

Xin Qiao

List of Publications by Year in descending order

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Version: 2024-02-01

39
papers

1,632
citations

471509

17
h-index

315739

38
g-index

40
all docs

40
docs citations

40
times ranked

1686
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide characterization of the G ₁ ± subunit gene family in Rosaceae and expression analysis of PbrGPAs under heat stress. <i>Gene</i> , 2022, 810, 146056.	2.2	2
2	Genome-wide identification and comparative analysis of the PYL gene family in eight Rosaceae species and expression analysis of seeds germination in pear. <i>BMC Genomics</i> , 2022, 23, 233.	2.8	8
3	The Origin and Evolution of RNase T2 Family and Gametophytic Self-incompatibility System in Plants. <i>Genome Biology and Evolution</i> , 2022, 14, .	2.5	5
4	Pervasive genome duplications across the plant tree of life and their links to major evolutionary innovations and transitions. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 3248-3256.	4.1	10
5	PbrCalS5, a callose synthase protein, is involved in pollen tube growth in <i>Pyrus bretschneideri</i> . <i>Planta</i> , 2022, 256, .	3.2	4
6	Characterization of the pectin methylesterase inhibitor gene family in Rosaceae and role of PbrPMEI23/39/41 in methylesterified pectin distribution in pear pollen tube. <i>Planta</i> , 2021, 253, 118.	3.2	13
7	Transcriptome and Resequencing Analyses Provide Insight into Differences in Organic Acid Accumulation in Two Pear Varieties. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9622.	4.1	5
8	Identification and expression analysis of the PbrMLO gene family in pear, and functional verification of PbrMLO23. <i>Journal of Integrative Agriculture</i> , 2021, 20, 2410-2423.	3.5	2
9	Genome-wide survey of G ₁ ³ subunit gene family in eight Rosaceae and expression analysis of PbrGGs in pear (<i>Pyrus bretschneideri</i>). <i>BMC Plant Biology</i> , 2021, 21, 471.	3.6	1
10	Genome-wide Identification and Evolution of the PP2C Gene Family in Eight Rosaceae Species and Expression Analysis Under Stress in <i>Pyrus bretschneideri</i> . <i>Frontiers in Genetics</i> , 2021, 12, 770014.	2.3	14
11	Multi-Omics Analysis Reveals the Dynamic Changes of RNA N6-Methyladenosine in Pear (<i>Pyrus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 <i>Microbiology</i> , 2021, 12, 803512.	3.5	3
12	Genome-Wide Identification and Comparative Analysis of the ASR Gene Family in the Rosaceae and Expression Analysis of PbrASRs During Fruit Development. <i>Frontiers in Genetics</i> , 2021, 12, 792250.	2.3	4
13	Genome-wide comparative analysis of the BAHD superfamily in seven Rosaceae species and expression analysis in pear (<i>Pyrus bretschneideri</i>). <i>BMC Plant Biology</i> , 2020, 20, 14.	3.6	22
14	Characterization of the pectin methyl-esterase gene family and its function in controlling pollen tube growth in pear (<i>Pyrus bretschneideri</i>). <i>Genomics</i> , 2020, 112, 2467-2477.	2.9	27
15	Genome-wide survey of sucrose non-fermenting 1-related protein kinase 2 in Rosaceae and expression analysis of PbrSnRK2 in response to ABA stress. <i>BMC Genomics</i> , 2020, 21, 781.	2.8	11
16	Comprehensive genomic analysis of the RNase T2 gene family in Rosaceae and expression analysis in <i>Pyrus bretschneideri</i> . <i>Plant Systematics and Evolution</i> , 2020, 306, 1.	0.9	7
17	Genome-wide identification of lysin motif containing protein family genes in eight rosaceae species, and expression analysis in response to pathogenic fungus <i>Botryosphaeria dothidea</i> in Chinese white pear. <i>BMC Genomics</i> , 2020, 21, 612.	2.8	9
18	Genome-wide identification and comparative analysis of the ADH gene family in Chinese white pear (<i>Pyrus bretschneideri</i>) and other Rosaceae species. <i>Genomics</i> , 2020, 112, 3484-3496.	2.9	20

