

zhongshan Gao

List of Publications by Year in descending order

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#	ARTICLE	IF	CITATIONS
1	Comparative Transcriptome Analysis Reveals Sex-Biased Expression of Hormone-Related Genes at an Early Stage of Sex Differentiation in Red Bayberry (<i>Morella rubra</i>). <i>Horticulturae</i> , 2022, 8, 183.	2.8	3
2	Effects of Exogenous Application of GA4+7 and NAA on Sugar Accumulation and Related Gene Expression in Peach Fruits During Developing and Ripening Stages. <i>Journal of Plant Growth Regulation</i> , 2021, 40, 962-973.	5.1	8
3	China Consensus Document on Allergy Diagnostics. <i>Allergy, Asthma and Immunology Research</i> , 2021, 13, 177.	2.9	17
4	Peach allergen Pru p 1 content is generally low in fruit but with large variation in different varieties. <i>Clinical and Translational Allergy</i> , 2021, 11, e12034.	3.2	3
5	Genome-Wide Analysis of MYB Gene Family in Chinese Bayberry (<i>Morella rubra</i>) and Identification of Members Regulating Flavonoid Biosynthesis. <i>Frontiers in Plant Science</i> , 2021, 12, 691384.	3.6	40
6	MrTPS3 and MrTPS20 Are Responsible for β -Caryophyllene and α -Pinene Production, Respectively, in Red Bayberry (<i>Morella rubra</i>). <i>Frontiers in Plant Science</i> , 2021, 12, 798086.	3.6	5
7	Single Nucleotide Polymorphism Detection for Peach Gummosis Disease Resistance by Genome-Wide Association Study. <i>Frontiers in Plant Science</i> , 2021, 12, 763618.	3.6	4
8	Selection of Pru p 3 hypoallergenic peach and nectarine varieties. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2020, 75, 1256-1260.	5.7	4
9	Variation in IgE binding potencies of seven <i>Artemisia</i> species depending on content of major allergens. <i>Clinical and Translational Allergy</i> , 2020, 10, 50.	3.2	10
10	Toward personalization of asthma treatment according to trigger factors. <i>Journal of Allergy and Clinical Immunology</i> , 2020, 145, 1529-1534.	2.9	30
11	Construction of an anchoring SSR marker genetic linkage map and detection of a sex-linked region in two dioecious populations of red bayberry. <i>Horticulture Research</i> , 2020, 7, 53.	6.3	23
12	The red bayberry genome and genetic basis of sex determination. <i>Plant Biotechnology Journal</i> , 2019, 17, 397-409.	8.3	61
13	Genome-wide identification and analysis of the MADS-box gene family and its potential role in fruit development and ripening in red bayberry (<i>Morella rubra</i>). <i>Gene</i> , 2019, 717, 144045.	2.2	13
14	<i>Prunus</i> genetics and applications after de novo genome sequencing: achievements and prospects. <i>Horticulture Research</i> , 2019, 6, 58.	6.3	121
15	Localization of Four Allergens in <i>Artemisia</i> Pollen by Immunofluorescent Antibodies. <i>International Archives of Allergy and Immunology</i> , 2019, 179, 165-172.	2.1	5
16	<i>Artemisia</i> pollen allergy in China: Component-resolved diagnosis reveals allergic asthma patients have significant multiple allergen sensitization. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2019, 74, 284-293.	5.7	54
17	PeachVar-DB: A Curated Collection of Genetic Variations for the Interactive Analysis of Peach Genome Data. <i>Plant and Cell Physiology</i> , 2018, 59, e2-e2.	3.1	12
18	Identification of a 62 kDa major allergen from <i>Artemisia</i> pollen as a putative galactose oxidase. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2018, 73, 1041-1052.	5.7	15

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19	Acyl-CoA oxidase 1 is involved in $\hat{1}^3$ -decalactone release from peach (<i>Prunus persica</i>) fruit. <i>Plant Cell Reports</i> , 2017, 36, 829-842.	5.6	27
20	Identification of differentially expressed genes in flower, leaf and bulb scale of <i>Lilium</i> oriental hybrid "Sorbonne" and putative control network for scent genes. <i>BMC Genomics</i> , 2017, 18, 899.	2.8	18
21	IgE-binding potencies of three peach Pru p 1 isoforms. <i>Molecular Nutrition and Food Research</i> , 2016, 60, 2457-2466.	3.3	12
22	Quantification of Peach Fruit Allergen Lipid Transfer Protein by a Double Monoclonal Antibody-based Sandwich ELISA. <i>Food Analytical Methods</i> , 2016, 9, 823-830.	2.6	15
23	Whole-Genome Analysis of Diversity and SNP-Major Gene Association in Peach Germplasm. <i>PLoS ONE</i> , 2015, 10, e0136803.	2.5	98
24	Genetic diversity of male and female Chinese bayberry (<i>Myrica rubra</i>) populations and identification of sex-associated markers. <i>BMC Genomics</i> , 2015, 16, 394.	2.8	31
25	Identification of volatile and softening-related genes using digital gene expression profiles in melting peach. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	1.6	31
26	Selection of generally applicable SSR markers for evaluation of genetic diversity and identity in <i>Lilium</i> . <i>Biochemical Systematics and Ecology</i> , 2015, 61, 278-285.	1.3	13
27	Evaluation of the Role of IgE Responses to Der p 1 and Der p 2 in Chinese House Dust Mite-Allergic Patients. <i>International Archives of Allergy and Immunology</i> , 2015, 167, 203-210.	2.1	21
28	De Novo Assembled Transcriptome Analysis and SSR Marker Development of a Mixture of Six Tissues from <i>Lilium</i> Oriental Hybrid "Sorbonne". <i>Plant Molecular Biology Reporter</i> , 2015, 33, 281-293.	1.8	54
29	Development of 107 SSR markers from whole genome shotgun sequences of Chinese bayberry (<i>Myrica</i>) Tj ETQq1 1 0.784314 rgBT /Ove 15, 997-1005.	2.8	17
30	Transcriptome and proteomic analysis of mango (<i>Mangifera indica</i> Linn) fruits. <i>Journal of Proteomics</i> , 2014, 105, 19-30.	2.4	80
31	Peach genetic resources: diversity, population structure and linkage disequilibrium. <i>BMC Genetics</i> , 2013, 14, 84.	2.7	78
32	The PpLTP1 Primary Allergen Gene is Highly Conserved in Peach and Has Small Variations in Other <i>Prunus</i> Species. <i>Plant Molecular Biology Reporter</i> , 2013, 32, 652.	1.8	0
33	Peach allergy in China: A dominant role for mugwort pollen lipid transfer protein as a primary sensitizer. <i>Journal of Allergy and Clinical Immunology</i> , 2013, 131, 224-226.e3.	2.9	85
34	In vitro selection of glyphosate-tolerant variants from long-term callus cultures of <i>Zoysia matrella</i> [L.] Merr. <i>Plant Cell, Tissue and Organ Culture</i> , 2012, 111, 199-207.	2.3	9
35	Development of simple sequence repeat (SSR) markers from a genome survey of Chinese bayberry (<i>Myrica rubra</i>). <i>BMC Genomics</i> , 2012, 13, 201.	2.8	133
36	Anaphylaxis and generalized urticaria from eating Chinese bayberry fruit. <i>Journal of Zhejiang University: Science B</i> , 2012, 13, 851-854.	2.8	6

