

# HemI: A Toolkit for Illustrating Heatmaps

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Proteomic profiling of host-biofilm interactions in an oral infection model resembling the periodontal pocket. <i>Scientific Reports</i> , 2015, 5, 15999.	1.6	30
2	Effects of Common Data Errors in Electronic Health Records on Emergency Department Operational Performance Metrics: A Monte Carlo Simulation. <i>Academic Emergency Medicine</i> , 2015, 22, 1085-1092.	0.8	15
3	Priming maize resistance by its neighbors: activating 1,4-benzoxazine-3-ones synthesis and defense gene expression to alleviate leaf disease. <i>Frontiers in Plant Science</i> , 2015, 6, 830.	1.7	33
4	Genome-specific differential gene expressions in resynthesized Brassica allotetraploids from pair-wise crosses of three cultivated diploids revealed by RNA-seq. <i>Frontiers in Plant Science</i> , 2015, 6, 957.	1.7	31
5	Genome-Wide Analysis of the Fasciclin-Like Arabinogalactan Protein Gene Family Reveals Differential Expression Patterns, Localization, and Salt Stress Response in Populus. <i>Frontiers in Plant Science</i> , 2015, 6, 1140.	1.7	55
6	Phosphoproteomic Analysis of the Highly-Metastatic Hepatocellular Carcinoma Cell Line, MHCC97-H. <i>International Journal of Molecular Sciences</i> , 2015, 16, 4209-4225.	1.8	22
7	SILAC-based quantitative proteomics identified lysosome as a fast response target to PDT agent Gd-N induced oxidative stress in human ovarian cancer IGROV1 cells. <i>Molecular BioSystems</i> , 2015, 11, 3059-3067.	2.9	6
8	Comparison of the Seasonal Variations of Synechococcus Assemblage Structures in Estuarine Waters and Coastal Waters of Hong Kong. <i>Applied and Environmental Microbiology</i> , 2015, 81, 7644-7655.	1.4	69
9	Diet- and Genetically-induced Obesity Produces Alterations in the Microbiome, Inflammation and Wnt Pathway in the Intestine of Apc <sup>+/1638N</sup> Mice: Comparisons and Contrasts. <i>Journal of Cancer</i> , 2016, 7, 1780-1790.	1.2	61
10	A Genome-Scale Investigation of How Sequence, Function, and Tree-Based Gene Properties Influence Phylogenetic Inference. <i>Genome Biology and Evolution</i> , 2016, 8, 2565-2580.	1.1	70
11	La docencia actual de la Ética en las universidades jesuitas. <i>Arbor</i> , 2016, 192, 360.	0.1	1
12	Transcriptome-Based Analysis of Dof Family Transcription Factors and Their Responses to Abiotic Stress in Tea Plant ( <i>Camellia sinensis</i> ). <i>International Journal of Genomics</i> , 2016, 2016, 1-15.	0.8	20
13	Transcriptome Analysis Identifies Key Candidate Genes Mediating Purple Ovary Coloration in Asiatic Hybrid Lilies. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1881.	1.8	12
14	Gene Turnover Contributes to the Evolutionary Adaptation of <i>Acidithiobacillus caldus</i> : Insights from Comparative Genomics. <i>Frontiers in Microbiology</i> , 2016, 7, 1960.	1.5	35
15	Systematic Analysis of the 4-Coumarate:Coenzyme A Ligase (4CL) Related Genes and Expression Profiling during Fruit Development in the Chinese Pear. <i>Genes</i> , 2016, 7, 89.	1.0	51
16	Interspecies and Intraspecies Analysis of Trehalose Contents and the Biosynthesis Pathway Gene Family Reveals Crucial Roles of Trehalose in Osmotic-Stress Tolerance in Cassava. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1077.	1.8	39
17	Genome-Wide Analysis of the Synonymous Codon Usage Patterns in <i>Riemerella anatispestifer</i> . <i>International Journal of Molecular Sciences</i> , 2016, 17, 1304.	1.8	26
18	Comprehensive Transcriptome Analysis of Sex-Biased Expressed Genes Reveals Discrete Biological and Physiological Features of Male and Female <i>Schistosoma japonicum</i> . <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004684.	1.3	43

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19	Heat Shock Factor Genes of Tall Fescue and Perennial Ryegrass in Response to Temperature Stress by RNA-Seq Analysis. <i>Frontiers in Plant Science</i> , 2015, 6, 1226.	1.7	39
20	Expression of the Grape VqSTS21 Gene in Arabidopsis Confers Resistance to Osmotic Stress and Biotrophic Pathogens but Not Botrytis cinerea. <i>Frontiers in Plant Science</i> , 2016, 7, 1379.	1.7	23
21	Genome-Wide Identification, Localization, and Expression Analysis of Proanthocyanidin-Associated Genes in Brassica. <i>Frontiers in Plant Science</i> , 2016, 7, 1831.	1.7	14
22	GPS-PAIL: prediction of lysine acetyltransferase-specific modification sites from protein sequences. <i>Scientific Reports</i> , 2016, 6, 39787.	1.6	88
23	OsSGL, a novel pleiotropic stress-related gene enhances grain length and yield in rice. <i>Scientific Reports</i> , 2016, 6, 38157.	1.6	38
24	Redirecting abiraterone metabolism to fine-tune prostate cancer anti-androgen therapy. <i>Nature</i> , 2016, 533, 547-551.	13.7	138
25	Effects of dietary fibre source on microbiota composition in the large intestine of suckling piglets. <i>FEMS Microbiology Letters</i> , 2016, 363, fnw138.	0.7	55
26	Photosynthetic and physiological responses of mangroves under an environmental deterioration. <i>Acta Physiologiae Plantarum</i> , 2016, 38, 1.	1.0	2
27	Discovery of biomarkers for oxidative stress based on cellular metabolomics. <i>Biomarkers</i> , 2016, 21, 449-457.	0.9	16
28	Genome-wide identification and characterization of the Dof gene family in moso bamboo ( <i>Phyllostachys heterocycla</i> var. <i>pubescens</i> ). <i>Genes and Genomics</i> , 2016, 38, 733-745.	0.5	14
29	Characterization of Rice Group 3 LEA Genes in Developmental Stages and Under Abiotic Stress. <i>Plant Molecular Biology Reporter</i> , 2016, 34, 1003-1015.	1.0	6
30	Identification and differential regulation of microRNAs in response to methyl jasmonate treatment in <i>Lycoris aurea</i> by deep sequencing. <i>BMC Genomics</i> , 2016, 17, 789.	1.2	25
31	Distinct distribution patterns of prokaryotes between sediment and water in the Yellow River estuary. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 9683-9697.	1.7	61
32	Genome-wide analysis of RNA-interference pathway in <i>Brassica napus</i> , and the expression profile of BnAGOs in response to <i>Sclerotinia sclerotiorum</i> infection. <i>European Journal of Plant Pathology</i> , 2016, 146, 565-579.	0.8	10
33	Exploring and visualizing multidimensional data in translational research platforms. <i>Briefings in Bioinformatics</i> , 2016, 18, bbw080.	3.2	25
34	Comparative proteomic analysis provides novel insight into the interaction between resistant vs susceptible tomato cultivars and TYLCV infection. <i>BMC Plant Biology</i> , 2016, 16, 162.	1.6	22
35	Effect of exogenous GA 3 and its inhibitor paclobutrazol on floral formation, endogenous hormones, and flowering-associated genes in 'Fuji' apple ( <i>Malus domestica</i> Borkh.). <i>Plant Physiology and Biochemistry</i> , 2016, 107, 178-186.	2.8	92
36	Analysis of proteome dynamics inside the silk gland lumen of <i>Bombyx mori</i> . <i>Scientific Reports</i> , 2016, 6, 21158.	1.6	36

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37	The impact of P2Y12 promoter DNA methylation on the recurrence of ischemic events in Chinese patients with ischemic cerebrovascular disease. <i>Scientific Reports</i> , 2016, 6, 34570.	1.6	14
38	The NF- $\kappa$ B/RGL2 module integrates GA and ABA signalling to regulate seed germination in Arabidopsis. <i>Nature Communications</i> , 2016, 7, 12768.	5.8	216
39	OUP accepted manuscript. <i>Nucleic Acids Research</i> , 2017, 45, D264-D270.	6.5	62
40	Current and Evolving Methods to Visualize Biological Data in Cancer Research. <i>Journal of the National Cancer Institute</i> , 2016, 108, djw031.	3.0	18
41	Shifts of archaeal community structure in soil along an elevation gradient in a reservoir water level fluctuation zone. <i>Journal of Soils and Sediments</i> , 2016, 16, 2728-2739.	1.5	21
42	Rhizoma Coptidis alkaloids alleviate hyperlipidemia in B6 mice by modulating gut microbiota and bile acid pathways. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2016, 1862, 1696-1709.	1.8	111
43	Abundant members of Scavenger receptors family and their identification, characterization and expression against <i>Vibrio alginolyticus</i> infection in juvenile <i>Larimichthys crocea</i> . <i>Fish and Shellfish Immunology</i> , 2016, 50, 297-309.	1.6	7
44	Transcriptome analysis of the <i>Taxodium</i> Zhongshanshan 405™ roots in response to salinity stress. <i>Plant Physiology and Biochemistry</i> , 2016, 100, 156-165.	2.8	31
45	Comparative UPLC-QTOF-MS-based metabolomics and bioactivities analyses of <i>Garcinia oblongifolia</i> . <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2016, 1011, 179-195.	1.2	34
46	Impacts of addition of natural zeolite or a nitrification inhibitor on antibiotic resistance genes during sludge composting. <i>Water Research</i> , 2016, 91, 339-349.	5.3	255
47	Drought priming induces thermo-tolerance to post-anthesis high-temperature in offspring of winter wheat. <i>Environmental and Experimental Botany</i> , 2016, 127, 26-36.	2.0	51
48	Identification and Characterization of Novel Chitin-Binding Proteins from the Larval Cuticle of Silkworm, <i>Bombyx mori</i> . <i>Journal of Proteome Research</i> , 2016, 15, 1435-1445.	1.8	44
49	Illumina MiSeq sequencing reveals long-term impacts of single-walled carbon nanotubes on microbial communities of wastewater treatment systems. <i>Bioresource Technology</i> , 2016, 211, 209-215.	4.8	33
50	Meta-Prediction of <i>MTHFR</i> Gene Polymorphism Mutations and Associated Risk for Colorectal Cancer. <i>Biological Research for Nursing</i> , 2016, 18, 357-369.	1.0	23
51	Evolution of DUF1313 family members across plant species and their association with maize photoperiod sensitivity. <i>Genomics</i> , 2016, 107, 199-207.	1.3	9
52	Cloning, mRNA expression and transcriptional regulation of five retinoid X receptor subtypes in yellow catfish <i>Pelteobagrus fulvidraco</i> by insulin. <i>General and Comparative Endocrinology</i> , 2016, 225, 133-141.	0.8	10
53	Transcriptomics-based identification of <i>WRKY</i> genes and characterization of a salt and hormone-responsive <i>PgWRKY1</i> gene in <i>Panax ginseng</i> . <i>Acta Biochimica Et Biophysica Sinica</i> , 2016, 48, 117-131.	0.9	27
54	A next-generation microarray further reveals stage-enriched gene expression pattern in the blood fluke <i>Schistosoma japonicum</i> . <i>Parasites and Vectors</i> , 2017, 10, 19.	1.0	16

