

Jinggui Fang

List of Publications by Year in descending order

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140
papers

3,976
citations

117453

34
h-index

155451

55
g-index

143
all docs

143
docs citations

143
times ranked

3923
citing authors

#	ARTICLE	IF	CITATIONS
1	Effects of ethylene on berry ripening and anthocyanin accumulation of ‘Fujiminori’ grape in protected cultivation. <i>Journal of the Science of Food and Agriculture</i> , 2022, 102, 1124-1136.	1.7	10
2	VvERF17 mediates chlorophyll degradation by transcriptional activation of chlorophyll catabolic genes in grape berry skin. <i>Environmental and Experimental Botany</i> , 2022, 193, 104678.	2.0	11
3	Metabolomic profiling of brassinolide and abscisic acid in response to high-temperature stress. <i>Plant Cell Reports</i> , 2022, 41, 935-946.	2.8	5
4	Genome-wide association study of the candidate genes for grape berry shape-related traits. <i>BMC Plant Biology</i> , 2022, 22, 42.	1.6	6
5	Systematic analysis reveals O-methyltransferase gene family members involved in flavonoid biosynthesis in grape. <i>Plant Physiology and Biochemistry</i> , 2022, 173, 33-45.	2.8	8
6	Comparative Transcriptomic and Metabolomic Profiling of Grapevine Leaves (cv. Kyoho) upon Infestation of Grasshopper and <i>Botrytis cinerea</i> . <i>Plant Molecular Biology Reporter</i> , 2022, 40, 539-555.	1.0	3
7	Jasmonate increases terpene synthase expression, leading to strawberry resistance to <i>Botrytis cinerea</i> infection. <i>Plant Cell Reports</i> , 2022, 41, 1243-1260.	2.8	12
8	DNA and Histone Methylation Regulates Different Types of Fruit Ripening by Transcriptome and Proteome Analyses. <i>Journal of Agricultural and Food Chemistry</i> , 2022, 70, 3541-3556.	2.4	12
9	Transcriptome and metabolite integrated analysis reveals that exogenous ethylene controls berry ripening processes in grapevine. <i>Food Research International</i> , 2022, 155, 111084.	2.9	14
10	Characterization and regulatory mechanism analysis of VvmiR156a and VvAGL80 pair during grapevine flowering and parthenocarp process induced by gibberellin. <i>Plant Genome</i> , 2022, 15, e20181.	1.6	2
11	Transcriptomic Analysis Elaborates the Resistance Mechanism of Grapevine Rootstocks against Salt Stress. <i>Plants</i> , 2022, 11, 1167.	1.6	4
12	Transcriptional Profiling of Resistant and Susceptible Cultivars of Grapevine (<i>Vitis L.</i>) Reveals Hypersensitive Responses to <i>Plasmopara viticola</i> . <i>Frontiers in Microbiology</i> , 2022, 13, 846504.	1.5	5
13	Genome-wide identification and expression analysis of magnesium transporter gene family in grape (<i>Vitis vinifera</i>). <i>BMC Plant Biology</i> , 2022, 22, 217.	1.6	8
14	Effect of Silver Nitrate (AgNO ₃) and Nano-Silver (Ag-NPs) on Physiological Characteristics of Grapes and Quality during Storage Period. <i>Horticulturae</i> , 2022, 8, 419.	1.2	9
15	Copper stress in grapevine: Consequences, responses, and a novel mitigation strategy using 5-aminolevulinic acid. <i>Environmental Pollution</i> , 2022, 307, 119561.	3.7	8
16	Transcriptional and metabolite analysis reveal a shift in fruit quality in response to calcium chloride treatment on "Kyoho" grapevine. <i>Journal of Food Science and Technology</i> , 2021, 58, 2246-2257.	1.4	7
17	Overproduction of ROS: underlying molecular mechanism of scavenging and redox signaling. , 2021, , 347-382.		5
18	Preferential water uptake and differences in the anatomical structure of the distal end of grape berry may jointly lead to cracking in vitro soaking. <i>Horticulture Environment and Biotechnology</i> , 2021, 62, 353-365.	0.7	1

