

# Tetsuya Sakurai

## List of Publications by Citations

**Source:** <https://exaly.com/author-pdf/8161040/tetsuya-sakurai-publications-by-citations.pdf>

**Version:** 2024-04-25

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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

89  
papers

12,425  
citations

50  
h-index

90  
g-index

90  
ext. papers

13,968  
ext. citations

7.1  
avg, IF

5.14  
L-index

#	Paper	IF	Citations
89	Genome sequence of the palaeopolyploid soybean. <i>Nature</i> , <b>2010</b> , 463, 178-83	50.4	2997
88	Monitoring the expression profiles of 7000 Arabidopsis genes under drought, cold and high-salinity stresses using a full-length cDNA microarray. <i>Plant Journal</i> , <b>2002</b> , 31, 279-92	6.9	1501
87	Empirical analysis of transcriptional activity in the Arabidopsis genome. <i>Science</i> , <b>2003</b> , 302, 842-6	33.3	782
86	Functional annotation of a full-length Arabidopsis cDNA collection. <i>Science</i> , <b>2002</b> , 296, 141-5	33.3	588
85	Comparative genomics in salt tolerance between Arabidopsis and aRabidopsis-related halophyte salt cress using Arabidopsis microarray. <i>Plant Physiology</i> , <b>2004</b> , 135, 1697-709	6.6	497
84	The AtGenExpress hormone and chemical treatment data set: experimental design, data evaluation, model data analysis and data access. <i>Plant Journal</i> , <b>2008</b> , 55, 526-542	6.9	383
83	Monitoring the expression pattern of around 7,000 Arabidopsis genes under ABA treatments using a full-length cDNA microarray. <i>Functional and Integrative Genomics</i> , <b>2002</b> , 2, 282-91	3.8	353
82	The AtGenExpress hormone and chemical treatment data set: experimental design, data evaluation, model data analysis and data access. <i>Plant Journal</i> , <b>2008</b> , 55, 526-42	6.9	238
81	Monitoring expression profiles of Arabidopsis gene expression during rehydration process after dehydration using ca 7000 full-length cDNA microarray. <i>Plant Journal</i> , <b>2003</b> , 34, 868-87	6.9	223
80	RIKEN tandem mass spectral database (ReSpect) for phytochemicals: a plant-specific MS/MS-based data resource and database. <i>Phytochemistry</i> , <b>2012</b> , 82, 38-45	4	214
79	Widely targeted metabolomics based on large-scale MS/MS data for elucidating metabolite accumulation patterns in plants. <i>Plant and Cell Physiology</i> , <b>2009</b> , 50, 37-47	4.9	205
78	Curated genome annotation of Oryza sativa ssp. japonica and comparative genome analysis with Arabidopsis thaliana. <i>Genome Research</i> , <b>2007</b> , 17, 175-83	9.7	200
77	Genome-wide analysis of alternative pre-mRNA splicing in Arabidopsis thaliana based on full-length cDNA sequences. <i>Nucleic Acids Research</i> , <b>2004</b> , 32, 5096-103	20.1	195
76	Identification of cis-acting promoter elements in cold- and dehydration-induced transcriptional pathways in Arabidopsis, rice, and soybean. <i>DNA Research</i> , <b>2012</b> , 19, 37-49	4.5	183
75	A collection of 11 800 single-copy Ds transposon insertion lines in Arabidopsis. <i>Plant Journal</i> , <b>2004</b> , 37, 897-905	6.9	183
74	Identification of Arabidopsis genes regulated by high light-stress using cDNA microarray. <i>Photochemistry and Photobiology</i> , <b>2003</b> , 77, 226-33	3.6	166
73	AtMetExpress development: a phytochemical atlas of Arabidopsis development. <i>Plant Physiology</i> , <b>2010</b> , 152, 566-78	6.6	149

