Chun-Xiang Fu

List of Publications by Year
in descending order

51 papers	2,915 citations	257450 24 h-index	182427 51 g-index
52 all docs	52 docs citations	52 times ranked	3556 citing authors

#	Article	IF	Citations
1	PAMP-INDUCED SECRETED PEPTIDE 3 modulates salt tolerance through RECEPTOR-LIKE KINASE 7 in plants. Plant Cell, 2022, 34, 927-944.	6.6	21
2	Downregulation of miR156-Targeted PvSPL6 in Switchgrass Delays Flowering and Increases Biomass Yield. Frontiers in Plant Science, 2022, 13, 834431.	3.6	4
3	Down-regulation of <i>PvSAMS</i> impairs <i>S</i>-adenosyl-L-methionine and lignin biosynthesis, and improves cell wall digestibility in switchgrass. Journal of Experimental Botany, 2022, 73, 4157-4169.	4.8	6
4	<i>LATERAL BRANCHING OXIDOREDUCTASE</i>, one novel target gene of Squamosa Promoter Binding Proteinâ€like 2, regulates tillering in switchgrass. New Phytologist, 2022, 235, 563-575.	7.3	7
5	Conduction of a chemical structure-guided metabolic phenotype analysis method targeting phenylpropane pathway via LC-MS: Ginkgo biloba and soybean as examples. Food Chemistry, 2022, 390, 133155.	8.2	6
6	Genetic manipulation of bermudagrass photosynthetic biosynthesis using <scp><i>Agrobacteriumâ€mediated</i></scp> transformation. Physiologia Plantarum, 2022, 174, e13710.	5.2	4
7	Genome-Wide Identification of Switchgrass Laccases Involved in Lignin Biosynthesis and Heavy-Metal Responses. International Journal of Molecular Sciences, 2022, 23, 6530.	4.1	7
8	<i>Escherichia coli</i> segments its controls on carbonâ€dependent gene expression into global and specific regulations. Microbial Biotechnology, 2021, 14, 1084-1106.	4.2	4
9	Ginkgo biloba. Trends in Genetics, 2021, 37, 488-489.	6.7	10
10	Highly efficient detoxification of dinitrotoluene by transgenic switchgrass overexpressing bacterial <i>nitroreductase</i>. Plant, Cell and Environment, 2021, 44, 3173-3183.	5.7	4
11	Establishment of an efficient Agrobacterium-mediated genetic transformation system in halophyte Puccinellia tenuiflora. Molecular Breeding, 2021, 41, 1.	2.1	6
12	Exogenous proanthocyanidins improve tolerance of Cu-toxicity by amelioration of oxidative damage and re-programming of gene expression in Medicago sativa. PLoS ONE, 2021, 16, e0259100.	2.5	3
13	Gain of Spontaneous clpX Mutations Boosting Motility via Adaption to Environments in Escherichia coli. Frontiers in Bioengineering and Biotechnology, 2021, 9, 772397.	4.1	3
14	Overexpression of PvWOX3a in switchgrass promotes stem development and increases plant height. Horticulture Research, 2021, 8, 252.	6.3	11
15	MYB20, MYB42, MYB43, and MYB85 Regulate Phenylalanine and Lignin Biosynthesis during Secondary Cell Wall Formation. Plant Physiology, 2020, 182, 1272-1283.	4.8	154
16	Efficient Genome Editing in Populus Using CRISPR/Cas12a. Frontiers in Plant Science, 2020, 11, 593938.	3.6	36
17	Characterization of Two New brown midrib1 Mutations From an EMS-Mutagenic Maize Population for Lignocellulosic Biomass Utilization. Frontiers in Plant Science, 2020, 11, 594798.	3.6	5
18	MiR156 regulates anthocyanin biosynthesis through SPL targets and other microRNAs in poplar. Horticulture Research, 2020, 7, 118.	6.3	90