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19	The role of <i>VvMYBA2r</i> and <i>VvMYBA2w</i> alleles of the <i>MYBA2</i> locus in the regulation of anthocyanin biosynthesis for molecular breeding of grape (<i>Vitis</i> spp.) skin coloration. <i>Plant Biotechnology Journal</i> , 2021, 19, 1216-1239.	4.1	39
20	Characterization and Action Mechanism Analysis of <i>VvmiR156b/c/d-VvSPL9</i> Module Responding to Multiple-Hormone Signals in the Modulation of Grape Berry Color Formation. <i>Foods</i> , 2021, 10, 896.	1.9	16
21	Expressional diversity of grapevine 3-Hydroxy-3-methylglutaryl-CoA reductase (<i>VvHMGR</i>) in different grapes genotypes. <i>BMC Plant Biology</i> , 2021, 21, 279.	1.6	12
22	Identification of GH17 gene family in <i>Vitis vinifera</i> and expression analysis of GH17 under various adversities. <i>Physiology and Molecular Biology of Plants</i> , 2021, 27, 1423-1436.	1.4	3
23	Molecular Evaluation of Kyoho Grape Leaf and Berry Characteristics Influenced by Different NPK Fertilizers. <i>Plants</i> , 2021, 10, 1578.	1.6	4
24	Transcriptome and metabolite profiling reveal that spraying calcium fertilizer reduces grape berry cracking by modulating the flavonoid biosynthetic metabolic pathway. <i>Food Chemistry Molecular Sciences</i> , 2021, 2, 100025.	0.9	10
25	Profiling Analysis of Volatile and Non-volatile Compounds in <i>Vitis Vinifera</i> Berries (cv. Chardonnay) and Spontaneous Bud Mutation. <i>Frontiers in Nutrition</i> , 2021, 8, 715528.	1.6	7
26	Identification of miRNAs-mediated seed and stone-hardening regulatory networks and their signal pathway of GA-induced seedless berries in grapevine (<i>V. vinifera</i> L.). <i>BMC Plant Biology</i> , 2021, 21, 442.	1.6	4
27	Multi-omics analyses on the response mechanisms of "Shine Muscat" grapevine to low degree of excess copper stress (Low-ECS). <i>Environmental Pollution</i> , 2021, 286, 117278.	3.7	13
28	Integrative Analyses of Metabolomes and Transcriptomes Provide Insights into Flavonoid Variation in Grape Berries. <i>Journal of Agricultural and Food Chemistry</i> , 2021, 69, 12354-12367.	2.4	23
29	"The PLCP gene family of grapevine (<i>Vitis vinifera</i> L.): characterization and differential expression in response to <i>Plasmopara Viticola</i> ". <i>BMC Plant Biology</i> , 2021, 21, 499.	1.6	7
30	Strawberry Proteome Responses to Controlled Hot and Cold Stress Partly Mimic Post-harvest Storage Temperature Effects on Fruit Quality. <i>Frontiers in Nutrition</i> , 2021, 8, 812666.	1.6	11
31	Comparative Analysis of Cuticular Wax in Various Grape Cultivars During Berry Development and After Storage. <i>Frontiers in Nutrition</i> , 2021, 8, 817796.	1.6	9
32	Brassinosteroid Regulates 3-Hydroxy-3-methylglutaryl CoA Reductase to Promote Grape Fruit Development. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 11987-11996.	2.4	21
33	Transcriptome analysis of strawberry fruit in response to exogenous arginine. <i>Planta</i> , 2020, 252, 82.	1.6	16
34	The Effect of Ethylene on the Color Change and Resistance to <i>Botrytis cinerea</i> Infection in "Kyoho" Grape Fruits. <i>Foods</i> , 2020, 9, 892.	1.9	24
35	Demethylation alters transcriptome profiling of buds and leaves in "Kyoho" grape. <i>BMC Plant Biology</i> , 2020, 20, 544.	1.6	7
36	Comparative transcriptome analysis provides insight into regulation pathways and temporal and spatial expression characteristics of grapevine (<i>Vitis vinifera</i>) dormant buds in different nodes. <i>BMC Plant Biology</i> , 2020, 20, 390.	1.6	13

