

Daisuke Shibata

List of Publications by Year in descending order

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Version: 2024-02-01

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	MassBank: a public repository for sharing mass spectral data for life sciences. <i>Journal of Mass Spectrometry</i> , 2010, 45, 703-714.	1.6	1,831
2	Omics-based identification of Arabidopsis Myb transcription factors regulating aliphatic glucosinolate biosynthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 6478-6483.	7.1	666
3	ATTED-II: a database of co-expressed genes and cis elements for identifying co-regulated gene groups in Arabidopsis. <i>Nucleic Acids Research</i> , 2007, 35, D863-D869.	14.5	343
4	Metabolite annotations based on the integration of mass spectral information. <i>Plant Journal</i> , 2008, 54, 949-962.	5.7	286
5	Role of the Putative Membrane-Bound Endo-1,4- β -Glucanase KORRIGAN in Cell Elongation and Cellulose Synthesis in Arabidopsis thaliana. <i>Plant and Cell Physiology</i> , 2001, 42, 251-263.	3.1	185
6	Large-scale analysis of full-length cDNAs from the tomato (<i>Solanum lycopersicum</i>) cultivar Micro-Tom, a reference system for the Solanaceae genomics. <i>BMC Genomics</i> , 2010, 11, 210.	2.8	179
7	KaPPA-View. A Web-Based Analysis Tool for Integration of Transcript and Metabolite Data on Plant Metabolic Pathway Maps. <i>Plant Physiology</i> , 2005, 138, 1289-1300.	4.8	155
8	Pathway engineering of Brassica napus seeds using multiple key enzyme genes involved in ketocarotenoid formation. <i>Journal of Experimental Botany</i> , 2009, 60, 1319-1332.	4.8	139
9	An Arabidopsis Sigma Factor (SIG2)-Dependent Expression of Plastid-Encoded tRNAs in Chloroplasts. <i>Plant and Cell Physiology</i> , 2001, 42, 1034-1043.	3.1	129
10	<i>Arabidopsis</i> Cotyledon-Specific Chloroplast Biogenesis Factor CYO1 Is a Protein Disulfide Isomerase. <i>Plant Cell</i> , 2007, 19, 3157-3169.	6.6	118
11	Clarification of Pathway-Specific Inhibition by Fourier Transform Ion Cyclotron Resonance/Mass Spectrometry-Based Metabolic Phenotyping Studies. <i>Plant Physiology</i> , 2006, 142, 398-413.	4.8	107
12	Technical Focus-Agrobacterium-mediated plant transformation with large DNA fragments. <i>Trends in Plant Science</i> , 2000, 5, 354-357.	8.8	91
13	CoP: a database for characterizing co-expressed gene modules with biological information in plants. <i>Bioinformatics</i> , 2010, 26, 1267-1268.	4.1	72
14	KaPPA-View4: a metabolic pathway database for representation and analysis of correlation networks of gene co-expression and metabolite co-accumulation and omics data. <i>Nucleic Acids Research</i> , 2011, 39, D677-D684.	14.5	69
15	Differential metabolomics unraveling light/dark regulation of metabolic activities in Arabidopsis cell culture. <i>Planta</i> , 2007, 227, 57-66.	3.2	67
16	Genome sequencing and functional genomics approaches in tomato. <i>Journal of General Plant Pathology</i> , 2005, 71, 1-7.	1.0	66
17	Potent PPAR α Activator Derived from Tomato Juice, 13-oxo-9,11-Octadecadienoic Acid, Decreases Plasma and Hepatic Triglyceride in Obese Diabetic Mice. <i>PLoS ONE</i> , 2012, 7, e31317.	2.5	62
18	Chloroplast development in Arabidopsis thaliana requires the nuclear-encoded transcription factor Sigma B. <i>FEBS Letters</i> , 2000, 485, 178-182.	2.8	55