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55	Transcriptome profiling of spleen provides insights into the antiviral mechanism in <i>Schizothorax prenanti</i> after poly (I: C) challenge. <i>Fish and Shellfish Immunology</i> , 2017, 62, 13-23.	1.6	30
56	Anthocyanin biosynthesis regulation of DhMYB2 and DhbHLH1 in <i>Dendrobium</i> hybrids petals. <i>Plant Physiology and Biochemistry</i> , 2017, 112, 335-345.	2.8	59
57	Comparative RNA-seq analysis of transcriptome dynamics during petal development in <i>Rosa chinensis</i> . <i>Scientific Reports</i> , 2017, 7, 43382.	1.6	44
58	High flavonoid accompanied with high starch accumulation triggered by nutrient starvation in bioenergy crop duckweed ( <i>Landoltia punctata</i> ). <i>BMC Genomics</i> , 2017, 18, 166.	1.2	29
59	The effect of environmental contamination on the community structure and fructification of ectomycorrhizal fungi. <i>MicrobiologyOpen</i> , 2017, 6, e00396.	1.2	7
60	MYBs affect the variation in the ratio of anthocyanin and flavanol in fruit peel and flesh in response to shade. <i>Journal of Photochemistry and Photobiology B: Biology</i> , 2017, 168, 40-49.	1.7	20
61	Dietary fibres modulate the composition and activity of butyrate-producing bacteria in the large intestine of suckling piglets. <i>Antonie Van Leeuwenhoek</i> , 2017, 110, 687-696.	0.7	43
62	Transcriptomic analysis of the biosynthesis, recycling, and distribution of ascorbic acid during leaf development in tea plant ( <i>Camellia sinensis</i> (L.) O. Kuntze). <i>Scientific Reports</i> , 2017, 7, 46212.	1.6	32
63	Antibacterial evaluation of <i>Salvia miltiorrhizae</i> on <i>Escherichia coli</i> by microcalorimetry coupled with chemometrics. <i>AMB Express</i> , 2017, 7, 65.	1.4	6
64	Inhibition of neurotensin receptor 1 induces intrinsic apoptosis via let-7a-3p/Bcl-w axis in glioblastoma. <i>British Journal of Cancer</i> , 2017, 116, 1572-1584.	2.9	35
65	Genome-wide identification, phylogeny and expression analyses of SCARECROW-LIKE(SCL) genes in millet ( <i>Setaria italica</i> ). <i>Physiology and Molecular Biology of Plants</i> , 2017, 23, 629-640.	1.4	6
66	Effect of <i>Trichoderma harzianum</i> on maize rhizosphere microbiome and biocontrol of <i>Fusarium</i> Stalk rot. <i>Scientific Reports</i> , 2017, 7, 1771.	1.6	140
67	The heterogeneity of composition and assembly processes of the microbial community between different nutrient loading lake zones in Taihu Lake. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 5913-5923.	1.7	49
68	Comparative morphology and transcriptome analysis reveals distinct functions of the primary and secondary laticifer cells in the rubber tree. <i>Scientific Reports</i> , 2017, 7, 3126.	1.6	17
69	Profiles and drivers of antibiotic resistance genes distribution in one-stage and two-stage sludge anaerobic digestion based on microwave-H <sub>2</sub> O <sub>2</sub> pretreatment. <i>Bioresource Technology</i> , 2017, 241, 573-581.	4.8	42
70	Heavy mineral compositions and zircon U-Pb ages of Cenozoic sandstones in the SW Qaidam basin, northern Tibetan Plateau: Implications for provenance and tectonic setting. <i>Journal of Asian Earth Sciences</i> , 2017, 146, 233-250.	1.0	26
71	Time-series transcriptomic analysis of the deep-sea bacterium <i>Shewanella piezotolerans</i> WP3 in response to high salinity stress. <i>Marine Genomics</i> , 2017, 34, 23-26.	0.4	2
72	Metabolic adaptation to the aqueous leaf extract of <i>Moringa oleifera</i> Lam.-supplemented diet is related to the modulation of gut microbiota in mice. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 5115-5130.	1.7	24

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73	Cytological and Molecular Characterization of <i>ZmWAK</i> -Mediated Head-Smut Resistance in Maize. <i>Molecular Plant-Microbe Interactions</i> , 2017, 30, 455-465.	1.4	29
74	Three dimensional approach to investigating biological effects along energetic ion beam pathways. <i>Scientific Reports</i> , 2017, 7, 44732.	1.6	0
75	Diversity and composition of bacterial community in the rhizosphere sediments of submerged macrophytes revealed by 454 pyrosequencing. <i>Annals of Microbiology</i> , 2017, 67, 313-319.	1.1	15
76	Discovery and identification of potential biomarkers for alcohol-induced oxidative stress based on cellular metabolomics. <i>Biomedical Chromatography</i> , 2017, 31, e3907.	0.8	9
77	Transcriptome Analysis of Sugarcane Response to the Infection by Sugarcane Steak Mosaic Virus (SCSMV). <i>Tropical Plant Biology</i> , 2017, 10, 45-55.	1.0	21
78	Rapid Production of Virus Protein Microarray Using Protein Microarray Fabrication through Gene Synthesis (PAGES). <i>Molecular and Cellular Proteomics</i> , 2017, 16, 288-299.	2.5	8
79	A Phase II Study of Methotrexate, Etoposide, Dexamethasone and Pegaspargase Sandwiched with Radiotherapy in the Treatment of Newly Diagnosed, Stage IE to IIE Extranodal Natural-Killer/T-Cell Lymphoma, Nasal-Type. <i>EBioMedicine</i> , 2017, 25, 41-49.	2.7	45
80	Synergistic Effect in Core Microbiota Associated with Sulfur Metabolism in Spontaneous Chinese Liquor Fermentation. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	54
81	Proper land use for heavy metal-polluted soil based on enzyme activity analysis around a Pb-Zn mine in Feng County, China. <i>Environmental Science and Pollution Research</i> , 2017, 24, 28152-28164.	2.7	50
82	Genome-wide identification of glycosyltransferases converting phloretin to phloridzin in <i>Malus</i> species. <i>Plant Science</i> , 2017, 265, 131-145.	1.7	53
83	ALK is a therapeutic target for lethal sepsis. <i>Science Translational Medicine</i> , 2017, 9, .	5.8	90
84	Comprehensive Analysis of Acylcarnitine Species in <i>db/db</i> Mouse Using a Novel Method of High-Resolution Parallel Reaction Monitoring Reveals Widespread Metabolic Dysfunction Induced by Diabetes. <i>Analytical Chemistry</i> , 2017, 89, 10368-10375.	3.2	33
85	Identification and expression analysis of <i>LATERAL ORGAN BOUNDARIES DOMAIN</i> ( <i>LBD</i> ) transcription factor genes in <i>Fragaria vesca</i> . <i>Canadian Journal of Plant Science</i> , 2017, , .	0.3	4
86	Quantitative Proteomics and Targeted Fatty Acids Analysis Reveal the Damage of Triptolide in Liver and Kidney. <i>Proteomics</i> , 2017, 17, 1700001.	1.3	20
87	Simultaneous degradation of tetracycline by a microbial fuel cell and its toxicity evaluation by zebrafish. <i>RSC Advances</i> , 2017, 7, 44226-44233.	1.7	39
88	Exploring the Genomic Diversity and Cariogenic Differences of <i>Streptococcus mutans</i> Strains Through Pan-Genome and Comparative Genome Analysis. <i>Current Microbiology</i> , 2017, 74, 1200-1209.	1.0	23
89	Effects of subchronic exposure to waterborne cadmium on H-P-I axis hormones and related genes in rare minnows ( <i>Gobiocypris rarus</i> ). <i>Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology</i> , 2017, 202, 1-11.	1.3	7
90	A distinct serum metabolic signature of distant metastatic papillary thyroid carcinoma. <i>Clinical Endocrinology</i> , 2017, 87, 844-852.	1.2	33

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91	In silico genome-wide identification, phylogeny and expression analysis of the R2R3-MYB gene family in <i>Medicago truncatula</i> . <i>Journal of Integrative Agriculture</i> , 2017, 16, 1576-1591.	1.7	38
92	Fate of antimicrobial resistance genes in response to application of poultry and swine manure in simulated manure-soil microcosms and manure-pond microcosms. <i>Environmental Science and Pollution Research</i> , 2017, 24, 20949-20958.	2.7	15
93	Sugar and organic acid composition of apricot and their contribution to sensory quality and consumer satisfaction. <i>Scientia Horticulturae</i> , 2017, 225, 553-560.	1.7	58
94	Quantitative proteomic analysis of host responses triggered by <i>Mycobacterium tuberculosis</i> infection in human macrophage cells. <i>Acta Biochimica Et Biophysica Sinica</i> , 2017, 49, 835-844.	0.9	23
95	Molecular Characterization and Co-expression Analysis of the SnRK2 Gene Family in Sugarcane ( <i>Saccharum officinarum</i> L.). <i>Scientific Reports</i> , 2017, 7, 17659.	1.6	23
96	Medical examination powers miR-194-5p as a biomarker for postmenopausal osteoporosis. <i>Scientific Reports</i> , 2017, 7, 16726.	1.6	15
97	Massive expansion and differential evolution of small heat shock proteins with wheat ( <i>Triticum</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 50	1.6	17
98	Genome-wide identification, functional and evolutionary analysis of terpene synthases in pineapple. <i>Computational Biology and Chemistry</i> , 2017, 70, 40-48.	1.1	11
99	Transcriptomic Profiling Reveals Differentially Expressed Genes Associated with Pine Wood Nematode Resistance in Masson Pine ( <i>Pinus massoniana</i> Lamb.). <i>Scientific Reports</i> , 2017, 7, 4693.	1.6	58
100	High efficiency microbial electrosynthesis of acetate from carbon dioxide by a self-assembled electroactive biofilm. <i>Bioresource Technology</i> , 2017, 243, 573-582.	4.8	70
101	The Gut Bacterial Community Composition of Wild <i>Cervus albirostris</i> (White-Lipped Deer) Detected by the 16S Ribosomal RNA Gene Sequencing. <i>Current Microbiology</i> , 2017, 74, 1100-1107.	1.0	14
102	The community structure of <i>Methanomassiliicoccales</i> in the rumen of Chinese goats and its response to a high-grain diet. <i>Journal of Animal Science and Biotechnology</i> , 2017, 8, 47.	2.1	19
103	Variation in Floral Scent Compositions of Different Lily Hybrid Groups. <i>Journal of the American Society for Horticultural Science</i> , 2017, 142, 175-183.	0.5	18
104	MZH29 is a novel potent inhibitor that overcomes drug resistance FLT3 mutations in acute myeloid leukemia. <i>Leukemia</i> , 2017, 31, 913-921.	3.3	20
105	Characterization of the LBD gene family in <i>Brachypodium</i> : a phylogenetic and transcriptional study. <i>Plant Cell Reports</i> , 2017, 36, 61-79.	2.8	16
106	Phylogeography and pigment type diversity of <i>Synechococcus</i> cyanobacteria in surface waters of the northwestern pacific ocean. <i>Environmental Microbiology</i> , 2017, 19, 142-158.	1.8	40
107	In vivo effects of metal ions on conformation and mechanical performance of silkworm silks. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017, 1861, 567-576.	1.1	44
108	Metabolic responses of <i>Haliotis diversicolor</i> to <i>Vibrio parahaemolyticus</i> infection. <i>Fish and Shellfish Immunology</i> , 2017, 60, 265-274.	1.6	55

