

# Lin Li

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6472352/publications.pdf>

Version: 2024-02-01

22  
papers

1,696  
citations

687363

13  
h-index

677142

22  
g-index

22  
all docs

22  
docs citations

22  
times ranked

2188  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide discovery and characterization of maize long non-coding RNAs. <i>Genome Biology</i> , 2014, 15, R40.	9.6	419
2	Characterization of a global germplasm collection and its potential utilization for analysis of complex quantitative traits in maize. <i>Molecular Breeding</i> , 2011, 28, 511-526.	2.1	324
3	Genetic analysis and characterization of a new maize association mapping panel for quantitative trait loci dissection. <i>Theoretical and Applied Genetics</i> , 2010, 121, 417-431.	3.6	176
4	A large-scale circular <i>scRNA</i> profiling reveals universal molecular mechanisms responsive to drought stress in maize and <i>Arabidopsis</i> . <i>Plant Journal</i> , 2019, 98, 697-713.	5.7	99
5	The Genetic Basis of Plant Architecture in 10 Maize Recombinant Inbred Line Populations. <i>Plant Physiology</i> , 2017, 175, 858-873.	4.8	97
6	Circular RNAs mediated by transposons are associated with transcriptomic and phenotypic variation in maize. <i>New Phytologist</i> , 2018, 217, 1292-1306.	7.3	92
7	Genome-wide recombination dynamics are associated with phenotypic variation in maize. <i>New Phytologist</i> , 2016, 210, 1083-1094.	7.3	88
8	Mendelian and Non-Mendelian Regulation of Gene Expression in Maize. <i>PLoS Genetics</i> , 2013, 9, e1003202.	3.5	84
9	QTL-Seq Accelerates QTL Fine Mapping through QTL Partitioning and Whole-Genome Sequencing of Bulk Segregant Samples. <i>Molecular Plant</i> , 2019, 12, 426-437.	8.3	75
10	Population-level analysis reveals the widespread occurrence and phenotypic consequence of DNA methylation variation not tagged by genetic variation in maize. <i>Genome Biology</i> , 2019, 20, 243.	8.8	65
11	Co-expression network analysis of duplicate genes in maize ( <i>Zea mays</i> L.) reveals no subgenome bias. <i>BMC Genomics</i> , 2016, 17, 875.	2.8	36
12	Using Interactome Big Data to Crack Genetic Mysteries and Enhance Future Crop Breeding. <i>Molecular Plant</i> , 2021, 14, 77-94.	8.3	34
13	Genome-Wide Identification and Characterization of Small Peptides in Maize. <i>Frontiers in Plant Science</i> , 2021, 12, 695439.	3.6	16
14	New lncRNA annotation reveals extensive functional divergence of the transcriptome in maize. <i>Journal of Integrative Plant Biology</i> , 2019, 61, 394-405.	8.5	15
15	Large-scale translome profiling annotates the functional genome and reveals the key role of genic 3' untranslated regions in translomic variation in plants. <i>Plant Communications</i> , 2021, 2, 100181.	7.7	15
16	Complexity of genetic mechanisms conferring nonuniformity of recombination in maize. <i>Scientific Reports</i> , 2017, 7, 1205.	3.3	14
17	Down-regulation of OsMYB103L distinctively alters beta-1,4-glucan polymerization and cellulose microfibrils assembly for enhanced biomass enzymatic saccharification in rice. <i>Biotechnology for Biofuels</i> , 2021, 14, 245.	6.2	14
18	Circular RNAs exhibit extensive intraspecific variation in maize. <i>Planta</i> , 2019, 250, 69-78.	3.2	11

#	ARTICLE	IF	CITATIONS
19	Trait ontology analysis based on association mapping studies bridges the gap between crop genomics and Phenomics. <i>BMC Genomics</i> , 2019, 20, 443.	2.8	8
20	Dynamic patterns of circular and linear RNAs in maize hybrid and parental lines. <i>Theoretical and Applied Genetics</i> , 2020, 133, 593-604.	3.6	5
21	Dynamic patterns of the transcriptome in a hybrid triplet show translational fractionation of the maize subgenomes. <i>Crop Journal</i> , 2021, , .	5.2	5
22	Single-molecule long-read sequencing reveals extensive genomic and transcriptomic variation between maize and its wild relative teosinte ( <i>Zea mays</i> ssp. <i>parviglumis</i> ). <i>Molecular Ecology Resources</i> , 2022, 22, 272-282.	4.8	4