Akio Miyao

List of Publications by Year
in descending order

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 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
2	Cytosolic Glutamine Synthetase GS1;3 Is Involved in Rice Grain Ripening and Germination. Frontiers in Plant Science, 2022, 13, 835835.	3.6	12
3	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
4	Detection of Transposition Events from Next-Generation Sequencing Data. Methods in Molecular Biology, 2021, 2250, 123-129.	0.9	0
5	Polymorphic edge detection (PED): two efficient methods of polymorphism detection from next-generation sequencing data. BMC Bioinformatics, 2019, 20, 362.	2.6	3
6	Specification of the basal region identity after asymmetric zygotic division requires mitogen-activated protein kinase 6 in rice. Development (Cambridge), 2019, 146, .	2.5	12
7	Characterisation of a rice vacuolar invertase isoform, OsINV2, for growth and yield-related traits. Functional Plant Biology, 2019, 46, 777.	2.1	5
8	The urea transporter DUR3 contributes to rice production under nitrogenâ€deficient and field conditions. Physiologia Plantarum, 2019, 167, 75-89.	5.2	15
9	A rice Serine/Threonine receptor-like kinase regulates arbuscular mycorrhizal symbiosis at the peri-arbuscular membrane. Nature Communications, 2018, 9, 4677.	12.8	45
10	Genetic Evidence for the Role of a Rice Vacuolar Invertase as a Molecular Sink Strength Determinant. Rice, 2018, 11, 6.	4.0	46
11	Loss of function mutations in the rice chromomethylase Os<scp>CMT</scp>3a cause a burst of transposition. Plant Journal, 2015, 83, 1069-1081.	5.7	56
12	Transposon-mediated mutagenesis and its application to plant breeding. Ikushugaku Kenkyu, 2015, 17, 77-87.	0.3	0
13	OsATG7 is required for autophagy-dependent lipid metabolism in rice postmeiotic anther development. Autophagy, 2014, 10, 878-888.	9.1	176
14	Reverseâ€genetic approach to verify physiological roles of rice phytoalexins: characterization of a knockdown mutant of <scp>OsCPS4</scp> phytoalexin biosynthetic gene in rice. Physiologia Plantarum, 2014, 150, 55-62.	5.2	71
15	Transposon Insertion Finder (TIF): a novel program for detection of de novo transpositions of transposable elements. BMC Bioinformatics, 2014, 15, 71.	2.6	43
16	Phenotypic analyses of rice lse2 and lse3 mutants that exhibit hyperaccumulation of starch in the leaf blades. Rice, 2014, 7, 32.	4.0	5
17	Response of an aspartic protease gene OsAP77 to fungal, bacterial and viral infections in rice. Rice, 2014, 7, 9.	4.0	20
18	Isolation of a novel mutant gene for soil-surface rooting in rice (Oryza sativa L.). Rice, 2013, 6, 30.	4.0	24

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19	RICE SALT SENSITIVE3 Forms a Ternary Complex with JAZ and Class-C bHLH Factors and Regulates Jasmonate-Induced Gene Expression and Root Cell Elongation Â. Plant Cell, 2013, 25, 1709-1725.	6.6	107
20	Disruption of a rice gene for Î±-glucan water dikinase, OsGWD1, leads to hyperaccumulation of starch in leaves but exhibits limited effects on growth. Frontiers in Plant Science, 2013, 4, 147.	3.6	55
21	Identification of Transcription Factors Involved in Rice Secondary Cell Wall Formation. Plant and Cell Physiology, 2013, 54, 1791-1802.	3.1	105
22	COLLAPSED ABNORMAL POLLEN1Gene Encoding the Arabinokinase-Like Protein Is Involved in Pollen Development in Rice Â Â Â. Plant Physiology, 2013, 162, 858-871.	4.8	45
23	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
24	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
25	CAD2 deficiency causes both brown midrib and gold hull and internode phenotypes in Oryza sativa L. cv. Nipponbare. Plant Biotechnology, 2013, 30, 365-373.	1.0	29
26	Molecular Spectrum of Somaclonal Variation in Regenerated Rice Revealed by Whole-Genome Sequencing. Plant and Cell Physiology, 2012, 53, 256-264.	3.1	114
27	Cryptochrome and Phytochrome Cooperatively but Independently Reduce Active Gibberellin Content in Rice Seedlings under Light Irradiation. Plant and Cell Physiology, 2012, 53, 1570-1582.	3.1	48
28	Nonredundant Regulation of Rice Arbuscular Mycorrhizal Symbiosis by Two Members of the PHOSPHATE TRANSPORTER1 Gene Family. Plant Cell, 2012, 24, 4236-4251.	6.6	306
29	Regulation of a Proteinaceous Elicitor-induced Ca2+ Influx and Production of Phytoalexins by a Putative Voltage-gated Cation Channel, OsTPC1, in Cultured Rice Cells. Journal of Biological Chemistry, 2012, 287, 9931-9939.	3.4	39
30	A rice calciumâ€dependent protein kinase OsCPK12 oppositely modulates saltâ€stress tolerance and blast disease resistance. Plant Journal, 2012, 69, 26-36.	5.7	269
31	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
32	An ATP-binding cassette subfamily G full transporter is essential for the retention of leaf water in both wild barley and rice. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 12354-12359.	7.1	134
33	RSS1 regulates the cell cycle and maintains meristematic activity under stress conditions in rice. Nature Communications, 2011, 2, 278.	12.8	87
34	A loss-of-function mutation of rice DENSE PANICLE 1 causes semi-dwarfness and slightly increased number of spikelets. Breeding Science, 2011, 61, 17-25.	1.9	45
35	Negative feedback regulation of microbe-associated molecular pattern-induced cytosolic Ca2+ transients by protein phosphorylation. Journal of Plant Research, 2011, 124, 415-424.	2.4	18
36	Isolation, fine mapping and expression profiling of a lesion mimic genotype, spl NF4050-8 that confers blast resistance in rice. Theoretical and Applied Genetics, 2011, 122, 831-854.	3.6	6

