

# Youxiong Que

## List of Publications by Year in descending order

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106  
papers

2,730  
citations

186265

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111  
docs citations

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times ranked

2224  
citing authors

#	ARTICLE	IF	CITATIONS
1	Comprehensive Selection of Reference Genes for Gene Expression Normalization in Sugarcane by Real Time Quantitative RT-PCR. PLoS ONE, 2014, 9, e97469.	2.5	121
2	Genome sequencing of Sporisorium scitamineum provides insights into the pathogenic mechanisms of sugarcane smut. BMC Genomics, 2014, 15, 996.	2.8	112
3	A Global View of Transcriptome Dynamics during Sporisorium scitamineum Challenge in Sugarcane by RNA-seq. PLoS ONE, 2014, 9, e106476.	2.5	108
4	The choice of reference genes for assessing gene expression in sugarcane under salinity and drought stresses. Scientific Reports, 2014, 4, 7042.	3.3	100
5	ScChi, Encoding an Acidic Class III Chitinase of Sugarcane, Confers Positive Responses to Biotic and Abiotic Stresses in Sugarcane. International Journal of Molecular Sciences, 2014, 15, 2738-2760.	4.1	82
6	Isolation of a Novel Peroxisomal Catalase Gene from Sugarcane, Which Is Responsive to Biotic and Abiotic Stresses. PLoS ONE, 2014, 9, e84426.	2.5	81
7	Establishment and application of a loop-mediated isothermal amplification (LAMP) system for detection of cry1Ac transgenic sugarcane. Scientific Reports, 2014, 4, 4912.	3.3	77
8	Species-Specific Detection and Identification of Fusarium Species Complex, the Causal Agent of Sugarcane Pokkah Boeng in China. PLoS ONE, 2014, 9, e104195.	2.5	70
9	Identification, Phylogeny and Transcript of Chitinase Family Genes in Sugarcane. Scientific Reports, 2015, 5, 10708.	3.3	63
10	miRNA alteration is an important mechanism in sugarcane response to low-temperature environment. BMC Genomics, 2017, 18, 833.	2.8	61
11	The alcohol dehydrogenase gene family in sugarcane and its involvement in cold stress regulation. BMC Genomics, 2020, 21, 521.	2.8	57
12	Comparative proteomics reveals that central metabolism changes are associated with resistance against Sporisorium scitamineum in sugarcane. BMC Genomics, 2016, 17, 800.	2.8	53
13	Isolation and Characterization of ScGluD2, a New Sugarcane beta-1,3-Glucanase D Family Gene Induced by Sporisorium scitamineum, ABA, H <sub>2</sub> O <sub>2</sub> , NaCl, and CdCl <sub>2</sub> Stresses. Frontiers in Plant Science, 2016, 7, 1348.	3.6	51
14	Early Selection for Smut Resistance in Sugarcane Using Pathogen Proliferation and Changes in Physiological and Biochemical Indices. Frontiers in Plant Science, 2016, 7, 1133.	3.6	49
15	A cytosolic glucose-6-phosphate dehydrogenase gene, ScG6PDH, plays a positive role in response to various abiotic stresses in sugarcane. Scientific Reports, 2014, 4, 7090.	3.3	46
16	A class III WRKY transcription factor in sugarcane was involved in biotic and abiotic stress responses. Scientific Reports, 2020, 10, 20964.	3.3	46
17	Transgenic Sugarcane with a cry1Ac Gene Exhibited Better Phenotypic Traits and Enhanced Resistance against Sugarcane Borer. PLoS ONE, 2016, 11, e0153929.	2.5	45
18	Genetic Analysis of Diversity within a Chinese Local Sugarcane Germplasm Based on Start Codon Targeted Polymorphism. BioMed Research International, 2014, 2014, 1-10.	1.9	44

