

# Atsushi Fukushima

## List of Publications by Year in descending order

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65  
papers

4,612  
citations

101543

36  
h-index

106344

65  
g-index

66  
all docs

66  
docs citations

66  
times ranked

6462  
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcript Profiling of an Arabidopsis PSEUDO RESPONSE REGULATOR Arrhythmic Triple Mutant Reveals a Role for the Circadian Clock in Cold Stress Response. <i>Plant and Cell Physiology</i> , 2009, 50, 447-462.	3.1	249
2	Metabolomics reveals comprehensive reprogramming involving two independent metabolic responses of Arabidopsis to UV-B light. <i>Plant Journal</i> , 2011, 67, 354-369.	5.7	249
3	Acetate-mediated novel survival strategy against drought in plants. <i>Nature Plants</i> , 2017, 3, 17097.	9.3	232
4	Impact of clock-associated <i>Arabidopsis</i> pseudo-response regulators in metabolic coordination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 7251-7256.	7.1	228
5	Metabolomic correlation-network modules in Arabidopsis based on a graph-clustering approach. <i>BMC Systems Biology</i> , 2011, 5, 1.	3.0	215
6	Integrated omics approaches in plant systems biology. <i>Current Opinion in Chemical Biology</i> , 2009, 13, 532-538.	6.1	201
7	Metabolomic approaches toward understanding nitrogen metabolism in plants. <i>Journal of Experimental Botany</i> , 2011, 62, 1439-1453.	4.8	198
8	Compensation for Systematic Cross-Contribution Improves Normalization of Mass Spectrometry Based Metabolomics Data. <i>Analytical Chemistry</i> , 2009, 81, 7974-7980.	6.5	173
9	Application of a metabolomic method combining one-dimensional and two-dimensional gas chromatography-time-of-flight/mass spectrometry to metabolic phenotyping of natural variants in rice. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2007, 855, 71-79.	2.3	169
10	DiffCorr: An R package to analyze and visualize differential correlations in biological networks. <i>Gene</i> , 2013, 518, 209-214.	2.2	168
11	Two glycosyltransferases involved in anthocyanin modification delineated by transcriptome independent component analysis in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2012, 69, 154-167.	5.7	164
12	Physiological Roles of the $\beta$ -Substituted Alanine Synthase Gene Family in Arabidopsis. <i>Plant Physiology</i> , 2008, 146, 310-320.	4.8	161
13	Metabolomics data reveal a crucial role of cytosolic glutamine synthetase 1;1 in coordinating metabolic balance in rice. <i>Plant Journal</i> , 2011, 66, 456-466.	5.7	133
14	Using Metabolomic Approaches to Explore Chemical Diversity in Rice. <i>Molecular Plant</i> , 2015, 8, 58-67.	8.3	119
15	Unbiased characterization of genotype-dependent metabolic regulations by metabolomic approach in <i>Arabidopsis thaliana</i> . <i>BMC Systems Biology</i> , 2007, 1, 53.	3.0	116
16	Covering Chemical Diversity of Genetically-Modified Tomatoes Using Metabolomics for Objective Substantial Equivalence Assessment. <i>PLoS ONE</i> , 2011, 6, e16989.	2.5	110
17	Light Controls Protein Localization through Phytochrome-Mediated Alternative Promoter Selection. <i>Cell</i> , 2017, 171, 1316-1325.e12.	28.9	99
18	Antagonistic regulation of the gibberellic acid response during stem growth in rice. <i>Nature</i> , 2020, 584, 109-114.	27.8	98

