

Rentao Song

List of Publications by Year in descending order

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91
papers

8,217
citations

126858

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48277

88
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92
all docs

92
docs citations

92
times ranked

8935
citing authors

#	ARTICLE	IF	CITATIONS
1	The map-based sequence of the rice genome. <i>Nature</i> , 2005, 436, 793-800.	13.7	3,365
2	CARPEL FACTORY, a Dicer Homolog, and HEN1, a Novel Protein, Act in microRNA Metabolism in <i>Arabidopsis thaliana</i> . <i>Current Biology</i> , 2002, 12, 1484-1495.	1.8	1,125
3	Gene expression of a gene family in maize based on noncollinear haplotypes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 9055-9060.	3.3	248
4	In-Depth View of Structure, Activity, and Evolution of Rice Chromosome 10. <i>Science</i> , 2003, 300, 1566-1569.	6.0	245
5	A New Opaque Variant of Maize by a Single Dominant RNA-Interference-Inducing Transgene. <i>Genetics</i> , 2003, 165, 387-397.	1.2	188
6	High-efficiency CRISPR/Cas9 multiplex gene editing using the glycine tRNA-processing system-based strategy in maize. <i>BMC Biotechnology</i> , 2016, 16, 58.	1.7	162
7	Mosaic Organization of Orthologous Sequences in Grass Genomes. <i>Genome Research</i> , 2002, 12, 1549-1555.	2.4	130
8	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.	3.1	130
9	Comparative sequence analysis of <i>MONOCULM1</i> -orthologous regions in 14 <i>Oryza</i> genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 2071-2076.	3.3	119
10	Sequence, Regulation, and Evolution of the Maize 22-kD Zein Gene Family. <i>Genome Research</i> , 2001, 11, 1817-1825.	2.4	118
11	<i>Dek35</i> Encodes a PPR Protein that Affects <i>cis</i> -Splicing of Mitochondrial <i>nad4</i> Intron 1 and Seed Development in Maize. <i>Molecular Plant</i> , 2017, 10, 427-441.	3.9	106
12	OPAQUE11 Is a Central Hub of the Regulatory Network for Maize Endosperm Development and Nutrient Metabolism. <i>Plant Cell</i> , 2018, 30, 375-396.	3.1	103
13	Isolation of High Quality RNA from Cereal Seeds Containing High Levels of Starch. <i>Phytochemical Analysis</i> , 2012, 23, 159-163.	1.2	101
14	<i>Opaque1</i> Encodes a Myosin XI Motor Protein That Is Required for Endoplasmic Reticulum Motility and Protein Body Formation in Maize Endosperm. <i>Plant Cell</i> , 2012, 24, 3447-3462.	3.1	99
15	<i>Retracted: Proline responding1</i> Plays a Critical Role in Regulating General Protein Synthesis and the Cell Cycle in Maize. <i>Plant Cell</i> , 2014, 26, 2582-2600.	3.1	99
16	Coupling of the hydrogen and polyhydroxyalkanoates (PHA) production through anaerobic digestion from Taihu blue algae. <i>Bioresource Technology</i> , 2010, 101, 4508-4512.	4.8	93
17	<i>E+</i> subgroup PPR protein defective kernel 36 is required for multiple mitochondrial transcripts editing and seed development in maize and <i>Arabidopsis</i> . <i>New Phytologist</i> , 2017, 214, 1563-1578.	3.5	85
18	Mitochondrial Function and Maize Kernel Development Requires <i>Dek2</i> , a Pentatricopeptide Repeat Protein Involved in <i>nad1</i> mRNA Splicing. <i>Genetics</i> , 2017, 205, 239-249.	1.2	82

