Daisuke Shibata

List of Publications by Year
in descending order

50 papers	5,296 citations	186265 28 h-index	206112 48 g-index
51 all docs	51 docs citations	51 times ranked	7665 citing authors

#	Article	IF	Citations
1	Introduction of a long synthetic repetitive DNA sequence into cultured tobacco cells. Plant Biotechnology, 2022, 39, 101-110.	1.0	2
2	Metagenomic mining and structure-function studies of a hyper-thermostable cellobiohydrolase from hot spring sediment. Communications Biology, 2022, 5, 247.	4.4	3
3	TOMATOMET: A metabolome database consists of 7118 accurate mass values detected in mature fruits of 25 tomato cultivars. Plant Direct, 2021, 5, e00318.	1.9	20
4	Development of the binary vector pTACAtg1 for stable gene expression in plant: Reduction of gene silencing in transgenic plants carrying the target gene with long flanking sequences. Plant Biotechnology, 2021, 38, 391-400.	1.0	0
5	An Artificial Conversion of Roots into Organs with Shoot Stem Characteristics by Inducing Two Transcription Factors. IScience, 2020, 23, 101332.	4.1	3
6	A Cytosol-Localized Geranyl Diphosphate Synthase from *Lithospermum erythrorhizon* and Its Molecular Evolution. Plant Physiology, 2020, 182, 1933-1945.	4.8	27
7	Comparative multi-omics analysis reveals diverse latex-based defense strategies against pests among latex-producing organs of the fig tree (Ficus carica). Planta, 2018, 247, 1423-1438.	3.2	31
8	Wide-range screening of anti-inflammatory compounds in tomato using LC-MS and elucidating the mechanism of their functions. PLoS ONE, 2018, 13, e0191203.	2.5	18
9	FlavonoidSearch: A system for comprehensive flavonoid annotation by mass spectrometry. Scientific Reports, 2017, 7, 1243.	3.3	41
10	Co-expressed Pathways DataBase for Tomato: a database to predict pathways relevant to a query gene. BMC Genomics, 2017, 18, 437.	2.8	12
11	Isolation of highly thermostable Î²-xylosidases from a hot spring soil microbial community using a metagenomic approach. DNA Research, 2017, 24, 649-656.	3.4	15
12	The Arabidopsis TAC Position Viewer: a highâ€resolution map of transformationâ€competent artificial chromosome (<scp>TAC</scp>) clones aligned with the *Arabidopsis thaliana* Columbiaâ€0 genome. Plant Journal, 2015, 83, 1114-1122.	5.7	4
13	Metabolonote: A Wiki-Based Database for Managing Hierarchical Metadata of Metabolome Analyses. Frontiers in Bioengineering and Biotechnology, 2015, 3, 38.	4.1	39
14	Tools and Databases of the KOMICS Web Portal for Preprocessing, Mining, and Dissemination of Metabolomics Data. BioMed Research International, 2014, 2014, 1-11.	1.9	38
15	An application of a relational database system for high-throughput prediction of elemental compositions from accurate mass values. Bioinformatics, 2013, 29, 290-291.	4.1	28
16	Precise Sequential DNA Ligation on A Solid Substrate: Solid-Based Rapid Sequential Ligation of Multiple DNA Molecules. DNA Research, 2013, 20, 583-592.	3.4	8
17	High-Throughput Cryopreservation of Plant Cell Cultures for Functional Genomics. Plant and Cell Physiology, 2012, 53, 943-952.	3.1	42
18	Potent PPARÎ± Activator Derived from Tomato Juice, 13-oxo-9,11-Octadecadienoic Acid, Decreases Plasma and Hepatic Triglyceride in Obese Diabetic Mice. PLoS ONE, 2012, 7, e31317.	2.5	62

