

# Renhai Peng

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1396967/publications.pdf>

Version: 2024-02-01

28  
papers

477  
citations

759233

12  
h-index

752698

20  
g-index

28  
all docs

28  
docs citations

28  
times ranked

475  
citing authors

#	ARTICLE	IF	CITATIONS
1	Protoplast Dissociation and Transcriptome Analysis Provides Insights to Salt Stress Response in Cotton. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2845.	4.1	13
2	Conservation and Divergence of Phosphoenolpyruvate Carboxylase Gene Family in Cotton. <i>Plants</i> , 2022, 11, 1482.	3.5	1
3	From Sequencing to Genome Editing for Cotton Improvement. <i>Trends in Biotechnology</i> , 2021, 39, 221-224.	9.3	27
4	Foxtail Millet: A New Model for C4 Plants. <i>Trends in Plant Science</i> , 2021, 26, 199-201.	8.8	50
5	Systematical characterization of YUCCA gene family in five cotton species, and potential functions of YUCCA22 gene in drought resistance of cotton. <i>Industrial Crops and Products</i> , 2021, 162, 113290.	5.2	8
6	Genome-wide identification of the MIOX gene family and their expression profile in cotton development and response to abiotic stress. <i>PLoS ONE</i> , 2021, 16, e0254111.	2.5	9
7	Functional Characterization of GhACX3 Gene Reveals Its Significant Role in Enhancing Drought and Salt Stress Tolerance in Cotton. <i>Frontiers in Plant Science</i> , 2021, 12, 658755.	3.6	15
8	DNA Methylation and RNA-Sequencing Analysis Show Epigenetic Function During Grain Filling in Foxtail Millet ( <i>Setaria italica</i> L.). <i>Frontiers in Plant Science</i> , 2021, 12, 741415.	3.6	4
9	Identification of the Golden-2-like transcription factors gene family in <i>Gossypium hirsutum</i> . <i>PeerJ</i> , 2021, 9, e12484.	2.0	9
10	GhGLK1 a Key Candidate Gene From GARP Family Enhances Cold and Drought Stress Tolerance in Cotton. <i>Frontiers in Plant Science</i> , 2021, 12, 759312.	3.6	17
11	High throughput deep sequencing elucidates the important role of lncRNAs in Foxtail millet response to herbicides. <i>Genomics</i> , 2020, 112, 4463-4473.	2.9	8
12	Transcriptome Analysis Provides Insights into Grain Filling in Foxtail Millet ( <i>Setaria italica</i> L.). <i>International Journal of Molecular Sciences</i> , 2020, 21, 5031.	4.1	10
13	Identification of a genome-specific repetitive element in the <i>Gossypium</i> D genome. <i>PeerJ</i> , 2020, 8, e8344.	2.0	2
14	Genome-wide analysis of the cotton G-coupled receptor proteins (GPCR) and functional analysis of GTOM1, a novel cotton GPCR gene under drought and cold stress. <i>BMC Genomics</i> , 2019, 20, 651.	2.8	21
15	Functional characterization of Gh_A08G1120 (GH3.5) gene reveal their significant role in enhancing drought and salt stress tolerance in cotton. <i>BMC Genetics</i> , 2019, 20, 62.	2.7	39
16	Genome-Wide Mining and Identification of Protein Kinase Gene Family Impacts Salinity Stress Tolerance in Highly Dense Genetic Map Developed from Interspecific Cross between <i>G. hirsutum</i> L. and <i>G. darwinii</i> G. Watt. <i>Agronomy</i> , 2019, 9, 560.	3.0	21
17	Knockdown of Cytochrome P450 Genes Gh_D07G1197 and Gh_A13G2057 on Chromosomes D07 and A13 Reveals Their Putative Role in Enhancing Drought and Salt Stress Tolerance in <i>Gossypium hirsutum</i> . <i>Genes</i> , 2019, 10, 226.	2.4	52
18	RNA-Sequencing, Physiological and RNAi Analyses Provide Insights into the Response Mechanism of the ABC-Mediated Resistance to <i>Verticillium dahliae</i> Infection in Cotton. <i>Genes</i> , 2019, 10, 110.	2.4	31

#	ARTICLE	IF	CITATIONS
19	Genome-wide identification, characterization, and expression analysis of superoxide dismutase (SOD) genes in foxtail millet ( <i>Setaria italica</i> L.). <i>3 Biotech</i> , 2018, 8, 486.	2.2	23
20	Construction and characterization of a bacterial artificial chromosome library for <i>Gossypium mustelinum</i> . <i>PLoS ONE</i> , 2018, 13, e0196847.	2.5	3
21	Genome-Wide Analysis of Multidrug and Toxic Compound Extrusion ( <i>MATE</i> ) Family in <i>Gossypium raimondii</i> and <i>Gossypium arboreum</i> and Its Expression Analysis Under Salt, Cadmium, and Drought Stress. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2483-2500.	1.8	56
22	Genome-Wide Survey and Comparative Analysis of Long Terminal Repeat (LTR) Retrotransposon Families in Four <i>Gossypium</i> Species. <i>Scientific Reports</i> , 2018, 8, 9399.	3.3	11
23	Cytogenetic maps of homoeologous chromosomes A h01 and D h01 and their integration with the genome assembly in <i>Gossypium hirsutum</i> . <i>Comparative Cytogenetics</i> , 2017, 11, 405-420.	0.8	2
24	A <i>Gossypium</i> BAC clone contains key repeat components distinguishing sub-genome of allotetraploidy cottons. <i>Molecular Cytogenetics</i> , 2016, 9, 27.	0.9	6
25	Genome-wide characterization and comparative analysis of the MLO gene family in cotton. <i>Plant Physiology and Biochemistry</i> , 2016, 103, 106-119.	5.8	12
26	Construction of cytogenetic map of <i>Gossypium herbaceum</i> chromosome 1 and its integration with genetic maps. <i>Molecular Cytogenetics</i> , 2015, 8, 2.	0.9	8
27	Construction of a bacterial artificial chromosome library for <i>Gossypium herbaceum</i> var. <i>africanum</i> . <i>Science Bulletin</i> , 2013, 58, 3199-3201.	1.7	4
28	Individual chromosome identification, chromosomal collinearity and genetic-physical integrated map in <i>Gossypium darwinii</i> and four D genome cotton species revealed by BAC-FISH. <i>Genes and Genetic Systems</i> , 2012, 87, 233-241.	0.7	15