Shuen-Fang Lo

List of Publications by Year
in descending order

20 papers	1,287 citations	759055 12 h-index	794469 19 g-index
20 all docs	20 docs citations	20 times ranked	2133 citing authors

#	Article	IF	Citations
1	A Novel Class of Gibberellin 2-Oxidases Control Semidwarfism, Tillering, and Root Development in Rice. Plant Cell, 2008, 20, 2603-2618.	3.1	410
2	Sourceâ€“Sink Communication: Regulated by Hormone, Nutrient, and Stress Cross-Signaling. Trends in Plant Science, 2015, 20, 844-857.	4.3	259
3	A rice gene activation/knockout mutant resource for high throughput functional genomics. Plant Molecular Biology, 2007, 63, 351-364.	2.0	197
4	Ectopic expression of specific <scp>GA</scp>2 oxidase mutants promotes yield and stress tolerance in rice. Plant Biotechnology Journal, 2017, 15, 850-864.	4.1	97
5	A late embryogenesis abundant protein <scp>HVA</scp>1 regulated by an inducible promoter enhances root growth and abiotic stress tolerance in rice without yield penalty. Plant Biotechnology Journal, 2015, 13, 105-116.	4.1	69
6	Serotonin accumulation in transgenic rice by over-expressing tryptophan decarboxlyase results in a dark brown phenotype and stunted growth. Plant Molecular Biology, 2012, 78, 525-543.	2.0	56
7	Genetic resources offer efficient tools for rice functional genomics research. Plant, Cell and Environment, 2016, 39, 998-1013.	2.8	42
8	Increasing Leaf Vein Density by Mutagenesis: Laying the Foundations for C4 Rice. PLoS ONE, 2014, 9, e94947.	1.1	36
9	<i>Rice Big Grain 1 </i>promotes cell division to enhance organ development, stress tolerance and grain yield. Plant Biotechnology Journal, 2020, 18, 1969-1983.	4.1	25
10	How does rice cope with too little oxygen during its early life?. New Phytologist, 2021, 229, 36-41.	3.5	25
11	Candidate regulators of Early Leaf Development in Maize Perturb Hormone Signalling and Secondary Cell Wall Formation When Constitutively Expressed in Rice. Scientific Reports, 2017, 7, 4535.	1.6	18
12	Large-scale phenomics analysis of a T-DNA tagged mutant population. GigaScience, 2017, 6, 1-7.	3.3	15
13	Ectopic expression of OsMADS45 activates the upstream genes Hd3a and RFT1 at an early development stage causing early flowering in rice. , 2013, 54, 12.		10
14	Lack of Genotype and Phenotype Correlation in a Rice T-DNA Tagged Line Is Likely Caused by Introgression in the Seed Source. PLoS ONE, 2016, 11, e0155768.	1.1	7
15	The Nucleotideâ€Dependent Interactome of Rice Heterotrimeric Gâ€Protein Î± â€Subunit. Proteomics, 2019, 19, 1800385.	1.3	6
16	Comparisons within the Rice GA 2-Oxidase Gene Family Revealed Three Dominant Paralogs and a Functional Attenuated Gene that Led to the Identification of Four Amino Acid Variants Associated with GA Deactivation Capability. Rice, 2021, 14, 70.	1.7	5
17	EAT-Rice: A predictive model for flanking gene expression of T-DNA insertion activation-tagged rice mutants by machine learning approaches. PLoS Computational Biology, 2019, 15, e1006942.	1.5	4
18	Ectopic Expression of WINDING 1 Leads to Asymmetrical Distribution of Auxin and a Spiral Phenotype in Rice. Plant and Cell Physiology, 2017, 58, 1494-1506.	1.5	3

#	Article	IF	Citations
19	Using Machine Learning Approaches to Predict Target Gene Expression in Rice T-DNA Insertional Mutants. Frontiers in Genetics, 2021, 12, 798107.	1.1	2
20	Closer vein spacing by ectopic expression of nucleotide-binding and leucine-rich repeat proteins in rice leaves. Plant Cell Reports, 2022, 41, 319-335.	2.8	1