder (TIF): a novel program for detection of de novo transpositions of transposable elements. <i>BMC Bioinformatics</i> , 2014, 15, 71.	2.6	43
61	Physiological and genetic analyses of aluminium tolerance in rice, focusing on root growth during germination. <i>Journal of Inorganic Biochemistry</i> , 2005, 99, 1837-1844.	3.5	42
62	Regulation of a Proteinaceous Elicitor-induced Ca ²⁺ Influx and Production of Phytoalexins by a Putative Voltage-gated Cation Channel, OsTPC1, in Cultured Rice Cells. <i>Journal of Biological Chemistry</i> , 2012, 287, 9931-9939.	3.4	39
63	Isolation of a novel lateral-rootless mutant in rice (<i>Oryza sativa</i> L.) with reduced sensitivity to auxin. <i>Plant Science</i> , 2006, 170, 70-77.	3.6	38
64	Pdk1 Kinase Regulates Basal Disease Resistance Through the OsOx1a-OsPti1a Phosphorylation Cascade in Rice. <i>Plant and Cell Physiology</i> , 2010, 51, 2082-2091.	3.1	36
65	Mapping of Sequence-Tagged Sites in Rice by Single Strand Conformation Polymorphism. <i>DNA Research</i> , 1994, 1, 271-277.	3.4	33
66	The plastid sigma factor SIG1 maintains photosystem I activity via regulated expression of the <i>psaA</i> operon in rice chloroplasts. <i>Plant Journal</i> , 2007, 52, 124-132.	5.7	32
67	Characterization and Genetic Mapping of Simple Sequence Repeats in the Rice Genome. <i>DNA Research</i> , 1996, 3, 233-238.	3.4	31
68	Production and characterization of a large population of cDNA-overexpressing transgenic rice plants using Gateway-based full-length cDNA expression libraries. <i>Breeding Science</i> , 2010, 60, 575-585.	1.9	31
69	CAD2 deficiency causes both brown midrib and gold hull and internode phenotypes in <i>Oryza sativa</i> L. cv. Nipponbare. <i>Plant Biotechnology</i> , 2013, 30, 365-373.	1.0	29
70	<i>Bacillus subtilis</i> spoVE gene is transcribed by sigma E-associated RNA polymerase. <i>Journal of Bacteriology</i> , 1993, 175, 4081-4086.	2.2	28
71	Root hairless 2 (<i>rth2</i>) mutant represents a loss-of-function allele of the cellulose synthase-like gene OsCSLD1 in rice (<i>Oryza sativa</i> L.). <i>Breeding Science</i> , 2011, 61, 225-233.	1.9	27
72	Saturation mapping with subclones of YACs: DNA marker production targeting the rice blast disease resistance gene, Pi-b. <i>Theoretical and Applied Genetics</i> , 1997, 94, 170-176.	3.6	26

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73	SSD1, which encodes a plant-specific novel protein, controls plant elongation by regulating cell division in rice. Proceedings of the Japan Academy Series B: Physical and Biological Sciences, 2010, 86, 265-273.	3.8	24
74	Rice TOGO Browser: A Platform to Retrieve Integrated Information on Rice Functional and Applied Genomics. Plant and Cell Physiology, 2011, 52, 230-237.	3.1	24
75	Isolation of a novel mutant gene for soil-surface rooting in rice (<i>Oryza sativa</i> L.). Rice, 2013, 6, 30.	4.0	24
76	Two Novel Nuclear Genes, OsSIG5 and OsSIG6, Encoding Potential Plastid Sigma Factors of RNA Polymerase in Rice: Tissue-Specific and Light-Responsive Gene Expression. Plant and Cell Physiology, 2007, 48, 186-192.	3.1	21
77	Response of an aspartic protease gene OsAP77 to fungal, bacterial and viral infections in rice. Rice, 2014, 7, 9.	4.0	20
78	The rice wound-inducible transcription factor RERJ1 sharing same signal transduction pathway with OsMYC2 is necessary for defense response to herbivory and bacterial blight. Plant Molecular Biology, 2022, 109, 651-666.	3.9	19
79	Plant Biotechniques Series (9). Systematic screening of mutants of rice by sequencing retrotransposon-insertion sites.. Plant Biotechnology, 1998, 15, 253-256.	1.0	19
80	Isolation and characterization of a short lateral root mutant in rice (<i>Oryza sativa</i> L.). Plant Science, 2003, 165, 895-903.	3.6	18
