

Hui Chen

List of Publications by Year in descending order

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Version: 2024-02-01

61
papers

2,342
citations

279701

23
h-index

223716

46
g-index

63
all docs

63
docs citations

63
times ranked

2039
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	Genome-wide investigation of the AP2/ERF gene family in tartary buckwheat (<i>Fagopyum Tataricum</i>). <i>BMC Plant Biology</i> , 2019, 19, 84.	1.6	91
3	Genome-wide analysis of the NAC transcription factor family in Tartary buckwheat (<i>Fagopyrum</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.2	90
4	MYB Gene Family in Potato (<i>Solanum tuberosum</i> L.): Genome-Wide Identification of Hormone-Responsive Reveals Their Potential Functions in Growth and Development. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4847.	1.8	74
5	Genome-wide identification, expression analysis and functional study of the GRAS gene family in Tartary buckwheat (<i>Fagopyrum tataricum</i>). <i>BMC Plant Biology</i> , 2019, 19, 342.	1.6	72
6	Overexpression of a tartary buckwheat R2R3-MYB transcription factor gene, FtMYB9, enhances tolerance to drought and salt stresses in transgenic <i>Arabidopsis</i> . <i>Journal of Plant Physiology</i> , 2017, 214, 81-90.	1.6	68
7	Insights into the correlation between Physiological changes in and seed development of tartary buckwheat (<i>Fagopyrum tataricum</i> Gaertn.). <i>BMC Genomics</i> , 2018, 19, 648.	1.2	62
8	Overexpression of a Tartary Buckwheat Gene, FtBHLH3, Enhances Drought/Oxidative Stress Tolerance in Transgenic <i>Arabidopsis</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 625.	1.7	60
9	Genome-Wide Investigation of the Auxin Response Factor Gene Family in Tartary Buckwheat (<i>Fagopyrum tataricum</i>). <i>International Journal of Molecular Sciences</i> , 2018, 19, 3526.	1.8	60
10	Characterization of two tartary buckwheat R2R3-MYB transcription factors and their regulation of proanthocyanidin biosynthesis. <i>Physiologia Plantarum</i> , 2014, 152, 431-440.	2.6	56
11	A R2R3-MYB transcription factor gene, FtMYB13, from Tartary buckwheat improves salt/drought tolerance in <i>Arabidopsis</i> . <i>Plant Physiology and Biochemistry</i> , 2018, 132, 238-248.	2.8	47
12	Tartary buckwheat FtMYB10 encodes an R2R3-MYB transcription factor that acts as a novel negative regulator of salt and drought response in transgenic <i>Arabidopsis</i> . <i>Plant Physiology and Biochemistry</i> , 2016, 109, 387-396.	2.8	41
13	Basic helix-loop-helix (bHLH) gene family in Tartary buckwheat (<i>Fagopyrum tataricum</i>): Genome-wide identification, phylogeny, evolutionary expansion and expression analyses. <i>International Journal of Biological Macromolecules</i> , 2020, 155, 1478-1490.	3.6	41
14	Identification, isolation and expression analysis of eight stress-related R2R3-MYB genes in tartary buckwheat (<i>Fagopyrum tataricum</i>). <i>Plant Cell Reports</i> , 2016, 35, 1385-1396.	2.8	37
15	Anthocyanins accumulate in tartary buckwheat (<i>Fagopyrum tataricum</i>) sprout in response to cold stress. <i>Acta Physiologiae Plantarum</i> , 2015, 37, 1.	1.0	36
16	A WRKY transcription factor, FtWRKY46, from Tartary buckwheat improves salt tolerance in transgenic <i>Arabidopsis thaliana</i> . <i>Plant Physiology and Biochemistry</i> , 2020, 147, 43-53.	2.8	36
17	Genome-wide identification of the SPL gene family in Tartary Buckwheat (<i>Fagopyrum tataricum</i>) and expression analysis during fruit development stages. <i>BMC Plant Biology</i> , 2019, 19, 299.	1.6	35
18	Genome-wide investigation of the MADS gene family and dehulling genes in tartary buckwheat (<i>Fagopyrum tataricum</i>). <i>Planta</i> , 2019, 249, 1301-1318.	1.6	34