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19	Expression and evolutionary analysis of soluble inorganic pyrophosphatase gene family in pear and four other Rosaceae species. <i>Plant Systematics and Evolution</i> , 2020, 306, 1.	0.9	5
20	Comparative analysis of the P-type ATPase gene family in seven Rosaceae species and an expression analysis in pear (<i>Pyrus bretschneideri</i> Rehd.). <i>Genomics</i> , 2020, 112, 2550-2563.	2.9	14
21	Genome-wide survey and expression analysis of the SLAC/SLAH gene family in pear (<i>Pyrus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 10	2.9	10
22	Unbiased subgenome evolution following a recent whole-genome duplication in pear (<i>Pyrus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 622 T	6.3	54
23	Gene duplication and evolution in recurring polyploidization“diploidization cycles in plants. <i>Genome Biology</i> , 2019, 20, 38.	8.8	542
24	The unique evolutionary pattern of the Hydroxyproline-rich glycoproteins superfamily in Chinese white pear (<i>Pyrus bretschneideri</i>). <i>BMC Plant Biology</i> , 2018, 18, 36.	3.6	6
25	Characterisation of the whole-genome wide hexokinase gene family unravels the functional divergence in pear (<i>Pyrus bretschneideri</i> Rehd.). <i>Journal of Horticultural Science and Biotechnology</i> , 2018, 93, 244-254.	1.9	6
26	Dynamic transcriptome analysis of root nitrate starvation and re-supply provides insights into nitrogen metabolism in pear (<i>Pyrus bretschneideri</i>). <i>Plant Science</i> , 2018, 277, 322-333.	3.6	15
27	Different Modes of Gene Duplication Show Divergent Evolutionary Patterns and Contribute Differently to the Expansion of Gene Families Involved in Important Fruit Traits in Pear (<i>Pyrus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10	3.6	10
28	Chemical Composition and Crystal Morphology of Epicuticular Wax in Mature Fruits of 35 Pear (<i>Pyrus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	3.6	52
29	Evolution, expression analysis, and functional verification of <i>Catharanthus roseus</i> RLK1-like kinase (CrRLK1L) family proteins in pear (<i>Pyrus bretschneideri</i>). <i>Genomics</i> , 2017, 109, 290-301.	2.9	25
30	A New Insight into the Evolution and Functional Divergence of SWEET Transporters in Chinese White Pear (<i>Pyrus bretschneideri</i>). <i>Plant and Cell Physiology</i> , 2017, 58, 839-850.	3.1	87
31	Genome-wide analysis and characterization of molecular evolution of the HCT gene family in pear (<i>Pyrus bretschneideri</i>). <i>Plant Systematics and Evolution</i> , 2017, 303, 71-90.	0.9	23
32	Expansion and evolutionary patterns of cysteine-rich peptides in plants. <i>BMC Genomics</i> , 2017, 18, 610.	2.8	18
33	Genome-wide identification of the<i>MADS-box</i> transcription factor family in pear (<i>Pyrus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 38	2.0	38
34	F-box genes: Genome-wide expansion, evolution and their contribution to pollen growth in pear (<i>Pyrus bretschneideri</i>). <i>Plant Science</i> , 2016, 253, 164-175.	3.6	42
35	Genome-Wide Identification, Evolution and Functional Divergence of MYB Transcription Factors in Chinese White Pear (<i>Pyrus bretschneideri</i>). <i>Plant and Cell Physiology</i> , 2016, 57, 824-847.	3.1	89
36	Genome-Wide Function, Evolutionary Characterization and Expression Analysis of Sugar Transporter Family Genes in Pear (<i>Pyrus bretschneideri</i>Rehd). <i>Plant and Cell Physiology</i> , 2015, 56, 1721-1737.	3.1	74

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37	Genome-wide identification and comparative analysis of the heat shock transcription factor family in Chinese white pear (<i>Pyrus bretschneideri</i>) and five other Rosaceae species. <i>BMC Plant Biology</i> , 2015, 15, 12.	3.6	138
38	Identification of miRNAs involved in pear fruit development and quality. <i>BMC Genomics</i> , 2014, 15, 953.	2.8	102
39	Characterization of the lipoxygenase (LOX) gene family in the Chinese white pear (<i>Pyrus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	2.8	49