

# Gui-Xian Xia

## List of Publications by Year in descending order

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43  
papers

7,786  
citations

201674

27  
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254184

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docs citations

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times ranked

16365  
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#	ARTICLE	IF	CITATIONS
1	<i>GhADF6</i> -mediated actin reorganization is associated with defence against <i>Verticillium dahliae</i> infection in cotton. <i>Molecular Plant Pathology</i> , 2021, 22, 1656-1667.	4.2	10
2	Cotton plant defence against a fungal pathogen is enhanced by expanding <i>BLADE-ON-PETIOLE1</i> expression beyond lateral-organ boundaries. <i>Communications Biology</i> , 2019, 2, 238.	4.4	20
3	The Cotton Apoplastic Protein <i>CRR1</i> Stabilizes Chitinase 28 to Facilitate Defense against the Fungal Pathogen <i>Verticillium dahliae</i> . <i>Plant Cell</i> , 2019, 31, 520-536.	6.6	85
4	iTRAQ-based proteomics analysis of autophagy-mediated immune responses against the vascular fungal pathogen <i>Verticillium dahliae</i> in <i>Arabidopsis</i> . <i>Autophagy</i> , 2018, 14, 598-618.	9.1	35
5	Ectopic expression of <i>SsPETE2</i> , a plastocyanin from <i>Suaeda salsa</i> , improves plant tolerance to oxidative stress. <i>Plant Science</i> , 2018, 268, 1-10.	3.6	21
6	The potato transcription factor <i>StbZIP61</i> regulates dynamic biosynthesis of salicylic acid in defense against <i>Phytophthora infestans</i> infection. <i>Plant Journal</i> , 2018, 95, 1055-1068.	5.7	50
7	Overexpression of <i>GhFIM2</i> propels cotton fiber development by enhancing actin bundle formation. <i>Journal of Integrative Plant Biology</i> , 2017, 59, 531-534.	8.5	18
8	Overexpression of <i>GhPFN2</i> enhances protection against <i>Verticillium dahliae</i> invasion in cotton. <i>Science China Life Sciences</i> , 2017, 60, 861-867.	4.9	14
9	iTRAQ-based proteomic analysis of defence responses triggered by the necrotrophic pathogen <i>Rhizoctonia solani</i> in cotton. <i>Journal of Proteomics</i> , 2017, 152, 226-235.	2.4	28
10	Functional Characterization of a Dihydroflavanol 4-Reductase from the Fiber of Upland Cotton ( <i>Gossypium hirsutum</i> ). <i>Molecules</i> , 2016, 21, 32.	3.8	13
11	iTRAQ Protein Profile Differential Analysis of Dormant and Germinated Grassbur Twin Seeds Reveals that Ribosomal Synthesis and Carbohydrate Metabolism Promote Germination Possibly Through the PI3K Pathway. <i>Plant and Cell Physiology</i> , 2016, 57, 1244-1256.	3.1	8
12	Rice Plasma Membrane Proteomics Reveals <i>Magnaporthe oryzae</i> Promotes Susceptibility by Sequential Activation of Host Hormone Signaling Pathways. <i>Molecular Plant-Microbe Interactions</i> , 2016, 29, 902-913.	2.6	29
13	The two domains of cotton <i>WLM1a</i> protein are functionally divergent. <i>Science China Life Sciences</i> , 2016, 59, 206-212.	4.9	10
14	Guidelines for the use and interpretation of assays for monitoring autophagy (3rd edition). <i>Autophagy</i> , 2016, 12, 1-222.	9.1	4,701
15	The cotton <i>MYB108</i> forms a positive feedback regulation loop with <i>CML11</i> and participates in the defense response against <i>Verticillium dahliae</i> infection. <i>Journal of Experimental Botany</i> , 2016, 67, 1935-1950.	4.8	87
16	The Thioredoxin <i>GbNRX1</i> Plays a Crucial Role in Homeostasis of Apoplastic Reactive Oxygen Species in Response to <i>Verticillium dahliae</i> Infection in Cotton. <i>Plant Physiology</i> , 2016, 170, 2392-2406.	4.8	132
17	Functional characterization of an anthocyanidin reductase gene from the fibers of upland cotton ( <i>Gossypium hirsutum</i> ). <i>Planta</i> , 2015, 241, 1075-1089.	3.2	33
18	The mitochondrial malate dehydrogenase 1 gene <i>GhmMDH1</i> is involved in plant and root growth under phosphorus deficiency conditions in cotton. <i>Scientific Reports</i> , 2015, 5, 10343.	3.3	42

