

# Yuanda Lv

## List of Publications by Year in descending order

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31  
papers

1,297  
citations

430874

18  
h-index

526287

27  
g-index

34  
all docs

34  
docs citations

34  
times ranked

2052  
citing authors

#	ARTICLE	IF	CITATIONS
1	The population genetics of structural variants in grapevine domestication. <i>Nature Plants</i> , 2019, 5, 965-979.	9.3	229
2	Genome-Wide Characterization of <i>cis</i> -Acting DNA Targets Reveals the Transcriptional Regulatory Framework of <i>Opaque2</i> in Maize. <i>Plant Cell</i> , 2015, 27, 532-545.	6.6	130
3	Comparative Transcriptome Profiling of a Resistant vs. Susceptible Tomato ( <i>Solanum lycopersicum</i> ) Cultivar in Response to Infection by Tomato Yellow Leaf Curl Virus. <i>PLoS ONE</i> , 2013, 8, e80816.	2.5	126
4	Genome-wide identification and functional prediction of nitrogen-responsive intergenic and intronic long non-coding RNAs in maize ( <i>Zea mays</i> L.). <i>BMC Genomics</i> , 2016, 17, 350.	2.8	107
5	OPAQUE11 Is a Central Hub of the Regulatory Network for Maize Endosperm Development and Nutrient Metabolism. <i>Plant Cell</i> , 2018, 30, 375-396.	6.6	103
6	Genome-wide identification of housekeeping genes in maize. <i>Plant Molecular Biology</i> , 2014, 86, 543-554.	3.9	68
7	Characterization of Rice Black-Streaked Dwarf Virus- and Rice Stripe Virus-Derived siRNAs in Singly and Doubly Infected Insect Vector <i>Laodelphax striatellus</i> . <i>PLoS ONE</i> , 2013, 8, e66007.	2.5	59
8	Evolutionary Genomics of Structural Variation in Asian Rice ( <i>Oryza sativa</i> ) Domestication. <i>Molecular Biology and Evolution</i> , 2020, 37, 3507-3524.	8.9	58
9	Development of novel InDel markers and genetic diversity in <i>Chenopodium quinoa</i> through whole-genome re-sequencing. <i>BMC Genomics</i> , 2017, 18, 685.	2.8	47
10	Maize transposable elements contribute to long non-coding RNAs that are regulatory hubs for abiotic stress response. <i>BMC Genomics</i> , 2019, 20, 864.	2.8	47
11	The NIN-like protein 5 (ZmNLP5) transcription factor is involved in modulating the nitrogen response in maize. <i>Plant Journal</i> , 2020, 102, 353-368.	5.7	41
12	Gene Body Methylation in Plants: Mechanisms, Functions, and Important Implications for Understanding Evolutionary Processes. <i>Genome Biology and Evolution</i> , 2022, 14, .	2.5	39
13	Genome-wide analysis of maize NLP transcription factor family revealed the roles in nitrogen response. <i>Plant Growth Regulation</i> , 2018, 84, 95-105.	3.4	37
14	mInDel: a high-throughput and efficient pipeline for genome-wide InDel marker development. <i>BMC Genomics</i> , 2016, 17, 290.	2.8	28
15	Proteome-wide lysine acetylation identification in developing rice ( <i>Oryza sativa</i> ) seeds and protein co-modification by acetylation, succinylation, ubiquitination, and phosphorylation. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2018, 1866, 451-463.	2.3	28
16	Transcriptome Sequencing and Differential Gene Expression Analysis of Delayed Gland Morphogenesis in <i>Gossypium australe</i> during Seed Germination. <i>PLoS ONE</i> , 2013, 8, e75323.	2.5	26
17	Aberrant phenotype and transcriptome expression during fiber cell wall thickening caused by the mutation of the <i>Im</i> gene in immature fiber ( <i>im</i> ) mutant in <i>Gossypium hirsutum</i> L. <i>BMC Genomics</i> , 2014, 15, 94.	2.8	25
18	Mining, characterization, and exploitation of EST-derived microsatellites in <i>Gossypium barbadense</i> . <i>Science Bulletin</i> , 2010, 55, 1889-1893.	1.7	19

#	ARTICLE	IF	CITATIONS
19	Genome-Wide Analysis of Small RNA and Novel MicroRNA Discovery during Fiber and Seed Initial Development in <i>Gossypium hirsutum</i> L. PLoS ONE, 2013, 8, e69743.	2.5	17
20	Gene coexpression network analysis reveals the role of SRS genes in senescence leaf of maize ( <i>Zea mays</i> L.). <i>Plant Physiology</i> , 2015, 167, 1010-1020.	0.7	16
21	Characterization of expressed sequence tags from developing fibers of <i>Gossypium barbadense</i> and evaluation of insertion-deletion variation in tetraploid cultivated cotton species. BMC Genomics, 2013, 14, 170.	2.8	8
22	Identification and characterization of presence/absence variation in maize genotype Mo17. <i>Genes and Genomics</i> , 2015, 37, 503-515.	1.4	7
23	Identification and Characterization of Secondary Wall-Associated NAC Genes and Their Involvement in Hormonal Responses in Tobacco ( <i>Nicotiana tabacum</i> ). <i>Frontiers in Plant Science</i> , 2021, 12, 712254.	3.6	5
24	The Landscape of Alternative Splicing Regulating Potassium Use Efficiency in <i>Nicotiana tabacum</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 774829.	3.6	5
25	Comprehensive Transcriptome Analysis Uncovers Hub Long Non-coding RNAs Regulating Potassium Use Efficiency in <i>Nicotiana tabacum</i> . <i>Frontiers in Plant Science</i> , 2022, 13, 777308.	3.6	5
26	Comprehensive Transcriptome Analysis of GS3 Near-Isogenic Lines During Panicle Development in Rice ( <i>Oryza sativa</i> L.). <i>Frontiers in Genetics</i> , 2022, 13, 857143.	2.3	5
27	Principle and Strategy of DNA Fingerprint Identification of Plant Variety. <i>Molecular Plant Breeding</i> , 0, .	0.0	3
28	Transcriptome Profiling of Transposon-Derived Long Non-coding RNAs Response to Hormone in Strawberry Fruit Development. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	3
29	Systematic Identification and Validation of Housekeeping and Tissue-Specific Genes in Allotetraploid <i>Chenopodium quinoa</i> . <i>Horticulturae</i> , 2021, 7, 235.	2.8	1
30	Gene coexpression network analysis reveals the role of genes in senescence leaf of maize ( <i>Z. mays</i> L.). <i>Journal of Genetics</i> , 2020, 99, .	0.7	1
31	Construction of BAC contig maps of homoeologous chromosomes A12 and D12 of <i>Gossypium hirsutum</i> L. acc. TM-1. <i>Molecular Cytogenetics</i> , 2015, 8, 55.	0.9	0