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19	Dynamic metabolic changes during fruit maturation in Jatropha curcas L.. Plant Biotechnology, 2012, 29, 175-178.	1.0	12
20	KaPPA-View4: a metabolic pathway database for representation and analysis of correlation networks of gene co-expression and metabolite co-accumulation and omics data. Nucleic Acids Research, 2011, 39, D677-D684.	14.5	69
21	Large-scale analysis of full-length cDNAs from the tomato (Solanum lycopersicum) cultivar Micro-Tom, a reference system for the Solanaceae genomics. BMC Genomics, 2010, 11, 210.	2.8	179
22	MassBank: a public repository for sharing mass spectral data for life sciences. Journal of Mass Spectrometry, 2010, 45, 703-714.	1.6	1,831
23	CoP: a database for characterizing co-expressed gene modules with biological information in plants. Bioinformatics, 2010, 26, 1267-1268.	4.1	72
24	Pathway engineering of Brassica napus seeds using multiple key enzyme genes involved in ketocarotenoid formation. Journal of Experimental Botany, 2009, 60, 1319-1332.	4.8	139
25	Metabolite annotations based on the integration of mass spectral information. Plant Journal, 2008, 54, 949-962.	5.7	286
26	Efficient and High-Throughput Vector Construction and Agrobacterium-Mediated Transformation of Arabidopsis thaliana Suspension-Cultured Cells for Functional Genomics. Plant and Cell Physiology, 2008, 49, 242-250.	3.1	43
27	Metabolite Profiling of Chalcones and Flavanones in Tomato Fruit. Japanese Society for Horticultural Science, 2008, 77, 94-102.	0.8	37
28	Cryopreservation and metabolic profiling analysis of Arabidopsis T87 suspension-cultured cells. Cryo-Letters, 2008, 29, 427-36.	0.3	9
29	ATTED-II: a database of co-expressed genes and cis elements for identifying co-regulated gene groups in Arabidopsis. Nucleic Acids Research, 2007, 35, D863-D869.	14.5	343
30	*Arabidopsis* Cotyledon-Specific Chloroplast Biogenesis Factor CYO1 Is a Protein Disulfide Isomerase. Plant Cell, 2007, 19, 3157-3169.	6.6	118
31	Omics-based identification of Arabidopsis Myb transcription factors regulating aliphatic glucosinolate biosynthesis. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 6478-6483.	7.1	666
32	Genomic Databases for Tomato. Plant Biotechnology, 2007, 24, 17-25.	1.0	15
33	Differential metabolomics unraveling light/dark regulation of metabolic activities in Arabidopsis cell culture. Planta, 2007, 227, 57-66.	3.2	67
34	MiBASE: A database of a miniature tomato cultivar Micro-Tom. Plant Biotechnology, 2006, 23, 195-198.	1.0	28
35	Beta-Cyanoalanine Synthase as a Molecular Marker for Induced Resistance by Fungal Glycoprotein Elicitor and Commercial Plant Activators. Phytopathology, 2006, 96, 908-916.	2.2	47
36	Clarification of Pathway-Specific Inhibition by Fourier Transform Ion Cyclotron Resonance/Mass Spectrometry-Based Metabolic Phenotyping Studies. Plant Physiology, 2006, 142, 398-413.	4.8	107

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37	Genome sequencing and functional genomics approaches in tomato. Journal of General Plant Pathology, 2005, 71, 1-7.	1.0	66
38	Catalog of Micro-Tom tomato responses to common fungal, bacterial, and viral pathogens. Journal of General Plant Pathology, 2005, 71, 8-22.	1.0	46
39	KaPPA-View. A Web-Based Analysis Tool for Integration of Transcript and Metabolite Data on Plant Metabolic Pathway Maps. Plant Physiology, 2005, 138, 1289-1300.	4.8	155
40	Expressed sequence tags of full-length cDNA clones from the miniature tomato (Lycopersicon) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 622	1.0	17
41	Distinctive Features of Plant Organs Characterized by Global Analysis of Gene Expression in Arabidopsis. DNA Research, 2004, 11, 11-25.	3.4	27
42	Identification of anther-specific genes in a cruciferous model plant, Arabidopsis thaliana, by using a combination of Arabidopsis macroarray and mRNA derived from Brassica oleracea. Sexual Plant Reproduction, 2003, 15, 213-220.	2.2	47
43	Analysis of gene expression inArabidopsis thalianaby array hybridization with genomic DNA fragments aligned along chromosomal regions. Plant Journal, 2002, 30, 247-255.	5.7	7
44	An Arabidopsis Sigma Factor (SIG2)-Dependent Expression of Plastid-Encoded tRNAs in Chloroplasts. Plant and Cell Physiology, 2001, 42, 1034-1043.	3.1	129
45	Role of the Putative Membrane-Bound Endo-1,4-Î²-Glucanase KORRIGAN in Cell Elongation and Cellulose Synthesis in Arabidopsis thaliana. Plant and Cell Physiology, 2001, 42, 251-263.	3.1	185
46	Technical Focus-Agrobacterium-mediated plant transformation with large DNA fragments. Trends in Plant Science, 2000, 5, 354-357.	8.8	91
47	Chloroplast development in Arabidopsis thaliana requires the nuclear-encoded transcription factor Sigma B. FEBS Letters, 2000, 485, 178-182.	2.8	55
48	A Sequence-ready Contig Map of the Top Arm of Arabidopsis thaliana Chromosome 3. DNA Research, 1999, 6, 117-121.	3.4	7
49	Establishment of framework P1 clones for map-based cloning and genome sequencing: direct RFLP mapping of large clones. Gene, 1998, 225, 31-38.	2.2	3
50	A Novel Conversion of Roots into Organs with Shoot Stem Characteristics by Inducing Two Transcription Factors. SSRN Electronic Journal, 0, , .	0.4	0