Qi You

List of Publications by Year
in descending order

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	agriGO v2.0: a GO analysis toolkit for the agricultural community, 2017 update. Nucleic Acids Research, 2017, 45, W122-W129.	14.5	1,872
2	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
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	JAZ7 negatively regulates dark-induced leaf senescence in*Arabidopsis*. Journal of Experimental Botany, 2016, 67, 751-762.	4.8	113
5	PCSD: a plant chromatin state database. Nucleic Acids Research, 2018, 46, D1157-D1167.	14.5	107
6	ccNET: Database of co-expression networks with functional modules for diploid and polyploid*Gossypium*. Nucleic Acids Research, 2017, 45, D1090-D1099.	14.5	89
7	Co-expression Gene Network Analysis and Functional Module Identification in Bamboo Growth and Development. Frontiers in Genetics, 2018, 9, 574.	2.3	85
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	PlantEAR: Functional Analysis Platform for Plant EAR Motif-Containing Proteins. Frontiers in Genetics, 2018, 9, 590.	2.3	52
10	SorghumFDB: sorghum functional genomics database with multidimensional network analysis. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw099.	3.0	47
11	Co-expression network analyses identify functional modules associated with development and stress response in Gossypium arboreum. Scientific Reports, 2016, 6, 38436.	3.3	46
12	Precise spatio–temporal modulation of <scp>ACC</scp> synthase by <scp>MPK</scp>6 cascade mediates the response of rose flowers to rehydration. Plant Journal, 2014, 79, 941-950.	5.7	39
13	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
14	Bidirectional Promoter-Based CRISPR-Cas9 Systems for Plant Genome Editing. Frontiers in Plant Science, 2019, 10, 1173.	3.6	39
15	SIFGD: Setaria italica Functional Genomics Database. Molecular Plant, 2015, 8, 967-970.	8.3	37
16	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
17	GraP: platform for functional genomics analysis of Gossypium raimondii. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav047.	3.0	14
18	Histone modifications facilitate the coexpression of bidirectional promoters in rice. BMC Genomics, 2016, 17, 768.	2.8	10

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19	Genome-wide comparative analysis of H3K4me3 profiles between diploid and allotetraploid cotton to refine genome annotation. Scientific Reports, 2017, 7, 9098.	3.3	10
20	Evaluation and application of tools for the identification of known microRNAs in plants. Applications in Plant Sciences, 2021, 9, e11414.	2.1	8
21	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