Tetsuya Sakurai

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

89	12,425	50	90
papers	citations	h-index	g-index
90	13,968	7.1	5.14
ext. papers	ext. citations	avg, IF	L-index

#	Paper	IF	Citations
89	Development of Blade Cells and Rhizoid Cells Aseptically Isolated from the Multicellular Leafy Seaweed <i>Gayralia oxysperma</i>. *Cytologia*, **2022**, 87, 17-22	0.9	1
88	Metabolite/phytohormone-gene regulatory networks in soybean organs under dehydration conditions revealed by integration analysis. *Plant Journal*, **2020**, 103, 197-211	6.9	5
87	A genome resource for green millet Setaria viridis enables discovery of agronomically valuable loci. *Nature Biotechnology*, **2020**, 38, 1203-1210	44.5	43
86	Transcriptional alterations during proliferation and lignification in Phyllostachys nigra cells. *Scientific Reports*, **2018**, 8, 11347	4.9	7
85	Identification of Arabidopsis genic and non-genic promoters by paired-end sequencing of TSS tags. *Plant Journal*, **2017**, 90, 587-605	6.9	14
84	Alga-PrAS (Algal Protein Annotation Suite): A Database of Comprehensive Annotation in Algal Proteomes. *Plant and Cell Physiology*, **2017**, 58, e6	4.9	8
83	Design of an optimal promoter involved in the heat-induced transcriptional pathway in Arabidopsis, soybean, rice and maize. *Plant Journal*, **2017**, 89, 671-680	6.9	16
82	Draft genome assembly and annotation of Glycyrrhiza uralensis, a medicinal legume. *Plant Journal*, **2017**, 89, 181-194	6.9	94
81	Diurnal Transcriptome and Gene Network Represented through Sparse Modeling in. *Frontiers in Plant Science*, **2017**, 8, 2055	6.2	9
80	Analysis of single nucleotide polymorphisms based on RNA sequencing data of diverse bio-geographical accessions in barley. *Scientific Reports*, **2016**, 6, 33199	4.9	10
79	Efficient and Heritable Targeted Mutagenesis in Mosses Using the CRISPR/Cas9 System. *Plant and Cell Physiology*, **2016**, 57, 2600-2610	4.9	24
78	Chemical Assignment of Structural Isomers of Sulfur-Containing Metabolites in Garlic by Liquid Chromatography-Fourier Transform Ion Cyclotron Resonance-Mass Spectrometry. *Journal of Nutrition*, **2016**, 146, 397S-402S	4.1	24
77	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	2.6	21
76	Genome-wide analysis reveals phytohormone action during cassava storage root initiation. *Plant Molecular Biology*, **2015**, 88, 531-43	4.6	29
75	Transcriptome analysis of thermogenic Arum concinnatum reveals the molecular components of floral scent production. *Scientific Reports*, **2015**, 5, 8753	4.9	21
74	Transcriptome analysis of hormone-induced gene expression in Brachypodium distachyon. *Scientific Reports*, **2015**, 5, 14476	4.9	31
73	Content of intrinsic disorder influences the outcome of cell-free protein synthesis. *Scientific Reports*, **2015**, 5, 14079	4.9	7

(2012-2015)

72	In Silico Analysis of Correlations between Protein Disorder and Post-Translational Modifications in Algae. *International Journal of Molecular Sciences*, **2015**, 16, 19812-35	6.3	16
71	Whole transcriptome analysis using next-generation sequencing of sterile-cultured Eisenia andrei for immune system research. *PLoS ONE*, **2015**, 10, e0118587	3.7	5
70	Plant-PrAS: a database of physicochemical and structural properties and novel functional regions in plant proteomes. *Plant and Cell Physiology*, **2015**, 56, e11	4.9	13
69	Determination of growth stages and metabolic profiles in Brachypodium distachyon for comparison of developmental context with Triticeae crops. *Proceedings of the Royal Society B: Biological Sciences*, **2015**, 282,	4.4	16
68	ppdb: plant promoter database version 3.0. *Nucleic Acids Research*, **2014**, 42, D1188-92	20.1	50
67	Correlations between predicted protein disorder and post-translational modifications in plants. *Bioinformatics*, **2014**, 30, 1095-1103	7.2	31
66	RARGE II: an integrated phenotype database of Arabidopsis mutant traits using a controlled vocabulary. *Plant and Cell Physiology*, **2014**, 55, e4	4.9	19
65	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, 686-96	4.9	67
64	Combination of liquid chromatography-Fourier transform ion cyclotron resonance-mass spectrometry with 13C-labeling for chemical assignment of sulfur-containing metabolites in onion bulbs. *Analytical Chemistry*, **2013**, 85, 1310-5	7.8	68
63	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	4.9	27
62	PRIMe Update: innovative content for plant metabolomics and integration of gene expression and metabolite accumulation. *Plant and Cell Physiology*, **2013**, 54, e5	4.9	72
61	UniVIO: a multiple omics database with hormonome and transcriptome data from rice. *Plant and Cell Physiology*, **2013**, 54, e9	4.9	31
60	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, 151-62	4.5	23
59	Glycyrrhiza uralensis transcriptome landscape and study of phytochemicals. *Plant and Cell Physiology*, **2013**, 54, 697-710	4.9	62
58	Genome-wide discovery and information resource development of DNA polymorphisms in cassava. *PLoS ONE*, **2013**, 8, e74056	3.7	10
57	Large-scale collection and analysis of full-length cDNAs from Brachypodium distachyon and integration with Pooideae sequence resources. *PLoS ONE*, **2013**, 8, e75265	3.7	25
56	Identification of cis-acting promoter elements in cold- and dehydration-induced transcriptional pathways in Arabidopsis, rice, and soybean. *DNA Research*, **2012**, 19, 37-49	4.5	183
55	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	4.5	54