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109	Combining paired analytical metabolomics and common garden trial to study the metabolism and gene variation of <i>Ginkgo biloba</i> L. cultivated varieties. <i>RSC Advances</i> , 2017, 7, 55309-55317.	1.7	5
110	Transcriptomic profiling and genetic analyses reveal novel key regulators of cellulase and xylanase gene expression in <i>Penicillium oxalicum</i> . <i>Biotechnology for Biofuels</i> , 2017, 10, 279.	6.2	49
111	Comparative Analysis of Compatibility Effects on Invigorating Blood Circulation for <i>Cyperus Rhizoma</i> Series of Herb Pairs Using Untargeted Metabolomics. <i>Frontiers in Pharmacology</i> , 2017, 8, 677.	1.6	16
112	Heat Stress Regulates the Expression of Genes at Transcriptional and Post-Transcriptional Levels, Revealed by RNA-seq in <i>Brachypodium distachyon</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 2067.	1.7	38
113	Genome Wide Identification and Characterization of Apple bHLH Transcription Factors and Expression Analysis in Response to Drought and Salt Stress. <i>Frontiers in Plant Science</i> , 2017, 8, 480.	1.7	148
114	Histological Characteristics, Cell Wall Hydrolytic Enzymes Activity and Candidate Genes Expression Associated with Seed Shattering of <i>Elymus sibiricus</i> Accessions. <i>Frontiers in Plant Science</i> , 2017, 08, 606.	1.7	19
115	Genome Wide Identification and Expression Profiling of Ethylene Receptor Genes during Soybean Nodulation. <i>Frontiers in Plant Science</i> , 2017, 8, 859.	1.7	7
116	Generation, Annotation, and Analysis of a Large-Scale Expressed Sequence Tag Library from <i>Arabidopsis pumila</i> to Explore Salt-Responsive Genes. <i>Frontiers in Plant Science</i> , 2017, 8, 955.	1.7	16
117	Accurate Digitization of the Chlorophyll Distribution of Individual Rice Leaves Using Hyperspectral Imaging and an Integrated Image Analysis Pipeline. <i>Frontiers in Plant Science</i> , 2017, 8, 1238.	1.7	21
118	Identification and Expression Profile of CYPome in Perennial Ryegrass and Tall Fescue in Response to Temperature Stress. <i>Frontiers in Plant Science</i> , 2017, 8, 1519.	1.7	39
119	microRNAs and Their Targets in Apple ( <i>Malus domestica</i> cv. 'Fuji') Involved in Response to Infection of Pathogen <i>Valsa mali</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 2081.	1.7	13
120	Chemosensory genes in the antennal transcriptome of two syrphid species, <i>Episyrphus balteatus</i> and <i>Eupeodes corollae</i> (Diptera: Syrphidae). <i>BMC Genomics</i> , 2017, 18, 586.	1.2	64
121	Genome-Wide Analysis of CCA1-Like Proteins in Soybean and Functional Characterization of GmMYB138a. <i>International Journal of Molecular Sciences</i> , 2017, 18, 2040.	1.8	18
122	Comparative Analysis of Fruit Ripening-Related miRNAs and Their Targets in Blueberry Using Small RNA and Degradome Sequencing. <i>International Journal of Molecular Sciences</i> , 2017, 18, 2767.	1.8	36
123	Genome-Wide Analysis of the Biosynthesis and Deactivation of Gibberellin-Dioxygenases Gene Family in <i>Camellia sinensis</i> (L.) O. Kuntze. <i>Genes</i> , 2017, 8, 235.	1.0	34
124	Genome-Wide Identification and Structural Analysis of bZIP Transcription Factor Genes in <i>Brassica napus</i> . <i>Genes</i> , 2017, 8, 288.	1.0	68
125	Involvement of MicroRNAs in Probiotics-Induced Reduction of the Cecal Inflammation by <i>Salmonella Typhimurium</i> . <i>Frontiers in Immunology</i> , 2017, 8, 704.	2.2	40
126	Comparative Genomics Unravels the Functional Roles of Co-occurring Acidophilic Bacteria in Bioleaching Heaps. <i>Frontiers in Microbiology</i> , 2017, 8, 790.	1.5	17



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127	Unraveling Core Functional Microbiota in Traditional Solid-State Fermentation by High-Throughput Amplicons and Metatranscriptomics Sequencing. <i>Frontiers in Microbiology</i> , 2017, 8, 1294.	1.5	181
128	Microbiome-Metabolome Responses to a High-Grain Diet Associated with the Hind-Gut Health of Goats. <i>Frontiers in Microbiology</i> , 2017, 8, 1764.	1.5	41
129	llumina Sequencing Approach to Characterize Thiamine Metabolism Related Bacteria and the Impacts of Thiamine Supplementation on Ruminant Microbiota in Dairy Cows Fed High-Grain Diets. <i>Frontiers in Microbiology</i> , 2017, 8, 1818.	1.5	85
130	Basin Scale Variation on the Composition and Diversity of Archaea in the Pacific Ocean. <i>Frontiers in Microbiology</i> , 2017, 8, 2057.	1.5	21
131	High Fat Diet Alters Gut Microbiota and the Expression of Paneth Cell-Antimicrobial Peptides Preceding Changes of Circulating Inflammatory Cytokines. <i>Mediators of Inflammation</i> , 2017, 2017, 1-9.	1.4	116
132	Signal Factors Secreted by 2D and Spheroid Mesenchymal Stem Cells and by Cocultures of Mesenchymal Stem Cells Derived Microvesicles and Retinal Photoreceptor Neurons. <i>Stem Cells International</i> , 2017, 2017, 1-13.	1.2	25
133	Identification of differentially expressed genes in flower, leaf and bulb scale of <i>Lilium oriental</i> hybrid "Sorbonne" and putative control network for scent genes. <i>BMC Genomics</i> , 2017, 18, 899.	1.2	18
134	Structure of Pigment Metabolic Pathways and Their Contributions to White Tepal Color Formation of Chinese <i>Narcissus tazetta</i> var. <i>chinensis</i> cv <i>Jinzhanyintai</i> . <i>International Journal of Molecular Sciences</i> , 2017, 18, 1923.	1.8	17
135	Identification, classification, and transcription profiles of the B-type response regulator family in pear. <i>PLoS ONE</i> , 2017, 12, e0171523.	1.1	28
136	Identification and characterization of CONSTANS-like (COL) gene family in upland cotton ( <i>Gossypium</i> ) Tj ETQq1 1 0.784314 $\mu$ gBT /Over	1.1	26
137	MiRNAs regulate oxidative stress related genes via binding to the 3' UTR and TATA-box regions: a new hypothesis for cataract pathogenesis. <i>BMC Ophthalmology</i> , 2017, 17, 142.	0.6	37
138	Wild Silkworm Cocoon Contains More Metabolites Than Domestic Silkworm Cocoon to Improve Its Protection. <i>Journal of Insect Science</i> , 2017, 17, .	0.6	11
139	Transcriptome-wide elucidation of liposomal formulations for anticancer drug delivery. <i>International Journal of Nanomedicine</i> , 2017, Volume 12, 8557-8572.	3.3	1
140	Quantitative Phosphoproteomic Analysis Provides Insight into the Response to Short-Term Drought Stress in <i>Ammopiptanthus mongolicus</i> Roots. <i>International Journal of Molecular Sciences</i> , 2017, 18, 2158.	1.8	17
141	Proteomic profiling of early degenerative retina of RCS rats. <i>International Journal of Ophthalmology</i> , 2017, 10, 878-889.	0.5	6
142	The Citrus Transcription Factor CsMADS6 Modulates Carotenoid Metabolism by Directly Regulating Carotenogenic Genes. <i>Plant Physiology</i> , 2018, 176, 2657-2676.	2.3	184
143	Dissolved organic matter release in overlying water and bacterial community shifts in biofilm during the decomposition of <i>Myriophyllum verticillatum</i> . <i>Science of the Total Environment</i> , 2018, 633, 929-937.	3.9	70
144	Responses of microbial capacity and community on the performance of mesophilic co-digestion of food waste and waste activated sludge in a high-frequency feeding CSTR. <i>Bioresource Technology</i> , 2018, 260, 85-94.	4.8	25

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145	Genome-Wide Association Studies of Image Traits Reveal Genetic Architecture of Drought Resistance in Rice. <i>Molecular Plant</i> , 2018, 11, 789-805.	3.9	151
146	Analysis of synonymous codon usage bias in helicase gene from <i>Autographa californica</i> multiple nucleopolyhedrovirus. <i>Genes and Genomics</i> , 2018, 40, 767-780.	0.5	14
147	Transcriptome-wide identification and expression profile analysis of the bHLH family genes in <i>Camellia sinensis</i> . <i>Functional and Integrative Genomics</i> , 2018, 18, 489-503.	1.4	47
148	Specific Upregulation of a Cotton Phytoene Synthase Gene Produces Golden Cottonseeds with Enhanced Provitamin A. <i>Scientific Reports</i> , 2018, 8, 1348.	1.6	14
149	Effects of water flow on submerged macrophyte-biofilm systems in constructed wetlands. <i>Scientific Reports</i> , 2018, 8, 2650.	1.6	25
150	Chronic impacts of oxytetracycline on mesophilic anaerobic digestion of excess sludge: Inhibition of hydrolytic acidification and enrichment of antibiotic resistome. <i>Environmental Pollution</i> , 2018, 238, 1017-1026.	3.7	41
151	Contamination level, chemical fraction and ecological risk of heavy metals in sediments from Daya Bay, South China Sea. <i>Marine Pollution Bulletin</i> , 2018, 128, 132-139.	2.3	78
152	Bioinformatic identification of chemoresistance-associated microRNAs in breast cancer based on microarray data. <i>Oncology Reports</i> , 2018, 39, 1003-1010.	1.2	45
153	Modulation of gut microbiota by dietary supplementation with tuna oil and algae oil alleviates the effects of D-galactose-induced ageing. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 2791-2801.	1.7	21
154	DNA methylation changes and evolution of RNA-based duplication in <i>Sus scrofa</i> : based on a two-step strategy. <i>Epigenomics</i> , 2018, 10, 199-218.	1.0	6
155	Developing a low fishmeal diet for juvenile Pacific white shrimp, <i>Litopenaeus vannamei</i> , using the nutritional value of FM as the reference profile. <i>Aquaculture Nutrition</i> , 2018, 24, 1184-1197.	1.1	20
156	Could FlhF be a key element that controls <i>Campylobacter jejuni</i> flagella biosynthesis in the initial assembly stage?. <i>Microbiological Research</i> , 2018, 207, 240-248.	2.5	20
157	Transcriptome sequencing and comparative analysis of differentially-expressed isoforms in the roots of <i>Halogeton glomeratus</i> under salt stress. <i>Gene</i> , 2018, 646, 159-168.	1.0	27
158	Simulated Digestion and Fermentation in Vitro by Human Gut Microbiota of Polysaccharides from Bee Collected Pollen of Chinese Wolfberry. <i>Journal of Agricultural and Food Chemistry</i> , 2018, 66, 898-907.	2.4	127
159	iUUCD 2.0: an update with rich annotations for ubiquitin and ubiquitin-like conjugations. <i>Nucleic Acids Research</i> , 2018, 46, D447-D453.	6.5	57
160	ZmWRKY79 positively regulates maize phytoalexin biosynthetic gene expression and is involved in stress response. <i>Journal of Experimental Botany</i> , 2018, 69, 497-510.	2.4	51
161	Mechanisms of the active components from Korean pine nut preventing and treating d-galactose-induced aging rats. <i>Biomedicine and Pharmacotherapy</i> , 2018, 103, 680-690.	2.5	9
162	Comparative genome analysis of 52 fish species suggests differential associations of repetitive elements with their living aquatic environments. <i>BMC Genomics</i> , 2018, 19, 141.	1.2	89

