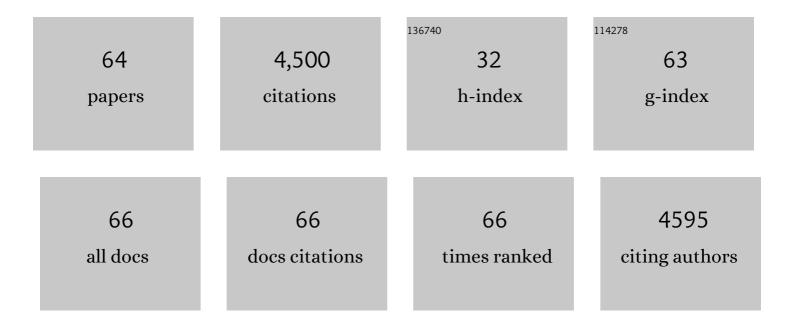
## Xiao-Quan Qi

List of Publications by Year in descending order

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Χιλο-ΟιιλΝ Οι

#	Article	lF	CITATIONS
1	Genomeâ€wide investigation and transcriptional profiling of the oxidosqualene cyclase ( <i>OSC</i> ) genes in wheat ( <i>Triticum aestivum</i> ). Journal of Systematics and Evolution, 2022, 60, 1378-1392.	1.6	2
2	Diverse triterpene skeletons are derived from the expansion and divergent evolution of 2,3-oxidosqualene cyclases in plants. Critical Reviews in Biochemistry and Molecular Biology, 2022, 57, 113-132.	2.3	26
3	Jujube metabolome selection determined the edible properties acquired during domestication. Plant Journal, 2022, 109, 1116-1133.	2.8	25
4	AtPQT11, a P450 enzyme, detoxifies paraquat via N-demethylation. Journal of Genetics and Genomics, 2022, 49, 1169-1173.	1.7	5
5	Improving bread wheat yield through modulating an unselected AP2/ERF gene. Nature Plants, 2022, 8, 930-939.	4.7	23
6	Mining plant metabolomes: Methods, applications, and perspectives. Plant Communications, 2021, 2, 100238.	3.6	16
7	Mapping causal genes and genetic interactions for agronomic traits using a large F2 population in rice. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	5
8	Expansion within the CYP71D subfamily drives the heterocyclization of tanshinones synthesis in Salvia miltiorrhiza. Nature Communications, 2021, 12, 685.	5.8	94
9	Cytochrome P450 family member CYP96B5 hydroxylates alkanes to primary alcohols and is involved in rice leaf cuticular wax synthesis. New Phytologist, 2020, 225, 2094-2107.	3.5	25
10	Characterization of a 2,3â€oxidosqualene cyclase in the toosendanin biosynthetic pathway of <i>Melia toosendan</i> . Physiologia Plantarum, 2020, 170, 528-536.	2.6	14
11	QPMASS: A parallel peak alignment and quantification software for the analysis of large-scale gas chromatography-mass spectrometry (GC-MS)-based metabolomics datasets. Journal of Chromatography A, 2020, 1620, 460999.	1.8	14
12	Improvement of multiplex semi-nested PCR system for screening of rare mutations by high-throughput sequencing. BioTechniques, 2019, 67, 294-298.	0.8	1
13	Orthologous receptor kinases quantitatively affect the host status of barley to leaf rust fungi. Nature Plants, 2019, 5, 1129-1135.	4.7	37
14	An Efficient System for <i>Ds</i> Transposon Tagging in <i>Brachypodium distachyon</i> . Plant Physiology, 2019, 180, 56-65.	2.3	3
15	<i>CsMYB60</i> is a key regulator of flavonols and proanthocyanidans that determine the colour of fruit spines in cucumber. Journal of Experimental Botany, 2019, 70, 69-84.	2.4	40
16	Acclimation-induced metabolic reprogramming contributes to rapid desiccation tolerance acquisition in Boea hygrometrica. Environmental and Experimental Botany, 2018, 148, 70-84.	2.0	23
17	Deficiency of a triterpene pathway results in humidity-sensitive genic male sterility in rice. Nature Communications, 2018, 9, 604.	5.8	50
18	Transcriptomic and metabolic flux analyses reveal shift of metabolic patterns during rice grain development. BMC Systems Biology, 2018, 12, 47.	3.0	10