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19	A Novel L-ascorbate Peroxidase 6 Gene, ScAPX6, Plays an Important Role in the Regulation of Response to Biotic and Abiotic Stresses in Sugarcane. <i>Frontiers in Plant Science</i> , 2017, 8, 2262.	3.6	44
20	Transcriptome Profile Analysis of Sugarcane Responses to <i>Sporisorium scitamineum</i> Infection Using Solexa Sequencing Technology. <i>BioMed Research International</i> , 2013, 2013, 1-9.	1.9	42
21	<i>ScMT2-1-3</i> , a Metallothionein Gene of Sugarcane, Plays an Important Role in the Regulation of Heavy Metal Tolerance/Accumulation. <i>BioMed Research International</i> , 2013, 2013, 1-12.	1.9	41
22	Transgenic Sugarcane Resistant to <i>Sorghum mosaic virus</i> Based on Coat Protein Gene Silencing by RNA Interference. <i>BioMed Research International</i> , 2015, 2015, 1-9.	1.9	40
23	Transcripts and low nitrogen tolerance: Regulatory and metabolic pathways in sugarcane under low nitrogen stress. <i>Environmental and Experimental Botany</i> , 2019, 163, 97-111.	4.2	40
24	Differential Protein Expression in Sugarcane during Sugarcane- <i>Sporisorium scitamineum</i> Interaction Revealed by 2-DE and MALDI-TOF-TOF/MS. <i>Comparative and Functional Genomics</i> , 2011, 2011, 1-10.	2.0	39
25	A Novel Non-specific Lipid Transfer Protein Gene from Sugarcane (NsLTPs), Obviously Responded to Abiotic Stresses and Signaling Molecules of SA and MeJA. <i>Sugar Tech</i> , 2017, 19, 17-25.	1.8	36
26	Plant jasmonate ZIM domain genes: shedding light on structure and expression patterns of JAZ gene family in sugarcane. <i>BMC Genomics</i> , 2017, 18, 771.	2.8	35
27	Biplot evaluation of test environments and identification of mega-environment for sugarcane cultivars in China. <i>Scientific Reports</i> , 2015, 5, 15505.	3.3	34
28	Small RNA sequencing reveals a role for sugarcane miRNAs and their targets in response to <i>Sporisorium scitamineum</i> infection. <i>BMC Genomics</i> , 2017, 18, 325.	2.8	34
29	Loop-mediated isothermal amplification (LAMP) based detection of <i>Colletotrichum falcatum</i> causing red rot in sugarcane. <i>Molecular Biology Reports</i> , 2015, 42, 1309-1316.	2.3	32
30	The Physiological and Agronomic Responses to Nitrogen Dosage in Different Sugarcane Varieties. <i>Frontiers in Plant Science</i> , 2019, 10, 406.	3.6	31
31	Genetic Diversity Analysis of Sugarcane Germplasm Based on Fluorescence-Labeled Simple Sequence Repeat Markers and a Capillary Electrophoresis-based Genotyping Platform. <i>Sugar Tech</i> , 2016, 18, 380-390.	1.8	30
32	Highly Polymorphic Microsatellite DNA Markers for Sugarcane Germplasm Evaluation and Variety Identity Testing. <i>Sugar Tech</i> , 2011, 13, 129-136.	1.8	28
33	Transcriptional analysis identifies major pathways as response components to <i>Sporisorium scitamineum</i> stress in sugarcane. <i>Gene</i> , 2018, 678, 207-218.	2.2	28
34	<i>Gelsemium elegans</i> Benth: Chemical Components, Pharmacological Effects, and Toxicity Mechanisms. <i>Molecules</i> , 2021, 26, 7145.	3.8	28
35	Sugarcane Smut: Current Knowledge and the Way Forward for Management. <i>Journal of Fungi (Basel)</i> , 2021, 7, 1074.	3.5	27
36	Selection of Suitable Endogenous Reference Genes for Relative Copy Number Detection in Sugarcane. <i>International Journal of Molecular Sciences</i> , 2014, 15, 8846-8862.	4.1	26