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19	The ZmZIP22 Transcription Factor Regulates 27-kD β -Zein Gene Transcription during Maize Endosperm Development. <i>Plant Cell</i> , 2018, 30, 2402-2424.	3.1	65
20	Diversity of methanogenic archaea in a biogas reactor fed with swine feces as the mono-substrate by mcrA analysis. <i>Microbiological Research</i> , 2011, 166, 27-35.	2.5	63
21	ZmMADS47 Regulates Zein Gene Transcription through Interaction with Opaque2. <i>PLoS Genetics</i> , 2016, 12, e1005991.	1.5	62
22	Contiguous Genomic DNA Sequence Comprising the 19-kD Zein Gene Family from Maize. <i>Plant Physiology</i> , 2002, 130, 1626-1635.	2.3	61
23	Overexpression of two cambium-abundant Chinese fir (<i>Cunninghamia lanceolata</i>) expansin genes <i>CLEXPA1</i> and <i>CLEXPA2</i> affect growth and development in transgenic tobacco and increase the amount of cellulose in stem cell walls. <i>Plant Biotechnology Journal</i> , 2011, 9, 486-502.	4.1	56
24	Editing of Mitochondrial Transcripts <i>nad3</i> and <i>cox2</i> by Dek10 Is Essential for Mitochondrial Function and Maize Plant Development. <i>Genetics</i> , 2017, 205, 1489-1501.	1.2	56
25	Maize <i>Dek37</i> Encodes a P-type PPR Protein That Affects <i>cis</i> -Splicing of Mitochondrial <i>nad2</i> Intron 1 and Seed Development. <i>Genetics</i> , 2018, 208, 1069-1082.	1.2	55
26	Reductive degradation of chloramphenicol using bioelectrochemical system (BES): A comparative study of abiotic cathode and biocathode. <i>Bioresource Technology</i> , 2013, 143, 699-702.	4.8	53
27	Identification and Characterization of Maize floury4 as a Novel Semidominant Opaque Mutant That Disrupts Protein Body Assembly. <i>Plant Physiology</i> , 2014, 165, 582-594.	2.3	52
28	Maize opaque10 Encodes a Cereal-Specific Protein That Is Essential for the Proper Distribution of Zeins in Endosperm Protein Bodies. <i>PLoS Genetics</i> , 2016, 12, e1006270.	1.5	43
29	Expressional profiling study revealed unique expressional patterns and dramatic expressional divergence of maize β -zein super gene family. <i>Plant Molecular Biology</i> , 2009, 69, 649-659.	2.0	41
30	Maize <i>reas1</i> Mutant Stimulates Ribosome Use Efficiency and Triggers Distinct Transcriptional and Translational Responses. <i>Plant Physiology</i> , 2016, 170, 971-988.	2.3	41
31	Maize endosperm development. <i>Journal of Integrative Plant Biology</i> , 2021, 63, 613-627.	4.1	40
32	Expression of the sorghum 10-member kafirin gene cluster in maize endosperm. <i>Nucleic Acids Research</i> , 2004, 32, e189-e189.	6.5	39
33	<i>Dek42</i> encodes an RNA-binding protein that affects alternative pre-mRNA splicing and maize kernel development. <i>Journal of Integrative Plant Biology</i> , 2019, 61, 728-748.	4.1	38
34	The regulation of zein biosynthesis in maize endosperm. <i>Theoretical and Applied Genetics</i> , 2020, 133, 1443-1453.	1.8	38
35	Maize <i>Dek15</i> Encodes the Cohesin-Loading Complex Subunit SCC4 and Is Essential for Chromosome Segregation and Kernel Development. <i>Plant Cell</i> , 2019, 31, 465-485.	3.1	35
36	Maize pentatricopeptide repeat protein DEK41 affects cis-splicing of mitochondrial <i>nad4</i> intron 3 and is required for normal seed development. <i>Journal of Experimental Botany</i> , 2019, 70, 3795-3808.	2.4	35

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37	Two transposable element insertions are causative mutations for the major domestication gene teosinte branched 1 in modern maize. <i>Cell Research</i> , 2011, 21, 1267-1270.	5.7	33
38	Comprehensive proteomic analysis of developing protein bodies in maize (<i>Zea mays</i>) endosperm provides novel insights into its biogenesis. <i>Journal of Experimental Botany</i> , 2016, 67, 6323-6335.	2.4	28
39	A Sequence-Indexed <i>Mutator</i> Insertional Library for Maize Functional Genomics Study. <i>Plant Physiology</i> , 2019, 181, 1404-1414.	2.3	28
40	Maize <i>Dek44</i> Encodes Mitochondrial Ribosomal Protein L9 and Is Required for Seed Development. <i>Plant Physiology</i> , 2019, 180, 2106-2119.	2.3	28
41	Maize kernel development. <i>Molecular Breeding</i> , 2021, 41, 1.	1.0	28
42	Cloning and characterization of two novel chloroplastic glycerol-3-phosphate dehydrogenases from <i>Dunaliella viridis</i> . <i>Plant Molecular Biology</i> , 2009, 71, 193-205.	2.0	25
43	High segregation distortion in maize B73 x teosinte crosses. <i>Genetics and Molecular Research</i> , 2012, 11, 693-706.	0.3	25
44	Isolation and characterization of a sodium-dependent phosphate transporter gene in <i>Dunaliella viridis</i> . <i>Biochemical and Biophysical Research Communications</i> , 2006, 340, 95-104.	1.0	24
45	An expression analysis of 57 transcription factors derived from ESTs of developing seeds in Maize (<i>Zea</i>) Tj ETQq1 1.0.784314.rgBT/O	2.8	24
46	The cloning and characterization of two ammonium transporters in the salt-resistant green alga, <i>Dunaliella viridis</i> . <i>Molecular Biology Reports</i> , 2011, 38, 4797-4804.	1.0	24
47	Cloning, characterization and genetic engineering of FLC homolog in <i>Thellungiella halophila</i> . <i>Biochemical and Biophysical Research Communications</i> , 2006, 347, 707-714.	1.0	23
48	A SnRK1- <i>Zm</i> RFWD3-Opaque2 Signaling Axis Regulates Diurnal Nitrogen Accumulation in Maize Seeds. <i>Plant Cell</i> , 2020, 32, 2823-2841.	3.1	22
49	<i>Zea mays</i> Taxilin Protein Negatively Regulates Opaque-2 Transcriptional Activity by Causing a Change in Its Sub-Cellular Distribution. <i>PLoS ONE</i> , 2012, 7, e43822.	1.1	20
50	Divergence in centromere structure distinguishes related genomes in <i>Coix lacryma-jobi</i> and its wild relative. <i>Chromosoma</i> , 2010, 119, 89-98.	1.0	19
51	Characterization of a glutamine synthetase gene <i>DvGS2</i> from <i>Dunaliella viridis</i> and biochemical identification of <i>DvGS2</i> -transgenic <i>Arabidopsis thaliana</i> . <i>Gene</i> , 2014, 536, 407-415.	1.0	18
52	Morphology and stability changes of recombinant TMV particles caused by a cysteine residue in the foreign peptide fused to the coat protein. <i>Journal of Virological Methods</i> , 2007, 140, 212-217.	1.0	17
53	The endoglucanase from <i>Bacillus subtilis</i> BEC-1 bears halo-tolerant, acidophilic and dithiothreitol-stimulated enzyme activity. <i>World Journal of Microbiology and Biotechnology</i> , 2011, 27, 2863-2871.	1.7	16
54	Maize <i>Dek33</i> encodes a pyrimidine reductase in riboflavin biosynthesis that is essential for oil-body formation and ABA biosynthesis during seed development. <i>Journal of Experimental Botany</i> , 2019, 70, 5173-5187.	2.4	16