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37	Characterization of the regulation mechanism of grapevine microRNA172 family members during flower development. <i>BMC Plant Biology</i> , 2020, 20, 409.	1.6	0
38	Genome-wide identification and characterization of gibberellin metabolic and signal transduction (GA) Tj ETQq0 0 0 rgBT /Overlock 10 T Biology, 2020, 20, 384.	1.6	10
39	Chitinase family genes in grape differentially expressed in a manner specific to fruit species in response to <i>Botrytis cinerea</i> . <i>Molecular Biology Reports</i> , 2020, 47, 7349-7363.	1.0	10
40	Integrative transcriptomics and metabolomics data exploring the effect of chitosan on postharvest grape resistance to <i>Botrytis cinerea</i> . <i>Postharvest Biology and Technology</i> , 2020, 167, 111248.	2.9	46
41	Comprehensive Sequence Analysis of IQD Gene Family and their Expression Profiling in Grapevine (<i>Vitis</i> Tj ETQq1 1,0,784314 rgBT /Oe	1.0	12
42	Characterization and temporalâ€”spatial expression analysis of LEC1 gene in the development of seedless berries in grape induced by gibberellin. <i>Plant Growth Regulation</i> , 2020, 90, 585-596.	1.8	5
43	Genome-wide identification and analysis of B-BOX gene family in grapevine reveal its potential functions in berry development. <i>BMC Plant Biology</i> , 2020, 20, 72.	1.6	41
44	Effect of the Methylation Level on the Grape Fruit Development Process. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 2099-2115.	2.4	23
45	Comparative study of DAM, Dof, and WRKY gene families in fourteen species and their expression in <i>Vitis vinifera</i> . <i>3 Biotech</i> , 2020, 10, 72.	1.1	7
46	Triacantanol Promotes the Fruit Development and Retards Fruit Senescence in Strawberry: A Transcriptome Analysis. <i>Plants</i> , 2020, 9, 488.	1.6	14
47	Characterization of DNA methylation variations during fruit development and ripening of <i>Vitis vinifera</i> (cv. â€”Fujiminoriâ€”™). <i>Physiology and Molecular Biology of Plants</i> , 2020, 26, 617-637.	1.4	13
48	Genome-Wide Identification and Expression Profiling of the Polygalacturonase (PG) and Pectin Methylesterase (PME) Genes in Grapevine (<i>Vitis vinifera</i> L.). <i>International Journal of Molecular Sciences</i> , 2019, 20, 3180.	1.8	37
49	Integrated metatranscriptome and transcriptome reveals the microbial community composition and physiological function of xylem sap on grapevine during bleeding period. <i>Genes and Genomics</i> , 2019, 41, 1095-1111.	0.5	9
50	VvmiR160s/VvARFs interaction and their spatio-temporal expression/cleavage products during GA-induced grape parthenocarpy. <i>BMC Plant Biology</i> , 2019, 19, 111.	1.6	25
51	Physiological and transcriptional variations inducing complex adaptive mechanisms in grapevine by salt stress. <i>Environmental and Experimental Botany</i> , 2019, 162, 455-467.	2.0	42
52	Identification of copper (Cu) stress-responsive grapevine microRNAs and their target genes by high-throughput sequencing. <i>Royal Society Open Science</i> , 2019, 6, 180735.	1.1	19
53	Molecular Evaluation of Vitality and Survival Rate of Dormant Kyoho Grape Seedlings: A Step toward Molecular Farming. <i>Plants</i> , 2019, 8, 577.	1.6	1
54	Drought stress revealed physiological, biochemical and gene-expressional variations in â€”Yoshihimeâ€”™ peach (<i>Prunus Persica</i> L) cultivar. <i>Journal of Plant Interactions</i> , 2018, 13, 83-90.	1.0	75

