

# Fei He

## List of Publications by Year in descending order

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Version: 2024-02-01

43  
papers

3,587  
citations

236925

25  
h-index

243625

44  
g-index

51  
all docs

51  
docs citations

51  
times ranked

5268  
citing authors

#	ARTICLE	IF	CITATIONS
1	KBase: The United States Department of Energy Systems Biology Knowledgebase. <i>Nature Biotechnology</i> , 2018, 36, 566-569.	17.5	955
2	Exogenous spermidine improves seed germination of sweet corn via involvement in phytohormone interactions, H <sub>2</sub> O <sub>2</sub> and relevant gene expression. <i>BMC Plant Biology</i> , 2017, 17, 1.	3.6	314
3	<i>Badh2</i> , Encoding Betaine Aldehyde Dehydrogenase, Inhibits the Biosynthesis of 2-Acetyl-1-Pyrroline, a Major Component in Rice Fragrance. <i>Plant Cell</i> , 2008, 20, 1850-1861.	6.6	267
4	Transgenerational CRISPR-Cas9 Activity Facilitates Multiplex Gene Editing in Allopolyploid Wheat. <i>CRISPR Journal</i> , 2018, 1, 65-74.	2.9	248
5	Exome sequencing highlights the role of wild-relative introgression in shaping the adaptive landscape of the wheat genome. <i>Nature Genetics</i> , 2019, 51, 896-904.	21.4	225
6	Gene editing and mutagenesis reveal inter-cultivar differences and additivity in the contribution of TaGW2 homologues to grain size and weight in wheat. <i>Theoretical and Applied Genetics</i> , 2018, 131, 2463-2475.	3.6	142
7	The <i>Bifidobacterium dentium</i> Bd1 Genome Sequence Reflects Its Genetic Adaptation to the Human Oral Cavity. <i>PLoS Genetics</i> , 2009, 5, e1000785.	3.5	141
8	The genetic architecture of genome-wide recombination rate variation in allopolyploid wheat revealed by nested association mapping. <i>Plant Journal</i> , 2018, 95, 1039-1054.	5.7	97
9	Gene editing of the wheat homologs of <i>TONNEAU1</i> recruiting motif encoding gene affects grain shape and weight in wheat. <i>Plant Journal</i> , 2019, 100, 251-264.	5.7	97
10	Cold plasma treatment and exogenous salicylic acid priming enhances salinity tolerance of <i>Oryza sativa</i> seedlings. <i>Protoplasma</i> , 2019, 256, 79-99.	2.1	90
11	De Novo Inference of Systems-Level Mechanistic Models of Development from Live-Imaging-Based Phenotype Analysis. <i>Cell</i> , 2014, 156, 359-372.	28.9	89
12	Genetic analysis and morphological identification of pilus-like structures in members of the genus <i>Bifidobacterium</i> . <i>Microbial Cell Factories</i> , 2011, 10, S16.	4.0	84
13	Analysis of Complete Nucleotide Sequences of 12 <i>Gossypium</i> Chloroplast Genomes: Origin and Evolution of Allotetraploids. <i>PLoS ONE</i> , 2012, 7, e37128.	2.5	78
14	The prediction of protein-protein interaction networks in rice blast fungus. <i>BMC Genomics</i> , 2008, 9, 519.	2.8	77
15	The Regulatory Landscape of Lineage Differentiation in a Metazoan Embryo. <i>Developmental Cell</i> , 2015, 34, 592-607.	7.0	53
16	Regulation of ZnO nanoparticles-induced physiological and molecular changes by seed priming with humic acid in <i>Oryza sativa</i> seedlings. <i>Plant Growth Regulation</i> , 2017, 83, 27-41.	3.4	51
17	Large-scale atlas of microarray data reveals the distinct expression landscape of different tissues in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2016, 86, 472-480.	5.7	39
18	Maize annexin genes <i>ZmANN33</i> and <i>ZmANN35</i> encode proteins that function in cell membrane recovery during seed germination. <i>Journal of Experimental Botany</i> , 2019, 70, 1183-1195.	4.8	37