72	PRIME: a Web site that assembles tools for metabolomics and transcriptomics. <i>In Silico Biology</i> , <b>2008</b> , 8, 339-45	2	141
71	sORF finder: a program package to identify small open reading frames with high coding potential. <i>Bioinformatics</i> , <b>2010</b> , 26, 399-400	7.2	130
70	Monitoring expression profiles of Arabidopsis genes during cold acclimation and deacclimation using DNA microarrays. <i>Functional and Integrative Genomics</i> , <b>2006</b> , 6, 212-34	3.8	118
69	Identification of plant promoter constituents by analysis of local distribution of short sequences. <i>BMC Genomics</i> , <b>2007</b> , 8, 67	4.5	117
68	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. <i>Plant Molecular Biology</i> , <b>2004</b> , 56, 29-55	4.6	115
67	RARTF: database and tools for complete sets of Arabidopsis transcription factors. <i>DNA Research</i> , <b>2005</b> , 12, 247-56	4.5	115
66	Systematic approaches to using the FOX hunting system to identify useful rice genes. <i>Plant Journal</i> , <b>2009</b> , 57, 883-94	6.9	99
65	A trial of phenome analysis using 4000 Ds-insertional mutants in gene-coding regions of Arabidopsis. <i>Plant Journal</i> , <b>2006</b> , 47, 640-51	6.9	96
64	Draft genome assembly and annotation of Glycyrrhiza uralensis, a medicinal legume. <i>Plant Journal</i> , <b>2017</b> , 89, 181-194	6.9	94
63	RCH1, a locus in Arabidopsis that confers resistance to the hemibiotrophic fungal pathogen Colletotrichum higginsianum. <i>Molecular Plant-Microbe Interactions</i> , <b>2004</b> , 17, 749-62	3.6	93
62	A new resource of locally transposed Dissociation elements for screening gene-knockout lines in silico on the Arabidopsis genome. <i>Plant Physiology</i> , <b>2002</b> , 129, 1695-9	6.6	91
61	Sequencing and analysis of approximately 40,000 soybean cDNA clones from a full-length-enriched cDNA library. <i>DNA Research</i> , <b>2008</b> , 15, 333-46	4.5	86
60	Heterogeneity of Arabidopsis core promoters revealed by high-density TSS analysis. <i>Plant Journal</i> , <b>2009</b> , 60, 350-62	6.9	81
59	TriFLDB: a database of clustered full-length coding sequences from Triticeae with applications to comparative grass genomics. <i>Plant Physiology</i> , <b>2009</b> , 150, 1135-46	6.6	80
58	Transcriptome analysis using a high-density oligomicroarray under drought stress in various genotypes of cassava: an important tropical crop. <i>DNA Research</i> , <b>2012</b> , 19, 335-45	4.5	79
57	Sequencing analysis of 20,000 full-length cDNA clones from cassava reveals lineage specific expansions in gene families related to stress response. <i>BMC Plant Biology</i> , <b>2007</b> , 7, 66	5.3	78
56	In silico analysis of transcription factor repertoire and prediction of stress responsive transcription factors in soybean. <i>DNA Research</i> , <b>2009</b> , 16, 353-69	4.5	76
55	The cDNA microarray analysis using an Arabidopsis pad3 mutant reveals the expression profiles and classification of genes induced by Alternaria brassicicola attack. <i>Plant and Cell Physiology</i> , <b>2003</b> , 44, 377-87	4.9	76