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55	Genome-wide analysis of autophagy-related genes (ARGs) in grapevine and plant tolerance to copper stress. <i>Planta</i> , 2018, 247, 1449-1463.	1.6	38
56	Genome-wide Characterization and Expression Analysis of Sugar Transporter Family Genes in Woodland Strawberry. <i>Plant Genome</i> , 2018, 11, 170103.	1.6	39
57	Transcriptome Sequence Analysis Elaborates a Complex Defensive Mechanism of Grapevine (<i>Vitis</i>) Tj ETQq1 1 0.784314 rgBT /Overl	1.8	48
58	Genome-Wide Identification of PIFs in Grapes (<i>Vitis vinifera</i> L.) and Their Transcriptional Analysis under Lighting/Shading Conditions. <i>Genes</i> , 2018, 9, 451.	1.0	19
59	Characterization of Vv-miR156: Vv-SPL pairs involved in the modulation of grape berry development and ripening. <i>Molecular Genetics and Genomics</i> , 2018, 293, 1333-1354.	1.0	30
60	Analysis of the regulation networks in grapevine reveals response to waterlogging stress and candidate gene-marker selection for damage severity. <i>Royal Society Open Science</i> , 2018, 5, 172253.	1.1	23
61	In silico identification and computational characterization of endogenous small interfering RNAs from diverse grapevine tissues and stages. <i>Genes and Genomics</i> , 2018, 40, 801-817.	0.5	2
62	Changes of Anthocyanin Component Biosynthesis in "Summer Black"™ Grape Berries after the Red Flesh Mutation Occurred. <i>Journal of Agricultural and Food Chemistry</i> , 2018, 66, 9209-9218.	2.4	40
63	Coloring biology in grape skin: a prospective strategy for molecular farming. <i>Physiologia Plantarum</i> , 2018, 164, 429-441.	2.6	26
64	Chloroplast based genetic diversity among Chinese grapes genotypes. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2017, 28, 565-569.	0.7	6
65	Abscisic acid, sucrose, and auxin coordinately regulate berry ripening process of the Fujiminori grape. <i>Functional and Integrative Genomics</i> , 2017, 17, 441-457.	1.4	78
66	Characterization of miR061 and its target genes in grapevine responding to exogenous gibberellic acid. <i>Functional and Integrative Genomics</i> , 2017, 17, 537-549.	1.4	12
67	Role of microRNAs and their target genes in salinity response in plants. <i>Plant Growth Regulation</i> , 2017, 82, 377-390.	1.8	23
68	Insights into grapevine defense response against drought as revealed by biochemical, physiological and RNA-Seq analysis. <i>Scientific Reports</i> , 2017, 7, 13134.	1.6	107
69	Enzyme activities and gene expression of starch metabolism provide insights into grape berry development. <i>Horticulture Research</i> , 2017, 4, 17018.	2.9	28
70	Grapevine immune signaling network in response to drought stress as revealed by transcriptomic analysis. <i>Plant Physiology and Biochemistry</i> , 2017, 121, 187-195.	2.8	56
71	Characterization of miRNAs responsive to exogenous ethylene in grapevine berries at whole genome level. <i>Functional and Integrative Genomics</i> , 2017, 17, 213-235.	1.4	19
72	Ectopic expression of CSD1 and CSD2 targeting genes of miR398 in grapevine is associated with oxidative stress tolerance. <i>Functional and Integrative Genomics</i> , 2017, 17, 697-710.	1.4	36

