Takashi Kuromori

List of Publications by Year in descending order

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60 papers

6,887 citations

39 h-index 56 g-index

62 all docs

62 docs citations

62 times ranked 8626 citing authors

| # | Article | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Molecular Basis of the Core Regulatory Network in ABA Responses: Sensing, Signaling and Transport. Plant and Cell Physiology, 2010, 51, 1821-1839. | 3.1 | 800 |
| 2 | ABC transporter AtABCG25 is involved in abscisic acid transport and responses. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 2361-2366. | 7.1 | 494 |
| 3 | Genetic Definition and Sequence Analysis of <i>Arabidopsis</i> Centromeres. Science, 1999, 286, 2468-2474. | 12.6 | 417 |
| 4 | ABA-Hypersensitive Germination3 Encodes a Protein Phosphatase 2C (AtPP2CA) That Strongly Regulates Abscisic Acid Signaling during Germination among Arabidopsis Protein Phosphatase 2Cs. Plant Physiology, 2006, 140, 115-126. | 4.8 | 344 |
| 5 | AtIPT3 is a Key Determinant of Nitrate-Dependent Cytokinin Biosynthesis in Arabidopsis. Plant and Cell Physiology, 2004, 45, 1053-1062. | 3.1 | 343 |
| 6 | ABA Transport and Plant Water Stress Responses. Trends in Plant Science, 2018, 23, 513-522. | 8.8 | 343 |
| 7 | A Heterocomplex of Iron Superoxide Dismutases Defends Chloroplast Nucleoids against Oxidative Stress and Is Essential for Chloroplast Development in <i>Arabidopsis</i> . Plant Cell, 2008, 20, 3148-3162. | 6.6 | 270 |
| 8 | Acetate-mediated novel survival strategy against drought in plants. Nature Plants, 2017, 3, 17097. | 9.3 | 232 |
| 9 | MS/MS spectral tagâ€based annotation of nonâ€targeted profile of plant secondary metabolites. Plant Journal, 2009, 57, 555-577. | 5.7 | 208 |
| 10 | Arabidopsis SPO11â€2 functions with SPO11â€1 in meiotic recombination. Plant Journal, 2006, 48, 206-216. | 5.7 | 206 |
| 11 | A collection of 11 800 single-copyDstransposon insertion lines inArabidopsis. Plant Journal, 2004, 37, 897-905. | 5.7 | 203 |
| 12 | Drought Stress Responses and Resistance in Plants: From Cellular Responses to Long-Distance Intercellular Communication. Frontiers in Plant Science, 2020, 11, 556972. | 3.6 | 199 |
| 13 | Arabidopsis mutants of <i>AtABCG22</i> , an ABC transporter gene, increase water transpiration and drought susceptibility. Plant Journal, 2011, 67, 885-894. | 5.7 | 164 |
| 14 | Two glycosyltransferases involved in anthocyanin modification delineated by transcriptome independent component analysis in <i>Arabidopsis thaliana</i> . Plant Journal, 2012, 69, 154-167. | 5.7 | 164 |
| 15 | Global Patterns of Human DNA Sequence Variation in a 10-kb Region on Chromosome 1. Molecular Biology and Evolution, 2001, 18, 214-222. | 8.9 | 157 |
| 16 | AtPHT4;4 is a chloroplast-localized ascorbate transporter in Arabidopsis. Nature Communications, 2015, 6, 5928. | 12.8 | 145 |
| 17 | Multiple loss-of-function of Arabidopsis gibberellin receptor AtGID1s completely shuts down a gibberellin signal. Plant Journal, 2007, 50, 958-966. | 5.7 | 136 |
| 18 | Analysis of ABA Hypersensitive Germination2 revealed the pivotal functions of PARN in stress response in Arabidopsis. Plant Journal, 2005, 44, 972-984. | 5.7 | 131 |