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19	Genome-wide identification, phylogeny, evolutionary expansion and expression analyses of bZIP transcription factor family in tartary buckwheat. <i>BMC Genomics</i> , 2019, 20, 483.	1.2	32
20	Isolation and identification of flavonoid-producing endophytic fungi from medicinal plant <i>Conyza blinii</i> H. Lv that exhibit higher antioxidant and antibacterial activities. <i>PeerJ</i> , 2020, 8, e8978.	0.9	31
21	Improved thermostability and enzyme activity of a recombinant phyA mutant phytase from <i>Aspergillus niger</i> N25 by directed evolution and site-directed mutagenesis. <i>Enzyme and Microbial Technology</i> , 2018, 108, 74-81.	1.6	29
22	Tartary buckwheat transcription factor FtbZIP83 improves the drought/salt tolerance of <i>Arabidopsis</i> via an ABA-mediated pathway. <i>Plant Physiology and Biochemistry</i> , 2019, 144, 312-323.	2.8	28
23	Genome-wide identification and expression analysis of the trihelix transcription factor family in tartary buckwheat (<i>Fagopyrum tataricum</i>). <i>BMC Plant Biology</i> , 2019, 19, 344.	1.6	26
24	The jasmonate-responsive transcription factor CbWRKY24 regulates terpenoid biosynthetic genes to promote saponin biosynthesis in <i>Conyza blinii</i> H. Lv.. <i>Journal of Genetics</i> , 2018, 97, 1379-1388.	0.4	25
25	Genome-wide investigation of the ZF-HD gene family in Tartary buckwheat (<i>Fagopyrum tataricum</i>). <i>BMC Plant Biology</i> , 2019, 19, 248.	1.6	25
26	Genome-wide investigation of the heat shock transcription factor (Hsf) gene family in Tartary buckwheat (<i>Fagopyrum tataricum</i>). <i>BMC Genomics</i> , 2019, 20, 871.	1.2	24
27	Improving Phytase Enzyme Activity in a Recombinant phyA Mutant Phytase from <i>Aspergillus niger</i> N25 by Error-Prone PCR. <i>Applied Biochemistry and Biotechnology</i> , 2012, 166, 549-562.	1.4	22
28	The Potential Role of Auxin and Abscisic Acid Balance and FtARF2 in the Final Size Determination of Tartary Buckwheat Fruit. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2755.	1.8	22
29	Extraction of polysaccharides from <i>Amaranthus hybridus</i> L. by hot water and analysis of their antioxidant activity. <i>PeerJ</i> , 2019, 7, e7149.	0.9	22
30	Site-Directed Mutagenesis Improves the Thermostability and Catalytic Efficiency of <i>Aspergillus niger</i> N25 Phytase Mutated by I44E and T252R. <i>Applied Biochemistry and Biotechnology</i> , 2013, 171, 900-915.	1.4	20
31	Validation of reference genes for gene expression studies in tartary buckwheat (<i>Fagopyrum</i>) Tj ETQq1 1 0.784314 rgBT / Overlock 18	0.9	18
32	Purification, characterization and antioxidant activities in vitro of polysaccharides from <i>Amaranthus hybridus</i> L.. <i>PeerJ</i> , 2020, 8, e9077.	0.9	17
33	Diversity, Chemical Constituents, and Biological Activities of Endophytic Fungi Isolated From <i>Ligusticum chuanxiong</i> Hort. <i>Frontiers in Microbiology</i> , 2021, 12, 771000.	1.5	17
34	Genome-wide investigation of WRKY transcription factors in Tartary buckwheat (<i>Fagopyrum</i>) Tj ETQq0 0 0 rgBT / Overlock 10 Tf 50 1	0.9	15
35	Karyotype and genetic relationship based on RAPD markers of six wild buckwheat species (<i>Fagopyrum</i>) Tj ETQq1 1 0.784314 rgBT / Overlock 14	0.8	14
36	Expression, purification and characterization of a phyA m -phyCs fusion phytase. <i>Journal of Zhejiang University: Science B</i> , 2008, 9, 536-545.	1.3	13

