

# Lei Gao

## List of Publications by Year in descending order

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49  
papers

3,416  
citations

257357

24  
h-index

175177

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55  
all docs

55  
docs citations

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times ranked

5249  
citing authors

#	ARTICLE	IF	CITATIONS
1	<i>TRANS-ACTING SIRNA3</i>-derived short interfering RNAs confer cleavage of mRNAs in rice. <i>Plant Physiology</i> , 2022, 188, 347-362.	2.3	6
2	OsRLR4 binds to the <i>OsAUX1</i> promoter to negatively regulate primary root development in rice. <i>Journal of Integrative Plant Biology</i> , 2022, 64, 118-134.	4.1	7
3	Origin, evolution and diversification of plant ARGONAUTE proteins. <i>Plant Journal</i> , 2022, 109, 1086-1097.	2.8	24
4	Arabidopsis RBV is a conserved WD40 repeat protein that promotes microRNA biogenesis and ARGONAUTE1 loading. <i>Nature Communications</i> , 2022, 13, 1217.	5.8	19
5	Mechanism for the genomic and functional evolution of the MIR2118 family in the grass lineage. <i>New Phytologist</i> , 2022, 233, 1915-1930.	3.5	5
6	NAD <sup>+</sup> -capped RNAs are widespread in rice ( <i>Oryza sativa</i> ) and spatiotemporally modulated during development. <i>Science China Life Sciences</i> , 2022, 65, 2121-2124.	2.3	4
7	Plant miR397 and its functions. <i>Functional Plant Biology</i> , 2021, 48, 361.	1.1	37
8	Widespread occurrence of microRNA-mediated target cleavage on membrane-bound polysomes. <i>Genome Biology</i> , 2021, 22, 15.	3.8	19
9	ZmFdC2 Encoding a Ferredoxin Protein With C-Terminus Extension Is Indispensable for Maize Growth. <i>Frontiers in Plant Science</i> , 2021, 12, 646359.	1.7	2
10	RiboNT: A Noise-Tolerant Predictor of Open Reading Frames from Ribosome-Protected Footprints. <i>Life</i> , 2021, 11, 701.	1.1	8
11	Comparative ribosome profiling reveals distinct translational landscapes of salt-sensitive and -tolerant rice. <i>BMC Genomics</i> , 2021, 22, 612.	1.2	10
12	Distinct Evolutionary Profiles and Functions of microRNA156 and microRNA529 in Land Plants. <i>International Journal of Molecular Sciences</i> , 2021, 22, 11100.	1.8	8
13	Genome-wide mRNA and small RNA transcriptome profiles uncover cultivar- and tissue-specific changes induced by cadmium in <i>Brassica parachinensis</i> . <i>Environmental and Experimental Botany</i> , 2020, 180, 104207.	2.0	7
14	High-Throughput Sequencing-Based Identification of Arabidopsis miRNAs Induced by <i>Phytophthora capsici</i> Infection. <i>Frontiers in Microbiology</i> , 2020, 11, 1094.	1.5	15
15	Genome-Wide Transcript and Small RNA Profiling Reveals Transcriptomic Responses to Heat Stress. <i>Plant Physiology</i> , 2019, 181, 609-629.	2.3	49
16	The PROTEIN PHOSPHATASE4 Complex Promotes Transcription and Processing of Primary microRNAs in Arabidopsis. <i>Plant Cell</i> , 2019, 31, 486-501.	3.1	51
17	SnRK2s at the Crossroads of Growth and Stress Responses. <i>Trends in Plant Science</i> , 2019, 24, 672-676.	4.3	39
18	AUSPP: A universal short-read pre-processing package. <i>Journal of Bioinformatics and Computational Biology</i> , 2019, 17, 1950037.	0.3	3

