

Hao Yin

List of Publications by Year in descending order

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34
papers

2,575
citations

430754

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377752

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docs citations

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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. <i>BMC Plant Biology</i> , 2022, 22, . | 1.6 | 5 |
| 2 | 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 |
| 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. <i>Functional Plant Biology</i> , 2020, 47, 156. | 1.1 | 6 |
| 4 | PbrPOE21 inhibits pear pollen tube growth in vitro by altering apical reactive oxygen species content. <i>Planta</i> , 2020, 252, 43. | 1.6 | 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. <i>BMC Genomics</i> , 2020, 21, 612. | 1.2 | 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. <i>Genomics</i> , 2020, 112, 3484-3496. | 1.3 | 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 | 1.3 | 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. <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 8319-8331. | 2.4 | 15 |
| 9 | 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 |
| 10 | Single-pollen-cell sequencing for gamete-based phased diploid genome assembly in plants. <i>Genome Research</i> , 2019, 29, 1889-1899. | 2.4 | 28 |
| 11 | 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 |
| 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 | 2.9 | 54 |
| 13 | Gene duplication and evolution in recurring polyploidization–diploidization cycles in plants. <i>Genome Biology</i> , 2019, 20, 38. | 3.8 | 542 |
| 14 | 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 |
| 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 | 1.3 | 10 |
| 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 | 1.7 | 52 |
| 17 | Diversification and independent domestication of Asian and European pears. <i>Genome Biology</i> , 2018, 19, 77. | 3.8 | 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. <i>Scientia Horticulturae</i> , 2017, 218, 198-204. | 1.7 | 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. | 1.3 | 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. | 2.9 | 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. | 1.3 | 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. | 1.7 | 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. | 1.7 | 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. | 1.0 | 32 |
| 25 | Gene-expression profile of developing pollen tube of <i>Pyrus bretschneideri</i> . <i>Gene Expression Patterns</i> , 2016, 20, 11-21. | 0.3 | 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. | 1.6 | 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. | 0.6 | 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. | 1.6 | 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. | 0.6 | 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. | 1.3 | 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 rgBT1/Overload610 Tf S | | |
| 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. | 2.4 | 171 |
| 33 | The genome of the pear (<i>Pyrus bretschneideri</i> Rehd.). <i>Genome Research</i> , 2013, 23, 396-408. | 2.4 | 832 |
| 34 | TARE1, a Mutated Copia-Like LTR Retrotransposon Followed by Recent Massive Amplification in Tomato. <i>PLoS ONE</i> , 2013, 8, e68587. | 1.1 | 20 |