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19	Identification of anther-specific genes in a cruciferous model plant, <i>Arabidopsis thaliana</i> , by using a combination of <i>Arabidopsis</i> macroarray and mRNA derived from <i>Brassica oleracea</i> . <i>Sexual Plant Reproduction</i> , 2003, 15, 213-220.	2.2	47
20	Beta-Cyanoalanine Synthase as a Molecular Marker for Induced Resistance by Fungal Glycoprotein Elicitor and Commercial Plant Activators. <i>Phytopathology</i> , 2006, 96, 908-916.	2.2	47
21	Catalog of Micro-Tom tomato responses to common fungal, bacterial, and viral pathogens. <i>Journal of General Plant Pathology</i> , 2005, 71, 8-22.	1.0	46
22	Efficient and High-Throughput Vector Construction and <i>Agrobacterium</i> -Mediated Transformation of <i>Arabidopsis thaliana</i> Suspension-Cultured Cells for Functional Genomics. <i>Plant and Cell Physiology</i> , 2008, 49, 242-250.	3.1	43
23	High-Throughput Cryopreservation of Plant Cell Cultures for Functional Genomics. <i>Plant and Cell Physiology</i> , 2012, 53, 943-952.	3.1	42
24	FlavonoidSearch: A system for comprehensive flavonoid annotation by mass spectrometry. <i>Scientific Reports</i> , 2017, 7, 1243.	3.3	41
25	Metabolonote: A Wiki-Based Database for Managing Hierarchical Metadata of Metabolome Analyses. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 38.	4.1	39
26	Tools and Databases of the KOMICS Web Portal for Preprocessing, Mining, and Dissemination of Metabolomics Data. <i>BioMed Research International</i> , 2014, 2014, 1-11.	1.9	38
27	Metabolite Profiling of Chalcones and Flavanones in Tomato Fruit. <i>Japanese Society for Horticultural Science</i> , 2008, 77, 94-102.	0.8	37
28	Comparative multi-omics analysis reveals diverse latex-based defense strategies against pests among latex-producing organs of the fig tree (<i>Ficus carica</i>). <i>Planta</i> , 2018, 247, 1423-1438.	3.2	31
29	MiBASE: A database of a miniature tomato cultivar Micro-Tom. <i>Plant Biotechnology</i> , 2006, 23, 195-198.	1.0	28
30	An application of a relational database system for high-throughput prediction of elemental compositions from accurate mass values. <i>Bioinformatics</i> , 2013, 29, 290-291.	4.1	28
31	Distinctive Features of Plant Organs Characterized by Global Analysis of Gene Expression in <i>Arabidopsis</i> . <i>DNA Research</i> , 2004, 11, 11-25.	3.4	27
32	A Cytosol-Localized Geranyl Diphosphate Synthase from <i>Lithospermum erythrorhizon</i> and Its Molecular Evolution. <i>Plant Physiology</i> , 2020, 182, 1933-1945.	4.8	27
33	TOMATOMET: A metabolome database consists of 7118 accurate mass values detected in mature fruits of 25 tomato cultivars. <i>Plant Direct</i> , 2021, 5, e00318.	1.9	20
34	Wide-range screening of anti-inflammatory compounds in tomato using LC-MS and elucidating the mechanism of their functions. <i>PLoS ONE</i> , 2018, 13, e0191203.	2.5	18
35	Expressed sequence tags of full-length cDNA clones from the miniature tomato (<i>Lycopersicon</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.0	17
36	Genomic Databases for Tomato. <i>Plant Biotechnology</i> , 2007, 24, 17-25.	1.0	15

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37	Isolation of highly thermostable β -xylosidases from a hot spring soil microbial community using a metagenomic approach. <i>DNA Research</i> , 2017, 24, 649-656.	3.4	15
38	Co-expressed Pathways DataBase for Tomato: a database to predict pathways relevant to a query gene. <i>BMC Genomics</i> , 2017, 18, 437.	2.8	12
39	Dynamic metabolic changes during fruit maturation in <i>Jatropha curcas</i> L.. <i>Plant Biotechnology</i> , 2012, 29, 175-178.	1.0	12
40	Cryopreservation and metabolic profiling analysis of <i>Arabidopsis</i> T87 suspension-cultured cells. <i>Cryo-Letters</i> , 2008, 29, 427-36.	0.3	9
41	Precise Sequential DNA Ligation on A Solid Substrate: Solid-Based Rapid Sequential Ligation of Multiple DNA Molecules. <i>DNA Research</i> , 2013, 20, 583-592.	3.4	8
42	A Sequence-ready Contig Map of the Top Arm of <i>Arabidopsis thaliana</i> Chromosome 3. <i>DNA Research</i> , 1999, 6, 117-121.	3.4	7
43	Analysis of gene expression in <i>Arabidopsis thaliana</i> by array hybridization with genomic DNA fragments aligned along chromosomal regions. <i>Plant Journal</i> , 2002, 30, 247-255.	5.7	7
44	The <i>Arabidopsis</i> TAC Position Viewer: a high-resolution map of transformation-competent artificial chromosome (<sc>TAC</sc>) clones aligned with the <i>Arabidopsis thaliana</i> Columbia genome. <i>Plant Journal</i> , 2015, 83, 1114-1122.	5.7	4
45	Establishment of framework P1 clones for map-based cloning and genome sequencing: direct RFLP mapping of large clones. <i>Gene</i> , 1998, 225, 31-38.	2.2	3
46	An Artificial Conversion of Roots into Organs with Shoot Stem Characteristics by Inducing Two Transcription Factors. <i>IScience</i> , 2020, 23, 101332.	4.1	3
47	Metagenomic mining and structure-function studies of a hyper-thermostable cellobiohydrolase from hot spring sediment. <i>Communications Biology</i> , 2022, 5, 247.	4.4	3
48	Introduction of a long synthetic repetitive DNA sequence into cultured tobacco cells. <i>Plant Biotechnology</i> , 2022, 39, 101-110.	1.0	2
49	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. <i>Plant Biotechnology</i> , 2021, 38, 391-400.	1.0	0
50	A Novel Conversion of Roots into Organs with Shoot Stem Characteristics by Inducing Two Transcription Factors. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0