

Hao Yin

List of Publications by Year in descending order

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34
papers

2,575
citations

430754

18
h-index

377752

34
g-index

35
all docs

35
docs citations

35
times ranked

2515
citing authors

#	ARTICLE	IF	CITATIONS
1	The genome of the pear (<i>Pyrus bretschneideri</i> Rehd.). <i>Genome Research</i> , 2013, 23, 396-408.	2.4	832
2	Gene duplication and evolution in recurring polyploidization–diploidization cycles in plants. <i>Genome Biology</i> , 2019, 20, 38.	3.8	542
3	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.	2.4	171
4	Diversification and independent domestication of Asian and European pears. <i>Genome Biology</i> , 2018, 19, 77.	3.8	149
5	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.	1.6	138
6	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>) <i>Tj ETQq0 0 0 rgBT / Overlock 10 Tf 50 537</i>	1.7	52
7	Unbiased subgenome evolution following a recent whole-genome duplication in pear (<i>Pyrus</i>) <i>Tj ETQq1 1 0.784314 rgBT / Overlock 10 Tf 54</i>	2.9	54
8	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.	1.3	52
9	Chemical Composition and Crystal Morphology of Epicuticular Wax in Mature Fruits of 35 Pear (<i>Pyrus</i>) <i>Tj ETQq1 1 0.784314 rgBT / Overlock 10 Tf 52</i>	1.7	52
10	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.	2.9	51
11	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.	1.7	45
12	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.	1.7	42
13	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. <i>Scientia Horticulturae</i> , 2017, 218, 198-204.	1.7	42
14	Gene-expression profile of developing pollen tube of <i>Pyrus bretschneideri</i> . <i>Gene Expression Patterns</i> , 2016, 20, 11-21.	0.3	40
15	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.	1.0	32
16	Single-pollen-cell sequencing for gamete-based phased diploid genome assembly in plants. <i>Genome Research</i> , 2019, 29, 1889-1899.	2.4	28
17	Comparative Genomic Analysis Reveals Multiple Long Terminal Repeats, Lineage-Specific Amplification, and Frequent Interelement Recombination for Cassandra Retrotransposon in Pear (<i>Pyrus</i>) <i>Tj ETQq1 1 0.784314 rgBT / Overlock 10 Tf 50</i>	1.7	50
18	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.	1.3	25

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19	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.	1.6	22
20	TARE1, a Mutated Copia-Like LTR Retrotransposon Followed by Recent Massive Amplification in Tomato. <i>PLoS ONE</i> , 2013, 8, e68587.	1.1	20
21	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.	1.3	20
22	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.	1.6	16
23	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.	1.7	15
24	Transcriptomic and Gas Chromatography-Mass Spectrometry Metabolomic Profiling Analysis of the Epidermis Provides Insights into Cuticular Wax Regulation in Developing 'Yuluxiang' Pear Fruit. <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 8319-8331.	2.4	15
25	Identification of Shaker K+ channel family members in Rosaceae and a functional exploration of PbrKAT1. <i>Planta</i> , 2019, 250, 1911-1925.	1.6	14
26	Genome-wide survey and expression analysis of the SLAC/SLAH gene family in pear (<i>Pyrus</i>). <i>Tree Genetics and Genomes</i> , 2015, 11, 1046-1062.	1.3	10
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.	0.6	9
28	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.	1.2	9
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.	0.6	6
30	PbrSLAH3 is a nitrate-selective anion channel which is modulated by calcium-dependent protein kinase 32 in pear. <i>BMC Plant Biology</i> , 2019, 19, 190.	1.6	6
31	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. <i>Functional Plant Biology</i> , 2020, 47, 156.	1.1	6
32	Genome-wide identification and comparative evolutionary analysis of sorbitol metabolism pathway genes in four Rosaceae species and three model plants. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	5
33	PbrPOE21 inhibits pear pollen tube growth in vitro by altering apical reactive oxygen species content. <i>Planta</i> , 2020, 252, 43.	1.6	3
34	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.	1.3	2