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19	Metabolomic Screening Applied to Rice FOX Arabidopsis Lines Leads to the Identification of a Gene-Changing Nitrogen Metabolism. <i>Molecular Plant</i> , 2010, 3, 125-142.	8.3	87
20	Metabolic Reprogramming in Leaf Lettuce Grown Under Different Light Quality and Intensity Conditions Using Narrow-Band LEDs. <i>Scientific Reports</i> , 2018, 8, 7914.	3.3	77
21	HEAT INDUCIBLE LIPASE1 Remodels Chloroplastic Monogalactosyldiacylglycerol by Liberating $\pm$ -Linolenic Acid in Arabidopsis Leaves under Heat Stress. <i>Plant Cell</i> , 2018, 30, 1887-1905.	6.6	71
22	Recent Progress in the Development of Metabolome Databases for Plant Systems Biology. <i>Frontiers in Plant Science</i> , 2013, 4, 73.	3.6	68
23	Exploring Tomato Gene Functions Based on Coexpression Modules Using Graph Clustering and Differential Coexpression Approaches. <i>Plant Physiology</i> , 2012, 158, 1487-1502.	4.8	63
24	Effects of molybdenum deficiency and defects in molybdate transporter MOT1 on transcript accumulation and nitrogen/sulphur metabolism in Arabidopsis thaliana. <i>Journal of Experimental Botany</i> , 2011, 62, 1483-1497.	4.8	55
25	Integrated network analysis and effective tools in plant systems biology. <i>Frontiers in Plant Science</i> , 2014, 5, 598.	3.6	55
26	Periodicity in prokaryotic and eukaryotic genomes identified by power spectrum analysis. <i>Gene</i> , 2002, 300, 203-211.	2.2	54
27	Transcriptional and metabolic programs following exposure of plants to UV-B irradiation. <i>Plant Signaling and Behavior</i> , 2011, 6, 1987-1992.	2.4	54
28	A network perspective on nitrogen metabolism from model to crop plants using integrated omics approaches. <i>Journal of Experimental Botany</i> , 2014, 65, 5619-5630.	4.8	54
29	Lack of cytosolic glutamine synthetase1;2 in vascular tissues of axillary buds causes severe reduction in their outgrowth and disorder of metabolic balance in rice seedlings. <i>Plant Journal</i> , 2015, 81, 347-356.	5.7	53
30	Third DWF1 paralog in Solanaceae, sterol <sup>24</sup> -isomerase, branches withanolide biosynthesis from the general phytosterol pathway. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E8096-E8103.	7.1	51
31	Transcriptome data modeling for targeted plant metabolic engineering. <i>Current Opinion in Biotechnology</i> , 2013, 24, 285-290.	6.6	50
32	Metabolomic Characterization of Knockout Mutants in Arabidopsis: Development of a Metabolite Profiling Database for Knockout Mutants in Arabidopsis. <i>Plant Physiology</i> , 2014, 165, 948-961.	4.8	49
33	Integrated analysis of transcriptome and metabolome of Arabidopsis albino or pale green mutants with disrupted nuclear-encoded chloroplast proteins. <i>Plant Molecular Biology</i> , 2014, 85, 411-428.	3.9	48
34	Assessing metabolomic and chemical diversity of a soybean lineage representing 35 years of breeding. <i>Metabolomics</i> , 2015, 11, 261-270.	3.0	48
35	High-Throughput Sequencing and De Novo Assembly of Red and Green Forms of the <i>Perilla frutescens</i> var. <i>crispa</i> Transcriptome. <i>PLoS ONE</i> , 2015, 10, e0129154.	2.5	40
36	Consolidating metabolite identifiers to enable contextual and multi-platform metabolomics data analysis. <i>BMC Bioinformatics</i> , 2010, 11, 214.	2.6	38