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|----|--|------|-----------|
| 19 | Intertissue Signal Transfer of Abscisic Acid from Vascular Cells to Guard Cells Â. Plant Physiology, 2014, 164, 1587-1592. | 4.8 | 123 |
| 20 | A trial of phenome analysis using 4000Ds-insertional mutants in gene-coding regions of Arabidopsis. Plant Journal, 2006, 47, 640-651. | 5.7 | 110 |
| 21 | A New Resource of Locally Transposed DissociationElements for Screening Gene-Knockout Lines in Silico on the Arabidopsis Genome. Plant Physiology, 2002, 129, 1695-1699. | 4.8 | 103 |
| 22 | The Glycerophosphoryl Diester Phosphodiesterase-Like Proteins SHV3 and its Homologs Play Important Roles in Cell Wall Organization. Plant and Cell Physiology, 2008, 49, 1522-1535. | 3.1 | 103 |
| 23 | Regulatory Gene Networks in Drought Stress Responses and Resistance in Plants. Advances in Experimental Medicine and Biology, 2018, 1081, 189-214. | 1.6 | 91 |
| 24 | Cytological and Biochemical Analysis of COF1, an Arabidopsis Mutant of an ABC Transporter Gene. Plant and Cell Physiology, 2007, 48, 1524-1533. | 3.1 | 84 |
| 25 | Phenome Analysis in Plant Species Using Loss-of-Function and Gain-of-Function Mutants. Plant and Cell Physiology, 2009, 50, 1215-1231. | 3.1 | 83 |
| 26 | An Arabidopsis chloroplast-targeted Hsp101 homologue, APG6, has an essential role in chloroplast development as well as heat-stress response. Plant Journal, 2006, 48, 249-260. | 5.7 | 81 |
| 27 | Evolutionary Persistence of Functional Compensation by Duplicate Genes in Arabidopsis. Genome Biology and Evolution, 2009, 1, 409-414. | 2.5 | 81 |
| 28 | Functional Compensation of Primary and Secondary Metabolites by Duplicate Genes in Arabidopsis thaliana. Molecular Biology and Evolution, 2011, 28, 377-382. | 8.9 | 76 |
| 29 | RARGE: a large-scale database of RIKEN Arabidopsis resources ranging from transcriptome to phenome. Nucleic Acids Research, 2004, 33, D647-D650. | 14.5 | 73 |
| 30 | Loss of NECROTIC SPOTTED LESIONS 1 associates with cell death and defense responses in Arabidopsis thaliana. Plant Molecular Biology, 2006, 62, 29-42. | 3.9 | 68 |
| 31 | Expression and Interaction Analysis of Arabidopsis Skp1-Related Genes. Plant and Cell Physiology, 2004, 45, 83-91. | 3.1 | 67 |
| 32 | Quantitative trait loci analysis of nitrate storage in Arabidopsis leading to an investigation of the contribution of the anion channel gene, AtCLC-c, to variation in nitrate levels. Journal of Experimental Botany, 2004, 55, 2005-2014. | 4.8 | 65 |
| 33 | The Chloroplast Function Database: a largeâ€scale collection of Arabidopsis <i>Ds/Spm</i> â€or Tâ€DNAâ€tagged homozygous lines for nuclearâ€encoded chloroplast proteins, and their systematic phenotype analysis. Plant Journal, 2010, 61, 529-542. | 5.7 | 60 |
| 34 | A Resource of 5,814 Dissociation Transposon-tagged and Sequence-indexed Lines of Arabidopsis Transposed from Start Loci on Chromosome 5. Plant and Cell Physiology, 2005, 46, 1149-1153. | 3.1 | 58 |
| 35 | Top-down Phenomics of Arabidopsis thaliana. Journal of Biological Chemistry, 2007, 282, 18532-18541. | 3.4 | 58 |
| 36 | Increased Expression and Protein Divergence in Duplicate Genes Is Associated with Morphological Diversification. PLoS Genetics, 2009, 5, e1000781. | 3.5 | 50 |