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37	Overview of Allergen Sources in China. <i>Advanced Topics in Science and Technology in China</i> , 2012, , 59-79.	0.1	2
38	Diversity arrays technology (DArT) markers in apple for genetic linkage maps. <i>Molecular Breeding</i> , 2012, 29, 645-660.	2.1	41
39	Multidisciplinary Approaches to Allergy Prevention. <i>Advanced Topics in Science and Technology in China</i> , 2012, , 33-55.	0.1	1
40	Allergen Protein Families and Cross-Reactivity. <i>Advanced Topics in Science and Technology in China</i> , 2012, , 81-90.	0.1	1
41	Recombinant Allergens and Applications. <i>Advanced Topics in Science and Technology in China</i> , 2012, , 131-146.	0.1	0
42	Fruit Allergy and Genetic and Genomic Tools to Select Hypoallergenic Fruit Cultivars. <i>Advanced Topics in Science and Technology in China</i> , 2012, , 359-383.	0.1	0
43	Genetic Diversity and Identity of Chinese Loquat Cultivars/Accessions (<i>Eriobotrya japonica</i>) Using Apple SSR Markers. <i>Plant Molecular Biology Reporter</i> , 2011, 29, 197-208.	1.8	52
44	Cultivar Identification and Genetic Diversity of Chinese Bayberry (<i>Myrica rubra</i>) Accessions Based on Fluorescent SSR Markers. <i>Plant Molecular Biology Reporter</i> , 2011, 29, 554-562.	1.8	24
45	Saturating the Prunus (stone fruits) genome with candidate genes for fruit quality. <i>Molecular Breeding</i> , 2011, 28, 667-682.	2.1	53
46	Callus induction, plant regeneration, and long-term maintenance of embryogenic cultures in <i>Zoysia matrella</i> [L.] Merr. <i>Plant Cell, Tissue and Organ Culture</i> , 2011, 104, 187-192.	2.3	29
47	In vitro selection of salt tolerant variants following ⁶⁰ Co gamma irradiation of long-term callus cultures of <i>Zoysia matrella</i> [L.] Merr.. <i>Plant Cell, Tissue and Organ Culture</i> , 2011, 107, 493-500.	2.3	26
48	Differential transcript abundance and genotypic variation of four putative allergen-encoding gene families in melting peach. <i>Tree Genetics and Genomes</i> , 2011, 7, 903-916.	1.6	20
49	Evaluation of the genetic diversity of Asian peach accessions using a selected set of SSR markers. <i>Scientia Horticulturae</i> , 2010, 125, 622-629.	3.6	40
50	Development of SNP markers and haplotype analysis of the candidate gene for <i>rhg1</i> , which confers resistance to soybean cyst nematode in soybean. <i>Molecular Breeding</i> , 2009, 24, 63-76.	2.1	28
51	Development and characterization of microsatellite markers for Chinese bayberry (<i>Myrica rubra</i> Sieb.) Tj ETQq1 1 0,784314 rgBT /Ove	1.5	22
52	Genetic Diversity of Chinese Bayberry (<i>Myrica rubra</i> Sieb. et Zucc.) Accessions Revealed by Amplified Fragment Length Polymorphism. <i>Hortscience: A Publication of the American Society for Horticultural Science</i> , 2009, 44, 487-491.	1.0	26
53	Assessment of allelic diversity in intron-containing Mal d 1 genes and their association to apple allergenicity. <i>BMC Plant Biology</i> , 2008, 8, 116.	3.6	45
54	Genomic characterization of putative allergen genes in peach/almond and their synteny with apple. <i>BMC Genomics</i> , 2008, 9, 543.	2.8	61

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55	An Anthocyanin-Related Glutathione S-Transferase, MrGST1, Plays an Essential Role in Fruit Coloration in Chinese Bayberry (<i>Morella rubra</i>). <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	7