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37	Selection of Reference Genes for Normalization of MicroRNA Expression by RT-qPCR in Sugarcane Buds under Cold Stress. <i>Frontiers in Plant Science</i> , 2016, 7, 86.	3.6	26
38	Sugarcane Ratooning Ability: Research Status, Shortcomings, and Prospects. <i>Biology</i> , 2021, 10, 1052.	2.8	26
39	A sugarcane R2R3-MYB transcription factor gene is alternatively spliced during drought stress. <i>Scientific Reports</i> , 2017, 7, 41922.	3.3	25
40	Expression Characteristics and Functional Analysis of the ScWRKY3 Gene from Sugarcane. <i>International Journal of Molecular Sciences</i> , 2018, 19, 4059.	4.1	25
41	Transcriptional Insights into the Sugarcane-Sorghum mosaic virus Interaction. <i>Tropical Plant Biology</i> , 2018, 11, 163-176.	1.9	25
42	A TaqMan Real-Time PCR Assay for Detection and Quantification of <i>Sporisorium scitamineum</i> in Sugarcane. <i>Scientific World Journal</i> , The, 2013, 2013, 1-9.	2.1	24
43	Foreign cry1Ac gene integration and endogenous borer stress-related genes synergistically improve insect resistance in sugarcane. <i>BMC Plant Biology</i> , 2018, 18, 342.	3.6	24
44	Sugarcane calcineurin B-like (CBL) genes play important but versatile roles in regulation of responses to biotic and abiotic stresses. <i>Scientific Reports</i> , 2020, 10, 167.	3.3	24
45	Genetic Diversity Analysis of Sugarcane Parents in Chinese Breeding Programmes Using gSSR Markers. <i>Scientific World Journal</i> , The, 2013, 2013, 1-11.	2.1	23
46	Development of Loop-Mediated Isothermal Amplification for Detection of <i>Leifsonia xyli</i> subsp. <i>xyli</i> in Sugarcane. <i>BioMed Research International</i> , 2013, 2013, 1-8.	1.9	22
47	Cry1Ac Transgenic Sugarcane Does Not Affect the Diversity of Microbial Communities and Has No Significant Effect on Enzyme Activities in Rhizosphere Soil within One Crop Season. <i>Frontiers in Plant Science</i> , 2016, 7, 265.	3.6	22
48	Detection of Bar Transgenic Sugarcane with a Rapid and Visual Loop-Mediated Isothermal Amplification Assay. <i>Frontiers in Plant Science</i> , 2016, 7, 279.	3.6	22
49	Rational regional distribution of sugarcane cultivars in China. <i>Scientific Reports</i> , 2015, 5, 15721.	3.3	21
50	A sugarcane pathogenesis-related protein, ScPR10, plays a positive role in defense responses under <i>Sporisorium scitamineum</i> , SrMV, SA, and MeJA stresses. <i>Plant Cell Reports</i> , 2017, 36, 1427-1440.	5.6	21
51	Identification of cold-related miRNAs in sugarcane by small RNA sequencing and functional analysis of a cold inducible ScmiR393 to cold stress. <i>Environmental and Experimental Botany</i> , 2018, 155, 464-476.	4.2	21
52	New insights into the evolution and functional divergence of the CIPK gene family in <i>Saccharum</i> . <i>BMC Genomics</i> , 2020, 21, 868.	2.8	21
53	A sugarcane smut fungus effector simulates the host endogenous elicitor peptide to suppress plant immunity. <i>New Phytologist</i> , 2022, 233, 919-933.	7.3	21
54	A PIP-mediated osmotic stress signaling cascade plays a positive role in the salt tolerance of sugarcane. <i>BMC Plant Biology</i> , 2021, 21, 589.	3.6	21

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55	Straw retention efficiently improves fungal communities and functions in the fallow ecosystem. <i>BMC Microbiology</i> , 2021, 21, 52.	3.3	20
56	Genome-wide identification, characterization and expression analysis of the carotenoid cleavage oxygenase (CCO) gene family in <i>Saccharum</i> . <i>Plant Physiology and Biochemistry</i> , 2021, 162, 196-210.	5.8	20
57	Identification and Characterization of a New Fungal Pathogen Causing Twisted Leaf Disease of Sugarcane in China. <i>Plant Disease</i> , 2015, 99, 325-332.	1.4	19
58	Particle Bombardment of the cry2A Gene Cassette Induces Stem Borer Resistance in Sugarcane. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1692.	4.1	19
59	High-level coproduction, purification and characterisation of laccase and exopolysaccharides by <i>Coriolus versicolor</i> . <i>Food Chemistry</i> , 2014, 159, 208-213.	8.2	17
60	Genome-wide identification, phylogeny, and expression analysis of Sec14-like P1TP gene family in sugarcane. <i>Plant Cell Reports</i> , 2019, 38, 637-655.	5.6	17
61	Development and application of a rapid and visual loop-mediated isothermal amplification for the detection of <i>Sporisorium scitamineum</i> in sugarcane. <i>Scientific Reports</i> , 2016, 6, 23994.	3.3	15
62	The Role of Sugarcane Catalase Gene ScCAT2 in the Defense Response to Pathogen Challenge and Adversity Stress. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2686.	4.1	15
63	Identification and evaluation of PCR reference genes for host and pathogen in sugarcane- <i>Sporisorium scitamineum</i> interaction system. <i>BMC Genomics</i> , 2018, 19, 479.	2.8	14
64	A dynamic degradome landscape on miRNAs and their predicted targets in sugarcane caused by <i>Sporisorium scitamineum</i> stress. <i>BMC Genomics</i> , 2019, 20, 57.	2.8	13
65	ScAOC1, an allene oxide cyclase gene, confers defense response to biotic and abiotic stresses in sugarcane. <i>Plant Cell Reports</i> , 2020, 39, 1785-1801.	5.6	13
66	First Report of <i>Phoma</i> sp. Causing Twisting and Curling of Crown Leaves of Sugarcane in Mainland of China. <i>Plant Disease</i> , 2014, 98, 850-850.	1.4	12
67	Genome-Wide Characterization of Lectin Receptor Kinases in <i>Saccharum spontaneum</i> L. and Their Responses to <i>Stagonospora tainanensis</i> Infection. <i>Plants</i> , 2021, 10, 322.	3.5	11
68	The CaCA superfamily genes in <i>Saccharum</i> : comparative analysis and their functional implications in response to biotic and abiotic stress. <i>BMC Genomics</i> , 2021, 22, 549.	2.8	11
69	A comprehensive survey of the aldehyde dehydrogenase gene superfamily in <i>Saccharum</i> and the role of ScALDH2B-1 in the stress response. <i>Environmental and Experimental Botany</i> , 2022, 194, 104725.	4.2	11
70	Economic Impact of Stem Borer-Resistant Genetically Modified Sugarcane in Guangxi and Yunnan Provinces of China. <i>Sugar Tech</i> , 2016, 18, 537-545.	1.8	10
71	Characterization of the sugarcane MYC gene family and the negative regulatory role of ShMYC4 in response to pathogen stress. <i>Industrial Crops and Products</i> , 2022, 176, 114292.	5.2	10
72	Isolating QTL controlling sugarcane leaf blight resistance using a two-way pseudo-testcross strategy. <i>Crop Journal</i> , 2022, 10, 1131-1140.	5.2	10