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55	Maize pentatricopeptide repeat protein DEK53 is required for mitochondrial RNA editing at multiple sites and seed development. <i>Journal of Experimental Botany</i> , 2020, 71, 6246-6261.	2.4	16
56	Genome-wide identification, splicing, and expression analysis of the myosin gene family in maize (<i>Zea mays</i> L.). <i>Plant Physiology</i> , 2020, 184, 1000-1010.	2.4	14
57	<i>Dek40</i> Encodes a PBAC4 Protein Required for 20S Proteasome Biogenesis and Seed Development. <i>Plant Physiology</i> , 2019, 180, 2120-2132.	2.3	14
58	<i>ENB1</i> encodes a cellulose synthase 5 that directs synthesis of cell wall ingrowths in maize basal endosperm transfer cells. <i>Plant Cell</i> , 2022, 34, 1054-1074.	3.1	13
59	Molecular cloning and characterization of a vacuolar H ⁺ -pyrophosphatase from <i>Dunaliella viridis</i> . <i>Molecular Biology Reports</i> , 2011, 38, 3375-3382.	1.0	12
60	<i>shrunken4</i> is a mutant allele of <i>ZmYSL2</i> that affects aleurone development and starch synthesis in maize. <i>Genetics</i> , 2021, 218, .	1.2	12
61	Maize seed storage proteins.. , 2017, , 175-189.		12
62	The amplification and evolution of orthologous 22-kDa β -prolamin tandemly arrayed genes in coix, sorghum and maize genomes. <i>Plant Molecular Biology</i> , 2010, 74, 631-643.	2.0	11
63	Construction of a <i>Coix</i> BAC library and isolation of the 22-kDa β -coixin gene cluster. <i>Genome</i> , 2010, 53, 667-674.	0.9	11
64	Comparative Study between the CRISPR/Cpf1 (Cas12a) and CRISPR/Cas9 Systems for Multiplex Gene Editing in Maize. <i>Agriculture (Switzerland)</i> , 2021, 11, 429.	1.4	11
65	OsFY, a Homolog of AtFY, Encodes a Protein that Can Interact with OsFCA-1 ³ in Rice (<i>Oryza sativa</i> L.). <i>Acta Biochimica Et Biophysica Sinica</i> , 2006, 38, 492-499.	0.9	10
66	Characterization of duplicated <i>Dunaliella viridis</i> SPT1 genes provides insights into early gene divergence after duplication. <i>Gene</i> , 2008, 423, 36-42.	1.0	10
67	An Induced Hypersensitive-Like Response Limits Expression of Foreign Peptides via a Recombinant TMV-Based Vector in a Susceptible Tobacco. <i>PLoS ONE</i> , 2010, 5, e15087.	1.1	10
68	The characterization of two peroxiredoxin genes in <i>Dunaliella viridis</i> provides insights into antioxidative response to salt stress. <i>Plant Cell Reports</i> , 2011, 30, 1503-1512.	2.8	9
69	Sequencing and Analysis of a Genomic Fragment Provide an Insight into the <i>Dunaliella viridis</i> Genomic Sequence. <i>Acta Biochimica Et Biophysica Sinica</i> , 2006, 38, 812-820.	0.9	7
70	Molecular cloning and characterization of a trehalose-6-phosphate synthase/phosphatase from <i>Dunaliella viridis</i> . <i>Molecular Biology Reports</i> , 2011, 38, 2241-2248.	1.0	7
71	Maize ZmVPP5 is a truncated Vacuole H ⁺ -ATPase that confers hypersensitivity to salt stress. <i>Journal of Integrative Plant Biology</i> , 2016, 58, 518-528.	4.1	7
72	TMV recombinants encoding fused foreign transmembrane domains to the CP subunit caused local necrotic response on susceptible tobacco. <i>Virology</i> , 2006, 348, 253-259.	1.1	6