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73	Genome-wide identification and characterization of genes involved in carotenoid metabolic in three stages of grapevine fruit development. <i>Scientific Reports</i> , 2017, 7, 4216.	1.6	38
74	Genome-Wide Analysis of the Sucrose Synthase Gene Family in Grape (<i>Vitis vinifera</i>): Structure, Evolution, and Expression Profiles. <i>Genes</i> , 2017, 8, 111.	1.0	56
75	Naturally Occurring Anthocyanin, Structure, Functions and Biosynthetic Pathway in Fruit Plants. <i>Journal of Plant Biochemistry & Physiology</i> , 2017, 05, .	0.5	66
76	High Throughput Sequencing Advances and Future Challenges. <i>Journal of Plant Biochemistry & Physiology</i> , 2017, 05, .	0.5	6
77	RNA-Sequencing Reveals Biological Networks during Table Grapevine (‘Fujiminori’™) Fruit Development. <i>PLoS ONE</i> , 2017, 12, e0170571.	1.1	25
78	Applications of DNA Technologies in Agriculture. <i>Current Genomics</i> , 2016, 17, 379-386.	0.7	21
79	Characterization of WvPAL-like promoter from grapevine using transgenic tobacco plants. <i>Functional and Integrative Genomics</i> , 2016, 16, 595-617.	1.4	21
80	Calcium/calmodulin alleviates substrate inhibition in a strawberry UDP-glucosyltransferase involved in fruit anthocyanin biosynthesis. <i>BMC Plant Biology</i> , 2016, 16, 197.	1.6	32
81	Abscisic acid and sucrose regulate tomato and strawberry fruit ripening through the abscisic acid stress ripening transcription factor. <i>Plant Biotechnology Journal</i> , 2016, 14, 2045-2065.	4.1	207
82	Functional Analysis of WvBG1 During Fruit Development and Ripening of Grape. <i>Journal of Plant Growth Regulation</i> , 2016, 35, 987-999.	2.8	16
83	A characterization of grapevine of GRAS domain transcription factor gene family. <i>Functional and Integrative Genomics</i> , 2016, 16, 347-363.	1.4	16
84	Overexpression of Polyphenol Oxidase Gene in Strawberry Fruit Delays the Fungus Infection Process. <i>Plant Molecular Biology Reporter</i> , 2016, 34, 592-606.	1.0	32
85	Determination of the precise sequences of computationally predicted miRNAs in <i>Citrus reticulata</i> by miR-RACE and characterization of the related target genes using RLM-RACE. <i>Gene</i> , 2016, 575, 498-505.	1.0	3
86	Jasmonic acid involves in grape fruit ripening and resistant against <i>Botrytis cinerea</i> . <i>Functional and Integrative Genomics</i> , 2016, 16, 79-94.	1.4	87
87	Transcriptomic Analysis of Grapevine (cv. Summer Black) Leaf, Using the Illumina Platform. <i>PLoS ONE</i> , 2016, 11, e0147369.	1.1	20
88	Discovery of Conservation and Diversification of miR171 Genes by Phylogenetic Analysis based on Global Genomes. <i>Plant Genome</i> , 2015, 8, eplantgenome2014.10.0076.	1.6	64
89	Comparative transcriptome analysis of grapevine in response to copper stress. <i>Scientific Reports</i> , 2015, 5, 17749.	1.6	104
90	Genome-Wide Mapping and Analysis of Grapevine MicroRNAs and Their Potential Target Genes. <i>Plant Genome</i> , 2015, 8, eplantgenome2014.12.0091.	1.6	35

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91	Characterization of a Calmodulin-binding Transcription Factor from Strawberry (<i>Fragaria</i> ×) Tj ETQq1 1 0,784314 rgBT /Overlock_10 Tf 50 2	1.6	18
92	Transporters, chaperones, and P-type ATPases controlling grapevine copper homeostasis. <i>Functional and Integrative Genomics</i> , 2015, 15, 673-684.	1.4	21
93	Association between Chloroplast and Mitochondrial DNA sequences in Chinese <i>Prunus</i> genotypes (<i>Prunus persica</i> , <i>Prunus domestica</i> , and <i>Prunus avium</i>). <i>BMC Plant Biology</i> , 2015, 15, 4.	1.6	17
94	Functional conservation analysis and expression modes of grape anthocyanin synthesis genes responsive to low temperature stress. <i>Gene</i> , 2015, 574, 168-177.	1.0	35
95	An on-line high-performance liquid chromatography-diode-array detector-electrospray ionization-ion-trap-time-of-flight-mass spectrometry-total antioxidant capacity detection system applying two antioxidant methods for activity evaluation of the edible flowers from <i>Prunus mume</i> . <i>Journal of Chromatography A</i> , 2015, 1414, 88-102.	1.8	43
96	RLM-RACE, PPM-RACE, and qRT-PCR: An Integrated Strategy to Accurately Validate miRNA Target Genes. <i>Methods in Molecular Biology</i> , 2015, 1296, 175-186.	0.4	17
97	Characterization of Expression Patterns of Grapevine MicroRNA Family Members using MicroRNA Rapid Amplification of Complementary DNA Ends. <i>Plant Genome</i> , 2015, 8, eplantgenome2014.10.0069.	1.6	5
98	A Method for Validating MicroRNAs in Plants by miR-RACE. <i>Methods in Molecular Biology</i> , 2015, 1287, 139-145.	0.4	0
99	miR-RACE: An Effective Approach to Accurately Determine the Sequence of Computationally Identified miRNAs. <i>Methods in Molecular Biology</i> , 2015, 1296, 109-118.	0.4	0
100	Transcriptome-wide analysis of dynamic variations in regulation modes of grapevine microRNAs on their target genes during grapevine development. <i>Plant Molecular Biology</i> , 2014, 84, 269-285.	2.0	54
101	Grapevine microRNAs responsive to exogenous gibberellin. <i>BMC Genomics</i> , 2014, 15, 111.	1.2	58
102	Identification and bioinformatic analysis of signal responsive/calmodulin-binding transcription activators gene models in <i>Vitis vinifera</i> . <i>Molecular Biology Reports</i> , 2014, 41, 2937-2949.	1.0	35
103	Advances in identification and validation of plant microRNAs and their target genes. <i>Physiologia Plantarum</i> , 2014, 152, 203-218.	2.6	17
104	Genome-wide identification and analysis of FK506-binding protein gene family in peach (<i>Prunus</i>) Tj ETQq0 0 0 rgBT /Overlock_10 Tf 50 2	1.0	6
105	Microarray analysis of differentially expressed genes engaged in fruit development between table and wine grape. <i>Molecular Biology Reports</i> , 2014, 41, 4397-4412.	1.0	1
106	Characterization of regulatory mechanism of <i>Poncirus trifoliata</i> microRNAs on their target genes with an integrated strategy of newly developed PPM-RACE and RLM-RACE. <i>Gene</i> , 2014, 535, 42-52.	1.0	1
107	Cloning, expression, and characterization of miR058 and its target PPO during the development of grapevine berry stone. <i>Gene</i> , 2014, 548, 166-173.	1.0	22
108	Depiction of Grapevine Phenology by Gene Expression Information and a Test of its Workability in Guiding Fertilization. <i>Plant Molecular Biology Reporter</i> , 2014, 32, 1070-1084.	1.0	11