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163	Multi-element determination in <i>Schisandra chinensis fructus</i> by inductively coupled plasma mass spectrometry and the study of element transfer rules from herbs to decoctions. <i>Separation Science Plus</i> , 2018, 1, 135-143.	0.3	2
164	Stereoselective bioaccumulation of chiral PCB 91 in earthworm and its metabolomic and lipidomic responses. <i>Environmental Pollution</i> , 2018, 238, 421-430.	3.7	38
165	Strategies for the stable performance and rapid inhibition recovery of a thermophilic digester treating coffee wastes and the synergistic effects of microbes. <i>International Biodeterioration and Biodegradation</i> , 2018, 132, 114-121.	1.9	6
166	Effect of alkylglycerone phosphate synthase on the expression profile of circRNAs in the human thyroid cancer cell line FRO. <i>Oncology Letters</i> , 2018, 15, 7889-7899.	0.8	7
167	Wnt gene family members and their expression profiling in <i>Litopenaeus vannamei</i> . <i>Fish and Shellfish Immunology</i> , 2018, 77, 233-243.	1.6	36
168	Reveal the response of enzyme activities to heavy metals through in situ zymography. <i>Ecotoxicology and Environmental Safety</i> , 2018, 156, 106-115.	2.9	184
169	High efficiency microbial electrosynthesis of acetate from carbon dioxide using a novel graphene-nickel foam as cathode. <i>Journal of Chemical Technology and Biotechnology</i> , 2018, 93, 457-466.	1.6	54
170	De novo transcriptomic analysis during <i>Lentinula edodes</i> fruiting body growth. <i>Gene</i> , 2018, 641, 326-334.	1.0	44
171	Gene polymorphisms of DISC1 is associated with schizophrenia: Evidence from a meta-analysis. <i>Progress in Neuro-Psychopharmacology and Biological Psychiatry</i> , 2018, 81, 64-73.	2.5	28
172	Coal use embodied in globalized world economy: From source to sink through supply chain. <i>Renewable and Sustainable Energy Reviews</i> , 2018, 81, 978-993.	8.2	87
173	Behavior of antibiotic resistance genes under extremely high-level antibiotic selection pressures in pharmaceutical wastewater treatment plants. <i>Science of the Total Environment</i> , 2018, 612, 119-128.	3.9	95
174	A Comparative Proteome Profile of Female Mouse Gonads Suggests a Tight Link between the Electron Transport Chain and Meiosis Initiation. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 31-42.	2.5	7
175	Identification and genomic characterization of the emerging Senecavirus A in southeast China, 2017. <i>Transboundary and Emerging Diseases</i> , 2018, 65, 297-302.	1.3	22
176	Gene expression profile of <i>Ralstonia Solanacearum</i> for the rhizosphere ecological niche of <i>Solanum tuberosum</i> . <i>Journal of Phytopathology</i> , 2018, 166, 151-160.	0.5	1
177	Actin genes and their expression in pacific white shrimp, <i>Litopenaeus vannamei</i> . <i>Molecular Genetics and Genomics</i> , 2018, 293, 479-493.	1.0	12
178	Biodiesel production from microbial granules in sequencing batch reactor. <i>Bioresource Technology</i> , 2018, 249, 908-915.	4.8	37
179	Evolutionary relationships between seryl-histidine dipeptide and modern serine proteases from the analysis based on mass spectrometry and bioinformatics. <i>Amino Acids</i> , 2018, 50, 69-77.	1.2	5
180	Molecular characterization and expression analysis of WRKY family genes in <i>Dendrobium officinale</i> . <i>Genes and Genomics</i> , 2018, 40, 265-279.	0.5	14

#	ARTICLE	IF	CITATIONS
181	Characterization and Expression Profiling of Neuropeptides and G-Protein-Coupled Receptors (GPCRs) for Neuropeptides in the Asian Citrus Psyllid, <i>Diaphorina citri</i> (Hemiptera: Psyllidae). <i>International Journal of Molecular Sciences</i> , 2018, 19, 3912.	1.8	51
182	De Novo Analysis Reveals Transcriptomic Responses in <i>Eriobotrya japonica</i> Fruits during Postharvest Cold Storage. <i>Genes</i> , 2018, 9, 639.	1.0	19
183	Mining Late Embryogenesis Abundant (LEA) Family Genes in <i>Cleistogenes songorica</i> , a Xerophyte Perennial Desert Plant. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3430.	1.8	28
184	Functional annotation of extensively and divergently expressed miRNAs in suprachiasmatic nucleus of Clock <sup>019</sup> mutant mice. <i>Bioscience Reports</i> , 2018, 38, .	1.1	5
185	Genome-Wide Identification and Characterization of Pectin Methylesterase Inhibitor Genes in <i>Brassica oleracea</i> . <i>International Journal of Molecular Sciences</i> , 2018, 19, 3338.	1.8	9
186	Differential Expression Analysis of Olfactory Genes Based on a Combination of Sequencing Platforms and Behavioral Investigations in <i>Aphidius gifuensis</i> . <i>Frontiers in Physiology</i> , 2018, 9, 1679.	1.3	10
187	Characterization of Callose Deposition and Analysis of the Callose Synthase Gene Family of <i>Brassica napus</i> in Response to <i>Leptosphaeria maculans</i> . <i>International Journal of Molecular Sciences</i> , 2018, 19, 3769.	1.8	10
188	Transcriptome profiling of human oocytes experiencing recurrent total fertilization failure. <i>Scientific Reports</i> , 2018, 8, 17890.	1.6	16
189	A metabolomics and proteomics study of the <i>Lactobacillus plantarum</i> in the grass carp fermentation. <i>BMC Microbiology</i> , 2018, 18, 216.	1.3	28
190	Genome survey sequencing for the characterization of genetic background of <i>Dracaena cambodiana</i> and its defense response during dragon's blood formation. <i>PLoS ONE</i> , 2018, 13, e0209258.	1.1	16
191	Analysis of the transcriptome data in <i>Litopenaeus vannamei</i> reveals the immune basis and predicts the hub regulation-genes in response to high-pH stress. <i>PLoS ONE</i> , 2018, 13, e0207771.	1.1	20
192	Comparative analysis of cytokinin response factors in <i>Brassica</i> diploids and amphidiploids and insights into the evolution of <i>Brassica</i> species. <i>BMC Genomics</i> , 2018, 19, 728.	1.2	9
193	Complex gene response of herbicide-resistant <i>Enterobacter</i> strain NRS-1 under different glyphosate stresses. <i>3 Biotech</i> , 2018, 8, 422.	1.1	1
194	Occurrence, distribution and risk assessment of pesticides in a river-reservoir system. <i>Ecotoxicology and Environmental Safety</i> , 2018, 166, 320-327.	2.9	55
195	The annotation of repetitive elements in the genome of channel catfish ( <i>Ictalurus punctatus</i> ). <i>PLoS ONE</i> , 2018, 13, e0197371.	1.1	13
196	Insights into the impact of <i>flhF</i> inactivation on <i>Campylobacter jejuni</i> colonization of chick and mice gut. <i>BMC Microbiology</i> , 2018, 18, 149.	1.3	9
197	Multiplex Biomarker Screening Assay for Urinary Extracellular Vesicles Study: A Targeted Label-Free Proteomic Approach. <i>Scientific Reports</i> , 2018, 8, 15039.	1.6	35
198	Bacterial Carbon Cycling in the River Plume in the Northern South China Sea During Summer. <i>Journal of Geophysical Research: Oceans</i> , 2018, 123, 8106-8121.	1.0	15

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199	Differential Quantitative Determination of Site-Specific Intact N-Glycopeptides in Serum Haptoglobin between Hepatocellular Carcinoma and Cirrhosis Using LC-ETHcD-MS/MS. <i>Journal of Proteome Research</i> , 2018, 18, 359-371.	1.8	50
200	Identifying characteristic miRNAs-genes and risk pathways of multiple sclerosis based on bioinformatics analysis. <i>Oncotarget</i> , 2018, 9, 5287-5300.	0.8	19
201	Characterization of airborne antibiotic resistance genes from typical bioaerosol emission sources in the urban environment using metagenomic approach. <i>Chemosphere</i> , 2018, 213, 463-471.	4.2	71
202	Metabolic profiling of femoral muscle from rats at different periods of time after death. <i>PLoS ONE</i> , 2018, 13, e0203920.	1.1	16
203	VlbZIP30 of grapevine functions in dehydration tolerance via the abscisic acid core signaling pathway. <i>Horticulture Research</i> , 2018, 5, 49.	2.9	20
204	Transgenic Expression of A Venous Malformation Related Mutation, <i>TIE2-R849W</i> , Significantly Induces Multiple Malformations of Zebrafish. <i>International Journal of Medical Sciences</i> , 2018, 15, 385-394.	1.1	8
205	Comparative profiling of microRNAs and their effects on abiotic stress in wild-type and dark green leaf color mutant plants of <i>Anthurium andraeanum</i> "Sonate"™. <i>Plant Physiology and Biochemistry</i> , 2018, 132, 258-270.	2.8	8
206	<i>Pseudomonas aeruginosa</i> Quorum-Sensing and Type VI Secretion System Can Direct Interspecific Coexistence During Evolution. <i>Frontiers in Microbiology</i> , 2018, 9, 2287.	1.5	22
207	Transcriptome Analysis of <i>Novosphingobium pentaromativorans</i> US6-1 Reveals the Rsh Regulon and Potential Molecular Mechanisms of N-acyl-L-homoserine Lactone Accumulation. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2631.	1.8	8
208	A Smooth-Type, Phage-Resistant <i>Klebsiella pneumoniae</i> Mutant Strain Reveals that OmpC Is Indispensable for Infection by Phage GH-K3. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	29
209	Physiological responses of Chinese hamster ovary cells to a productivity-enhancing yeast extract. <i>Journal of Bioscience and Bioengineering</i> , 2018, 126, 636-643.	1.1	4
210	Genome-wide Identification and Expression Analyses of RPP13-like Genes in Barley. <i>Biochip Journal</i> , 2018, 12, 102-113.	2.5	18
211	Soil types influence the fate of antibiotic-resistant bacteria and antibiotic resistance genes following the land application of sludge composts. <i>Environment International</i> , 2018, 118, 34-43.	4.8	97
212	Silencing <i>Inc-ASAH2B-2</i> Inhibits Breast Cancer Cell Growth via the mTOR Pathway. <i>Anticancer Research</i> , 2018, 38, 3427-3434.	0.5	13
213	Identification and functional analysis of differentially expressed genes associated with cerebral ischemia/reperfusion injury through bioinformatics methods. <i>Molecular Medicine Reports</i> , 2018, 18, 1513-1523.	1.1	13
214	Characteristic and influencing factors of Taqman genotyping calling error. <i>Journal of Clinical Laboratory Analysis</i> , 2018, 32, e22613.	0.9	4
215	Seasonal distribution of nitrifiers and denitrifiers in urban river sediments affected by agricultural activities. <i>Science of the Total Environment</i> , 2018, 642, 1282-1291.	3.9	38
216	Enhanced stolon growth and metabolic adjustment in creeping bentgrass with elevated CO <sub>2</sub> concentration. <i>Environmental and Experimental Botany</i> , 2018, 155, 87-97.	2.0	19