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37	Root hairless 2 (rth2) mutant represents a loss-of-function allele of the cellulose synthase-like gene OsCSLD1 in rice (Oryza sativa L.). Breeding Science, 2011, 61, 225-233.	1.9	27
38	A Novel RNA-Recognition-Motif Protein Is Required for Premeiotic G1/S-Phase Transition in Rice (Oryza) Tj ETQq0 0 0 rgBT /Overlock 10 T	3.5	56
39	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
40	Unique features of the rice blast resistance Pish locus revealed by large scale retrotransposon-tagging. BMC Plant Biology, 2010, 10, 175.	3.6	94
41	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
42	The NAC transcription factor RIM1 of rice is a new regulator of jasmonate signaling. Plant Journal, 2010, 61, 804-815.	5.7	82
43	A rice fungal MAMPâ€responsive MAPK cascade regulates metabolic flow to antimicrobial metabolite synthesis. Plant Journal, 2010, 63, 599-612.	5.7	208
44	PANICLE PHYTOMER2 (PAP2), encoding a SEPALLATA subfamily MADS-box protein, positively controls spikelet meristem identity in rice. Plant and Cell Physiology, 2010, 51, 47-57.	3.1	174
45	Molecular cloning ofSdr4, a regulator involved in seed dormancy and domestication of rice. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 5792-5797.	7.1	272
46	Disruption of a gene for rice sucrose transporter, OsSUT1, impairs pollen function but pollen maturation is unaffected. Journal of Experimental Botany, 2010, 61, 3639-3646.	4.8	107
47	Pdk1 Kinase Regulates Basal Disease Resistance Through the OsOxi1â€“OsPti1a Phosphorylation Cascade in Rice. Plant and Cell Physiology, 2010, 51, 2082-2091.	3.1	36
48	Production and characterization of a large population of cDNA-overexpressing transgenic rice plants using Gateway-based full-length cDNA expression libraries. Breeding Science, 2010, 60, 575-585.	1.9	31
49	Low-Damage SF[sub 6] Plasma-Etching Condition for Planar GaN HEMTs. Journal of the Electrochemical Society, 2009, 156, H68.	2.9	3
50	MOSAIC FLORAL ORGANS1, anAGL6-Like MADS Box Gene, Regulates Floral Organ Identity and Meristem Fate in Rice. Plant Cell, 2009, 21, 3008-3025.	6.6	195
51	Disruption of a novel gene for a NACâ€domain protein in rice confers resistance to Rice dwarf virus. Plant Journal, 2009, 57, 615-625.	5.7	84
52	Characterization of pullulanase (PUL)-deficient mutants of rice (Oryza sativa L.) and the function of PUL on starch biosynthesis in the developing rice endosperm. Journal of Experimental Botany, 2009, 60, 1009-1023.	4.8	158
53	Isolation and mapping of three rice mutants that showed ectopic expression of KNOX genes in leaves. Plant Science, 2009, 177, 131-135.	3.6	12
54	Loss of cytosolic fructoseâ€1,6â€bisphosphatase limits photosynthetic sucrose synthesis and causes severe growth retardations in rice (Oryza sativa). Plant, Cell and Environment, 2008, 31, 1851-1863.	5.7	73

