

# Qi You

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3045692/publications.pdf>

Version: 2024-02-01

21  
papers

3,062  
citations

516710

16  
h-index

677142

22  
g-index

23  
all docs

23  
docs citations

23  
times ranked

5078  
citing authors

#	ARTICLE	IF	CITATIONS
1	Evaluation and application of tools for the identification of known microRNAs in plants. Applications in Plant Sciences, 2021, 9, e11414.	2.1	8
2	Bidirectional Promoter-Based CRISPR-Cas9 Systems for Plant Genome Editing. Frontiers in Plant Science, 2019, 10, 1173.	3.6	39
3	Plant Genome Editing Using FnCpf1 and LbCpf1 Nucleases at Redefined and Altered PAM Sites. Molecular Plant, 2018, 11, 999-1002.	8.3	136
4	PCSD: a plant chromatin state database. Nucleic Acids Research, 2018, 46, D1157-D1167.	14.5	107
5	PlantEAR: Functional Analysis Platform for Plant EAR Motif-Containing Proteins. Frontiers in Genetics, 2018, 9, 590.	2.3	52
6	Co-expression Gene Network Analysis and Functional Module Identification in Bamboo Growth and Development. Frontiers in Genetics, 2018, 9, 574.	2.3	85
7	A large-scale whole-genome sequencing analysis reveals highly specific genome editing by both Cas9 and Cpf1 (Cas12a) nucleases in rice. Genome Biology, 2018, 19, 84.	8.8	230
8	CRISPRMatch: An Automatic Calculation and Visualization Tool for High-throughput CRISPR Genome-editing Data Analysis. International Journal of Biological Sciences, 2018, 14, 858-862.	6.4	53
9	MCENet: A database for maize conditional co-expression network and network characterization collaborated with multi-dimensional omics levels. Journal of Genetics and Genomics, 2018, 45, 351-360.	3.9	39
10	agriGO v2.0: a GO analysis toolkit for the agricultural community, 2017 update. Nucleic Acids Research, 2017, 45, W122-W129.	14.5	1,872
11	A systemic identification approach for primary transcription start site of Arabidopsis miRNAs from multidimensional omics data. Functional and Integrative Genomics, 2017, 17, 353-363.	3.5	4
12	Genome-wide comparative analysis of H3K4me3 profiles between diploid and allotetraploid cotton to refine genome annotation. Scientific Reports, 2017, 7, 9098.	3.3	10
13	Genome-wide mapping of DNase I hypersensitive sites reveals chromatin accessibility changes in Arabidopsis euchromatin and heterochromatin regions under extended darkness. Scientific Reports, 2017, 7, 4093.	3.3	19
14	ccNET: Database of co-expression networks with functional modules for diploid and polyploid <i>Gossypium</i> . Nucleic Acids Research, 2017, 45, D1090-D1099.	14.5	89
15	Histone modifications facilitate the coexpression of bidirectional promoters in rice. BMC Genomics, 2016, 17, 768.	2.8	10
16	Co-expression network analyses identify functional modules associated with development and stress response in <i>Gossypium arboreum</i> . Scientific Reports, 2016, 6, 38436.	3.3	46
17	SorghumFDB: sorghum functional genomics database with multidimensional network analysis. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw099.	3.0	47
18	JAZ7 negatively regulates dark-induced leaf senescence in <i>Arabidopsis</i> . Journal of Experimental Botany, 2016, 67, 751-762.	4.8	113

#	ARTICLE	IF	CITATIONS
19	GraP: platform for functional genomics analysis of <i>Gossypium raimondii</i> . Database: the Journal of Biological Databases and Curation, 2015, 2015, bav047.	3.0	14
20	SIFGD: <i>Setaria italica</i> Functional Genomics Database. Molecular Plant, 2015, 8, 967-970.	8.3	37
21	Precise spatio-temporal modulation of ACC synthase by MPK6 cascade mediates the response of rose flowers to rehydration. Plant Journal, 2014, 79, 941-950.	5.7	39