Tetsuya Sakurai

List of Publications by Year
in descending order

		36203	48187
89 papers	**15,046** citations	**51** h-index	**88** g-index
90 all docs	**90** docs citations	**90** times ranked	**16154** citing authors

#	Article	IF	Citations
1	Genome sequence of the palaeopolyploid soybean. Nature, 2010, 463, 178-183.	13.7	3,854
2	Monitoring the expression profiles of 7000 Arabidopsis genes under drought, cold and high-salinity stresses using a full-length cDNA microarray. Plant Journal, 2002, 31, 279-292.	2.8	1,697
3	Empirical Analysis of Transcriptional Activity in the Arabidopsis Genome. Science, 2003, 302, 842-846.	6.0	853
4	Functional Annotation of a Full-Length Arabidopsis cDNA Collection. Science, 2002, 296, 141-145.	6.0	631
5	Comparative Genomics in Salt Tolerance between Arabidopsis and Arabidopsis-Related Halophyte Salt Cress Using Arabidopsis Microarray. Plant Physiology, 2004, 135, 1697-1709.	2.3	542
6	The AtGenExpress hormone and chemical treatment data set: experimental design, data evaluation, model data analysis and data access. Plant Journal, 2008, 55, 526-542.	2.8	467
7	Monitoring the expression pattern of around 7,000 Arabidopsis genes under ABA treatments using a full-length cDNA microarray. Functional and Integrative Genomics, 2002, 2, 282-291.	1.4	394
8	The AtGenExpress hormone- and chemical-treatment data set: Experimental design, data evaluation, model data analysis, and data access. Plant Journal, 2008, 55, 080414150319983.	2.8	307
9	RIKEN tandem mass spectral database (ReSpect) for phytochemicals: A plant-specific MS/MS-based data resource and database. Phytochemistry, 2012, 82, 38-45.	1.4	284
10	Widely Targeted Metabolomics Based on Large-Scale MS/MS Data for Elucidating Metabolite Accumulation Patterns in Plants. Plant and Cell Physiology, 2009, 50, 37-47.	1.5	264
11	Monitoring expression profiles ofArabidopsisgene expression during rehydration process after dehydration usingca. 7000 full-length cDNA microarray. Plant Journal, 2003, 34, 868-887.	2.8	263
12	Identification of Cis-Acting Promoter Elements in Cold- and Dehydration-Induced Transcriptional Pathways in Arabidopsis, Rice, and Soybean. DNA Research, 2012, 19, 37-49.	1.5	241
13	Genome-wide analysis of alternative pre-mRNA splicing in Arabidopsis thaliana based on full-length cDNA sequences. Nucleic Acids Research, 2004, 32, 5096-5103.	6.5	235
14	Curated genome annotation of Oryza sativa ssp. japonica and comparative genome analysis with Arabidopsis thaliana. Genome Research, 2007, 17, 175-183.	2.4	218
15	A collection of 11â€ƒ800 single-copyDstransposon insertion lines inArabidopsis. Plant Journal, 2004, 37, 897-905.	2.8	203
16	Identification of Arabidopsis Genes Regulated by High Lightâ€"Stress Using cDNA MicroarrayÂ¶. Photochemistry and Photobiology, 2003, 77, 226.	1.3	193
17	sORF finder: a program package to identify small open reading frames with high coding potential. Bioinformatics, 2010, 26, 399-400.	1.8	185
18	AtMetExpress Development: A Phytochemical Atlas of Arabidopsis Development Â. Plant Physiology, 2010, 152, 566-578.	2.3	161