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19	The RING Finger Protein NtRCP1 Is Involved in the Floral Transition in Tobacco ( <i>Nicotiana tabacum</i> ). <i>Journal of Genetics and Genomics</i> , 2015, 42, 311-317.	3.9	4
20	Cotton Major Latex Protein 28 Functions as a Positive Regulator of the Ethylene Responsive Factor 6 in Defense against <i>Verticillium dahliae</i> . <i>Molecular Plant</i> , 2015, 8, 399-411.	8.3	141
21	The Role of Autophagy during Development of the Oomycete Pathogen <i>Phytophthora infestans</i> . <i>Journal of Genetics and Genomics</i> , 2014, 41, 225-228.	3.9	9
22	Overexpression of AaPal, a peptidoglycan-associated lipoprotein from <i>Alkalomonas amylolytica</i> , improves salt and alkaline tolerance of <i>Escherichia coli</i> and <i>Arabidopsis thaliana</i> . <i>Biotechnology Letters</i> , 2014, 36, 601-607.	2.2	8
23	Augmin Triggers Microtubule-Dependent Microtubule Nucleation in Interphase Plant Cells. <i>Current Biology</i> , 2014, 24, 2708-2713.	3.9	78
24	The Dual Functions of WLIM1a in Cell Elongation and Secondary Wall Formation in Developing Cotton Fibers. <i>Plant Cell</i> , 2013, 25, 4421-4438.	6.6	144
25	The Tobacco <i>BLADE-ON-PETIOLE2</i> Gene Mediates Differentiation of the Corolla Abscission Zone by Controlling Longitudinal Cell Expansion. <i>Plant Physiology</i> , 2012, 159, 835-850.	4.8	59
26	Proteomic analysis of the sea-island cotton roots infected by wilt pathogen <i>Verticillium dahliae</i> . <i>Proteomics</i> , 2011, 11, 4296-4309.	2.2	90
27	Overexpression of a Profilin (GhPFN2) Promotes the Progression of Developmental Phases in Cotton Fibers. <i>Plant and Cell Physiology</i> , 2010, 51, 1276-1290.	3.1	70
28	Proteomic Identification of Differentially Expressed Proteins in the <i>Ligon lintless</i> Mutant of Upland Cotton ( <i>Gossypium hirsutum</i> L.). <i>Journal of Proteome Research</i> , 2010, 9, 1076-1087.	3.7	78
29	A Glutamic Acid-Rich Protein Identified in <i>Verticillium dahliae</i> from an Insertional Mutagenesis Affects Microsclerotial Formation and Pathogenicity. <i>PLoS ONE</i> , 2010, 5, e15319.	2.5	102
30	Down-regulation of <i>GhADF1</i> gene expression affects cotton fibre properties. <i>Plant Biotechnology Journal</i> , 2009, 7, 13-23.	8.3	87
31	Cloning and characterization of a calcium dependent protein kinase gene associated with cotton fiber development. <i>Plant Cell Reports</i> , 2008, 27, 1869-1875.	5.6	67
32	SsTypA1, a chloroplast-specific TypA/BipA-type GTPase from the halophytic plant <i>Suaeda salsa</i> , plays a role in oxidative stress tolerance. <i>Plant, Cell and Environment</i> , 2008, 31, 982-994.	5.7	36
33	Identification of genes preferentially expressed in cotton fibers: A possible role of calcium signaling in cotton fiber elongation. <i>Plant Science</i> , 2007, 173, 61-69.	3.6	32
34	Functional screening of salt stress-related genes from <i>Thellungiella halophila</i> using fission yeast system. <i>Physiologia Plantarum</i> , 2007, 129, 671-678.	5.2	13
35	Functional identification of cytokinesis-related genes from tobacco BY-2 cells. <i>Plant Cell Reports</i> , 2007, 26, 889-894.	5.6	5
36	Cloning and functional characterization of PpDBF1 gene encoding a DRE-binding transcription factor from <i>Physcomitrella patens</i> . <i>Planta</i> , 2007, 226, 827-838.	3.2	94

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37	Genetic transformation of green-colored cotton. <i>In Vitro Cellular and Developmental Biology - Plant</i> , 2006, 42, 439-444.	2.1	24
38	Ectopic Expression of the Cotton Non-symbiotic Hemoglobin Gene GhHbd1 Triggers Defense Responses and Increases Disease Tolerance in Arabidopsis. <i>Plant and Cell Physiology</i> , 2006, 47, 1058-1068.	3.1	70
39	GhHb1: A nonsymbiotic hemoglobin gene of cotton responsive to infection by <i>Verticillium dahliae</i> . <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2005, 1730, 103-113.	2.4	58
40	Functional characterization of <i>Gossypium hirsutum</i> profilin 1 gene (GhPFN1) in tobacco suspension cells. <i>Planta</i> , 2005, 222, 594-603.	3.2	48
41	Identification and characterization of a salt tolerance-responsive gene ( AtGRP9 ) of Arabidopsis *. <i>Progress in Natural Science: Materials International</i> , 2003, 13, 50-54.	4.4	1
42	ADF Proteins Are Involved in the Control of Flowering and Regulate F-Actin Organization, Cell Expansion, and Organ Growth in Arabidopsis. <i>Plant Cell</i> , 2001, 13, 1333-1346.	6.6	184
43	Actin Depolymerizing Factor (ADF/Cofilin) Enhances the Rate of Filament Turnover: Implication in Actin-based Motility. <i>Journal of Cell Biology</i> , 1997, 136, 1307-1322.	5.2	948