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19	Proteasome subunit RPT2a promotes PTGS through repressing RNA quality control in Arabidopsis. <i>Nature Plants</i> , 2019, 5, 1273-1282.	4.7	11
20	Prevalent cytidylation and uridylation of precursor miRNAs in Arabidopsis. <i>Nature Plants</i> , 2019, 5, 1260-1272.	4.7	19
21	MicroRNAs transcriptionally regulate promoter activity in <i>Arabidopsis thaliana</i> . <i>Journal of Integrative Plant Biology</i> , 2019, 61, 1128-1133.	4.1	20
22	The disease resistance protein SNC1 represses the biogenesis of microRNAs and phased siRNAs. <i>Nature Communications</i> , 2018, 9, 5080.	5.8	60
23	Conservation and divergence of small RNA pathways and microRNAs in land plants. <i>Genome Biology</i> , 2017, 18, 158.	3.8	91
24	ARGONAUTE10 promotes the degradation of miR165/6 through the SDN1 and SDN2 exonucleases in Arabidopsis. <i>PLoS Biology</i> , 2017, 15, e2001272.	2.6	81
25	The MBD7 complex promotes expression of methylated transgenes without significantly altering their methylation status. <i>ELife</i> , 2017, 6, .	2.8	18
26	POWERDRESS and HDA9 interact and promote histone H3 deacetylation at specific genomic sites in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 14858-14863.	3.3	111
27	Concerted genomic targeting of H3K27 demethylase REF6 and chromatin-remodeling ATPase BRM in Arabidopsis. <i>Nature Genetics</i> , 2016, 48, 687-693.	9.4	193
28	A partial loss-of-function mutation in an Arabidopsis RNA polymerase III subunit leads to pleiotropic defects. <i>Journal of Experimental Botany</i> , 2016, 67, 2219-2230.	2.4	17
29	SUVH1, a Su(var)3 $\Delta$ 9 family member, promotes the expression of genes targeted by DNA methylation. <i>Nucleic Acids Research</i> , 2016, 44, 608-620.	6.5	41
30	Genome-Wide Identification and Characterization of microRNAs in Developing Grains of Zea mays L.. <i>PLoS ONE</i> , 2016, 11, e0153168.	1.1	34
31	Biogenesis of phased siRNAs on membrane-bound polysomes in Arabidopsis. <i>ELife</i> , 2016, 5, .	2.8	104
32	The Arabidopsis SWI2/SNF2 Chromatin Remodeler BRAHMA Regulates Polycomb Function during Vegetative Development and Directly Activates the Flowering Repressor Gene SVP. <i>PLoS Genetics</i> , 2015, 11, e1004944.	1.5	111
33	Detection of Pol IV/RDR2-dependent transcripts at the genomic scale in <i>Arabidopsis</i> reveals features and regulation of siRNA biogenesis. <i>Genome Research</i> , 2015, 25, 235-245.	2.4	143
34	DNA Topoisomerase I Promotes Transcriptional Silencing of Transposable Elements through DNA Methylation and Histone Lysine 9 Dimethylation in Arabidopsis. <i>PLoS Genetics</i> , 2014, 10, e1004446.	1.5	26
35	DNA Topoisomerase I Affects Polycomb Group Protein-Mediated Epigenetic Regulation and Plant Development by Altering Nucleosome Distribution in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2014, 26, 2803-2817.	3.1	38
36	Roles of small siRNAs in soybean defense against <i>Phytophthora sojae</i> infection. <i>Plant Journal</i> , 2014, 79, 928-940.	2.8	122

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37	Genome-wide analysis of microRNAs in rubber tree ( <i>Hevea brasiliensis</i> L.) using high-throughput sequencing. <i>Planta</i> , 2012, 236, 437-445.	1.6	41
38	High throughput sequencing reveals novel and abiotic stress-regulated microRNAs in the inflorescences of rice. <i>BMC Plant Biology</i> , 2012, 12, 132.	1.6	157
39	Development of a luciferase-based reporter of transcriptional gene silencing that enables bidirectional mutant screening in <i>Arabidopsis thaliana</i> . <i>Silence: A Journal of RNA Regulation</i> , 2012, 3, 6.	8.0	8
40	Identification and comparative analysis of drought-associated microRNAs in two cowpea genotypes. <i>BMC Plant Biology</i> , 2011, 11, 127.	1.6	187
41	A fungal phylogeny based on 82 complete genomes using the composition vector method. <i>BMC Evolutionary Biology</i> , 2009, 9, 195.	3.2	194
42	Global Occurrence of Archaeal <i>amoA</i> Genes in Terrestrial Hot Springs. <i>Applied and Environmental Microbiology</i> , 2008, 74, 6417-6426.	1.4	189
43	Environmental Adaptation: Genomic Analysis of the Piezotolerant and Psychrotolerant Deep-Sea Iron Reducing Bacterium <i>Shewanella piezotolerans</i> WP3. <i>PLoS ONE</i> , 2008, 3, e1937.	1.1	123
44	Whole genome molecular phylogeny of large dsDNA viruses using composition vector method. <i>BMC Evolutionary Biology</i> , 2007, 7, 41.	3.2	89
45	Prokaryote phylogeny meets taxonomy: An exhaustive comparison of composition vector trees with systematic bacteriology. <i>Science in China Series C: Life Sciences</i> , 2007, 50, 587-599.	1.3	22
46	Test Data Sets and Evaluation of Gene Prediction Programs on the Rice Genome. <i>Journal of Computer Science and Technology</i> , 2005, 20, 446-453.	0.9	14
47	The Genomes of <i>Oryza sativa</i> : A History of Duplications. <i>PLoS Biology</i> , 2005, 3, e38.	2.6	808
48	Molecular phylogeny of coronaviruses including human SARS-CoV. <i>Science Bulletin</i> , 2003, 48, 1170-1174.	1.7	22
49	Molecular phylogeny of coronaviruses including human SARS-CoV. <i>Science Bulletin</i> , 2003, 48, 1170.	1.7	2