

Hao Yin

List of Publications by Year in descending order

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34
papers

2,575
citations

430874

18
h-index

377865

34
g-index

35
all docs

35
docs citations

35
times ranked

2515
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide identification and comparative evolutionary analysis of sorbitol metabolism pathway genes in four Rosaceae species and three model plants. BMC Plant Biology, 2022, 22, .	3.6	5
2	Genome-wide comparative analysis of the BAHD superfamily in seven Rosaceae species and expression analysis in pear (<i>Pyrus bretschneideri</i>). BMC Plant Biology, 2020, 20, 14.	3.6	22
3	Effects of palmitic acid (16:0), hexacosanoic acid (26:0), ethephon and methyl jasmonate on the cuticular wax composition, structure and expression of key gene in the fruits of three pear cultivars. Functional Plant Biology, 2020, 47, 156.	2.1	6
4	PbrPOE21 inhibits pear pollen tube growth in vitro by altering apical reactive oxygen species content. Planta, 2020, 252, 43.	3.2	3
5	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. BMC Genomics, 2020, 21, 612.	2.8	9
6	Genome-wide identification and comparative analysis of the ADH gene family in Chinese white pear (<i>Pyrus bretschneideri</i>) and other Rosaceae species. Genomics, 2020, 112, 3484-3496.	2.9	20
7	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 50 302 T	2.9	10
8	Transcriptomic and Gas Chromatography-Mass Spectrometry Metabolomic Profiling Analysis of the Epidermis Provides Insights into Cuticular Wax Regulation in Developing “Yuluxiang” Pear Fruit. Journal of Agricultural and Food Chemistry, 2019, 67, 8319-8331.	5.2	15
9	Identification of Shaker K ⁺ channel family members in Rosaceae and a functional exploration of PbrKAT1. Planta, 2019, 250, 1911-1925.	3.2	14
10	Single-pollen-cell sequencing for gamete-based phased diploid genome assembly in plants. Genome Research, 2019, 29, 1889-1899.	5.5	28
11	PbrSLAH3 is a nitrate-selective anion channel which is modulated by calcium-dependent protein kinase 32 in pear. BMC Plant Biology, 2019, 19, 190.	3.6	6
12	Unbiased subgenome evolution following a recent whole-genome duplication in pear (<i>Pyrus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 302 T	6.3	54
13	Gene duplication and evolution in recurring polyploidization-diploidization cycles in plants. Genome Biology, 2019, 20, 38.	8.8	542
14	Dynamic transcriptome analysis of root nitrate starvation and re-supply provides insights into nitrogen metabolism in pear (<i>Pyrus bretschneideri</i>). Plant Science, 2018, 277, 322-333.	3.6	15
15	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 Tf 50 302 T	3.6	52
16	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 50 302 T	3.6	52
17	Diversification and independent domestication of Asian and European pears. Genome Biology, 2018, 19, 77.	8.8	149
18	Construction of a high-density genetic linkage map in pear (<i>Pyrus communis</i> — <i>Pyrus pyrifolia nakai</i>) using SSRs and SNPs developed by SLAF-seq. Scientia Horticulturae, 2017, 218, 198-204.	3.6	42

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19	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
20	Chemical composition, crystal morphology and key gene expression of cuticular waxes of Asian pears at harvest and after storage. <i>Postharvest Biology and Technology</i> , 2017, 132, 71-80.	6.0	51
21	TGTT and AACA: two transcriptionally active LTR retrotransposon subfamilies with a specific LTR structure and horizontal transfer in four Rosaceae species. <i>Mobile DNA</i> , 2017, 8, 14.	3.6	2
22	Overexpression of a bHLH1 Transcription Factor of <i>Pyrus ussuriensis</i> Confers Enhanced Cold Tolerance and Increases Expression of Stress-Responsive Genes. <i>Frontiers in Plant Science</i> , 2016, 7, 441.	3.6	45
23	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
24	Genome-wide identification and comparative analysis of the cation proton antiporters family in pear and four other Rosaceae species. <i>Molecular Genetics and Genomics</i> , 2016, 291, 1727-1742.	2.1	32
25	Gene-expression profile of developing pollen tube of <i>Pyrus bretschneideri</i> . <i>Gene Expression Patterns</i> , 2016, 20, 11-21.	0.8	40
26	Genome-wide Annotation and Comparative Analysis of Long Terminal Repeat Retrotransposons between Pear Species of <i>P. bretschneideri</i> and <i>P. Communis</i> . <i>Scientific Reports</i> , 2015, 5, 17644.	3.3	16
27	Evaluation of new IRAP markers of pear and their potential application in differentiating bud sports and other Rosaceae species. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	1.6	9
28	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
29	Identification of differentially expressed genes using digital gene expression profiles in <i>Pyrus pyrifolia</i> Nakai cv. Hosui bud release following early defoliation. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	1.6	6
30	Genomic characterization, phylogenetic comparison and differential expression of the cyclic nucleotide-gated channels gene family in pear (<i>Pyrus bretschneideri</i> Rehd.). <i>Genomics</i> , 2015, 105, 39-52.	2.9	52
31	Comparative Genomic Analysis Reveals Multiple Long Terminal Repeats, Lineage-Specific Amplification, and Frequent Interelement Recombination for Cassandra Retrotransposon in Pear (<i>Pyrus</i>) Tj ETQq1 1 0.784314 rgBL4 Overload 610 Tf 5	0.784314	610
32	High-density genetic linkage map construction and identification of fruit-related QTLs in pear using SNP and SSR markers. <i>Journal of Experimental Botany</i> , 2014, 65, 5771-5781.	4.8	171
33	The genome of the pear (<i>Pyrus bretschneideri</i> Rehd.). <i>Genome Research</i> , 2013, 23, 396-408.	5.5	832
34	TARE1, a Mutated Copia-Like LTR Retrotransposon Followed by Recent Massive Amplification in Tomato. <i>PLoS ONE</i> , 2013, 8, e68587.	2.5	20