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109	tasiRNAdb: a database of ta-siRNA regulatory pathways. <i>Bioinformatics</i> , 2014, 30, 1045-1046.	1.8	72
110	Mining and comparison of the genes encoding the key enzymes involved in sugar biosynthesis in apple, grape, and sweet orange. <i>Scientia Horticulturae</i> , 2014, 165, 311-318.	1.7	27
111	Computational identification of microRNAs in the strawberry (<i>Fragaria</i> — <i>ananassa</i>) genome sequence and validation of their precise sequences by miR-RACE. <i>Gene</i> , 2014, 536, 151-162.	1.0	18
112	Characterization of target mRNAs for <i>Prunus persica</i> microRNAs using an integrated strategy of PLM-RACE, PPM-RACE and qRT-PCR. <i>Scientia Horticulturae</i> , 2014, 170, 8-16.	1.7	6
113	Genome-wide identification and analysis of FK506-binding protein family gene family in strawberry (<i>Fragaria</i> — <i>ananassa</i>). <i>Gene</i> , 2014, 534, 390-399.	1.0	8
114	Plant variety and cultivar identification: advances and prospects. <i>Critical Reviews in Biotechnology</i> , 2013, 33, 111-125.	5.1	94
115	Whole genome identification and analysis of FK506-binding protein family genes in grapevine (<i>Vitis</i>) Tj ETQq1 1 0.784314 rgBT /Overl	1.0	7
116	Characterization and expression profiling of selected microRNAs in tomato (<i>Solanum lycopersicon</i>) "Jiangshu14"™. <i>Molecular Biology Reports</i> , 2013, 40, 3503-3521.	1.0	8
117	Fruit skin color and the role of anthocyanin. <i>Acta Physiologiae Plantarum</i> , 2013, 35, 2879-2890.	1.0	110
118	Bioinformatics prediction of miRNAs in the <i>Prunus persica</i> genome with validation of their precise sequences by miR-RACE. <i>Journal of Plant Physiology</i> , 2013, 170, 80-92.	1.6	12
119	Characterization of target mRNAs for grapevine microRNAs with an integrated strategy of modified RLM-RACE, newly developed PPM-RACE and qPCRs. <i>Journal of Plant Physiology</i> , 2013, 170, 943-957.	1.6	40
120	Deep sequencing discovery of novel and conserved microRNAs in strawberry (<i>Fragaria</i> — <i>ananassa</i>). <i>Physiologia Plantarum</i> , 2013, 148, 387-396.	2.6	45
121	Evaluation of Genome Sequencing Quality in Selected Plant Species Using Expressed Sequence Tags. <i>PLoS ONE</i> , 2013, 8, e69890.	1.1	29
122	Identification of trans-acting siRNAs and their regulatory cascades in grapevine. <i>Bioinformatics</i> , 2012, 28, 2561-2568.	1.8	47
123	Microarray analysis of differentially expressed genes engaged in fruit development between <i>Prunus mume</i> and <i>Prunus armeniaca</i> . <i>Journal of Plant Physiology</i> , 2012, 169, 1776-1788.	1.6	10
124	Identification of microRNAs from Amur grape (<i>Vitis amurensis</i> Rupr.) by deep sequencing and analysis of microRNA variations with bioinformatics. <i>BMC Genomics</i> , 2012, 13, 122.	1.2	98
125	Validation and characterization of <i>Citrus sinensis</i> microRNAs and their target genes. <i>BMC Research Notes</i> , 2012, 5, 235.	0.6	18
126	Computational identification of microRNAs in peach expressed sequence tags and validation of their precise sequences by miR-RACE. <i>Molecular Biology Reports</i> , 2012, 39, 1975-1987.	1.0	31