54	RIKEN tandem mass spectral database (ReSpect) for phytochemicals: a plant-specific MS/MS-based data resource and database. *Phytochemistry*, **2012**, 82, 38-45	4	214
53	RIKEN Cassava Initiative: Establishment of a Cassava Functional Genomics Platform. *Tropical Plant Biology*, **2012**, 5, 110-116	1.6	9
52	Transcriptome analysis using a high-density oligomicroarray under drought stress in various genotypes of cassava: an important tropical crop. *DNA Research*, **2012**, 19, 335-45	4.5	79
51	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, 265-73	4.9	55
50	In silico analysis of transcription factor repertoires and prediction of stress-responsive transcription factors from six major gramineae plants. *DNA Research*, **2011**, 18, 321-32	4.5	38
49	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	4.9	55
48	Genome sequence of the palaeopolyploid soybean. *Nature*, **2010**, 463, 178-83	50.4	2997
47	The Chloroplast Function Database: a large-scale collection of Arabidopsis Ds/Spm- or T-DNA-tagged homozygous lines for nuclear-encoded chloroplast proteins, and their systematic phenotype analysis. *Plant Journal*, **2010**, 61, 529-42	6.9	54
46	LegumeTFDB: an integrative database of Glycine max, Lotus japonicus and Medicago truncatula transcription factors. *Bioinformatics*, **2010**, 26, 290-1	7.2	66
45	AtMetExpress development: a phytochemical atlas of Arabidopsis development. *Plant Physiology*, **2010**, 152, 566-78	6.6	149
44	sORF finder: a program package to identify small open reading frames with high coding potential. *Bioinformatics*, **2010**, 26, 399-400	7.2	130
43	Genome-wide analysis of two-component systems and prediction of stress-responsive two-component system members in soybean. *DNA Research*, **2010**, 17, 303-24	4.5	63
42	Toward genome-wide metabolotyping and elucidation of metabolic system: metabolic profiling of large-scale bioresources. *Journal of Plant Research*, **2010**, 123, 291-8	2.6	13
41	In silico analysis of transcription factor repertoire and prediction of stress responsive transcription factors in soybean. *DNA Research*, **2009**, 16, 353-69	4.5	76
40	Systematic approaches to using the FOX hunting system to identify useful rice genes. *Plant Journal*, **2009**, 57, 883-94	6.9	99
39	Heterogeneity of Arabidopsis core promoters revealed by high-density TSS analysis. *Plant Journal*, **2009**, 60, 350-62	6.9	81
38	TriFLDB: a database of clustered full-length coding sequences from Triticeae with applications to comparative grass genomics. *Plant Physiology*, **2009**, 150, 1135-46	6.6	80
37	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	4.9	205