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217	Linking abundance and community of microbial N <sub>2</sub> O-producers and N <sub>2</sub> O-reducers with enzymatic N <sub>2</sub> O production potential in a riparian zone. <i>Science of the Total Environment</i> , 2018, 642, 1090-1099.	3.9	51
218	$\langle \text{mml:math xmlns:mml}=\text{"http://www.w3.org/1998/Math/MathML"} \text{ id}=\text{"M1"} \rangle \langle \text{mml:mrow} \rangle \langle \text{mml:mi} \rangle \text{K} \langle \text{mml:mi} \rangle \langle \text{mml:mrow} \rangle \langle \text{mml:math} \rangle$ Nearest Neighbor Algorithm Coupled with Metabonomics to Study the Therapeutic Mechanism of Sendeng-4 in Adjuvant-Induced Rheumatoid Arthritis Rat. <i>Evidence-based Complementary and Alternative Medicine</i> , 2018, 2018, 1-9.	0.5	5
219	Reporting Results. , 2018, , 145-196.		0
220	Genome-wide analysis of the potato Hsp20 gene family: identification, genomic organization and expression profiles in response to heat stress. <i>BMC Genomics</i> , 2018, 19, 61.	1.2	183
221	Quantitative proteomic analysis reveals the involvement of mitochondrial proteins in tomato fruit ripening. <i>Postharvest Biology and Technology</i> , 2018, 145, 213-221.	2.9	12
222	Bisecting N-Acetylglucosamine Structures Inhibit Hypoxia-Induced Epithelial-Mesenchymal Transition in Breast Cancer Cells. <i>Frontiers in Physiology</i> , 2018, 9, 210.	1.3	26
223	Genome-Wide Identification and Characterization of WD40 Protein Genes in the Silkworm, <i>Bombyx mori</i> . <i>International Journal of Molecular Sciences</i> , 2018, 19, 527.	1.8	17
224	Genome-wide investigation of WRKY gene family in pineapple: evolution and expression profiles during development and stress. <i>BMC Genomics</i> , 2018, 19, 490.	1.2	246
225	Global Survey of Antibiotic Resistance Genes in Air. <i>Environmental Science &amp; Technology</i> , 2018, 52, 10975-10984.	4.6	227
226	Integrated Expression Profiles Analysis Reveals Correlations Between the IL-33/ST2 Axis and CD8+ T Cells, Regulatory T Cells, and Myeloid-Derived Suppressor Cells in Soft Tissue Sarcoma. <i>Frontiers in Immunology</i> , 2018, 9, 1179.	2.2	10
227	Pan-Genome Analysis Links the Hereditary Variation of <i>Leptospirillum ferriphilum</i> With Its Evolutionary Adaptation. <i>Frontiers in Microbiology</i> , 2018, 9, 577.	1.5	18
228	Comparative Transcriptome Analysis Between a Spontaneous Albino Mutant and Its Sibling Strain of <i>Cordyceps militaris</i> in Response to Light Stress. <i>Frontiers in Microbiology</i> , 2018, 9, 1237.	1.5	18
229	In Silico Genome-Wide Analysis Reveals the Potential Links Between Core Genome of <i>Acidithiobacillus thiooxidans</i> and Its Autotrophic Lifestyle. <i>Frontiers in Microbiology</i> , 2018, 9, 1255.	1.5	17
230	Sex-Based Differences in Gut Microbiota Composition in Response to Tuna Oil and Algae Oil Supplementation in a D-galactose-Induced Aging Mouse Model. <i>Frontiers in Aging Neuroscience</i> , 2018, 10, 187.	1.7	22
231	Stable STIM1 Knockdown in Self-Renewing Human Neural Precursors Promotes Premature Neural Differentiation. <i>Frontiers in Molecular Neuroscience</i> , 2018, 11, 178.	1.4	22
232	Genome-Wide Identification and Characterization of the Potato bHLH Transcription Factor Family. <i>Genes</i> , 2018, 9, 54.	1.0	112
233	Phenotype- and SSR-Based Estimates of Genetic Variation between and within Two Important <i>Elymus</i> Species in Western and Northern China. <i>Genes</i> , 2018, 9, 147.	1.0	23
234	Genome-Wide Analysis of the PYL Gene Family and Identification of PYL Genes That Respond to Abiotic Stress in <i>Brassica napus</i> . <i>Genes</i> , 2018, 9, 156.	1.0	55

#	ARTICLE	IF	CITATIONS
235	Exposure to Formaldehyde Perturbs the Mouse Gut Microbiome. <i>Genes</i> , 2018, 9, 192.	1.0	11
236	Meta-Prediction of MTHFR Gene Polymorphisms and Air Pollution on the Risk of Hypertensive Disorders in Pregnancy Worldwide. <i>International Journal of Environmental Research and Public Health</i> , 2018, 15, 326.	1.2	19
237	Genome-Wide Identification and Characterization of Tyrosine Kinases in the Silkworm, <i>Bombyx mori</i> . <i>International Journal of Molecular Sciences</i> , 2018, 19, 934.	1.8	4
238	Genome-Wide Screening and Characterization of the Dof Gene Family in Physic Nut ( <i>Jatropha curcas</i> ) Tj ETQq1 1 0.784314 rgBT /Ove	1.8	14
239	Occurrence, Distribution, and Risk Assessment of Antibiotics in a Subtropical River-Reservoir System. <i>Water (Switzerland)</i> , 2018, 10, 104.	1.2	50
240	Metabonomics and Molecular Biology-based Effects of Sugemule-3 in an Isoproterenol-induced Cardiovascular Disease Rat Model. <i>Chemical Research in Chinese Universities</i> , 2018, 34, 590-597.	1.3	1
241	A Zinc Finger Transcriptional Repressor Confers Pleiotropic Effects on Rice Growth and Drought Tolerance by Down-Regulating Stress-Responsive Genes. <i>Plant and Cell Physiology</i> , 2018, 59, 2129-2142.	1.5	42
242	Identification of aberrantly expressed F-box proteins in squamous-cell lung carcinoma. <i>Journal of Cancer Research and Clinical Oncology</i> , 2018, 144, 1509-1521.	1.2	25
243	Genome-wide analysis of GRAS transcription factor gene family in <i>Gossypium hirsutum</i> L.. <i>BMC Genomics</i> , 2018, 19, 348.	1.2	97
244	Genomic instability in adult men involved in processing electronic waste in Northern China. <i>Environment International</i> , 2018, 117, 69-81.	4.8	38
245	Uncovering potential anti-neuroinflammatory components of Modified Wuziyanzong Prescription through a target-directed molecular docking fingerprint strategy. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2018, 156, 328-339.	1.4	2
246	Transcriptome and metabolome analyses provide insights into root and root-released organic anion responses to phosphorus deficiency in oat. <i>Journal of Experimental Botany</i> , 2018, 69, 3759-3771.	2.4	42
247	Effects and molecular mechanisms of intrauterine infection/inflammation on lung development. <i>Respiratory Research</i> , 2018, 19, 93.	1.4	33
248	Enhanced biocontrol activity of cellulase from <i>Trichoderma harzianum</i> against <i>Fusarium graminearum</i> through activation of defense-related genes in maize. <i>Physiological and Molecular Plant Pathology</i> , 2018, 103, 130-136.	1.3	40
249	Bioinformatics approach reveals the key role of C&X&C motif chemokine receptor 2 in endometriosis development. <i>Molecular Medicine Reports</i> , 2018, 18, 2841-2849.	1.1	6
250	Traits-Based Integration of Multi-Species Inoculants Facilitates Shifts of Indigenous Soil Bacterial Community. <i>Frontiers in Microbiology</i> , 2018, 9, 1692.	1.5	29
251	Genome-Wide Identification, Molecular Evolution, and Expression Profiling Analysis of Pectin Methylesterase Inhibitor Genes in <i>Brassica campestris</i> ssp. <i>chinensis</i> . <i>International Journal of Molecular Sciences</i> , 2018, 19, 1338.	1.8	14
252	Effects of 5-Aminolevulinic Acid on Gene Expression, Immunity, and ATP Levels in Pacific White Shrimp, <i>Litopenaeus vannamei</i> . <i>Marine Biotechnology</i> , 2018, 20, 829-843.	1.1	10

#	ARTICLE	IF	CITATIONS
253	Genome-wide identification of the auxin/indole-3-acetic acid (Aux/IAA) gene family in pepper, its characterisation, and comprehensive expression profiling under environmental and phytohormones stress. <i>Scientific Reports</i> , 2018, 8, 12008.	1.6	17
254	Transcriptome Analysis of JA Signal Transduction, Transcription Factors, and Monoterpene Biosynthesis Pathway in Response to Methyl Jasmonate Elicitation in <i>Mentha canadensis</i> L.. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2364.	1.8	22
255	A genome-wide analysis of SWEET gene family in cotton and their expressions under different stresses. <i>Journal of Cotton Research</i> , 2018, 1, .	1.0	19
256	Comparative transcriptome analysis of genes involved in Na <sup>+</sup> transport in the leaves of halophyte <i>Halogeton glomeratus</i> . <i>Gene</i> , 2018, 678, 407-416.	1.0	3
257	Proceeding From in vivo Functions of Pheromone Receptors: Peripheral-Coding Perception of Pheromones From Three Closely Related Species, <i>Helicoverpa armigera</i> , <i>H. assulta</i> , and <i>Heliothis virescens</i> . <i>Frontiers in Physiology</i> , 2018, 9, 1188.	1.3	11
258	Enhanced catalytic activities and modified substrate preferences for taxoid 10 <sup>12</sup> -O-acetyl transferase mutants by engineering catalytic histidine residues. <i>Biotechnology Letters</i> , 2018, 40, 1245-1251.	1.1	6
259	Venom allergen-like protein 28 in <i>Clonorchis sinensis</i> : four epitopes on its surface and the potential role of Cys124 for its conformational stability. <i>Parasitology Research</i> , 2018, 117, 2521-2530.	0.6	2
260	Genome-wide analysis and expression profiles of glyoxalase gene families in Chinese cabbage ( <i>Brassica Tj ETQq1</i> 1,0,784314, ggBT / Over	1.1	18
261	Electroacupuncture at Guanyuan (CV 4), Zusanli (ST 36) and Baihui (DU 20) regulate the aging-related changes in gene expression profile of the hippocampus in sub-acutely aging rats. <i>PLoS ONE</i> , 2018, 13, e0191623.	1.1	2
262	Genome-wide identification of wheat ( <i>Triticum aestivum</i> ) expansins and expansin expression analysis in cold-tolerant and cold-sensitive wheat cultivars. <i>PLoS ONE</i> , 2018, 13, e0195138.	1.1	30
263	Molecular characterization and integrative genomic analysis of a panel of newly established penile cancer cell lines. <i>Cell Death and Disease</i> , 2018, 9, 684.	2.7	34
264	Oxidative damage and antioxidative indicators in 48h germinated rice embryos during the vitrification cryopreservation procedure. <i>Plant Cell Reports</i> , 2018, 37, 1325-1342.	2.8	18
265	Novel insight into the role of withering process in characteristic flavor formation of teas using transcriptome analysis and metabolite profiling. <i>Food Chemistry</i> , 2019, 272, 313-322.	4.2	133
266	Genomic and transcriptomic analyses of HD-Zip family transcription factors and their responses to abiotic stress in tea plant ( <i>Camellia sinensis</i> ). <i>Genomics</i> , 2019, 111, 1142-1151.	1.3	62
267	Identification and interaction analysis of key genes and microRNAs in atopic dermatitis by bioinformatics analysis. <i>Clinical and Experimental Dermatology</i> , 2019, 44, 257-264.	0.6	23
268	The SWEET family genes in strawberry: Identification and expression profiling during fruit development. <i>South African Journal of Botany</i> , 2019, 125, 176-187.	1.2	13
269	Genome-wide Identification, Classification, Expression and Duplication Analysis of GRAS Family Genes in <i>Juglans regia</i> L.. <i>Scientific Reports</i> , 2019, 9, 11643.	1.6	25
270	A 3-hydroxy-3-methylglutaryl-CoA synthase-based probe for the discovery of the acyltransferase-less type I polyketide synthases. <i>Environmental Microbiology</i> , 2019, 21, 4270-4282.	1.8	1