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19	PRIMe: a Web site that assembles tools for metabolomics and transcriptomics. In Silico Biology, 2008, 8, 339-45.	0.4	149
20	Draft genome assembly and annotation of <i>Glycyrrhiza uralensis</i>, a medicinal legume. Plant Journal, 2017, 89, 181-194.	2.8	148
21	Identification of plant promoter constituents by analysis of local distribution of short sequences. BMC Genomics, 2007, 8, 67.	1.2	142
22	Monitoring expression profiles of Arabidopsis genes during cold acclimation and deacclimation using DNA microarrays. Functional and Integrative Genomics, 2006, 6, 212-234.	1.4	137
23	Monitoring the expression profiles of genes induced by hyperosmotic, high salinity, and oxidative stress and abscisic acid treatment in Arabidopsis cell culture using a full-length cDNA microarray. Plant Molecular Biology, 2004, 56, 29-55.	2.0	130
24	RARTF: Database and Tools for Complete Sets of Arabidopsis Transcription Factors. DNA Research, 2005, 12, 247-256.	1.5	130
25	RCH1, a Locus in Arabidopsis That Confers Resistance to the Hemibiotrophic Fungal Pathogen Colletotrichum higginsianum. Molecular Plant-Microbe Interactions, 2004, 17, 749-762.	1.4	123
26	Systematic approaches to using the FOX hunting system to identify useful rice genes. Plant Journal, 2009, 57, 883-894.	2.8	121
27	A trial of phenome analysis using 4000Ds-insertional mutants in gene-coding regions of Arabidopsis. Plant Journal, 2006, 47, 640-651.	2.8	110
28	A New Resource of Locally Transposed DissociationElements for Screening Gene-Knockout Lines in Silico on the Arabidopsis Genome. Plant Physiology, 2002, 129, 1695-1699.	2.3	103
29	A genome resource for green millet Setaria viridis enables discovery of agronomically valuable loci. Nature Biotechnology, 2020, 38, 1203-1210.	9.4	103
30	Transcriptome Analysis Using a High-Density Oligomicroarray under Drought Stress in Various Genotypes of Cassava: An Important Tropical Crop. DNA Research, 2012, 19, 335-345.	1.5	101
31	Heterogeneity of Arabidopsis core promoters revealed by high‐density TSS analysis. Plant Journal, 2009, 60, 350-362.	2.8	99
32	Sequencing and Analysis of Approximately 40 000 Soybean cDNA Clones from a Full-Length-Enriched cDNA Library. DNA Research, 2008, 15, 333-346.	1.5	98
33	RIKEN Arabidopsis full-length (RAFL) cDNA and its applications for expression profiling under abiotic stress conditions. Journal of Experimental Botany, 2003, 55, 213-223.	2.4	94
34	Sequencing analysis of 20,000 full-length cDNA clones from cassava reveals lineage specific expansions in gene families related to stress response. BMC Plant Biology, 2007, 7, 66.	1.6	91
35	Coupling Deep Transcriptome Analysis with Untargeted Metabolic Profiling in Ophiorrhiza pumila to Further the Understanding of the Biosynthesis of the Anti-Cancer Alkaloid Camptothecin and Anthraquinones. Plant and Cell Physiology, 2013, 54, 686-696.	1.5	88
36	In silico Analysis of Transcription Factor Repertoire and Prediction of Stress Responsive Transcription Factors in Soybean. DNA Research, 2009, 16, 353-369.	1.5	87