36	The AtGenExpress hormone and chemical treatment data set: experimental design, data evaluation, model data analysis and data access. *Plant Journal*, **2008**, 55, 526-542	6.9	383
35	Large-scale collection and annotation of full-length enriched cDNAs from a model halophyte, Thellungiella halophila. *BMC Plant Biology*, **2008**, 8, 115	5.3	52
34	TriMEDB: a database to integrate transcribed markers and facilitate genetic studies of the tribe Triticeae. *BMC Plant Biology*, **2008**, 8, 72	5.3	16
33	Sequencing and analysis of approximately 40,000 soybean cDNA clones from a full-length-enriched cDNA library. *DNA Research*, **2008**, 15, 333-46	4.5	86
32	The AtGenExpress hormone and chemical treatment data set: experimental design, data evaluation, model data analysis and data access. *Plant Journal*, **2008**, 55, 526-42	6.9	238
31	PRIMe: a Web site that assembles tools for metabolomics and transcriptomics. *In Silico Biology*, **2008**, 8, 339-45	2	141
30	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	5.3	78
29	Identification of plant promoter constituents by analysis of local distribution of short sequences. *BMC Genomics*, **2007**, 8, 67	4.5	117
28	Curated genome annotation of Oryza sativa ssp. japonica and comparative genome analysis with Arabidopsis thaliana. *Genome Research*, **2007**, 17, 175-83	9.7	200
27	Functional annotation of 19,841 Populus nigra full-length enriched cDNA clones. *BMC Genomics*, **2007**, 8, 448	4.5	31
26	A flexible representation of omic knowledge for thorough analysis of microarray data. *Plant Methods*, **2006**, 2, 5	5.8	8
25	A trial of phenome analysis using 4000 Ds-insertional mutants in gene-coding regions of Arabidopsis. *Plant Journal*, **2006**, 47, 640-51	6.9	96
24	Monitoring expression profiles of Arabidopsis genes during cold acclimation and deacclimation using DNA microarrays. *Functional and Integrative Genomics*, **2006**, 6, 212-34	3.8	118
23	RARGE: a large-scale database of RIKEN Arabidopsis resources ranging from transcriptome to phenome. *Nucleic Acids Research*, **2005**, 33, D647-50	20.1	66
22	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, 1149-53	4.9	52
21	RARTF: database and tools for complete sets of Arabidopsis transcription factors. *DNA Research*, **2005**, 12, 247-56	4.5	115
20	A collection of 11 800 single-copy Ds transposon insertion lines in Arabidopsis. *Plant Journal*, **2004**, 37, 897-905	6.9	183
19	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	4.6	115

18	Comparative genomics in salt tolerance between Arabidopsis and aRabidopsis-related halophyte salt cress using Arabidopsis microarray. *Plant Physiology*, **2004**, 135, 1697-709	6.6	497
17	Genome-wide analysis of alternative pre-mRNA splicing in Arabidopsis thaliana based on full-length cDNA sequences. *Nucleic Acids Research*, **2004**, 32, 5096-103	20.1	195
16	RIKEN Arabidopsis full-length (RAFL) cDNA and its applications for expression profiling under abiotic stress conditions. *Journal of Experimental Botany*, **2004**, 55, 213-23	7	72
15	RCH1, a locus in Arabidopsis that confers resistance to the hemibiotrophic fungal pathogen Colletotrichum higginsianum. *Molecular Plant-Microbe Interactions*, **2004**, 17, 749-62	3.6	93
14	Expression profiles of Arabidopsis phospholipase A IIA gene in response to biotic and abiotic stresses. *Plant and Cell Physiology*, **2003**, 44, 1246-52	4.9	47
13	Identification of Arabidopsis genes regulated by high light-stress using cDNA microarray. *Photochemistry and Photobiology*, **2003**, 77, 226-33	3.6	166
12	Identification of Arabidopsis Genes Regulated by High LightStress Using cDNA Microarray¶. *Photochemistry and Photobiology*, **2003**, 77, 226-233	3.6	23
11	Monitoring expression profiles of Arabidopsis gene expression during rehydration process after dehydration using ca 7000 full-length cDNA microarray. *Plant Journal*, **2003**, 34, 868-87	6.9	223
10	Empirical analysis of transcriptional activity in the Arabidopsis genome. *Science*, **2003**, 302, 842-6	33.3	782
9	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, 377-87	4.9	76
8	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, 282-91	3.8	353
7	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, 279-92	6.9	1501
6	A new resource of locally transposed Dissociation elements for screening gene-knockout lines in silico on the Arabidopsis genome. *Plant Physiology*, **2002**, 129, 1695-9	6.6	91
5	Bipolar localization of putative photoreceptor protein for phototaxis in thermophilic cyanobacterium Synechococcus elongatus. *Plant and Cell Physiology*, **2002**, 43, 1585-8	4.9	10
4	Functional annotation of a full-length Arabidopsis cDNA collection. *Science*, **2002**, 296, 141-5	33.3	588
3	RIKEN Arabidopsis full-length cDNA database. *Trends in Plant Science*, **2002**, 7, 562-563	13.1	3
2	Genomic Analysis of Stress Respnse248-265		2
1	The Setaria viridis genome and diversity panel enables discovery of a novel domestication gene		9