

# Shoudong Zhang

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1116564/publications.pdf>

Version: 2024-02-01

20  
papers

2,806  
citations

623734

14  
h-index

752698

20  
g-index

23  
all docs

23  
docs citations

23  
times ranked

5153  
citing authors

#	ARTICLE	IF	CITATIONS
1	Dynamic regulation of genome-wide pre-mRNA splicing and stress tolerance by the Sm-like protein LSm5 in <i>Arabidopsis</i> . <i>Genome Biology</i> , 2014, 15, R1.	9.6	1,501
2	Genome-wide analysis of alternative splicing of pre-mRNA under salt stress in <i>Arabidopsis</i> . <i>BMC Genomics</i> , 2014, 15, 431.	2.8	234
3	An RNA polymerase II- and AGO4-associated protein acts in RNA-directed DNA methylation. <i>Nature</i> , 2010, 465, 106-109.	27.8	228
4	The Phloem-Delivered RNA Pool Contains Small Noncoding RNAs and Interferes with Translation. <i>Plant Physiology</i> , 2009, 150, 378-387.	4.8	224
5	m5C Methylation Guides Systemic Transport of Messenger RNA over Graft Junctions in Plants. <i>Current Biology</i> , 2019, 29, 2465-2476.e5.	3.9	149
6	A KH-Domain RNA-Binding Protein Interacts with FIERY2/CTD Phosphatase-Like 1 and Splicing Factors and Is Important for Pre-mRNA Splicing in <i>Arabidopsis</i> . <i>PLoS Genetics</i> , 2013, 9, e1003875.	3.5	88
7	MPB2C, a Microtubule-Associated Protein, Regulates Non-Cell-Autonomy of the Homeodomain Protein KNOTTED1. <i>Plant Cell</i> , 2007, 19, 3001-3018.	6.6	61
8	NAD tagSeq reveals that NAD <sup>+</sup> -capped RNAs are mostly produced from a large number of protein-coding genes in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 12072-12077.	7.1	61
9	New insights into <i>Arabidopsis</i> transcriptome complexity revealed by direct sequencing of native RNAs. <i>Nucleic Acids Research</i> , 2020, 48, 7700-7711.	14.5	57
10	Bisphenol S induced epigenetic and transcriptional changes in human breast cancer cell line MCF-7. <i>Environmental Pollution</i> , 2019, 246, 697-703.	7.5	42
11	Genome-wide DNA mutations in <i>Arabidopsis</i> plants after multigenerational exposure to high temperatures. <i>Genome Biology</i> , 2021, 22, 160.	8.8	35
12	PlaMoM: a comprehensive database compiles plant mobile macromolecules. <i>Nucleic Acids Research</i> , 2017, 45, D1021-D1028.	14.5	33
13	SNP calling using genotype model selection on high-throughput sequencing data. <i>Bioinformatics</i> , 2012, 28, 643-650.	4.1	22
14	Use of NAD tagSeq II to identify growth phase-dependent alterations in <i>E. coli</i> RNA NAD <sup>+</sup> capping. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	17
15	Applications and potentials of nanopore sequencing in the (epi)genome and (epi)transcriptome era. <i>Innovation(China)</i> , 2021, 2, 100153.	9.1	15
16	The caseinolytic protease complex component CLPC1 in <i>Arabidopsis</i> maintains proteome and RNA homeostasis in chloroplasts. <i>BMC Plant Biology</i> , 2018, 18, 192.	3.6	9
17	Two domain-disrupted <i>hda6</i> alleles have opposite epigenetic effects on transgenes and some endogenous targets. <i>Scientific Reports</i> , 2015, 5, 17832.	3.3	8
18	Editorial: New Insights Into Mechanisms of Epigenetic Modifiers in Plant Growth and Development. <i>Frontiers in Plant Science</i> , 2019, 10, 1661.	3.6	6

#	ARTICLE	IF	CITATIONS
19	AtHDA6 functions as an H3K18ac eraser to maintain pericentromeric CHG methylation in Arabidopsis thaliana. Nucleic Acids Research, 2021, 49, 9755-9767.	14.5	6
20	Analyzing and Predicting Phloem Mobility of Macromolecules with an Online Database. Methods in Molecular Biology, 2019, 2014, 433-438.	0.9	0