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73	Expression of bacterial glutamine synthetase gene in <i>Arabidopsis thaliana</i> increases the plant biomass and level of nitrogen utilization. <i>Biologia (Poland)</i> , 2015, 70, 1586-1596.	0.8	6
74	O11 is multi-functional regulator in maize endosperm. <i>Plant Signaling and Behavior</i> , 2018, 13, e1451709.	1.2	6
75	A specific cis-hairpin ribozyme facilitates infection of a TMV-based DNA vector in tobacco protoplasts. <i>Journal of Virological Methods</i> , 2003, 111, 101-109.	1.0	5
76	Characterization of a glutamine synthetase gene DvGS1 from <i>Dunaliella viridis</i> and investigation of the impact on expression of DvGS1 in transgenic <i>Arabidopsis thaliana</i> . <i>Molecular Biology Reports</i> , 2014, 41, 477-487.	1.0	5
77	A Transcriptional Roadmap for Seed Development in Maize. , 2012, , 81-97.		5
78	Accumulation of 22â€‰kDa Î±-zeinâ€‰mediated nonzein protein in protein body of maize endosperm. <i>New Phytologist</i> , 2022, 233, 265-281.	3.5	5
79	Construction of a BAC library from cucumber (<i>Cucumis sativus</i> L.) and identification of linkage group specific clones. <i>Progress in Natural Science: Materials International</i> , 2008, 18, 143-147.	1.8	4
80	Molecular characterization of a genomic interval with highly uneven recombination distribution on maize chromosome 10 L. <i>Genetica</i> , 2011, 139, 1109-1118.	0.5	4
81	Uncovering kappa-opioid receptor agonist-induced PAK1/2 phosphorylation by quantitative phosphoproteomics. <i>Biochemical and Biophysical Research Communications</i> , 2019, 516, 320-326.	1.0	4
82	An Ac transposon system based on maize chromosome 4S for isolating long-distance-transposed Ac tags in the maize genome. <i>Genetica</i> , 2010, 138, 1261-1270.	0.5	3
83	Expression of the 26S proteasome subunit RPN10 is upregulated by salt stress in <i>Dunaliella viridis</i> . <i>Journal of Plant Physiology</i> , 2010, 167, 1003-1008.	1.6	3
84	Pollen-Specific CRISPR/Cas9 System to Increase Heritable Gene Mutations in Maize. <i>Agriculture (Switzerland)</i> , 2021, 11, 751.	1.4	3
85	Cloning and characterization of a flowering time gene from <i>Thellungiella halophila</i> . <i>Acta Biochimica Et Biophysica Sinica</i> , 2008, 40, 747-753.	0.9	2
86	The growth improvement of DvGS2-transgenic <i>Arabidopsis thaliana</i> arises from the higher efficiency of nitrogen and carbon assimilation. <i>Plant Biotechnology Reports</i> , 2015, 9, 187-195.	0.9	2
87	Improved ethanol production in the presence of cadmium ions by a <i>Saccharomyces cerevisiae</i> transformed with a novel cadmium-resistance gene DvCRP1. <i>Environmental Technology (United Kingdom)</i> 14 0.784314 rgBT /Overlock		
88	High-resolution gene profiling of infection process indicates serine metabolism adaptation of <i>Fusarium graminearum</i> in host. <i>Science Bulletin</i> , 2017, 62, 758-760.	4.3	1
89	Establishment of a Bivector Genetic Transformation System in Recalcitrant Maize Inbred Lines. <i>Agriculture (Switzerland)</i> , 2021, 11, 663.	1.4	1
90	Characterization of an Ac transposon system based on apt1-m1 (Ac) on the long arm of maize chromosome 9. <i>Genetica</i> , 2012, 140, 337-347.	0.5	0

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91	The better growth phenotype of DvGS1-transgenic arabidopsis thaliana is attributed to the improved efficiency of nitrogen assimilation. Archives of Biological Sciences, 2015, 67, 1107-1118.	0.2	0