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55	OsRecQ1, a QDEâ€3 homologue in rice, is required for RNA silencing induced by particle bombardment for inverted repeat DNA, but not for doubleâ€stranded RNA. Plant Journal, 2008, 56, 274-286.	5.7	15
56	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. Plant and Cell Physiology, 2008, 49, 1659-1671.	3.1	103
57	Arbuscular Mycorrhizaâ€"Specific Signaling in Rice Transcends the Common Symbiosis Signaling Pathway. Plant Cell, 2008, 20, 2989-3005.	6.6	235
58	A Germ Cellâ€"Specific Gene of theARGONAUTEFamily Is Essential for the Progression of Premeiotic Mitosis and Meiosis during Sporogenesis in Rice. Plant Cell, 2007, 19, 2583-2594.	6.6	324
59	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
60	Characterization of SSIIIa-Deficient Mutants of Rice: The Function of SSIIIa and Pleiotropic Effects by SSIIIa Deficiency in the Rice Endosperm. Plant Physiology, 2007, 144, 2009-2023.	4.8	335
61	Rice Pti1a Negatively Regulates RAR1-Dependent Defense Responses. Plant Cell, 2007, 19, 2940-2951.	6.6	58
62	Curated genome annotation of Oryza sativa ssp. japonica and comparative genome analysis with Arabidopsis thaliana. Genome Research, 2007, 17, 175-183.	5.5	218
63	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. Plant and Cell Physiology, 2007, 48, 332-344.	3.1	60
64	Rice OsHKT2;1 transporter mediates large Na+ influx component into K+-starved roots for growth. EMBO Journal, 2007, 26, 3003-3014.	7.8	333
65	The plastid sigma factor SIG1 maintains photosystem I activity via regulated expression of the psaA operon in rice chloroplasts. Plant Journal, 2007, 52, 124-132.	5.7	32
66	A large-scale collection of phenotypic data describing an insertional mutant population to facilitate functional analysis of rice genes. Plant Molecular Biology, 2007, 63, 625-635.	3.9	131
67	A genome-wide gain-of-function analysis of rice genes using the FOX-hunting system. Plant Molecular Biology, 2007, 65, 357-371.	3.9	103
68	Isolation of a novel lateral-rootless mutant in rice (Oryza sativa L.) with reduced sensitivity to auxin. Plant Science, 2006, 170, 70-77.	3.6	38
69	Function and Characterization of Starch Synthase I Using Mutants in Rice. Plant Physiology, 2006, 140, 1070-1084.	4.8	339
70	Ethylene Promotes Submergence-Induced Expression of OsABA8ox1, a Gene that Encodes ABA 8'-Hydroxylase in Rice. Plant and Cell Physiology, 2006, 48, 287-298.	3.1	223
71	Physiological and genetic analyses of aluminium tolerance in rice, focusing on root growth during germination. Journal of Inorganic Biochemistry, 2005, 99, 1837-1844.	3.5	42
72	Identification of a putative voltage-gated Ca2+ channel as a key regulator of elicitor-induced hypersensitive cell death and mitogen-activated protein kinase activation in rice. Plant Journal, 2005, 42, 798-809.	5.7	120

