

# Yan Fu

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11595556/publications.pdf>

Version: 2024-02-01

16  
papers

5,712  
citations

567144

15  
h-index

940416

16  
g-index

16  
all docs

16  
docs citations

16  
times ranked

7679  
citing authors

#	ARTICLE	IF	CITATIONS
1	The B73 Maize Genome: Complexity, Diversity, and Dynamics. <i>Science</i> , 2009, 326, 1112-1115.	6.0	3,612
2	Maize Inbreds Exhibit High Levels of Copy Number Variation (CNV) and Presence/Absence Variation (PAV) in Genome Content. <i>PLoS Genetics</i> , 2009, 5, e1000734.	1.5	484
3	Genome-wide patterns of genetic variation among elite maize inbred lines. <i>Nature Genetics</i> , 2010, 42, 1027-1030.	9.4	439
4	Genome-wide analyses of alternative splicing in plants: Opportunities and challenges. <i>Genome Research</i> , 2008, 18, 1381-1392.	2.4	348
5	Mu Transposon Insertion Sites and Meiotic Recombination Events Co-Localize with Epigenetic Marks for Open Chromatin across the Maize Genome. <i>PLoS Genetics</i> , 2009, 5, e1000733.	1.5	196
6	Transcriptomic and Proteomic Analyses of Pericycle Cells of the Maize Primary Root. <i>Plant Physiology</i> , 2007, 145, 575-588.	2.3	144
7	Repeat subtraction-mediated sequence capture from a complex genome. <i>Plant Journal</i> , 2010, 62, 898-909.	2.8	89
8	Genetic Dissection of Intermated Recombinant Inbred Lines Using a New Genetic Map of Maize. <i>Genetics</i> , 2006, 174, 1671-1683.	1.2	79
9	Quality assessment of maize assembled genomic islands (MAGIs) and large-scale experimental verification of predicted genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 12282-12287.	3.3	67
10	Nearly Identical Paralogs: Implications for Maize ( <i>Zea mays</i> L.) Genome Evolution. <i>Genetics</i> , 2007, 175, 429-439.	1.2	60
11	A strategy for assembling the maize ( <i>Zea mays</i> L.) genome. <i>Bioinformatics</i> , 2004, 20, 140-147.	1.8	55
12	Evaluation of five ab initio gene prediction programs for the discovery of maize genes. <i>Plant Molecular Biology</i> , 2005, 57, 445-460.	2.0	45
13	Alternative splicing of anciently exonized 5S rRNA regulates plant transcription factor TFIIIA. <i>Genome Research</i> , 2009, 19, 913-921.	2.4	34
14	Comparative Transcriptome Profiling of Maize Coleoptilar Nodes during Shoot-Borne Root Initiation. <i>Plant Physiology</i> , 2013, 163, 419-430.	2.3	25
15	Types and Frequencies of Sequencing Errors in Methyl-Filtered and High C0t Maize Genome Survey Sequences. <i>Plant Physiology</i> , 2004, 135, 2040-2045.	2.3	24
16	High-Resolution Genotyping via Whole Genome Hybridizations to Microarrays Containing Long Oligonucleotide Probes. <i>PLoS ONE</i> , 2010, 5, e14178.	1.1	11