#	ARTICLE	IF	CITATIONS
271	Information visualisation methods and techniques: State-of-the-art and future directions. <i>Journal of Industrial Information Integration</i> , 2019, 16, 100102.	4.3	15
272	Comparative proteomic analysis of sex-biased proteins in ovary and testis at different stages of <i>Spodoptera litura</i> . <i>Journal of Proteomics</i> , 2019, 206, 103439.	1.2	1
273	Circulating miR-99b-5p as a novel predictor of erosion progression on high-resolution peripheral quantitative computed tomography in early rheumatoid arthritis: A prospective cohort study. <i>International Journal of Rheumatic Diseases</i> , 2019, 22, 1724-1733.	0.9	14
274	Genome-wide identification and expression profiling of odorant-binding proteins in the oriental fruit fly, <i>Bactrocera dorsalis</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2019, 31, 100605.	0.4	26
275	Genome-Wide Identification and Expression Analysis of Calcineurin B-Like Protein and Calcineurin B-Like Protein-Interacting Protein Kinase Family Genes in Tea Plant. <i>DNA and Cell Biology</i> , 2019, 38, 824-839.	0.9	29
276	Quantitative Proteomic Analysis Reveals Impaired Axonal Guidance Signaling in Human Postmortem Brain Tissues of Chronic Traumatic Encephalopathy. <i>Experimental Neurobiology</i> , 2019, 28, 362-375.	0.7	9
277	Quantitative proteomics reveals TMOD1-related proteins associated with water balance regulation. <i>PLoS ONE</i> , 2019, 14, e0219932.	1.1	5
278	Identification and Interaction Analysis of Significant Genes and MicroRNAs in <i>Pterygium</i> . <i>BioMed Research International</i> , 2019, 2019, 1-12.	0.9	10
279	A high performance liquid chromatography method for simultaneous detection of 20 bioactive components in tea extracts. <i>Electrophoresis</i> , 2019, 40, 2837-2844.	1.3	43
280	Transcriptional Profiling Reveals a Time-of-Day-Specific Role of REVEILLE 4/8 in Regulating the First Wave of Heat Shock-Induced Gene Expression in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2019, 31, 2353-2369.	3.1	79
281	Mitofusins regulate lipid metabolism to mediate the development of lung fibrosis. <i>Nature Communications</i> , 2019, 10, 3390.	5.8	93
282	<i>Arabidopsis</i> Histone Methyltransferase SUVH5 Is a Positive Regulator of Light-Mediated Seed Germination. <i>Frontiers in Plant Science</i> , 2019, 10, 841.	1.7	22
283	Recent Advances in Food Thawing Technologies. <i>Comprehensive Reviews in Food Science and Food Safety</i> , 2019, 18, 953-970.	5.9	83
284	The Composition and Assembly of Bacterial Communities across the Rhizosphere and Phyllosphere Compartments of <i>Phragmites Australis</i> . <i>Diversity</i> , 2019, 11, 98.	0.7	21
285	Bioinformatics approach reveals the critical role of TGF- $\beta$ 2 signaling pathway in pre-eclampsia development. <i>European Journal of Obstetrics, Gynecology and Reproductive Biology</i> , 2019, 240, 130-138.	0.5	13
286	Genome-wide identification, characterization, expression and enzyme activity analysis of coniferyl alcohol acetyltransferase genes involved in eugenol biosynthesis in <i>Prunus mume</i> . <i>PLoS ONE</i> , 2019, 14, e0223974.	1.1	20
287	Genome-Wide Identification and Analysis of the AP2 Transcription Factor Gene Family in Wheat ( <i>Triticum aestivum</i> L.). <i>Frontiers in Plant Science</i> , 2019, 10, 1286.	1.7	41
288	Knockdown of CaHSP60-6 confers enhanced sensitivity to heat stress in pepper ( <i>Capsicum annuum</i> L.). <i>Planta</i> , 2019, 250, 2127-2145.	1.6	29

#	ARTICLE	IF	CITATIONS
289	Variations of bacterial community during the decomposition of <i>Microcystis</i> under different temperatures and biomass. <i>BMC Microbiology</i> , 2019, 19, 207.	1.3	9
290	Simultaneous and sequential based co-fermentations of <i>Trichoderma asperellum</i> GDFS1009 and <i>Bacillus amyloliquefaciens</i> 1841: a strategy to enhance the gene expression and metabolites to improve the bio-control and plant growth promoting activity. <i>Microbial Cell Factories</i> , 2019, 18, 185.	1.9	25
291	Links of Extracellular Enzyme Activities, Microbial Metabolism, and Community Composition in the River-impacted Coastal Waters. <i>Journal of Geophysical Research G: Biogeosciences</i> , 2019, 124, 3507-3520.	1.3	12
292	G65V Substitution in Actin Disturbs Polymerization Leading to Inhibited Cell Elongation in Cotton. <i>Frontiers in Plant Science</i> , 2019, 10, 1486.	1.7	9
293	The ameliorative effect of the <i>Pyracantha fortuneana</i> (Maxim.) H. L. Li extract on intestinal barrier dysfunction through modulating glycolipid digestion and gut microbiota in high fat diet-fed rats. <i>Food and Function</i> , 2019, 10, 6517-6532.	2.1	23
294	Genome-Wide Identification and Transcriptional Expression of the METTL21C Gene Family in Chicken. <i>Genes</i> , 2019, 10, 628.	1.0	11
295	Denitrification is the main microbial N loss pathway on the Qinghai-Tibet Plateau above an elevation of 5000 m. <i>Science of the Total Environment</i> , 2019, 696, 133852.	3.9	21
296	Hippocampus Metabolic Disturbance and Autophagy Deficiency in Olfactory Bulbectomized Rats and the Modulatory Effect of Fluoxetine. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4282.	1.8	22
297	Urinary metabolic disturbance in the olfactory bulbectomized rats and the modulatory effects of fluoxetine. <i>Life Sciences</i> , 2019, 234, 116751.	2.0	12
298	Supplementation of triple viable probiotics combined with dietary intervention is associated with gut microbial improvement in humans on a high-fat diet. <i>Experimental and Therapeutic Medicine</i> , 2019, 18, 2262-2270.	0.8	13
299	Improving Chromosome Synthesis with a Semiquantitative Phenotypic Assay and Refined Assembly Strategy. <i>ACS Synthetic Biology</i> , 2019, 8, 2203-2211.	1.9	5
300	Identification of RING-H2 Gene Candidates Related to Wood Formation in Poplar. <i>Forests</i> , 2019, 10, 698.	0.9	1
301	Influence of nanoscale zero-valent iron and magnetite nanoparticles on anaerobic digestion performance and macrolide, aminoglycoside, $\beta$ -lactam resistance genes reduction. <i>Bioresource Technology</i> , 2019, 294, 122139.	4.8	79
302	MicroRNA-424 regulates cisplatin resistance of gastric cancer by targeting SMURF1 based on GEO database and primary validation in human gastric cancer tissues. <i>OncoTargets and Therapy</i> , 2019, Volume 12, 7623-7636.	1.0	30
303	Transcriptome analysis of the effect of GA3 in sugarcane culm. <i>3 Biotech</i> , 2019, 9, 376.	1.1	6
304	Multi-Evaluating Strategy for Siji-kangbingdu Mixture: Chemical Profiling, Fingerprint Characterization, and Quantitative Analysis. <i>Molecules</i> , 2019, 24, 3545.	1.7	15
305	A Hint of Primitive Mucosal Immunity in Shrimp through <i>Marsupenaeus japonicus</i> Gill C-Type Lectin. <i>Journal of Immunology</i> , 2019, 203, 2310-2318.	0.4	21
306	Population Genomics Insights into Adaptive Evolution and Ecological Differentiation in <i>Streptomyces</i> . <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	16

#	ARTICLE	IF	CITATIONS
307	Pilose antler polypeptides ameliorate inflammation and oxidative stress and improves gut microbiota in hypoxic-ischemic injured rats. <i>Nutrition Research</i> , 2019, 64, 93-108.	1.3	28
308	Decreased IL-17RB expression impairs CD11b+CD11c <sup>+</sup> myeloid cell accumulation in gastric mucosa and host defense during the early-phase of <i>Helicobacter pylori</i> infection. <i>Cell Death and Disease</i> , 2019, 10, 79.	2.7	7
309	Comparison of rhizosphere bacterial communities of reed and <i>Suaeda</i> in Shuangtaizi River Estuary, Northeast China. <i>Marine Pollution Bulletin</i> , 2019, 140, 171-178.	2.3	31
310	<i>Helicobacter pylori</i> downregulated tumor necrosis factor receptor-associated protein 1 mediates apoptosis of human gastric epithelial cells. <i>Journal of Cellular Physiology</i> , 2019, 234, 15698-15707.	2.0	7
311	The <i>EIL</i> transcription factor family in soybean: Genome-wide identification, expression profiling and genetic diversity analysis. <i>FEBS Open Bio</i> , 2019, 9, 629-642.	1.0	10
312	Genome-Wide Identification and Transcriptional Expression of the PAL Gene Family in Common Walnut ( <i>Juglans Regia</i> L.). <i>Genes</i> , 2019, 10, 46.	1.0	31
313	Understanding the regulation of overwintering diapause molecular mechanisms in <i>Culex pipiens pallens</i> through comparative proteomics. <i>Scientific Reports</i> , 2019, 9, 6485.	1.6	37
314	Genome-wide identification of stress-associated proteins (SAP) with A20/AN1 zinc finger domains associated with abiotic stresses responses in <i>Brassica napus</i> . <i>Environmental and Experimental Botany</i> , 2019, 165, 108-119.	2.0	34
315	Three Capsular Polysaccharide Synthesis-Related Glucosyltransferases, GT-1, GT-2 and WcaJ, Are Associated With Virulence and Phage Sensitivity of <i>Klebsiella pneumoniae</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 1189.	1.5	56
316	Sludge bio-drying followed by land application could control the spread of antibiotic resistance genes. <i>Environment International</i> , 2019, 130, 104906.	4.8	26
317	In silico genome-wide identification and comprehensive characterization of the BES1 gene family in soybean. <i>Heliyon</i> , 2019, 5, e01868.	1.4	14
318	Anammox and denitrification separately dominate microbial N-loss in water saturated and unsaturated soils horizons of riparian zones. <i>Water Research</i> , 2019, 162, 139-150.	5.3	78
319	Genome-Wide Analysis of the MADS-Box Transcription Factor Family in <i>Solanum lycopersicum</i> . <i>International Journal of Molecular Sciences</i> , 2019, 20, 2961.	1.8	69
320	Genome-wide characterization of aspartic protease (AP) gene family in <i>Populus trichocarpa</i> and identification of the potential PtAPs involved in wood formation. <i>BMC Plant Biology</i> , 2019, 19, 276.	1.6	23
321	Insights into transcriptional characteristics and homoeolog expression bias of embryo and de-embryonated kernels in developing grain through RNA-Seq and Iso-Seq. <i>Functional and Integrative Genomics</i> , 2019, 19, 919-932.	1.4	11
322	Manipulating the Expression of Small Secreted Protein 1 ( <i>Ssp1</i> ) Alters Patterns of Development and Metabolism in the White-Rot Fungus <i>Pleurotus ostreatus</i> . <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	10
323	iTRAQ-Based Quantitative Proteomic Profiling of <i>Staphylococcus aureus</i> Under Different Osmotic Stress Conditions. <i>Frontiers in Microbiology</i> , 2019, 10, 1082.	1.5	16
324	Genome-Wide Identification of the LAC Gene Family and Its Expression Analysis Under Stress in <i>Brassica napus</i> . <i>Molecules</i> , 2019, 24, 1985.	1.7	16

