

Qingpo Liu

List of Publications by Year in descending order

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34
papers

1,418
citations

331670

21
h-index

377865

34
g-index

35
all docs

35
docs citations

35
times ranked

2257
citing authors

#	ARTICLE	IF	CITATIONS
1	Demography and its effects on genomic variation in crop domestication. <i>Nature Plants</i> , 2018, 4, 512-520.	9.3	173
2	Dicer-like (DCL) proteins in plants. <i>Functional and Integrative Genomics</i> , 2009, 9, 277-286.	3.5	136
3	Comparative studies on codon usage pattern of chloroplasts and their host nuclear genes in four plant species. <i>Journal of Genetics</i> , 2005, 84, 55-62.	0.7	127
4	Molecular Identification and Analysis of Arsenite Stress-Responsive miRNAs in Rice. <i>Journal of Agricultural and Food Chemistry</i> , 2012, 60, 6524-6536.	5.2	90
5	Divergence in function and expression of the NOD26-like intrinsic proteins in plants. <i>BMC Genomics</i> , 2009, 10, 313.	2.8	76
6	Deleterious variants in Asian rice and the potential cost of domestication. <i>Molecular Biology and Evolution</i> , 2017, 34, msw296.	8.9	68
7	Molecular evolution of the MLO gene family in <i>Oryza sativa</i> and their functional divergence. <i>Gene</i> , 2008, 409, 1-10.	2.2	62
8	Genome-wide identification and analysis of miRNA-related single nucleotide polymorphisms (SNPs) in rice. <i>Rice</i> , 2013, 6, 10.	4.0	54
9	Synonymous codon usage bias in <i>Oryza sativa</i> . <i>Plant Science</i> , 2004, 167, 101-105.	3.6	51
10	Synonymous codon usage and gene function are strongly related in <i>Oryza sativa</i> . <i>BioSystems</i> , 2005, 80, 123-131.	2.0	47
11	Computational identification and phylogenetic analysis of the MAPK gene family in <i>Oryza sativa</i> . <i>Plant Physiology and Biochemistry</i> , 2007, 45, 6-14.	5.8	47
12	Analysis of codon usage pattern in the radioresistant bacterium <i>Deinococcus radiodurans</i> . <i>BioSystems</i> , 2006, 85, 99-106.	2.0	43
13	Involvement of miR528 in the Regulation of Arsenite Tolerance in Rice (<i>Oryza sativa</i> L.). <i>Journal of Agricultural and Food Chemistry</i> , 2015, 63, 8849-8861.	5.2	43
14	Computational identification of novel PR-1-type genes in <i>Oryza sativa</i> . <i>Journal of Genetics</i> , 2006, 85, 193-198.	0.7	42
15	The genome-wide dynamics of purging during selfing in maize. <i>Nature Plants</i> , 2019, 5, 980-990.	9.3	42
16	Analysis of factors shaping codon usage in the mitochondrion genome of. <i>Mitochondrion</i> , 2004, 4, 313-320.	3.4	34
17	Identification of rice TUBBY-like genes and their evolution. <i>FEBS Journal</i> , 2008, 275, 163-171.	4.7	30
18	Effect of silicate supplementation on the alleviation of arsenite toxicity in 93-11 (<i>Oryza sativa</i> L.) Tj ETQq0 0 0 rgBT/Overlock_10 Tf 50 6	5.3	26

#	ARTICLE	IF	CITATIONS
19	Mutational Bias and Translational Selection Shaping the Codon Usage Pattern of Tissue-Specific Genes in Rice. PLoS ONE, 2012, 7, e48295.	2.5	26
20	Functional divergence of the NIP III subgroup proteins involved altered selective constraints and positive selection. BMC Plant Biology, 2010, 10, 256.	3.6	23
21	The miR528- <i>AO</i> Module Confers Enhanced Salt Tolerance in Rice by Modulating the Ascorbic Acid and Abscisic Acid Metabolism and ROS Scavenging. Journal of Agricultural and Food Chemistry, 2021, 69, 8634-8648.	5.2	23
22	Novel miRNAs in the control of arsenite levels in rice. Functional and Integrative Genomics, 2012, 12, 649-658.	3.5	21
23	Evolutionary divergence of function and expression of laccase genes in plants. Journal of Genetics, 2020, 99, 1.	0.7	21
24	Comparative analysis of base biases around the stop codons in six eukaryotes. BioSystems, 2005, 81, 281-289.	2.0	18
25	Mutational bias is the driving force for shaping the synonymous codon usage pattern of alternatively spliced genes in rice (<i>Oryza sativa</i> L.). Molecular Genetics and Genomics, 2015, 290, 649-660.	2.1	18
26	Molecular Phylogeny, Evolution, and Functional Divergence of the LSD1-Like Gene Family: Inference from the Rice Genome. Journal of Molecular Evolution, 2007, 64, 354-363.	1.8	14
27	Genome-wide identification and evolutionary analysis of positively selected miRNA genes in domesticated rice. Molecular Genetics and Genomics, 2015, 290, 593-602.	2.1	13
28	The miR528-D3 Module Regulates Plant Height in Rice by Modulating the Gibberellin and Abscisic Acid Metabolisms. Rice, 2022, 15, .	4.0	13
29	Evolution and functional divergence of monocarboxylate transporter genes in vertebrates. Gene, 2008, 423, 14-22.	2.2	11
30	Computational identification and systematic analysis of the ACR gene family in <i>Oryza sativa</i> . Journal of Plant Physiology, 2006, 163, 445-451.	3.5	10
31	Computational identification and sequence analysis of stop codon readthrough genes in <i>Oryza sativa</i> . BioSystems, 2004, 77, 33-39.	2.0	7
32	Evolutionary divergence of function and expression of laccase genes in plants. Journal of Genetics, 2020, 99, .	0.7	4
33	Comparative studies on sequence characteristics around translation initiation codon in four eukaryotes. Journal of Genetics, 2005, 84, 317-322.	0.7	3
34	Gene Conversion and Positive Selection Driving the Evolution of the <i>Caenorhabditis</i> ssp. ZIM/HIM-8 Protein Family. Journal of Molecular Evolution, 2009, 68, 217-226.	1.8	2