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37	Enhanced antioxidant capacity and upregulated transporter genes contribute to the UV-B-induced increase in blinin in <i>Conyza blinii</i> . <i>Environmental Science and Pollution Research</i> , 2021, 28, 13275-13287.	2.7	12
38	A Review on Fruit and Vegetable Fermented Beverage-Benefits of Microbes and Beneficial Effects. <i>Food Reviews International</i> , 2023, 39, 4835-4872.	4.3	12
39	Tartary Buckwheat (<i>Fagopyrum tataricum</i>) NAC Transcription Factors FtNAC16 Negatively Regulates of Pod Cracking and Salinity Tolerant in <i>Arabidopsis</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 3197.	1.8	11
40	Genome-Wide Investigation of Major Enzyme-Encoding Genes in the Flavonoid Metabolic Pathway in Tartary Buckwheat (<i>Fagopyrum tataricum</i>). <i>Journal of Molecular Evolution</i> , 2021, 89, 269-286.	0.8	11
41	Î²â€œAmyrin synthase from <i>Conyza blinii</i> expressed in <i>Saccharomyces cerevisiae</i> . <i>FEBS Open Bio</i> , 2017, 7, 1575-1585.	1.0	10
42	Ferrous iron-induced increases in capitate glandular trichome density and upregulation of CbHO-1 contributes to increases in blinin content in <i>Conyza blinii</i> . <i>Planta</i> , 2020, 252, 81.	1.6	9
43	Optimal extraction, purification and antioxidant activity of total flavonoids from endophytic fungi of <i>Conyza blinii</i> H. L. v. <i>PeerJ</i> , 2021, 9, e11223.	0.9	9
44	Evaluation of a strawberry fermented beverage with potential health benefits. <i>PeerJ</i> , 2021, 9, e11974.	0.9	9
45	The jasmonate-responsive transcription factor regulates terpenoid biosynthetic genes to promote saponin biosynthesis in <i>H. L. v.</i> <i>Journal of Genetics</i> , 2018, 97, 1379-1388.	0.4	9
46	Evolutionary research on the expansin protein family during the plant transition to land provides new insights into the development of Tartary buckwheat fruit. <i>BMC Genomics</i> , 2021, 22, 252.	1.2	8
47	<i>Coix lacryma-jobi</i> chymotrypsin inhibitor displays antifungal activity. <i>Pesticide Biochemistry and Physiology</i> , 2019, 160, 49-57.	1.6	7
48	Cloning and expression analysis of 1-deoxy-D-xylulose-5-phosphate synthase gene from the medicinal plant <i>Conyza blinii</i> H. L. v. <i>Turkish Journal of Biology</i> , 2014, 38, 664-670.	2.1	6
49	Purification and properties of the chymotrypsin inhibitor from wild emmer wheat (<i>Triticum</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T <i>Biochemistry and Physiology</i> , 2017, 142, 141-147.	1.6	6
50	Molecular Evolution and Local Root Heterogeneous Expression of the <i>Chenopodium quinoa</i> ARF Genes Provide Insights into the Adaptive Domestication of Crops in Complex Environments. <i>Journal of Molecular Evolution</i> , 2021, 89, 287-301.	0.8	6
51	Hemin-induced increase in saponin content contributes to the alleviation of osmotic and cold stress damage to <i>Conyza blinii</i> in a heme oxygenase 1-dependent manner. <i>Journal of Zhejiang University: Science B</i> , 2021, 22, 682-694.	1.3	6
52	Research on homology modeling, molecular docking of the cellulase and highly expression of the key enzyme (Bgl) in <i>Pichia pastoris</i> . <i>International Journal of Biological Macromolecules</i> , 2018, 115, 1079-1087.	3.6	5
53	Ligand based 3D-QSAR model, pharmacophore, molecular docking and ADME to identify potential fibroblast growth factor receptor 1 inhibitors. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 7584-7597.	2.0	5
54	Interspecies Evolution and Networks Investigation of the Auxin Response Protein (AUX/IAA) Family Reveals the Adaptation Mechanisms of Halophytes Crops in Nitrogen Starvation Agroecological Environments. <i>Agriculture (Switzerland)</i> , 2021, 11, 780.	1.4	5

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55	Tartary buckwheat database (TBD): an integrative platform for gene analysis of and biological information on Tartary buckwheat. <i>Journal of Zhejiang University: Science B</i> , 2021, 22, 954-958.	1.3	5
56	Fe induces a dynamic and biased allocation of material flux within terpenoid metabolism controlled by CbNudix in <i>Conyza blinii</i> . <i>Plant and Soil</i> , 2021, 467, 421-436.	1.8	4
57	Involvement of several putative transporters of different families in $\hat{1}^2$ -cyclocitral-induced alleviation of cadmium toxicity in quinoa (<i>Chenopodium quinoa</i>) seedlings. <i>Journal of Hazardous Materials</i> , 2021, 419, 126474.	6.5	4
58	<i>Conyza blinii</i> responds to the changes of exogenous iron through auxin-terpenoids metabolism pathway. <i>Journal of Plant Interactions</i> , 2022, 17, 485-495.	1.0	4
59	Metal Tolerance Protein Encoding Gene Family in <i>Fagopyrum tartaricum</i> : Genome-Wide Identification, Characterization and Expression under Multiple Metal Stresses. <i>Plants</i> , 2022, 11, 850.	1.6	3
60	Cloning, identification, and functional analysis of chalcone isomerase gene and its promoter from Tartary buckwheat. <i>Acta Physiologiae Plantarum</i> , 2022, 44, .	1.0	2
61	Construction of <i>Aspergillus Oryzae</i> food-grade expression system based on auxotrophic markers. <i>Food Biotechnology</i> , 2021, 35, 310-326.	0.6	0