

# Changzheng Xu

## List of Publications by Year in descending order

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Version: 2024-02-01

27  
papers

1,209  
citations

516710

16  
h-index

580821

25  
g-index

28  
all docs

28  
docs citations

28  
times ranked

1653  
citing authors

#	ARTICLE	IF	CITATIONS
1	LOB Domain Proteins: Beyond Lateral Organ Boundaries. <i>Trends in Plant Science</i> , 2016, 21, 159-167.	8.8	124
2	Genome-wide investigation of pentatricopeptide repeat gene family in poplar and their expression analysis in response to biotic and abiotic stresses. <i>Scientific Reports</i> , 2018, 8, 2817.	3.3	115
3	PtoMYB170 positively regulates lignin deposition during wood formation in poplar and confers drought tolerance in transgenic Arabidopsis. <i>Tree Physiology</i> , 2017, 37, 1713-1726.	3.1	99
4	The <i>MicroRNA390</i> TRANS-ACTING SHORT INTERFERING RNA3 Module Mediates Lateral Root Growth under Salt Stress via the Auxin Pathway. <i>Plant Physiology</i> , 2018, 177, 775-791.	4.8	98
5	Proteomic analysis of roots growth and metabolic changes under phosphorus deficit in maize ( <i>Zea mays</i> L.) roots. <i>Journal of Proteomics</i> , 2019, 10, 1-14.	2.2	95
6	Auxin-mediated Aux/IAA-ARF-HB signaling cascade regulates secondary xylem development in <i>Populus</i> . <i>New Phytologist</i> , 2019, 222, 752-767.	7.3	85
7	Comparative proteome analyses of phosphorus responses in maize ( <i>Zea mays</i> L.) roots of wild-type and a low-P-tolerant mutant reveal root characteristics associated with phosphorus efficiency. <i>Plant Journal</i> , 2008, 55, 927-939.	5.7	81
8	Cooperative action of the paralogous maize lateral organ boundaries (LOB) domain proteins RTCS and RTCL in shoot-borne root formation. <i>New Phytologist</i> , 2015, 207, 1123-1133.	7.3	75
9	Phosphate starvation of maize inhibits lateral root formation and alters gene expression in the lateral root primordium zone. <i>BMC Plant Biology</i> , 2012, 12, 89.	3.6	71
10	Molecular interactions of ROOTLESS CONCERNING CROWN AND SEMINAL ROOTS, a LOB domain protein regulating shoot-borne root initiation in maize ( <i>Zea mays</i> L.). <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2012, 367, 1542-1551.	4.0	54
11	AUXIN RESPONSE FACTOR7 integrates gibberellin and auxin signaling via interactions between DELLA and AUX/IAA proteins to regulate cambial activity in poplar. <i>Plant Cell</i> , 2022, 34, 2688-2707.	6.6	46
12	Isolation and Functional Validation of Salinity and Osmotic Stress Inducible Promoter from the Maize Type-II H <sup>+</sup> -Pyrophosphatase Gene by Deletion Analysis in Transgenic Tobacco Plants. <i>PLoS ONE</i> , 2016, 11, e0154041.	2.5	41
13	Proteome profile of maize ( <i>Zea Mays</i> L.) leaf tissue at the flowering stage after long-term adjustment to rice black-streaked dwarf virus infection. <i>Gene</i> , 2011, 485, 106-113.	2.2	39
14	Kernel amino acid composition and protein content of introgression lines from <i>Zea mays</i> ssp. <i>mexicana</i> into cultivated maize. <i>Journal of Cereal Science</i> , 2008, 48, 387-393.	3.7	36
15	ZmSKS13, a cupredoxin domain-containing protein, is required for maize kernel development via modulation of redox homeostasis. <i>New Phytologist</i> , 2021, 229, 2163-2178.	7.3	20
16	Identification of a 467 bp Promoter of Maize Phosphatidylinositol Synthase Gene (ZmPIS) Which Confers High-Level Gene Expression and Salinity or Osmotic Stress Inducibility in Transgenic Tobacco. <i>Frontiers in Plant Science</i> , 2016, 7, 42.	3.6	19
17	Cytokinin signaling localized in phloem noncell-autonomously regulates cambial activity during secondary growth of <i>Populus</i> stems. <i>New Phytologist</i> , 2021, 230, 1476-1488.	7.3	19
18	Phosphoproteome and proteome analyses reveal low-phosphate mediated plasticity of root developmental and metabolic regulation in maize ( <i>Zea mays</i> L.). <i>Plant Physiology and Biochemistry</i> , 2014, 83, 232-242.	5.8	16

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19	Diversity of Stability, Localization, Interaction and Control of Downstream Gene Activity in the Maize Aux/IAA Protein Family. PLoS ONE, 2014, 9, e107346.	2.5	14
20	The microRNA476â€‹i>RFL</i> module regulates adventitious root formation through a mitochondriaâ€‹dependent pathway in <i>Populus</i>. New Phytologist, 2021, 230, 2011-2028.	7.3	14
21	Expression of <i>Ralstonia solanacearum</i> type III secretion system is dependent on a novel type 4 pili (T4P) assembly protein (TapV) but is T4P independent. Molecular Plant Pathology, 2020, 21, 777-793.	4.2	11
22	Heterologous Expression of Poplar WRKY18/35 Paralogs in Arabidopsis Reveals Their Antagonistic Regulation on Pathogen Resistance and Abiotic Stress Tolerance via Variable Hormonal Pathways. International Journal of Molecular Sciences, 2020, 21, 5440.	4.1	9
23	SH1-dependent maize seed development and starch synthesis via modulating carbohydrate flow and osmotic potential balance. BMC Plant Biology, 2020, 20, 264.	3.6	9
24	PtoMYB142, a poplar R2R3-MYB transcription factor, contributes to drought tolerance by regulating wax biosynthesis. Tree Physiology, 0, , .	3.1	9
25	Ionomics, transcriptomics and untargeted metabolomics analyses provide new insights into the Cd response and accumulation mechanisms of mulberry. Environmental and Experimental Botany, 2022, 196, 104821.	4.2	8
26	Dual Reproductive Cell-Specific Promoter-Mediated Split-Cre/LoxP System Suitable for Exogenous Gene Deletion in Hybrid Progeny of Transgenic Arabidopsis. International Journal of Molecular Sciences, 2021, 22, 5080.	4.1	2
27	Functional Characterization of RsRsgA for Ribosome Biosynthesis and Expression of the Type III Secretion System in Ralstonia solanacearum. Molecular Plant-Microbe Interactions, 2020, 33, 972-981.	2.6	0