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37	Genome-Wide Analysis of Two-Component Systems and Prediction of Stress-Responsive Two-Component System Members in Soybean. DNA Research, 2010, 17, 303-324.	1.5	87
38	TriFLDB: A Database of Clustered Full-Length Coding Sequences from Triticeae with Applications to Comparative Grass Genomics Â Â. Plant Physiology, 2009, 150, 1135-1146.	2.3	86
39	The cDNA Microarray Analysis Using an Arabidopsis pad3 Mutant Reveals the Expression Profiles and Classification of Genes Induced by Alternaria brassicicola Attack. Plant and Cell Physiology, 2003, 44, 377-387.	1.5	83
40	Glycyrrhiza uralensis Transcriptome Landscape and Study of Phytochemicals. Plant and Cell Physiology, 2013, 54, 697-710.	1.5	80
41	Combination of Liquid Chromatographyâ€"Fourier Transform Ion Cyclotron Resonance-Mass Spectrometry with ^{13}C-Labeling for Chemical Assignment of Sulfur-Containing Metabolites in Onion Bulbs. Analytical Chemistry, 2013, 85, 1310-1315.	3.2	77
42	PRIMe Update: Innovative Content for Plant Metabolomics and Integration of Gene Expression and Metabolite Accumulation. Plant and Cell Physiology, 2013, 54, e5-e5.	1.5	76
43	RARGE: a large-scale database of RIKEN Arabidopsis resources ranging from transcriptome to phenome. Nucleic Acids Research, 2004, 33, D647-D650.	6.5	73
44	Global Landscape of a Co-Expressed Gene Network in Barley and its Application to Gene Discovery in Triticeae Crops. Plant and Cell Physiology, 2011, 52, 785-803.	1.5	73
45	RiceFOX: A Database of Arabidopsis Mutant Lines Overexpressing Rice Full-Length cDNA that Contains a Wide Range of Trait Information to Facilitate Analysis of Gene Function. Plant and Cell Physiology, 2011, 52, 265-273.	1.5	72
46	LegumeTFDB: an integrative database of Glycine max, Lotus japonicus and Medicago truncatula transcription factors. Bioinformatics, 2010, 26, 290-291.	1.8	70
47	A second generation framework for the analysis of microsatellites in expressed sequence tags and the development of EST-SSR markers for a conifer, Cryptomeria japonica. BMC Genomics, 2012, 13, 136.	1.2	69
48	ppdb: plant promoter database version 3.0. Nucleic Acids Research, 2014, 42, D1188-D1192.	6.5	61
49	The Chloroplast Function Database: a largeâ€scale collection of Arabidopsis Ds/Spm â€•or Tâ€ÐNAâ€tagged homozygous lines for nuclearâ€encoded chloroplast proteins, and their systematic phenotype analysis. Plant Journal, 2010, 61, 529-542.	2.8	60
50	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.	1.5	58
51	Large-scale collection and annotation of full-length enriched cDNAs from a model halophyte, Thellungiella halophila. BMC Plant Biology, 2008, 8, 115.	1.6	57
52	Expression Profiles of Arabidopsis Phospholipase A IIA Gene in Response to Biotic and Abiotic Stresses. Plant and Cell Physiology, 2003, 44, 1246-1252.	1.5	50
53	In Silico Analysis of Transcription Factor Repertoires and Prediction of Stress-Responsive Transcription Factors from Six Major Gramineae Plants. DNA Research, 2011, 18, 321-332.	1.5	48
54	Identification of Arabidopsis Genes Regulated by High Light-Stress Using cDNA MicroarrayÂ¶. Photochemistry and Photobiology, 2003, 77, 226-233.	1.3	46

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55	Genome-wide analysis reveals phytohormone action during cassava storage root initiation. Plant Molecular Biology, 2015, 88, 531-543.	2.0	46
56	UniVIO: A Multiple Omics Database with Hormonome and Transcriptome Data from Rice. Plant and Cell Physiology, 2013, 54, e9-e9.	1.5	42
57	Transcriptome analysis of hormone-induced gene expression in Brachypodium distachyon. Scientific Reports, 2015, 5, 14476.	1.6	39
58	Correlations between predicted protein disorder and post-translational modifications in plants. Bioinformatics, 2014, 30, 1095-1103.	1.8	36
59	Efficient and Heritable Targeted Mutagenesis in Mosses Using the CRISPR/Cas9 System. Plant and Cell Physiology, 2016, 57, 2600-2610.	1.5	35
60	The Chloroplast Function Database II: A Comprehensive Collection of Homozygous Mutants and Their Phenotypic/Genotypic Traits for Nuclear-Encoded Chloroplast Proteins. Plant and Cell Physiology, 2013, 54, e2-e2.	1.5	34
61	Determination of growth stages and metabolic profiles in <i>Brachypodium distachyon</i> for comparison of developmental context with Triticeae crops. Proceedings of the Royal Society B: Biological Sciences, 2015, 282, 20150964.	1.2	33
62	Functional annotation of 19,841 Populus nigra full-length enriched cDNA clones. BMC Genomics, 2007, 8, 448.	1.2	32
63	RARGE II: An Integrated Phenotype Database of Arabidopsis Mutant Traits Using a Controlled Vocabulary. Plant and Cell Physiology, 2014, 55, e4-e4.	1.5	32
64	Transcriptome analysis of thermogenic Arum concinnatum reveals the molecular components of floral scent production. Scientific Reports, 2015, 5, 8753.	1.6	31
65	Transcriptional alterations during proliferation and lignification in Phyllostachys nigra cells. Scientific Reports, 2018, 8, 11347.	1.6	30
66	Diurnal Transcriptome and Gene Network Represented through Sparse Modeling in Brachypodium distachyon. Frontiers in Plant Science, 2017, 8, 2055.	1.7	29
67	Cassava (Manihot esculenta) transcriptome analysis in response to infection by the fungus Colletotrichum gloeosporioides using an oligonucleotide-DNA microarray. Journal of Plant Research, 2016, 129, 711-726.	1.2	28
68	Chemical Assignment of Structural Isomers of Sulfur-Containing Metabolites in Garlic by Liquid Chromatographyâ˜Fourier Transform Ion Cyclotron Resonanceâ˜Mass Spectrometry. Journal of Nutrition, 2016, 146, 397S-402S.	1.3	28
69	Design of an optimal promoter involved in the heatâ€induced transcriptional pathway in Arabidopsis, soybean, rice and maize. Plant Journal, 2017, 89, 671-680.	2.8	28
70	Large-Scale Collection and Analysis of Full-Length cDNAs from Brachypodium distachyon and Integration with Pooideae Sequence Resources. PLoS ONE, 2013, 8, e75265.	1.1	27
71	Identification of Arabidopsis genic and nonâ€genic promoters by pairedâ€end sequencing of <scp>TSS</scp> tags. Plant Journal, 2017, 90, 587-605.	2.8	26
72	TreeTFDB: An Integrative Database of the Transcription Factors from Six Economically Important Tree Crops for Functional Predictions and Comparative and Functional Genomics. DNA Research, 2013, 20, 151-162.	1.5	25