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19	Identification of key amino acid residues determining product specificity of 2,3â€oxidosqualene cyclase in <i>Oryza</i> species. New Phytologist, 2018, 218, 1076-1088.	3.5	39
20	Highly efficient generation of T-DNA insertion lines and isolation of flanking sequence tags (FSTs) of Brachypodium distachyon. Plant Biotechnology Reports, 2018, 12, 237-248.	0.9	3
21	Targeted mutagenesis in the medicinal plant Salvia miltiorrhiza. Scientific Reports, 2017, 7, 43320.	1.6	123
22	A brief view of international conference on plant cell wall biology 2017. Science Bulletin, 2017, 62, 1357-1358.	4.3	1
23	Discrimination and Quantification of True Biological Signals in Metabolomics Analysis Based on Liquid Chromatography-Mass Spectrometry. Molecular Plant, 2016, 9, 1217-1220.	3.9	19
24	Brachypodium distachyon T-DNA insertion lines: a model pathosystem to study nonhost resistance to wheat stripe rust. Scientific Reports, 2016, 6, 25510.	1.6	32
25	Analysis of the Genome Sequence of the Medicinal Plant Salvia miltiorrhiza. Molecular Plant, 2016, 9, 949-952.	3.9	255
26	Quantitative Resistance to Biotrophic Filamentous Plant Pathogens: Concepts, Misconceptions, and Mechanisms. Annual Review of Phytopathology, 2015, 53, 445-470.	3.5	201
27	Comparative physiological and metabolomic responses of four Brachypodium distachyon varieties contrasting in drought stress resistance. Acta Physiologiae Plantarum, 2015, 37, 1.	1.0	19
28	Functional divergence of diterpene syntheses in the medicinal plant Salvia miltiorrhiza Bunge. Plant Physiology, 2015, 169, pp.00695.2015.	2.3	118
29	Systematic Analysis and Identification of Stress-Responsive Genes of the NAC Gene Family in Brachypodium distachyon. PLoS ONE, 2015, 10, e0122027.	1.1	61
30	Biosynthesis, regulation, and domestication of bitterness in cucumber. Science, 2014, 346, 1084-1088.	6.0	388
31	Plant metabolomics and metabolic biology. Journal of Integrative Plant Biology, 2014, 56, 814-815.	4.1	7
32	Identification and fine mapping of quantitative trait loci for seed vigor in germination and seedling establishment in rice. Journal of Integrative Plant Biology, 2014, 56, 749-759.	4.1	91
33	Discovery of rare mutations in extensively pooled DNA samples using multiple target enrichment. Plant Biotechnology Journal, 2014, 12, 709-717.	4.1	13
34	Arabidopsis Plastidial Folylpolyglutamate Synthetase Is Required for Seed Reserve Accumulation and Seedling Establishment in Darkness. PLoS ONE, 2014, 9, e101905.	1.1	20
35	Modularity of Plant Metabolic Gene Clusters: A Trio of Linked Genes That Are Collectively Required for Acylation of Triterpenes in Oat Â. Plant Cell, 2013, 25, 1078-1092.	3.1	100