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127	An Efficient Identification of 68 Apple Cultivars Using a Cultivar Identification Diagram (CID) Strategy and RAPD Markers. <i>Horticultural Science and Technology</i> , 2012, 30, 549-556.	0.9	1
128	A novel strategy employed in identification of 25 important loquat cultivars using RAPD marker. <i>Caryologia</i> , 2011, 64, 265-271.	0.2	7
129	Characterization of microRNAs Identified in a Table Grapevine Cultivar with Validation of Computationally Predicted Grapevine miRNAs by miR-RACE. <i>PLoS ONE</i> , 2011, 6, e21259.	1.1	47
130	Computational identification of microRNAs in apple expressed sequence tags and validation of their precise sequences by miR-RACE. <i>Physiologia Plantarum</i> , 2011, 141, 56-70.	2.6	52
131	Deep sequencing of grapevine flower and berry short RNA library for discovery of novel microRNAs and validation of precise sequences of grapevine microRNAs deposited in miRBase. <i>Physiologia Plantarum</i> , 2011, 143, 64-81.	2.6	81
132	A mutation degree model for the identification of transcriptional regulatory elements. <i>BMC Bioinformatics</i> , 2011, 12, 262.	1.2	3
133	Deep sequencing discovery of novel and conserved microRNAs in trifoliate orange (<i>Citrus trifoliata</i>). <i>BMC Genomics</i> , 2010, 11, 431.	1.2	195
134	Analysis of expressed sequence tags from <i>Prunus mume</i> flower and fruit and development of simple sequence repeat markers. <i>BMC Genetics</i> , 2010, 11, 66.	2.7	24
135	MiR-RACE, a New Efficient Approach to Determine the Precise Sequences of Computationally Identified Trifoliate Orange (<i>Poncirus trifoliata</i>) MicroRNAs. <i>PLoS ONE</i> , 2010, 5, e10861.	1.1	55
136	Identification and characterization of 27 conserved microRNAs in citrus. <i>Planta</i> , 2009, 230, 671-685.	1.6	104
137	Genetic diversity of cowpea [<i>Vigna unguiculata</i> (L.) Walp.] in four West African and USA breeding programs as determined by AFLP analysis. <i>Genetic Resources and Crop Evolution</i> , 2007, 54, 1197-1209.	0.8	91
138	Genetic relationships among fruiting-mei (<i>Prunus mume</i> Sieb. et Zucc.) cultivars evaluated with AFLP and SNP markers. <i>Genome</i> , 2006, 49, 1256-1264.	0.9	31
139	(1) Genetic Diversity of Cowpea [<i>Vigna unguiculata</i> (L.) Walp.] Breeding Lines from Different Countries Determined by AFLP Markers. <i>Hortscience: A Publication of the American Society for Horticultural Science</i> , 2005, 40, 998A-998.	0.5	1
140	Validation of precise sequences of computationally identified microRNAs by miR-RACE. <i>Protocol Exchange</i> , 0, , .	0.3	0