

# Ting Lan

## List of Publications by Year in descending order

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Version: 2024-02-01

17  
papers

593  
citations

933264

10  
h-index

887953

17  
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18  
all docs

18  
docs citations

18  
times ranked

903  
citing authors

#	ARTICLE	IF	CITATIONS
1	Extensive Functional Diversification of the <i>Populus</i> Glutathione S-Transferase Supergene Family. <i>Plant Cell</i> , 2010, 21, 3749-3766.	3.1	185
2	Functional characterization of the late embryogenesis abundant (LEA) protein gene family from <i>Pinus tabulaeformis</i> (Pinaceae) in <i>Escherichia coli</i> . <i>Scientific Reports</i> , 2016, 6, 19467.	1.6	84
3	Genome-wide analysis of the LEA (late embryogenesis abundant) protein gene family in <i>Populus trichocarpa</i> . <i>Tree Genetics and Genomes</i> , 2013, 9, 253-264.	0.6	75
4	A Resource for Inactivation of MicroRNAs Using Short Tandem Target Mimic Technology in Model and Crop Plants. <i>Molecular Plant</i> , 2018, 11, 1400-1417.	3.9	52
5	Structural and Functional Evolution of Positively Selected Sites in Pine Glutathione S-Transferase Enzyme Family*. <i>Journal of Biological Chemistry</i> , 2013, 288, 24441-24451.	1.6	49
6	Genome-Wide Analysis of the Glutathione S-Transferase Gene Family in <i>Capsella rubella</i> : Identification, Expression, and Biochemical Functions. <i>Frontiers in Plant Science</i> , 2016, 7, 1325.	1.7	34
7	Extraribosomal Functions of Cytosolic Ribosomal Proteins in Plants. <i>Frontiers in Plant Science</i> , 2021, 12, 607157.	1.7	19
8	Arabidopsis RBV is a conserved WD40 repeat protein that promotes microRNA biogenesis and ARGONAUTE1 loading. <i>Nature Communications</i> , 2022, 13, 1217.	5.8	19
9	Genome-wide analysis of superoxide dismutase genes in <i>Larix kaempferi</i> . <i>Gene</i> , 2019, 686, 29-36.	1.0	18
10	Overexpression of <i>PtoCYCD3;3</i> Promotes Growth and Causes Leaf Wrinkle and Branch Appearance in <i>Populus</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 1288.	1.8	13
11	Plant cytoplasmic ribosomal proteins: an update on classification, nomenclature, evolution and resources. <i>Plant Journal</i> , 2022, 110, 292-318.	2.8	11
12	Distinct Evolutionary Profiles and Functions of microRNA156 and microRNA529 in Land Plants. <i>International Journal of Molecular Sciences</i> , 2021, 22, 11100.	1.8	8
13	MicroRNA Techniques: Valuable Tools for Agronomic Trait Analyses and Breeding in Rice. <i>Frontiers in Plant Science</i> , 2021, 12, 744357.	1.7	6
14	TRANS-ACTING SIRNA3-derived short interfering RNAs confer cleavage of mRNAs in rice. <i>Plant Physiology</i> , 2022, 188, 347-362.	2.3	6
15	High resolution RNA-seq profiling of genes encoding ribosomal proteins across different organs and developmental stages in <i>Arabidopsis thaliana</i> . <i>Plant Direct</i> , 2021, 5, e00320.	0.8	5
16	Mechanism for the genomic and functional evolution of the MIR2118 family in the grass lineage. <i>New Phytologist</i> , 2022, 233, 1915-1930.	3.5	5
17	Arabidopsis paralogous genes RPL23aA and RPL23aB encode functionally equivalent proteins. <i>BMC Plant Biology</i> , 2020, 20, 463.	1.6	4