

# Bo Wang

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2831757/publications.pdf>

Version: 2024-02-01

24  
papers

3,787  
citations

516215

16  
h-index

610482

24  
g-index

29  
all docs

29  
docs citations

29  
times ranked

5462  
citing authors

#	ARTICLE	IF	CITATIONS
1	A global survey of the transcriptome of the opium poppy ( <i>Papaver somniferum</i> ) based on single-molecule long-read isoform sequencing. <i>Plant Journal</i> , 2022, 110, 607-620.	2.8	5
2	SorghumBase: a web-based portal for sorghum genetic information and community advancement. <i>Planta</i> , 2022, 255, 35.	1.6	12
3	IAGS: Inferring Ancestor Genome Structure under a Wide Range of Evolutionary Scenarios. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	5
4	Gramene 2021: harnessing the power of comparative genomics and pathways for plant research. <i>Nucleic Acids Research</i> , 2021, 49, D1452-D1463.	6.5	83
5	Genome assembly and population genomic analysis provide insights into the evolution of modern sweet corn. <i>Nature Communications</i> , 2021, 12, 1227.	5.8	37
6	Chromosome-level genome assembly of a regenerable maize inbred line A188. <i>Genome Biology</i> , 2021, 22, 175.	3.8	32
7	Genome assembly of the Chinese maize elite inbred line RP125 and its EMS mutant collection provide new resources for maize genetics research and crop improvement. <i>Plant Journal</i> , 2021, 108, 40-54.	2.8	18
8	De novo assembly, annotation, and comparative analysis of 26 diverse maize genomes. <i>Science</i> , 2021, 373, 655-662.	6.0	282
9	Transcriptome analyses provide insights into the effect of temperature change on fiber quality of ramie. <i>Industrial Crops and Products</i> , 2020, 152, 112544.	2.5	6
10	Variant phasing and haplotypic expression from long-read sequencing in maize. <i>Communications Biology</i> , 2020, 3, 78.	2.0	20
11	Reviving the Transcriptome Studies: An Insight Into the Emergence of Single-Molecule Transcriptome Sequencing. <i>Frontiers in Genetics</i> , 2019, 10, 384.	1.1	112
12	Gramene 2018: unifying comparative genomics and pathway resources for plant research. <i>Nucleic Acids Research</i> , 2018, 46, D1181-D1189.	6.5	147
13	Construction of the third-generation <i>Zea mays</i> haplotype map. <i>GigaScience</i> , 2018, 7, 1-12.	3.3	191
14	A comparative transcriptional landscape of maize and sorghum obtained by single-molecule sequencing. <i>Genome Research</i> , 2018, 28, 921-932.	2.4	76
15	Extensive intraspecific gene order and gene structural variations between Mo17 and other maize genomes. <i>Nature Genetics</i> , 2018, 50, 1289-1295.	9.4	335
16	Improved maize reference genome with single-molecule technologies. <i>Nature</i> , 2017, 546, 524-527.	13.7	1,113
17	A Sorghum Mutant Resource as an Efficient Platform for Gene Discovery in Grasses. <i>Plant Cell</i> , 2016, 28, tpc.00373.2016.	3.1	113
18	Unveiling the complexity of the maize transcriptome by single-molecule long-read sequencing. <i>Nature Communications</i> , 2016, 7, 11708.	5.8	510

#	ARTICLE	IF	CITATIONS
19	Gramene 2016: comparative plant genomics and pathway resources. <i>Nucleic Acids Research</i> , 2016, 44, D1133-D1140.	6.5	138
20	Expression and functional analysis of genes encoding cytokinin receptor-like histidine kinase in maize ( <i>Zea mays</i> L.). <i>Molecular Genetics and Genomics</i> , 2014, 289, 501-512.	1.0	14
21	Maize ( <i>Zea mays</i> L.) seedling leaf nuclear proteome and differentially expressed proteins between a hybrid and its parental lines. <i>Proteomics</i> , 2014, 14, 1071-1087.	1.3	24
22	A novel histidine kinase gene, ZmHK9, mediate drought tolerance through the regulation of stomatal development in <i>Arabidopsis</i> . <i>Gene</i> , 2012, 501, 171-179.	1.0	17
23	Comparative Proteomic Analysis of Wheat Response to Powdery Mildew Infection in Wheat <i>Pm30</i> Near-Isogenic Lines. <i>Journal of Phytopathology</i> , 2012, 160, 229-236.	0.5	10
24	Genome-wide patterns of genetic variation among elite maize inbred lines. <i>Nature Genetics</i> , 2010, 42, 1027-1030.	9.4	439