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73	A Comprehensive Identification and Expression Analysis of VQ Motif-Containing Proteins in Sugarcane ( <i>Saccharum spontaneum</i> L.) under Phytohormone Treatment and Cold Stress. <i>International Journal of Molecular Sciences</i> , 2022, 23, 6334.	4.1	10
74	cDNA-SRAP and Its Application in Differential Gene Expression Analysis: A Case Study in <i>Erianthus arundinaceus</i> . <i>Journal of Biomedicine and Biotechnology</i> , 2012, 2012, 1-8.	3.0	9
75	Identification of smut-responsive genes in sugarcane using cDNA-SRAP. <i>Genetics and Molecular Research</i> , 2015, 14, 6808-6818.	0.2	9
76	Identification of quantitative trait loci controlling sucrose content based on an enriched genetic linkage map of sugarcane ( <i>Saccharum</i> spp. hybrids) cultivar "LCP 85-384". <i>Euphytica</i> , 2016, 207, 527-549.	1.2	9
77	Heterologous expression of a Glyoxalase I gene from sugarcane confers tolerance to several environmental stresses in bacteria. <i>PeerJ</i> , 2018, 6, e5873.	2.0	9
78	Genetic diversity of <i>Sporisorium scitamineum</i> in mainland China. <i>Sugar Tech</i> , 2004, 6, 267-271.	1.8	8
79	An autopolyploid-suitable polyBSA-seq strategy for screening candidate genetic markers linked to leaf blight resistance in sugarcane. <i>Theoretical and Applied Genetics</i> , 2022, 135, 623-636.	3.6	8
80	Cultivar Evaluation and Essential Test Locations Identification for Sugarcane Breeding in China. <i>Scientific World Journal</i> , The, 2014, 2014, 1-10.	2.1	7
81	Photosynthetic and Canopy Characteristics of Different Varieties at the Early Elongation Stage and Their Relationships with the Cane Yield in Sugarcane. <i>Scientific World Journal</i> , The, 2014, 2014, 1-9.	2.1	7
82	Productivity and Stability of Sugarcane Varieties in the 7th Round National Regional Trial of China. <i>Ying Yong Yu Huan Jing Sheng Wu Xue Bao = Chinese Journal of Applied and Environmental Biology</i> , 2012, 18, 734.	0.1	7
83	Systematic identification of miRNA-regulatory networks unveils their potential roles in sugarcane response to <i>Sorghum</i> mosaic virus infection. <i>BMC Plant Biology</i> , 2022, 22, 247.	3.6	7
84	Seasonal Variation of the Canopy Structure Parameters and Its Correlation with Yield-Related Traits in Sugarcane. <i>Scientific World Journal</i> , The, 2013, 2013, 1-11.	2.1	6
85	Independently Segregating Simple Sequence Repeats (SSR) Alleles in Polyploid Sugarcane. <i>Sugar Tech</i> , 2015, 17, 235-242.	1.8	6
86	SSR-Based Genetic Identity of Sugarcane Clones and its Potential Application in Breeding and Variety Extension. <i>Sugar Tech</i> , 2020, 22, 367-378.	1.8	6
87	Molecular variation of <i>Sporisorium scitamineum</i> in Mainland China revealed by internal transcribed spacers. <i>Genetics and Molecular Research</i> , 2015, 14, 7894-7909.	0.2	6
88	Utilization of a Sugarcane 100K Single Nucleotide Polymorphisms Microarray-Derived High-Density Genetic Map in Quantitative Trait Loci Mapping and Function Role Prediction of Genes Related to Chlorophyll Content in Sugarcane. <i>Frontiers in Plant Science</i> , 2021, 12, 817875.	3.6	6
89	ScMED7, a sugarcane mediator subunit gene, acts as a regulator of plant immunity and is responsive to diverse stress and hormone treatments. <i>Molecular Genetics and Genomics</i> , 2017, 292, 1363-1375.	2.1	5
90	Biogeographical Variation and Population Genetic Structure of <i>Sporisorium scitamineum</i> in Mainland China: Insights from ISSR and SP-SRAP Markers. <i>Scientific World Journal</i> , The, 2014, 2014, 1-13.	2.1	4