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19	Prediction of protein-protein interactions between <i>Ralstonia solanacearum</i> and <i>Arabidopsis thaliana</i> . <i>Amino Acids</i> , 2012, 42, 2363-2371.	2.7	36
20	Pan- and core- network analysis of co-expression genes in a model plant. <i>Scientific Reports</i> , 2016, 6, 38956.	3.3	36
21	Systematic comparison of lncRNAs with protein coding mRNAs in population expression and their response to environmental change. <i>BMC Plant Biology</i> , 2017, 17, 42.	3.6	36
22	Differential chromatin accessibility landscape reveals structural and functional features of the allopolyploid wheat chromosomes. <i>Genome Biology</i> , 2020, 21, 176.	8.8	35
23	Genomic variants affecting homoeologous gene expression dosage contribute to agronomic trait variation in allopolyploid wheat. <i>Nature Communications</i> , 2022, 13, 826.	12.8	31
24	A predicted protein-protein interaction network of the filamentous fungus <i>Neurospora crassa</i> . <i>Molecular BioSystems</i> , 2011, 7, 2278.	2.9	29
25	Can simple codon pair usage predict protein-protein interaction?. <i>Molecular BioSystems</i> , 2012, 8, 1396.	2.9	28
26	Transcriptome Analysis of Chilling-Imbibed Embryo Revealed Membrane Recovery Related Genes in Maize. <i>Frontiers in Plant Science</i> , 2016, 7, 1978.	3.6	28
27	E3 ubiquitin ligases promote progression of differentiation during <i>C. elegans</i> embryogenesis. <i>Developmental Biology</i> , 2015, 398, 267-279.	2.0	25
28	Differential Coexpression Analysis Reveals Extensive Rewiring of Arabidopsis Gene Coexpression in Response to <i>Pseudomonas syringae</i> Infection. <i>Scientific Reports</i> , 2016, 6, 35064.	3.3	25
29	Deciphering the Arabidopsis Floral Transition Process by Integrating a Protein-Protein Interaction Network and Gene Expression Data. <i>Plant Physiology</i> , 2010, 153, 1492-1505.	4.8	24
30	On-Off Thermo-responsive Coating Agent Containing Salicylic Acid Applied to Maize Seeds for Chilling Tolerance. <i>PLoS ONE</i> , 2015, 10, e0120695.	2.5	24
31	Divergent and convergent modes of interaction between wheat and <i>Puccinia graminis</i> f. sp. <i>tritici</i> isolates revealed by the comparative gene co-expression network and genome analyses. <i>BMC Genomics</i> , 2017, 18, 291.	2.8	20
32	PlaD: A Transcriptomics Database for Plant Defense Responses to Pathogens, Providing New Insights into Plant Immune System. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 283-293.	6.9	19
33	Large-scale transcriptome analysis reveals arabidopsis metabolic pathways are frequently influenced by different pathogens. <i>Plant Molecular Biology</i> , 2017, 94, 453-467.	3.9	16
34	Expanding the range of editable targets in the wheat genome using the variants of the Cas12a and Cas9 nucleases. <i>Plant Biotechnology Journal</i> , 2021, 19, 2428-2441.	8.3	16
35	Whole-genome sequencing of multiple isolates of <i>Puccinia triticina</i> reveals asexual lineages evolving by recurrent mutations. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	13
36	Multivariable regulation of gene expression plasticity in metazoans. <i>Open Biology</i> , 2019, 9, 190150.	3.6	11

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37	Large-Scale Public Transcriptomic Data Mining Reveals a Tight Connection between the Transport of Nitrogen and Other Transport Processes in Arabidopsis. <i>Frontiers in Plant Science</i> , 2016, 7, 1207.	3.6	9
38	Development of the Wheat Practical Haplotype Graph database as a resource for genotyping data storage and genotype imputation. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	7
39	The Haplotype-Based Analysis of <i>Aegilops tauschii</i> Introgression Into Hard Red Winter Wheat and Its Impact on Productivity Traits. <i>Frontiers in Plant Science</i> , 2021, 12, 716955.	3.6	6
40	DREISS: Using State-Space Models to Infer the Dynamics of Gene Expression Driven by External and Internal Regulatory Networks. <i>PLoS Computational Biology</i> , 2016, 12, e1005146.	3.2	6
41	An Important Role for Purifying Selection in Archaeal Genome Evolution. <i>MSystems</i> , 2017, 2, .	3.8	5
42	Combination of specific single chain antibody variable fragment and siRNA has a synergistic inhibitory effect on the propagation of avian influenza virus H5N1 in chicken cells. <i>Virology Journal</i> , 2014, 11, 208.	3.4	1
43	Critical roles of amino acids Ser231, His107 and Asp156 of <i>Staphylococcus sciuri</i> exfoliative toxin C (ExhC) in the induction of skin exfoliations in neonate mice. <i>Biologia (Poland)</i> , 2011, 66, 1189-1195.	1.5	0