Yan Fu

List of Publications by Year
in descending order

16 papers	5,712 citations	643344 15 h-index	1051228 16 g-index
16 all docs	16 docs citations	16 times ranked	8638 citing authors

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