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325	Determination of 21 free amino acids in 5 types of tea by ultra-high performance liquid chromatography coupled with tandem mass spectrometry (UHPLC-MS/MS) using a modified 6-aminoquinolyl-N-hydroxysuccinimidyl carbamate (AQC) method. <i>Journal of Food Composition and Analysis</i> , 2019, 81, 46-54.	1.9	30
326	Seasonality overwhelms aquacultural activity in determining the composition and assembly of the bacterial community in Lake Taihu, China. <i>Science of the Total Environment</i> , 2019, 683, 427-435.	3.9	49
327	What Changed on the Folliculogenesis in the Process of Mouse Ovarian Aging?. <i>BioMed Research International</i> , 2019, 2019, 1-10.	0.9	5
328	Polyploidy-related differential gene expression between diploid and synthesized allotriploid and allotetraploid hybrids of <i>Populus</i> . <i>Molecular Breeding</i> , 2019, 39, 1.	1.0	24
329	Genome-Wide Analysis of the D-type Cyclin Gene Family Reveals Differential Expression Patterns and Stem Development in the Woody Plant <i>Prunus mume</i> . <i>Forests</i> , 2019, 10, 147.	0.9	9
330	Genome-Wide Identification and Comparative Expression Profile Analysis of the Long-Chain Acyl-CoA synthetase (LACS) Gene Family in Two Different Oil Content Cultivars of <i>Brassica napus</i> . <i>Biochemical Genetics</i> , 2019, 57, 781-800.	0.8	11
331	Fine mapping and identification of the fuzzless gene <i>GaFz1</i> in DPL972 ( <i>Gossypium arboreum</i> ). <i>Theoretical and Applied Genetics</i> , 2019, 132, 2169-2179.	1.8	19
332	Transcriptional activation of <i>SIRT6</i> via <i>FKHRL1/FOXO3a</i> inhibits the Warburg effect in glioblastoma cells. <i>Cellular Signalling</i> , 2019, 60, 100-113.	1.7	24
333	Genome-Wide Identification and Transcriptional Expression Profiles of the F-box Gene Family in Common Walnut ( <i>Juglans regia</i> L.). <i>Forests</i> , 2019, 10, 275.	0.9	8
334	Genome-Wide Characterization and Expression Analysis of Soybean TGA Transcription Factors Identified a Novel TGA Gene Involved in Drought and Salt Tolerance. <i>Frontiers in Plant Science</i> , 2019, 10, 549.	1.7	97
335	iTRAQ-Based Quantitative Proteomics and Transcriptomics Provide Insights Into the Importance of Expansins During Root Development in Carrot. <i>Frontiers in Genetics</i> , 2019, 10, 247.	1.1	8
336	Effects of ball milling micronization on amino acids profile and antioxidant activities of <i>Polygonatumcyrtonea</i> Hua tuber powder. <i>Journal of Food Measurement and Characterization</i> , 2019, 13, 2106-2117.	1.6	7
337	Oxidative stress: One potential factor for arsenite-induced increase of N6-methyladenosine in human keratinocytes. <i>Environmental Toxicology and Pharmacology</i> , 2019, 69, 95-103.	2.0	51
338	Ocean Acidification Regulates the Activity, Community Structure, and Functional Potential of Heterotrophic Bacterioplankton in an Oligotrophic Gyre. <i>Journal of Geophysical Research C: Biogeosciences</i> , 2019, 124, 1001-1017.	1.3	10
339	ELF4 facilitates innate host defenses against <i>Plasmodium</i> by activating transcription of <i>Pf4</i> and <i>Ppbb</i> . <i>Journal of Biological Chemistry</i> , 2019, 294, 7787-7796.	1.6	6
340	Simultaneous Determination and Risk Assessment of Pyrrolizidine Alkaloids in <i>Artemisia capillaris</i> Thunb. by UPLC-MS/MS Together with Chemometrics. <i>Molecules</i> , 2019, 24, 1077.	1.7	8
342	Nano genome atlas (NGA) of body wide organ responses. <i>Biomaterials</i> , 2019, 205, 38-49.	5.7	16
343	Establishment of a human embryonic stem cell-based liver differentiation model for hepatotoxicity evaluations. <i>Ecotoxicology and Environmental Safety</i> , 2019, 174, 353-362.	2.9	17

#	ARTICLE	IF	CITATIONS
344	Integrated analysis of gene expression profiles identifies transcription factors potentially involved in psoriasis pathogenesis. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 12582-12594.	1.2	11
345	Population divergence of <i>Pseudomonas aeruginosa</i> can lead to the coexistence with <i>Escherichia coli</i> in animal suppurative lesions. <i>Veterinary Microbiology</i> , 2019, 231, 169-176.	0.8	4
346	Low doses of decitabine improve the chemotherapy efficacy against basal-like bladder cancer by targeting cancer stem cells. <i>Oncogene</i> , 2019, 38, 5425-5439.	2.6	19
347	Effect of green tea and mulberry leaf powders on the gut microbiota of chicken. <i>BMC Veterinary Research</i> , 2019, 15, 77.	0.7	29
348	Microbial mechanism underlying high and stable methane oxidation rates during mudflat reclamation with long-term rice cultivation: Illumina high-throughput sequencing-based data analysis. <i>Journal of Hazardous Materials</i> , 2019, 371, 332-341.	6.5	10
349	Distinct isoforms of Nrf1 diversely regulate different subsets of its cognate target genes. <i>Scientific Reports</i> , 2019, 9, 2960.	1.6	26
350	Impact of Wuyiencin Application on the Soil Microbial Community and Fate of Typical Antibiotic Resistance Genes. <i>Scientific Reports</i> , 2019, 9, 4016.	1.6	5
351	Lysophospholipid profiles of apolipoprotein E-deficient mice reveal potential lipid biomarkers associated with atherosclerosis progression using validated UPLC-QTRAP-MS/MS-based lipidomics approach. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2019, 171, 148-157.	1.4	8
352	Heterologous expression of HpBHY and CrBKT increases heat tolerance in <i>Physcomitrella patens</i> . <i>Plant Diversity</i> , 2019, 41, 266-274.	1.8	5
353	GmYUC2a mediates auxin biosynthesis during root development and nodulation in soybean. <i>Journal of Experimental Botany</i> , 2019, 70, 3165-3176.	2.4	49
354	Transcriptomic analysis of <i>de novo</i> folate biosynthetic genes in <i>Lactobacillus plantarum</i> strain 4_3 in fermented soybean. <i>Food and Function</i> , 2019, 10, 2426-2438.	2.1	6
355	Transcriptome analyses reveal key genes involved in skin color changes of 'Xinlimei' radish taproot. <i>Plant Physiology and Biochemistry</i> , 2019, 139, 528-539.	2.8	24
356	Genome-wide mining seed-specific candidate genes from peanut for promoter cloning. <i>PLoS ONE</i> , 2019, 14, e0214025.	1.1	10
357	Differential microRNA expression profiles determined by next-generation sequencing in three fulvestrant-resistant human breast cancer cell lines. <i>Oncology Letters</i> , 2019, 17, 3765-3776.	0.8	7
358	High-Throughput Sequencing Analysis of Microbial Profiles in the Dry Socket. <i>Journal of Oral and Maxillofacial Surgery</i> , 2019, 77, 1548-1556.	0.5	13
359	Genomic insights into HSFs as candidate genes for high-temperature stress adaptation and gene editing with minimal off-target effects in flax. <i>Scientific Reports</i> , 2019, 9, 5581.	1.6	18
360	Metabolomics analysis reveals global acetoin stress response of <i>Bacillus licheniformis</i> . <i>Metabolomics</i> , 2019, 15, 25.	1.4	39
361	Circadian Regulation of Alternative Splicing of Drought-Associated CIPK Genes in <i>Dendrobium catenatum</i> (Orchidaceae). <i>International Journal of Molecular Sciences</i> , 2019, 20, 688.	1.8	14

#	ARTICLE	IF	CITATIONS
362	Formation of nanoscale TeO and its effect on TeO <sub>3</sub> reduction in CH <sub>4</sub> -based membrane biofilm reactor. <i>Science of the Total Environment</i> , 2019, 655, 1232-1239.	3.9	14
363	A Comprehensive Comparative Study for the Authentication of the Kadsura Crude Drug. <i>Frontiers in Pharmacology</i> , 2019, 9, 1576.	1.6	8
364	Contrasting bacterial community structure in artificial pit mud-starter cultures of different qualities: a complex biological mixture for Chinese strong-flavor Baijiu production. <i>3 Biotech</i> , 2019, 9, 89.	1.1	19
365	Semi-supervised Aspect-level Sentiment Classification Model based on Variational Autoencoder. <i>Knowledge-Based Systems</i> , 2019, 171, 81-92.	4.0	58
366	Fermentation process of mulberry juice-whey based Tibetan kefir beverage production. <i>Czech Journal of Food Sciences</i> , 2018, 36, 494-501.	0.6	7
367	Genome-Wide Analysis of Members of the WRKY Gene Family and Their Cold Stress Response in <i>Prunus mume</i> . <i>Genes</i> , 2019, 10, 911.	1.0	29
368	Construction of the first high-density genetic linkage map and identification of seed yield-related QTLs and candidate genes in <i>Elymus sibiricus</i> , an important forage grass in Qinghai-Tibet Plateau. <i>BMC Genomics</i> , 2019, 20, 861.	1.2	12
369	Defining the function of SUMO system in pod development and abiotic stresses in Peanut. <i>BMC Plant Biology</i> , 2019, 19, 593.	1.6	12
370	Transcription Factor Atf1 Regulates Expression of Cellulase and Xylanase Genes during Solid-State Fermentation of Ascomycetes. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	27
371	Re-enforcing hypoxia-induced polyploid cardiomyocytes enter cytokinesis through activation of $\beta^2$ -catenin. <i>Scientific Reports</i> , 2019, 9, 17865.	1.6	11
372	Codon Usage in the Iflaviridae Family Is Not Diverse Though the Family Members Are Isolated from Diverse Host Taxa. <i>Viruses</i> , 2019, 11, 1087.	1.5	7
373	Effect of recycling the culture medium on biodiversity and population dynamics of bio-contaminants in <i>Spirulina platensis</i> mass culture systems. <i>Algal Research</i> , 2019, 44, 101718.	2.4	19
374	Whole Genome Re-sequencing Reveals Natural Variation and Adaptive Evolution of <i>Phytophthora sojae</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2792.	1.5	39
375	Genome-wide identification and expression profile of the MADS-box gene family in <i>Erigeron breviscapus</i> . <i>PLoS ONE</i> , 2019, 14, e0226599.	1.1	11
376	Mining and validating the expression pattern and prognostic value of acetylcholine receptors in non-small cell lung cancer. <i>Medicine (United States)</i> , 2019, 98, e15555.	0.4	11
377	Potential Effects of Awn Length Variation on Seed Yield and Components, Seed Dispersal and Germination Performance in Siberian Wildrye ( <i>Elymus sibiricus</i> L.). <i>Plants</i> , 2019, 8, 561.	1.6	17
378	Identification of cancer-type specific expression patterns for active aldehyde dehydrogenase (ALDH) isoforms in ALDEFLUOR assay. <i>Cell Biology and Toxicology</i> , 2019, 35, 161-177.	2.4	79
379	Complete nitrogen removal and electricity production in Thauera-dominated air-cathode single chambered microbial fuel cell. <i>Chemical Engineering Journal</i> , 2019, 356, 506-515.	6.6	142