81	Negative feedback regulation of microbe-associated molecular pattern-induced cytosolic Ca ²⁺ transients by protein phosphorylation. Journal of Plant Research, 2011, 124, 415-424.	2.4	18
82	Both OsRecQ1 and OsRDR1 Are Required for the Production of Small RNA in Response to DNA-Damage in Rice. PLoS ONE, 2013, 8, e55252.	2.5	18
83	Characterization of Chlorophyllide a Oxygenase (CAO) in Rice. Breeding Science, 2005, 55, 361-364.	1.9	17
84	In vivo expression of the Bacillus subtilis spoVE gene. Journal of Bacteriology, 1993, 175, 4071-4080.	2.2	16
85	Isolation and Characterization of Rice Phytochrome A Mutants. Plant Cell, 2001, 13, 521.	6.6	16
86	A pentatricopeptide repeat gene of rice is required for splicing of chloroplast transcripts and RNA editing of ndhA. Plant Biotechnology, 2013, 30, 57-64.	1.0	16
87	<i>OsRecQ1</i> , a <i>QDE3</i> homologue in rice, is required for RNA silencing induced by particle bombardment for inverted repeat DNA, but not for double-stranded RNA. Plant Journal, 2008, 56, 274-286.	5.7	15
88	The urea transporter DUR3 contributes to rice production under nitrogen-deficient and field conditions. Physiologia Plantarum, 2019, 167, 75-89.	5.2	15
89	A mycorrhiza-associated receptor-like kinase with an ancient origin in the green lineage. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	15
90	Analysis of rice RNA-dependent RNA polymerase 1 (OsRDR1) in virus-mediated RNA silencing after particle bombardment. Journal of General Plant Pathology, 2010, 76, 152-160.	1.0	14

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91	Screening of RAPD Markers Linked to the Photoperiod-Sensitivity Gene in Rice Chromosome 6 Using Bulk Segregant Analysis. <i>DNA Research</i> , 1995, 2, 101-106.	3.4	13
92	Isolation and mapping of three rice mutants that showed ectopic expression of KNOX genes in leaves. <i>Plant Science</i> , 2009, 177, 131-135.	3.6	12
93	Specification of the basal region identity after asymmetric zygotic division requires mitogen-activated protein kinase 6 in rice. <i>Development (Cambridge)</i> , 2019, 146, .	2.5	12
94	Cytosolic Glutamine Synthetase GS1;3 Is Involved in Rice Grain Ripening and Germination. <i>Frontiers in Plant Science</i> , 2022, 13, 835835.	3.6	12
95	Defects in root development and gravity response in the <i>aem1</i> mutant of rice are associated with reduced auxin efflux. <i>Journal of Plant Physiology</i> , 2005, 162, 678-685.	3.5	10
96	Isolation, fine mapping and expression profiling of a lesion mimic genotype, <i>spl NF4050-8</i> that confers blast resistance in rice. <i>Theoretical and Applied Genetics</i> , 2011, 122, 831-854.	3.6	6
97	Phenotypic analyses of rice <i>lse2</i> and <i>lse3</i> mutants that exhibit hyperaccumulation of starch in the leaf blades. <i>Rice</i> , 2014, 7, 32.	4.0	5
98	Characterisation of a rice vacuolar invertase isoform, <i>OsINV2</i> , for growth and yield-related traits. <i>Functional Plant Biology</i> , 2019, 46, 777.	2.1	5
99	Low-Damage SF[sub 6] Plasma-Etching Condition for Planar GaN HEMTs. <i>Journal of the Electrochemical Society</i> , 2009, 156, H68.	2.9	3
100	Polymorphic edge detection (PED): two efficient methods of polymorphism detection from next-generation sequencing data. <i>BMC Bioinformatics</i> , 2019, 20, 362.	2.6	3
101	Transposon-Insertion Lines of Rice for Analysis of Gene Function. , 2004, , 107-112.		1
102	Molecular Genetic Analysis of a <i>Tos17</i> -Tagged Mutant Line Related to Root Morphology in Rice. <i>Ikushugaku Kenkyu</i> , 2005, 7, 171-178.	0.3	1
103	Transposon-mediated mutagenesis and its application to plant breeding. <i>Ikushugaku Kenkyu</i> , 2015, 17, 77-87.	0.3	0
104	Detection of Transposition Events from Next-Generation Sequencing Data. <i>Methods in Molecular Biology</i> , 2021, 2250, 123-129.	0.9	0