54	PRIME Update: innovative content for plant metabolomics and integration of gene expression and metabolite accumulation. <i>Plant and Cell Physiology</i> , <b>2013</b> , 54, e5	4.9	72
53	RIKEN Arabidopsis full-length (RAFL) cDNA and its applications for expression profiling under abiotic stress conditions. <i>Journal of Experimental Botany</i> , <b>2004</b> , 55, 213-23	7	72
52	Combination of liquid chromatography-Fourier transform ion cyclotron resonance-mass spectrometry with <sup>13</sup> C-labeling for chemical assignment of sulfur-containing metabolites in onion bulbs. <i>Analytical Chemistry</i> , <b>2013</b> , 85, 1310-5	7.8	68
51	Coupling deep transcriptome analysis with untargeted metabolic profiling in <i>Ophiorrhiza pumila</i> to further the understanding of the biosynthesis of the anti-cancer alkaloid camptothecin and anthraquinones. <i>Plant and Cell Physiology</i> , <b>2013</b> , 54, 686-96	4.9	67
50	LegumeTFDB: an integrative database of Glycine max, Lotus japonicus and Medicago truncatula transcription factors. <i>Bioinformatics</i> , <b>2010</b> , 26, 290-1	7.2	66
49	RARGE: a large-scale database of RIKEN Arabidopsis resources ranging from transcriptome to phenome. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, D647-50	20.1	66
48	Genome-wide analysis of two-component systems and prediction of stress-responsive two-component system members in soybean. <i>DNA Research</i> , <b>2010</b> , 17, 303-24	4.5	63
47	<i>Glycyrrhiza uralensis</i> transcriptome landscape and study of phytochemicals. <i>Plant and Cell Physiology</i> , <b>2013</b> , 54, 697-710	4.9	62
46	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. <i>Plant and Cell Physiology</i> , <b>2011</b> , 52, 265-73	4.9	55
45	Global landscape of a co-expressed gene network in barley and its application to gene discovery in Triticeae crops. <i>Plant and Cell Physiology</i> , <b>2011</b> , 52, 785-803	4.9	55
44	A second generation framework for the analysis of microsatellites in expressed sequence tags and the development of EST-SSR markers for a conifer, <i>Cryptomeria japonica</i> . <i>BMC Genomics</i> , <b>2012</b> , 13, 136	4.5	54
43	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. <i>Plant Journal</i> , <b>2010</b> , 61, 529-42	6.9	54
42	Large-scale collection and annotation of full-length enriched cDNAs from a model halophyte, <i>Thellungiella halophila</i> . <i>BMC Plant Biology</i> , <b>2008</b> , 8, 115	5.3	52
41	A resource of 5,814 dissociation transposon-tagged and sequence-indexed lines of Arabidopsis transposed from start loci on chromosome 5. <i>Plant and Cell Physiology</i> , <b>2005</b> , 46, 1149-53	4.9	52
40	ppdb: plant promoter database version 3.0. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, D1188-92	20.1	50
39	Expression profiles of Arabidopsis phospholipase A IIA gene in response to biotic and abiotic stresses. <i>Plant and Cell Physiology</i> , <b>2003</b> , 44, 1246-52	4.9	47
38	A genome resource for green millet <i>Setaria viridis</i> enables discovery of agronomically valuable loci. <i>Nature Biotechnology</i> , <b>2020</b> , 38, 1203-1210	44.5	43
37	In silico analysis of transcription factor repertoires and prediction of stress-responsive transcription factors from six major gramineae plants. <i>DNA Research</i> , <b>2011</b> , 18, 321-32	4.5	38

36	Transcriptome analysis of hormone-induced gene expression in <i>Brachypodium distachyon</i> . <i>Scientific Reports</i> , <b>2015</b> , 5, 14476	4.9	31
35	Correlations between predicted protein disorder and post-translational modifications in plants. <i>Bioinformatics</i> , <b>2014</b> , 30, 1095-1103	7.2	31
34	UniVIO: a multiple omics database with hormone and transcriptome data from rice. <i>Plant and Cell Physiology</i> , <b>2013</b> , 54, e9	4.9	31
33	Functional annotation of 19,841 <i>Populus nigra</i> full-length enriched cDNA clones. <i>BMC Genomics</i> , <b>2007</b> , 8, 448	4.5	31
32	Genome-wide analysis reveals phytohormone action during cassava storage root initiation. <i>Plant Molecular Biology</i> , <b>2015</b> , 88, 531-43	4.6	29
31	The Chloroplast Function Database II: a comprehensive collection of homozygous mutants and their phenotypic/genotypic traits for nuclear-encoded chloroplast proteins. <i>Plant and Cell Physiology</i> , <b>2013</b> , 54, e2	4.9	27
30	Large-scale collection and analysis of full-length cDNAs from <i>Brachypodium distachyon</i> and integration with Pooideae sequence resources. <i>PLoS ONE</i> , <b>2013</b> , 8, e75265	3.7	25
29	Efficient and Heritable Targeted Mutagenesis in Mosses Using the CRISPR/Cas9 System. <i>Plant and Cell Physiology</i> , <b>2016</b> , 57, 2600-2610	4.9	24
28	Chemical Assignment of Structural Isomers of Sulfur-Containing Metabolites in Garlic by Liquid Chromatography-Fourier Transform Ion Cyclotron Resonance-Mass Spectrometry. <i>Journal of Nutrition</i> , <b>2016</b> , 146, 397S-402S	4.1	24
27	TreeTFDB: an integrative database of the transcription factors from six economically important tree crops for functional predictions and comparative and functional genomics. <i>DNA Research</i> , <b>2013</b> , 20, 151-62	4.5	23
26	Identification of Arabidopsis Genes Regulated by High Light Stress Using cDNA Microarray. <i>Photochemistry and Photobiology</i> , <b>2003</b> , 77, 226-233	3.6	23
25	Transcriptome analysis of thermogenic <i>Arum concinatum</i> reveals the molecular components of floral scent production. <i>Scientific Reports</i> , <b>2015</b> , 5, 8753	4.9	21
24	Cassava ( <i>Manihot esculenta</i> ) transcriptome analysis in response to infection by the fungus <i>Colletotrichum gloeosporioides</i> using an oligonucleotide-DNA microarray. <i>Journal of Plant Research</i> , <b>2016</b> , 129, 711-726	2.6	21
23	RARGE II: an integrated phenotype database of Arabidopsis mutant traits using a controlled vocabulary. <i>Plant and Cell Physiology</i> , <b>2014</b> , 55, e4	4.9	19
22	Design of an optimal promoter involved in the heat-induced transcriptional pathway in Arabidopsis, soybean, rice and maize. <i>Plant Journal</i> , <b>2017</b> , 89, 671-680	6.9	16
21	In Silico Analysis of Correlations between Protein Disorder and Post-Translational Modifications in Algae. <i>International Journal of Molecular Sciences</i> , <b>2015</b> , 16, 19812-35	6.3	16
20	Determination of growth stages and metabolic profiles in <i>Brachypodium distachyon</i> for comparison of developmental context with Triticeae crops. <i>Proceedings of the Royal Society B: Biological Sciences</i> , <b>2015</b> , 282,	4.4	16
19	TriMEDB: a database to integrate transcribed markers and facilitate genetic studies of the tribe Triticeae. <i>BMC Plant Biology</i> , <b>2008</b> , 8, 72	5.3	16