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| # | Article | IF | CITATIONS |
|----|--|------|-----------|
| 37 | Interâ€tissue and interâ€organ signaling in drought stress response and phenotyping of drought tolerance. Plant Journal, 2022, 109, 342-358. | 5.7 | 50 |
| 38 | Cloning of cDNAs from Arabidopsis thaliana that encode putative protein phosphatase 2C and a human DM-like protein by transformation of a fission yeast mutant. Nucleic Acids Research, 1994, 22, 5296-5301. | 14.5 | 47 |
| 39 | ABA transport factors found in Arabidopsis ABC transporters. Plant Signaling and Behavior, 2010, 5, 1124-1126. | 2.4 | 47 |
| 40 | Overexpression of AtABCG25 enhances the abscisic acid signal in guard cells and improves plant water use efficiency. Plant Science, 2016, 251, 75-81. | 3.6 | 45 |
| 41 | Evidence for potassium transport activity of Arabidopsis KEA1-KEA6. Scientific Reports, 2019, 9, 10040. | 3.3 | 42 |
| 42 | Arabidopsis mutant of AtABCG26, an ABC transporter gene, is defective in pollen maturation. Journal of Plant Physiology, 2011, 168, 2001-2005. | 3.5 | 35 |
| 43 | RARGE II: An Integrated Phenotype Database of Arabidopsis Mutant Traits Using a Controlled Vocabulary. Plant and Cell Physiology, 2014, 55, e4-e4. | 3.1 | 32 |
| 44 | SD3, an Arabidopsis thaliana Homolog of TIM21, Affects Intracellular ATP Levels and Seedling Development. Molecular Plant, 2012, 5, 461-471. | 8.3 | 31 |
| 45 | Members of the Arabidopsis 14-3-3 gene family trans-complement two types of defects in fission yeast. Plant Science, 2000, 158, 155-161. | 3.6 | 25 |
| 46 | Drought Stress Signaling Network. , 2014, , 383-409. | | 23 |
| 47 | Functional cloning of a cDNA encoding Mei2â€like protein from <i>Arabidopsis thaliana</i> using a fission yeast pheromone receptor deficient mutant. FEBS Letters, 1997, 413, 16-20. | 2.8 | 22 |
| 48 | SnRK1 Kinase and the NAC Transcription Factor SOG1 Are Components of a Novel Signaling Pathway Mediating the Low Energy Response Triggered by ATP Depletion. Frontiers in Plant Science, 2019, 10, 503. | 3.6 | 18 |
| 49 | PosMed-plus: An Intelligent Search Engine that Inferentially Integrates Cross-Species Information Resources for Molecular Breeding of Plants. Plant and Cell Physiology, 2009, 50, 1249-1259. | 3.1 | 17 |
| 50 | Toward genome-wide metabolotyping and elucidation of metabolic system: metabolic profiling of large-scale bioresources. Journal of Plant Research, 2010, 123, 291-298. | 2.4 | 13 |
| 51 | Functional relationship of AtABCG21 and AtABCG22 in stomatal regulation. Scientific Reports, 2017, 7, 12501. | 3.3 | 12 |
| 52 | Homologous chromosome pairing is completed in crossover defective atzip4 mutant. Biochemical and Biophysical Research Communications, 2008, 370, 98-103. | 2.1 | 9 |
| 53 | <i>Brachypodium</i> BdABCG25 is a homolog of <i>Arabidopsis</i> AtABCG25 involved in the transport of abscisic acid. FEBS Letters, 2021, 595, 954-959. | 2.8 | 8 |
| 54 | The Regulatory Networks of Plant Responses to Abscisic Acid. Advances in Botanical Research, 2011, , 201-248. | 1.1 | 6 |

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|----|---|-----|-----------|
| 55 | Stress Signaling Networks: Drought Stress. , 2013, , 1-23. | | 3 |
| 56 | Arabidopsis cDNA Clones Isolated by Transcomplementation of the Fission Yeast cAMP Phosphodiesterase Mutant. DNA Research, 2001, 8, 189-192. | 3.4 | 1 |
| 57 | Identification of a cDNA from Arabidopsis thaliana Encoding a Member of the Conserved SUG1 Protein Family by Complementation Screening in Fission Yeast Meiotic Mutants Plant Biotechnology, 2001, 18, 169-174. | 1.0 | 0 |
| 58 | Phenome analysis of root development in Arabidopsis. Plant Biotechnology, 2010, 27, 345-347. | 1.0 | 0 |
| 59 | ABA Transport by ABCG Transporter Proteins. Signaling and Communication in Plants, 2014, , 39-47. | 0.7 | 0 |
| 60 | Ds Transposon Mutant Lines for Saturation Mutagenesis of the Arabidopsis genome., 0,, 17-30. | | 0 |