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19	The nodulation and nyctinastic leaf movement is orchestrated by clock gene LHY in <i>Medicago truncatula</i>. Journal of Integrative Plant Biology, 2020, 62, 1880-1895.	8.5	26
20	Pyropia yezoensis genome reveals diverse mechanisms of carbon acquisition in the intertidal environment. Nature Communications, 2020, 11, 4028.	12.8	49
21	The miR396-GRFs Module Mediates the Prevention of Photo-oxidative Damage by Brassinosteroids during Seedling De-Etiolation in Arabidopsis. Plant Cell, 2020, 32, 2525-2542.	6.6	28
22	Efficient Generation of CRISPR/Cas9-Mediated Homozygous/Biallelic Medicago truncatula Mutants Using a Hairy Root System. Frontiers in Plant Science, 2020, 11, 294.	3.6	25
23	The developmental dynamics of the <i>Populus</i> stem transcriptome. Plant Biotechnology Journal, 2019, 17, 206-219.	8.3	112
24	Genome-wide characterization of SPL family in Medicago truncatula reveals the novel roles of miR156/SPL module in spiky pod development. BMC Genomics, 2019, 20, 552.	2.8	21
25	Genome-wide transcriptional adaptation to salt stress in Populus. BMC Plant Biology, 2019, 19, 367.	3.6	32
26	Genome-Wide Analysis of the<i>TCP</i>Gene Family in Switchgrass (<i>Panicum virgatum</i>L.). International Journal of Genomics, 2019, 2019, 1-13.	1.6	21
27	Mutation of 4-coumarate: coenzyme A ligase 1 gene affects lignin biosynthesis and increases the cell wall digestibility in maize brown midrib5 mutants. Biotechnology for Biofuels, 2019, 12, 82.	6.2	40
28	Efficient genetic transformation and <scp>CRISPR</scp>/Cas9â€mediated genome editing in <i>Lemna aequinoctialis</i>. Plant Biotechnology Journal, 2019, 17, 2143-2152.	8.3	28
29	Deciphering global gene expression and regulation strategy in <i>Escherichia coli</i> during carbon limitation. Microbial Biotechnology, 2019, 12, 360-376.	4.2	11
30	Metabolomics Integrated with Transcriptomics Reveals Redirection of the Phenylpropanoids Metabolic Flux in <i>Ginkgo biloba</i>. Journal of Agricultural and Food Chemistry, 2019, 67, 3284-3291.	5.2	85
31	Simultaneous regulation of <i>F5H</i> in <scp>COMT</scp>â€<scp>RNA</scp>i transgenic switchgrass alters effects of <i><scp>COMT</scp></i> suppression on syringyl lignin biosynthesis. Plant Biotechnology Journal, 2019, 17, 836-845.	8.3	54
32	PHB3 Maintains Root Stem Cell Niche Identity through ROS-Responsive AP2/ERF Transcription Factors in Arabidopsis. Cell Reports, 2018, 22, 1350-1363.	6.4	128
33	Alteration of <i>S</i>â€adenosylhomocysteine levels affects lignin biosynthesis in switchgrass. Plant Biotechnology Journal, 2018, 16, 2016-2026.	8.3	17
34	MicroRNA528 Affects Lodging Resistance of Maize by Regulating Lignin Biosynthesis under Nitrogen-Luxury Conditions. Molecular Plant, 2018, 11, 806-814.	8.3	136
35	Structural Characterization of Lignocresols from Transgenic and Wild-Type Switchgrass. Polymers, 2018, 10, 727.	4.5	2
36	Methylenetetrahydrofolate reductase modulates methyl metabolism and lignin monomer methylation in maize. Journal of Experimental Botany, 2018, 69, 3963-3973.	4.8	11

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37	Genome-Wide Identification, Phylogeny, and Expression Analysis of ARF Genes Involved in Vegetative Organs Development in Switchgrass. International Journal of Genomics, 2018, 2018, 1-13.	1.6	4
38	The <i>miR156</i>â€<i>SPL4</i> module predominantly regulates aerial axillary bud formation and controls shoot architecture. New Phytologist, 2017, 216, 829-840.	7.3	59
39	Genome-wide characterization of GRAS family genes in Medicago truncatula reveals their evolutionary dynamics and functional diversification. PLoS ONE, 2017, 12, e0185439.	2.5	39
40	Overexpression of the WOX gene STENOFOLIA improves biomass yield and sugar release in transgenic grasses and display altered cytokinin homeostasis. PLoS Genetics, 2017, 13, e1006649.	3.5	63
41	<scp>UDP</scp>â€glycosyltransferase 72B1 catalyzes the glucose conjugation of monolignols and is essential for the normal cell wall lignification in <i>Arabidopsis thaliana</i>. Plant Journal, 2016, 88, 26-42.	5.7	108
42	Switchgrass SBP-box transcription factors PvSPL1 and 2 function redundantly to initiate side tillers and affect biomass yield of energy crop. Biotechnology for Biofuels, 2016, 9, 101.	6.2	46
43	Metabolic engineering of 2-phenylethanol pathway producing fragrance chemical and reducing lignin in Arabidopsis. Plant Cell Reports, 2015, 34, 1331-1342.	5.6	7
44	Twoâ€year field analysis of reduced recalcitrance transgenic switchgrass. Plant Biotechnology Journal, 2014, 12, 914-924.	8.3	104
45	Cell wall polysaccharide distribution in Miscanthus lutarioriparius stem using immuno-detection. Plant Cell Reports, 2014, 33, 643-653.	5.6	15
46	Standardization of Switchgrass Sample Collection for Cell Wall and Biomass Trait Analysis. Bioenergy Research, 2013, 6, 755-762.	3.9	87
47	MlWRKY12, a novel Miscanthus transcription factor, participates in pith secondary cell wall formation and promotes flowering. Plant Science, 2013, 212, 1-9.	3.6	60
48	Overexpression of miR156 in switchgrass (<i>Panicum virgatum</i> L.) results in various morphological alterations and leads to improved biomass production. Plant Biotechnology Journal, 2012, 10, 443-452.	8.3	293
49	Genetic manipulation of lignin reduces recalcitrance and improves ethanol production from switchgrass. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 3803-3808.	7.1	585
50	Downregulation of Cinnamyl Alcohol Dehydrogenase (CAD) Leads to Improved Saccharification Efficiency in Switchgrass. Bioenergy Research, 2011, 4, 153-164.	3.9	156
51	Agrobacterium-Mediated Transformation of Switchgrass and Inheritance of the Transgenes. Bioenergy Research, 2009, 2, 275-283.	3.9	80