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37	Functional Analysis of a Rice Oxidosqualene Cyclase through Total Gene Synthesis. Molecular Plant, 2013, 6, 1726-1729.	3.9	9
38	Glycosyltransferases from oat (Avena) implicated in the acylation of avenacins Journal of Biological Chemistry, 2013, 288, 19644.	1.6	0
39	Glycosyltransferases from Oat (Avena) Implicated in the Acylation of Avenacins. Journal of Biological Chemistry, 2013, 288, 3696-3704.	1.6	35
40	Multiple samples alignment for GC-MS data in parallel on Sector/Sphere. Journal of Computer Applications, 2013, 33, 215-218.	0.1	1
41	Use of the Metabolomics Approach to Characterize Chinese Medicinal Material Huangqi. Molecular Plant, 2012, 5, 376-386.	3.9	95
42	Finding and Analyzing Plant Metabolic Gene Clusters. Methods in Enzymology, 2012, 517, 113-138.	0.4	20
43	Divergent evolution of oxidosqualene cyclases in plants. New Phytologist, 2012, 193, 1022-1038.	3.5	122
44	ldentification and Validation of a Major Quantitative Trait Locus for Slowâ€rusting Resistance to Stripe Rust in Wheat <sup>F</sup> . Journal of Integrative Plant Biology, 2012, 54, 330-344.	4.1	23
45	The phenotypic expression of QTLs for partial resistance to barley leaf rust during plant development. Theoretical and Applied Genetics, 2010, 121, 857-864.	1.8	20
46	Genes encoding hub and bottleneck enzymes of the Arabidopsis metabolic network preferentially retain homeologs through whole genome duplication. BMC Evolutionary Biology, 2010, 10, 145.	3.2	22
47	A Serine Carboxypeptidase-Like Acyltransferase Is Required for Synthesis of Antimicrobial Compounds and Disease Resistance in Oats Â. Plant Cell, 2009, 21, 2473-2484.	3.1	149
48	Signaling in Plant Disease Resistance and Symbiosis. Journal of Integrative Plant Biology, 2008, 50, 799-807.	4.1	37
49	<i>Sad3</i> and <i>Sad4</i> Are Required for Saponin Biosynthesis and Root Development in Oat. Plant Cell, 2008, 20, 201-212.	3.1	110
50	A different function for a member of an ancient and highly conserved cytochrome P450 family: From essential sterols to plant defense. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 18848-18853.	3.3	169
51	Ligation–mediated rolling–circle amplification–based approaches to single nucleotide polymorphism detection. Expert Review of Molecular Diagnostics, 2005, 5, 111-116.	1.5	14
52	A gene cluster for secondary metabolism in oat: Implications for the evolution of metabolic diversity in plants. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 8233-8238.	3.3	271
53	An integrated genetic map and a new set of simple sequence repeat markers for pearl millet, Pennisetum glaucum. Theoretical and Applied Genetics, 2004, 109, 1485-1493.	1.8	121
54	Dissecting plant secondary metabolism – constitutive chemical defences in cereals. New Phytologist, 2003, 159, 101-108.	3.5	85

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55	Construction of a BAC library of pearl millet, Pennisetum glaucum. Theoretical and Applied Genetics, 2001, 102, 1200-1205.	1.8	102
56	L-RCA (ligation-rolling circle amplification): a general method for genotyping of single nucleotide polymorphisms (SNPs). Nucleic Acids Research, 2001, 29, 116e-116.	6.5	97
57	A new class of oxidosqualene cyclases directs synthesis of antimicrobial phytoprotectants in monocots. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 13431-13436.	3.3	157
58	The evidence for abundance of QTLs for partial resistance to Puccinia hordei on the barley genome. Molecular Breeding, 2000, 6, 1-9.	1.0	52
59	Isolate-specific QTLs for partial resistance to Puccinia hordei in barley. Theoretical and Applied Genetics, 1999, 99, 877-884.	1.8	92
60	Use of locus-specific AFLP markers to construct a high-density molecular map in barley. Theoretical and Applied Genetics, 1998, 96, 376-384.	1.8	193
61	Identification of QTLs for partial resistance to leaf rust (Puccinia hordei) in barley. Theoretical and Applied Genetics, 1998, 96, 1205-1215.	1.8	162
62	Development of AFLP markers in barley. Molecular Genetics and Genomics, 1997, 254, 330-336.	2.4	104
63	Association between relationship measures based on AFLP markers, pedigree data and morphological traits in barley. Theoretical and Applied Genetics, 1997, 95, 1161-1168.	1.8	145
64	Comparison and integration of four barley genetic maps. Genome, 1996, 39, 379-394.	0.9	186