

# Zhaohua Peng

## List of Publications by Year in descending order

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29  
papers

1,295  
citations

394421

19  
h-index

454955

30  
g-index

33  
all docs

33  
docs citations

33  
times ranked

1755  
citing authors

#	ARTICLE	IF	CITATIONS
1	Global Analysis of UDP Glucose Pyrophosphorylase (UDPGP) Gene Family in Plants: Conserved Evolution Involved in Cell Death. <i>Frontiers in Plant Science</i> , 2021, 12, 681719.	3.6	5
2	Multi-locus genome-wide association studies for five yield-related traits in rice. <i>BMC Plant Biology</i> , 2021, 21, 364.	3.6	22
3	Genetic Diversity Relationship Between Grain Quality and Appearance in Rice. <i>Frontiers in Plant Science</i> , 2021, 12, 708996.	3.6	13
4	Dissecting Tumor Antigens and Immune Subtypes of Glioma to Develop mRNA Vaccine. <i>Frontiers in Immunology</i> , 2021, 12, 709986.	4.8	34
5	Uncovering the genetic mechanisms regulating panicle architecture in rice with GPWAS and GWAS. <i>BMC Genomics</i> , 2021, 22, 86.	2.8	23
6	Feeding Arsenic-Containing Rice Bran to Growing Pigs: Growth Performance, Arsenic Tissue Distribution, and Arsenic Excretion. <i>International Journal of Environmental Research and Public Health</i> , 2020, 17, 8530.	2.6	2
7	Genome-wide association studies of ionomic and agronomic traits in USDA mini core collection of rice and comparative analyses of different mapping methods. <i>BMC Plant Biology</i> , 2020, 20, 441.	3.6	25
8	Comprehensive Analysis of the Lysine Succinylome and Protein Co-modifications in Developing Rice Seeds. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 2359-2372.	3.8	22
9	Malonylome analysis in developing rice ( <i>Oryza sativa</i> ) seeds suggesting that protein lysine malonylation is well-conserved and overlaps with acetylation and succinylation substantially. <i>Journal of Proteomics</i> , 2018, 170, 88-98.	2.4	33
10	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
11	Proteome-wide Analysis of Lysine 2-hydroxyisobutyrylation in Developing Rice ( <i>Oryza sativa</i> ) Seeds. <i>Scientific Reports</i> , 2017, 7, 17486.	3.3	56
12	Comparative Proteomic Analysis of Cotton Fiber Development and Protein Extraction Method Comparison in Late Stage Fibers. <i>Proteomes</i> , 2016, 4, 7.	3.5	10
13	Proteome Profile of Starch Granules Purified from Rice ( <i>Oryza sativa</i> ) Endosperm. <i>PLoS ONE</i> , 2016, 11, e0168467.	2.5	36
14	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
15	Global Analysis of Lysine Acetylation Suggests the Involvement of Protein Acetylation in Diverse Biological Processes in Rice ( <i>Oryza sativa</i> ). <i>PLoS ONE</i> , 2014, 9, e89283.	2.5	102
16	Nuclear proteome response to cell wall removal in rice ( <i>Oryza sativa</i> ). <i>Proteome Science</i> , 2013, 11, 26.	1.7	19
17	Polycomb Group Gene OsFIE2 Regulates Rice ( <i>Oryza sativa</i> ) Seed Development and Grain Filling via a Mechanism Distinct from Arabidopsis. <i>PLoS Genetics</i> , 2013, 9, e1003322.	3.5	88
18	Differential Histone Modification and Protein Expression Associated with Cell Wall Removal and Regeneration in Rice ( <i>Oryza sativa</i> ). <i>Journal of Proteome Research</i> , 2011, 10, 551-563.	3.7	33

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19	Transcriptional dynamics during cell wall removal and regeneration reveals key genes involved in cell wall development in rice. <i>Plant Molecular Biology</i> , 2011, 77, 391-406.	3.9	17
20	ARR5 and ARR6 Mediate Tissue Specific Cross-talk between Auxin and Cytokinin in <i>Arabidopsis</i> . <i>American Journal of Plant Sciences</i> , 2011, 02, 549-553.	0.8	7
21	OsMADS6 plays an essential role in endosperm nutrient accumulation and is subject to epigenetic regulation in rice ( <i>Oryza sativa</i> ). <i>Plant Journal</i> , 2010, 64, 604-617.	5.7	90
22	Role of AUX1 in the control of organ identity during in vitro organogenesis and in mediating tissue specific auxin and cytokinin interaction in <i>Arabidopsis</i> . <i>Planta</i> , 2009, 229, 645-657.	3.2	34
23	Comparative analysis of proteome differential regulation during cell dedifferentiation in <i>Arabidopsis</i> . <i>Proteomics</i> , 2008, 8, 4303-4316.	2.2	26
24	Removal of high abundance proteins for nuclear subproteome studies in rice ( <i>Oryza</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 542	2.4	42
25	Proteome and Phosphoproteome Differential Expression under Salinity Stress in Rice ( <i>Oryza sativa</i> ) Roots. <i>Journal of Proteome Research</i> , 2007, 6, 1718-1727.	3.7	155
26	Proteome and phosphoproteome dynamic change during cell dedifferentiation in <i>Arabidopsis</i> . <i>Proteomics</i> , 2007, 7, 1473-1500.	2.2	51
27	Proteome and phosphoproteome analysis of chromatin associated proteins in rice ( <i>Oryza</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 65	2.2	65
28	Molecular Characterization of Subunit 6 of the COP9 Signalosome and Its Role in Multifaceted Developmental Processes in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2001, 13, 2393-2407.	6.6	79
29	A role of <i>Arabidopsis</i> COP9 signalosome in multifaceted developmental processes revealed by the characterization of its subunit 3. <i>Development (Cambridge)</i> , 2001, 128, 4277-4288.	2.5	69