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37	An MYB transcription factor regulating specialized metabolisms in <i>Ophiorrhiza pumila</i> . <i>Plant Biotechnology</i> , 2016, 33, 1-9.	1.0	35
38	Fruit setting rewires central metabolism via gibberellin cascades. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 23970-23981.	7.1	34
39	Defective cytokinin signaling reprograms lipid and flavonoid gene-to-metabolite networks to mitigate high salinity in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	34
40	Deciphering Starch Quality of Rice Kernels Using Metabolite Profiling and Pedigree Network Analysis. <i>Molecular Plant</i> , 2012, 5, 442-451.	8.3	29
41	eQTLs Regulating Transcript Variations Associated with Rapid Internode Elongation in Deepwater Rice. <i>Frontiers in Plant Science</i> , 2017, 8, 1753.	3.6	29
42	Comparative Characterization of the Leaf Tissue of <i>Physalis alkekengi</i> and <i>Physalis peruviana</i> Using RNA-seq and Metabolite Profiling. <i>Frontiers in Plant Science</i> , 2016, 7, 1883.	3.6	27
43	Integrative omics approaches revealed a crosstalk among phytohormones during tuberous root development in cassava. <i>Plant Molecular Biology</i> , 2022, 109, 249-269.	3.9	26
44	Cytosolic GLUTAMINE SYNTHETASE1;1 Modulates Metabolism and Chloroplast Development in Roots. <i>Plant Physiology</i> , 2020, 182, 1894-1909.	4.8	25
45	High Impact Gene Discovery: Simple Strand-Specific mRNA Library Construction and Differential Regulatory Analysis Based on Gene Co-Expression Network. <i>Methods in Molecular Biology</i> , 2018, 1830, 163-189.	0.9	24
46	Morphological and plant hormonal changes during parasitization by <i>Cuscuta japonica</i> on <i>Momordica charantia</i> . <i>Journal of Plant Interactions</i> , 2014, 9, 220-232.	2.1	23
47	Metabolite Signature during Short-Day Induced Growth Cessation in <i>Populus</i> . <i>Frontiers in Plant Science</i> , 2011, 2, 29.	3.6	20
48	Comparative metabolomics charts the impact of genotype-dependent methionine accumulation in <i>Arabidopsis thaliana</i> . <i>Amino Acids</i> , 2010, 39, 1013-1021.	2.7	19
49	Development of a Direct Headspace Collection Method from <i>Arabidopsis</i> Seedlings Using HS-SPME-GC-TOF-MS Analysis. <i>Metabolites</i> , 2013, 3, 223-242.	2.9	18
50	SVD-based Anatomy of Gene Expressions for Correlation Analysis in <i>Arabidopsis thaliana</i> . <i>DNA Research</i> , 2008, 15, 367-374.	3.4	17
51	Current challenges and future potential of tomato breeding using omics approaches. <i>Breeding Science</i> , 2013, 63, 31-41.	1.9	17
52	Reduction in sucrose contents by downregulation of fructose-1,6-bisphosphatase 2 causes tiller outgrowth cessation in rice mutants lacking glutamine synthetase1;2. <i>Rice</i> , 2018, 11, 65.	4.0	17
53	Metabolite and Phytohormone Profiling Illustrates Metabolic Reprogramming as an Escape Strategy of Deepwater Rice during Partially Submerged Stress. <i>Metabolites</i> , 2020, 10, 68.	2.9	17
54	Effects of Combined Low Glutathione with Mild Oxidative and Low Phosphorus Stress on the Metabolism of <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 1464.	3.6	16

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55	Maize specialized metabolome networks reveal organ-preferential mixed glycosides. Computational and Structural Biotechnology Journal, 2021, 19, 1127-1144.	4.1	15
56	Characterizing gene coexpression modules in <i>Oryza sativa</i> based on a graph-clustering approach. Plant Biotechnology, 2009, 26, 485-493.	1.0	12
57	Linkage between circadian clock and tricarboxylic acid cycle in <i>Arabidopsis</i> . Plant Signaling and Behavior, 2009, 4, 660-662.	2.4	11
58	A Systems Analysis With a Simplified Source-Sink Model Reveals Metabolic Reprogramming in a Pair of Source-to-Sink Organs During Early Fruit Development in Tomato by LED Light Treatments. Frontiers in Plant Science, 2018, 9, 1439.	3.6	9
59	Comparative co-expression network analysis extracts the <i>SIHSP70</i> gene affecting to shoot elongation of tomato. Plant Biotechnology, 2019, 36, 143-153.	1.0	8
60	Whole Transcriptome Analysis Using Next-Generation Sequencing of Sterile-Cultured <i>Eisenia andrei</i> for Immune System Research. PLoS ONE, 2015, 10, e0118587.	2.5	6
61	Development of RIKEN Plant Metabolome MetaDatabase. Plant and Cell Physiology, 2022, 63, 433-440.	3.1	6
62	Human uterus myoma and gene expression profiling: A novel in vitro model for studying secretory leukocyte protease inhibitor-mediated tumor invasion. Cancer Letters, 2016, 379, 84-93.	7.2	5
63	BioHackathon 2015: Semantics of data for life sciences and reproducible research. F1000Research, 2020, 9, 136.	1.6	5
64	Transcriptomic, Hormonomic and Metabolomic Analyses Highlighted the Common Modules Related to Photosynthesis, Sugar Metabolism and Cell Division in Parthenocarpic Tomato Fruits during Early Fruit Set. Cells, 2022, 11, 1420.	4.1	3
65	Application of Quantum Chemical Calculation for Prediction of Ultraviolet-vis Spectrum of Plant Self-protective Metabolites Produced by UV-B Irradiation. Journal of Computer Chemistry Japan, 2019, 18, 108-114.	0.1	0