18	Identification of Arabidopsis genic and non-genic promoters by paired-end sequencing of TSS tags. <i>Plant Journal</i> , <b>2017</b> , 90, 587-605	6.9	14
17	Plant-PrAS: a database of physicochemical and structural properties and novel functional regions in plant proteomes. <i>Plant and Cell Physiology</i> , <b>2015</b> , 56, e11	4.9	13
16	Toward genome-wide metabolotyping and elucidation of metabolic system: metabolic profiling of large-scale bioresources. <i>Journal of Plant Research</i> , <b>2010</b> , 123, 291-8	2.6	13
15	Analysis of single nucleotide polymorphisms based on RNA sequencing data of diverse bio-geographical accessions in barley. <i>Scientific Reports</i> , <b>2016</b> , 6, 33199	4.9	10
14	Genome-wide discovery and information resource development of DNA polymorphisms in cassava. <i>PLoS ONE</i> , <b>2013</b> , 8, e74056	3.7	10
13	Bipolar localization of putative photoreceptor protein for phototaxis in thermophilic cyanobacterium <i>Synechococcus elongatus</i> . <i>Plant and Cell Physiology</i> , <b>2002</b> , 43, 1585-8	4.9	10
12	Diurnal Transcriptome and Gene Network Represented through Sparse Modeling in. <i>Frontiers in Plant Science</i> , <b>2017</b> , 8, 2055	6.2	9
11	RIKEN Cassava Initiative: Establishment of a Cassava Functional Genomics Platform. <i>Tropical Plant Biology</i> , <b>2012</b> , 5, 110-116	1.6	9
10	The <i>Setaria viridis</i> genome and diversity panel enables discovery of a novel domestication gene		9
9	Alga-PrAS (Algal Protein Annotation Suite): A Database of Comprehensive Annotation in Algal Proteomes. <i>Plant and Cell Physiology</i> , <b>2017</b> , 58, e6	4.9	8
8	A flexible representation of omic knowledge for thorough analysis of microarray data. <i>Plant Methods</i> , <b>2006</b> , 2, 5	5.8	8
7	Transcriptional alterations during proliferation and lignification in <i>Phyllostachys nigra</i> cells. <i>Scientific Reports</i> , <b>2018</b> , 8, 11347	4.9	7
6	Content of intrinsic disorder influences the outcome of cell-free protein synthesis. <i>Scientific Reports</i> , <b>2015</b> , 5, 14079	4.9	7
5	Metabolite/phytohormone-gene regulatory networks in soybean organs under dehydration conditions revealed by integration analysis. <i>Plant Journal</i> , <b>2020</b> , 103, 197-211	6.9	5
4	Whole transcriptome analysis using next-generation sequencing of sterile-cultured <i>Eisenia andrei</i> for immune system research. <i>PLoS ONE</i> , <b>2015</b> , 10, e0118587	3.7	5
3	RIKEN Arabidopsis full-length cDNA database. <i>Trends in Plant Science</i> , <b>2002</b> , 7, 562-563	13.1	3
2	Genomic Analysis of Stress Response		2
1	Development of Blade Cells and Rhizoid Cells Aseptically Isolated from the Multicellular Leafy Seaweed <i>Gayralia oxysperma</i>. <i>Cytologia</i> , <b>2022</b> , 87, 17-22	0.9	1