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91	A Small GTP-Binding Gene ScRan from Sugarcane is Involved in Responses to Various Hormone Stresses and Sporisorium scitamineum Challenge. Sugar Tech, 2018, 20, 669-680.	1.8	4
92	A Comparative Study of Three Detection Techniques for <i>Leifsonia xyli</i> Subsp. <i>xyli</i> , the Causal Pathogen of Sugarcane Ratoon Stunting Disease. BioMed Research International, 2018, 2018, 1-11.	1.9	4
93	Suitable Reference Genes/miRNAs for qRT-PCR Normalization of Expression Analysis in Sugarcane Under Sorghum mosaic virus Infection. Sugar Tech, 2019, 21, 780-793.	1.8	4
94	The complete mitochondrial genome of sugarcane ( <i>Saccharum</i> spp.) variety FN15. Mitochondrial DNA Part B: Resources, 2020, 5, 2163-2165.	0.4	4
95	Genome-wide identification and expression analysis of the coronatine-insensitive 1 (COI1) gene family in response to biotic and abiotic stresses in <i>Saccharum</i> . BMC Genomics, 2022, 23, 38.	2.8	4
96	The complete mitochondrial genome sequence and phylogenetic analysis of sugarcane ( <i>Saccharum</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.4	3
97	Molecular cloning and expression analysis of a Mn-superoxide dismutase gene in sugarcane. African Journal of Biotechnology, 2012, 11, .	0.6	3
98	Characterization of silicon transporter gene family in <i>Saccharum</i> and functional analysis of the ShLsi6 gene in biotic stress. Gene, 2022, 822, 146331.	2.2	3
99	Expression analysis of transcription factors in sugarcane during cold stress. Brazilian Journal of Biology, 2021, 83, e242603.	0.9	3
100	Characterization and Phylogenetic Analyses of the Complete Mitochondrial Genome of Sugarcane ( <i>Saccharum</i> spp. Hybrids) Line A1. Diversity, 2022, 14, 333.	1.7	3
101	Genome-Wide Characterization of NLRs in <i>Saccharum spontaneum</i> L. and Their Responses to Leaf Blight in <i>Saccharum</i> . Agronomy, 2021, 11, 153.	3.0	2
102	Optimization of SCoT-PCR Reaction System, and Screening and Utilization of Polymorphic Primers in Sugarcane. Ying Yong Yu Huan Jing Sheng Wu Xue Bao = Chinese Journal of Applied and Environmental Biology, 2012, 18, 810.	0.1	2
103	Identification, Expression, and Functional Characterization of ScCaM in Response to Various Stresses in Sugarcane. Agronomy, 2021, 11, 2153.	3.0	2
104	The complete mitochondrial genome and phylogenetic analysis of sugarcane ( <i>Saccharum</i> spp. hybrids) line 15a-53. Mitochondrial DNA Part B: Resources, 2020, 5, 3389-3391.	0.4	1
105	Improved Drought and Salt Tolerance in Transgenic <i>Nicotiana benthamiana</i> by Overexpressing Sugarcane ScSEC14p Gene. Sugar Tech, 2021, 23, 326-335.	1.8	1
106	Identification of <i>Saccharum</i> CaM gene family and function characterization of ScCaM1 during cold and oxidant exposure in <i>Pichia pastoris</i> . Genes and Genomics, 2023, 45, 103-122.	1.4	1