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73	Analysis of single nucleotide polymorphisms based on RNA sequencing data of diverse bio-geographical accessions in barley. Scientific Reports, 2016, 6, 33199.	1.6	25
74	In Silico Analysis of Correlations between Protein Disorder and Post-Translational Modifications in Algae. International Journal of Molecular Sciences, 2015, 16, 19812-19835.	1.8	20
75	TriMEDB: A database to integrate transcribed markers and facilitate genetic studies of the tribe Triticeae. BMC Plant Biology, 2008, 8, 72.	1.6	18
76	Plant-PrAS: A Database of Physicochemical and Structural Properties and Novel Functional Regions in Plant Proteomes. Plant and Cell Physiology, 2015, 56, e11-e11.	1.5	15
77	Toward genome-wide metabolotyping and elucidation of metabolic system: metabolic profiling of large-scale bioresources. Journal of Plant Research, 2010, 123, 291-298.	1.2	13
78	RIKEN Cassava Initiative: Establishment of a Cassava Functional Genomics Platform. Tropical Plant Biology, 2012, 5, 110-116.	1.0	12
79	Genome-Wide Discovery and Information Resource Development of DNA Polymorphisms in Cassava. PLoS ONE, 2013, 8, e74056.	1.1	12
80	Bipolar Localization of Putative Photoreceptor Protein for Phototaxis in Thermophilic Cyanobacterium Synechococcus elongatus. Plant and Cell Physiology, 2002, 43, 1585-1588.	1.5	11
81	Alga-PrAS (Algal Protein Annotation Suite): A Database of Comprehensive Annotation in Algal Proteomes. Plant and Cell Physiology, 2017, 58, pcw212.	1.5	11
82	Metabolite/phytohormone–gene regulatory networks in soybean organs under dehydration conditions revealed by integration analysis. Plant Journal, 2020, 103, 197-211.	2.8	10
83	Content of intrinsic disorder influences the outcome of cell-free protein synthesis. Scientific Reports, 2015, 5, 14079.	1.6	9
84	A flexible representation of omic knowledge for thorough analysis of microarray data. Plant Methods, 2006, 2, 5.	1.9	8
85	Whole Transcriptome Analysis Using Next-Generation Sequencing of Sterile-Cultured Eisenia andrei for Immune System Research. PLoS ONE, 2015, 10, e0118587.	1.1	6
86	RIKEN Arabidopsis full-length cDNA database. Trends in Plant Science, 2002, 7, 562-563.	4.3	3
87	Development of Blade Cells and Rhizoid Cells Aseptically Isolated from the Multicellular Leafy Seaweed <i>Gayralia oxysperma</i>. Cytologia, 2022, 87, 17-22.	0.2	3
88	Genomic Analysis of Stress Respnse. , 0, , 248-265.		2
89	Draft Genome Sequence of Salinispora sp. Strain H7-4, Isolated from Deep-Sea Sediments of the Shikoku Basin. Microbiology Resource Announcements, 2020, 9, .	0.3	1