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73	The map-based sequence of the rice genome. Nature, 2005, 436, 793-800.	27.8	3,365
74	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. Plant Molecular Biology, 2005, 59, 125-135.	3.9	129
75	Distinct and Cooperative Functions of Phytochromes A, B, and C in the Control of Deetiolation and Flowering in Rice. Plant Cell, 2005, 17, 3311-3325.	6.6	287
76	Functional Diversification of the Two C-Class MADS Box Genes OSMADS3 and OSMADS58 in Oryza sativa. Plant Cell, 2005, 18, 15-28.	6.6	322
77	Defects in root development and gravity response in the aem1 mutant of rice are associated with reduced auxin efflux. Journal of Plant Physiology, 2005, 162, 678-685.	3.5	10
78	Characterization of Chlorophyllide a Oxygenase (CAO) in Rice. Breeding Science, 2005, 55, 361-364.	1.9	17
79	Molecular Genetic Analysis of a Tos17-Tagged Mutant Line Related to Root Morphology in Rice. Ikushugaku Kenkyu, 2005, 7, 171-178.	0.3	1
80	Function, Intracellular Localization and the Importance in Salt Tolerance of a Vacuolar Na+/H+ Antiporter from Rice. Plant and Cell Physiology, 2004, 45, 146-159.	3.1	397
81	Identification of a Putative Voltage-Gated Ca2+-permeable Channel (OsTPC1) Involved in Ca2+ Influx and Regulation of Growth and Development in Rice. Plant and Cell Physiology, 2004, 45, 693-702.	3.1	72
82	The Novel Gene HOMOLOGOUS PAIRING ABERRATION IN RICE MEIOSIS1 of Rice Encodes a Putative Coiled-Coil Protein Required for Homologous Chromosome Pairing in Meiosis. Plant Cell, 2004, 16, 1008-1020.	6.6	151
83	Loss-of-Function Mutations of the Rice GAMYB Gene Impair Î±-Amylase Expression in Aleurone and Flower Development. Plant Cell, 2004, 16, 33-44.	6.6	296
84	An Overview of Gibberellin Metabolism Enzyme Genes and Their Related Mutants in Rice. Plant Physiology, 2004, 134, 1642-1653.	4.8	643
85	An insertional mutation in the rice PAIR2 gene, the ortholog of Arabidopsis ASY1, results in a defect in homologous chromosome pairing during meiosis. Molecular Genetics and Genomics, 2004, 271, 121-129.	2.1	96
86	Transposon-Insertion Lines of Rice for Analysis of Gene Function. , 2004, , 107-112.		1
87	Three Distinct Rice Cellulose Synthase Catalytic Subunit Genes Required for Cellulose Synthesis in the Secondary Wall. Plant Physiology, 2003, 133, 73-83.	4.8	392
88	Isolation and characterization of a short lateral root mutant in rice (Oryza sativa L.). Plant Science, 2003, 165, 895-903.	3.6	18
89	Characterization of a Rice Chlorophyll-Deficient Mutant Using the T-DNA Gene-Trap System. Plant and Cell Physiology, 2003, 44, 463-472.	3.1	277
90	Target Site Specificity of the Tos17 Retrotransposon Shows a Preference for Insertion within Genes and against Insertion in Retrotransposon-Rich Regions of the Genome. Plant Cell, 2003, 15, 1771-1780.	6.6	493

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91	The MSP1 Gene Is Necessary to Restrict the Number of Cells Entering into Male and Female Sporogenesis and to Initiate Anther Wall Formation in Rice. Plant Cell, 2003, 15, 1728-1739.	6.6	291
92	Isolation and Characterization of Rice Phytochrome A Mutants. Plant Cell, 2001, 13, 521-534.	6.6	179
93	Screening of the Rice Viviparous Mutants Generated by Endogenous Retrotransposon Tos17 Insertion. Tagging of a Zeaxanthin Epoxidase Gene and a Novel OsTATCGene. Plant Physiology, 2001, 125, 1248-1257.	4.8	211
94	Isolation and Characterization of Rice Phytochrome A Mutants. Plant Cell, 2001, 13, 521.	6.6	16
95	Plant Biotechniques Series (9). Systematic screening of mutants of rice by sequencing retrotransposon-insertion sites.. Plant Biotechnology, 1998, 15, 253-256.	1.0	19
96	Saturation mapping with subclones of YACs: DNA marker production targeting the rice blast disease resistance gene, Pi-b. Theoretical and Applied Genetics, 1997, 94, 170-176.	3.6	26
97	Characterization and Genetic Mapping of Simple Sequence Repeats in the Rice Genome. DNA Research, 1996, 3, 233-238.	3.4	31
98	Screening of RAPD Markers Linked to the Photoperiod-Sensitivity Gene in Rice Chromosome 6 Using Bulked Segregant Analysis. DNA Research, 1995, 2, 101-106.	3.4	13
99	Mapping of Sequence-Tagged Sites in Rice by Single Strand Conformation Polymorphism. DNA Research, 1994, 1, 271-277.	3.4	33
100	Sequence-tagged sites (STSs) as standard landmarkers in the rice genome. Theoretical and Applied Genetics, 1994, 89, 728-734.	3.6	67
101	Determination of RAPD Markers in Rice and their Conversion into Sequence Tagged Sites (STSs) and STS-Specific Primers. DNA Research, 1994, 1, 139-148.	3.4	55
102	A 300 kilobase interval genetic map of rice including 883 expressed sequences. Nature Genetics, 1994, 8, 365-372.	21.4	578
103	Bacillus subtilis spoVE gene is transcribed by sigma E-associated RNA polymerase. Journal of Bacteriology, 1993, 175, 4081-4086.	2.2	28
104	In vivo expression of the Bacillus subtilis spoVE gene. Journal of Bacteriology, 1993, 175, 4071-4080.	2.2	16