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380	New Insights into Porcine Milk <i>N</i> -Glycome and the Potential Relation with Offspring Gut Microbiome. <i>Journal of Proteome Research</i> , 2019, 18, 1114-1124.	1.8	17
381	A newly identified cluster of glutathione <i>S</i> -transferase genes provides <i>Verticillium wilt</i> resistance in cotton. <i>Plant Journal</i> , 2019, 98, 213-227.	2.8	44
382	Quality assessment of <i>Astragali Radix</i> from different production areas by simultaneous determination of thirteen major compounds using tandem UV/charged aerosol detector. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2019, 165, 233-241.	1.4	14
383	Transcriptome analysis of spleen reveals the signal transduction of toll-like receptors after <i>Aeromonas hydrophila</i> infection in <i>Schizothorax prenanti</i> . <i>Fish and Shellfish Immunology</i> , 2019, 84, 816-824.	1.6	21
384	Consumption of florfenicol-medicated feed alters the composition of the channel catfish intestinal microbiota including enriching the relative abundance of opportunistic pathogens. <i>Aquaculture</i> , 2019, 501, 111-118.	1.7	39
385	Simultaneous quantification combined with multivariate statistical analysis of multiple chemical markers of Wu Ji Bai Feng Pill by UHPLC-MS/MS. <i>Journal of Food and Drug Analysis</i> , 2019, 27, 275-283.	0.9	10
386	Genotyping polymorphic microhaplotype markers through the Illumina® MiSeq platform for forensics. <i>Forensic Science International: Genetics</i> , 2019, 39, 1-7.	1.6	35
387	Rutin's natural source <i>Flos Sophorae</i> as potential antioxidant and improver of fungal community in Chinese sausages. <i>LWT - Food Science and Technology</i> , 2019, 101, 435-443.	2.5	31
388	Identification and comparison of oligopeptides during withering process of White tea by ultra-high pressure liquid chromatography coupled with quadrupole-orbitrap ultra-high resolution mass spectrometry. <i>Food Research International</i> , 2019, 121, 825-834.	2.9	18
389	Comparative Transcriptome Analysis Identifies Genes Involved in Diosgenin Biosynthesis in <i>Trigonella foenum-graecum</i> L. <i>Molecules</i> , 2019, 24, 140.	1.7	19
390	Different divergence events for three pairs of PEBPs in <i>Gossypium</i> as implied by evolutionary analysis. <i>Genes and Genomics</i> , 2019, 41, 445-458.	0.5	0
391	Understanding the Resistance Mechanism in <i>Brassica napus</i> to Clubroot Caused by <i>Plasmodiophora brassicae</i> . <i>Phytopathology</i> , 2019, 109, 810-818.	1.1	16
392	Analysis of transcriptional response in zebrafish eleutheroembryos exposed to climbazole: Signaling pathways and potential biomarkers. <i>Environmental Toxicology and Chemistry</i> , 2019, 38, 794-805.	2.2	20
393	Metagenomic Evidence for a <i>Methylocystis</i> Species Capable of Bioremediation of Diverse Heavy Metals. <i>Frontiers in Microbiology</i> , 2019, 9, 3297.	1.5	19
394	Genome-Wide Characterization and Identification of Trihelix Transcription Factor and Expression Profiling in Response to Abiotic Stresses in Rice ( <i>Oryza sativa</i> L.). <i>International Journal of Molecular Sciences</i> , 2019, 20, 251.	1.8	47
395	Genome-wide identification and characterization of novel microRNAs in seed development of soybean. <i>Bioscience, Biotechnology and Biochemistry</i> , 2019, 83, 233-242.	0.6	7
396	Effects of recombinant swollenin on the enzymatic hydrolysis, rumen fermentation, and rumen microbiota during in vitro incubation of agricultural straws. <i>International Journal of Biological Macromolecules</i> , 2019, 122, 348-358.	3.6	14
397	iEKP2.0: an update with rich annotations for eukaryotic protein kinases, protein phosphatases and proteins containing phosphoprotein-binding domains. <i>Nucleic Acids Research</i> , 2019, 47, D344-D350.	6.5	22

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398	Fate of microbial pollutants and evolution of antibiotic resistance in three types of soil amended with swine slurry. <i>Environmental Pollution</i> , 2019, 245, 353-362.	3.7	41
399	AsChip: A High-Throughput qPCR Chip for Comprehensive Profiling of Genes Linked to Microbial Cycling of Arsenic. <i>Environmental Science &amp; Technology</i> , 2019, 53, 798-807.	4.6	34
400	Diagnostic performance of plasma cytokine biosignature combination and MCP-1 as individual biomarkers for differentiating stages <i>Mycobacterium tuberculosis</i> infection. <i>Journal of Infection</i> , 2019, 78, 281-291.	1.7	30
401	The evaluation of lipids raw material resources with the fatty acid profile and morphological characteristics of <i>Idesia polycarpa</i> Maxim. var. <i>vestita</i> Diels fruit in harvesting. <i>Industrial Crops and Products</i> , 2019, 129, 114-122.	2.5	13
402	Evidence for co-selection of antibiotic resistance genes and mobile genetic elements in metal polluted urban soils. <i>Science of the Total Environment</i> , 2019, 656, 512-520.	3.9	183
403	Genome-wide identification of chitin-binding proteins and characterization of BmCBP1 in the silkworm, <i>Bombyx mori</i> . <i>Insect Science</i> , 2019, 26, 400-412.	1.5	10
404	<i>Arabidopsis</i> PEAPODs function with LIKE HETEROCHROMATIN PROTEIN1 to regulate lateral organ growth. <i>Journal of Integrative Plant Biology</i> , 2020, 62, 812-831.	4.1	13
405	DeepPhagy: a deep learning framework for quantitatively measuring autophagy activity in <i>Saccharomyces cerevisiae</i> . <i>Autophagy</i> , 2020, 16, 626-640.	4.3	18
406	Comparison of bacterial communities in gliadin-degraded sourdough (Khamir) sample and non-degraded sample. <i>Journal of Food Science and Technology</i> , 2020, 57, 375-380.	1.4	5
407	Increase in seed tannin extractability and oxidation using a freeze-thaw treatment in cool-climate grown red ( <i>Vitis vinifera</i> L.) cultivars. <i>Food Chemistry</i> , 2020, 308, 125571.	4.2	11
408	Evaluation of palatal support tissues for placement of orthodontic mini-implants in mouth breathers with high-narrow palates versus nose breathers with normal palates: a retrospective study. <i>Clinical Oral Investigations</i> , 2020, 24, 1259-1267.	1.4	6
409	Impact of different b-value combinations on radiomics features of apparent diffusion coefficient in cervical cancer. <i>Acta Radiologica</i> , 2020, 61, 568-576.	0.5	1
410	De novo biosynthesis of liquiritin in <i>Saccharomyces cerevisiae</i> . <i>Acta Pharmaceutica Sinica B</i> , 2020, 10, 711-721.	5.7	19
411	Biochemical characterization and expression analysis of lignification in two pear ( <i>Pyrus ussuriensis</i> ) Tj ETQq1 1 0.784314 rgBJ / Overl	1.0	14
412	Low-dose and same day use of polyethylene glycol improves image of video capsule endoscopy: A multicenter randomized clinical trial. <i>Journal of Gastroenterology and Hepatology (Australia)</i> , 2020, 35, 634-640.	1.4	15
413	Antibiotic contamination in a typical water-rich city in southeast China: a concern for drinking water resource safety. <i>Journal of Environmental Science and Health - Part B Pesticides, Food Contaminants, and Agricultural Wastes</i> , 2020, 55, 193-209.	0.7	17
414	Molecular Insights into the Insensitivity of Lepidopteran Pests to Cycloxyaprid. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 982-988.	2.4	5
415	Comparative Genomics Analysis of <i>Lactobacillus ruminis</i> from Different Niches. <i>Genes</i> , 2020, 11, 70.	1.0	27



#	ARTICLE	IF	CITATIONS
416	Exogenous phosphite application alleviates the adverse effects of heat stress and improves thermotolerance of potato ( <i>Solanum tuberosum</i> L.) seedlings. <i>Ecotoxicology and Environmental Safety</i> , 2020, 190, 110048.	2.9	22
417	Identification and comparative expression profiles of chemosensory genes in major chemoreception organs of a notorious pests, <i>Laodelphax striatellus</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2020, 33, 100646.	0.4	5
418	Characterization and comparison of CRISPR Loci in <i>Streptococcus thermophilus</i> . <i>Archives of Microbiology</i> , 2020, 202, 695-710.	1.0	10
419	Exogenous Melatonin and Abscisic Acid Expedite the Flavonoids Biosynthesis in Grape Berry of <i>Vitis vinifera</i> cv. Kyoho. <i>Molecules</i> , 2020, 25, 12.	1.7	39
420	SIFERL Interacts with S-Adenosylmethionine Synthetase to Regulate Fruit Ripening. <i>Plant Physiology</i> , 2020, 184, 2168-2181.	2.3	19
421	Comprehensive genomic characterization of NAC transcription factor family and their response to salt and drought stress in peanut. <i>BMC Plant Biology</i> , 2020, 20, 454.	1.6	27
422	Identification and expression profiling of MYB transcription factors related to l-theanine biosynthesis in <i>Camellia sinensis</i> . <i>International Journal of Biological Macromolecules</i> , 2020, 164, 4306-4317.	3.6	6
423	Identification of Metastasis-Associated Biomarkers in Synovial Sarcoma Using Bioinformatics Analysis. <i>Frontiers in Genetics</i> , 2020, 11, 530892.	1.1	5
424	HybridSucc: A Hybrid-learning Architecture for General and Species-specific Succinylation Site Prediction. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 194-207.	3.0	28
425	Transcriptome profiling reveals the occurrence mechanism of bisexual flowers in melon ( <i>Cucumis</i> ) Tj ETQq1 1 0.784314 rgBT /Overlo	1.7	10
426	Behaviors and related mechanisms of Zn resistance and antibiotic resistance genes during co-composting of erythromycin manufacturing wastes and pig manure. <i>Bioresource Technology</i> , 2020, 318, 124048.	4.8	15
427	DrLLPS: a data resource of liquid-liquid phase separation in eukaryotes. <i>Nucleic Acids Research</i> , 2020, 48, D288-D295.	6.5	112
428	Origin and evolution of emerging Liao ning Virus (genus Seadornavirus, family Reoviridae). <i>Virology Journal</i> , 2020, 17, 105.	1.4	1
429	The Impact of Mutations in SARS-CoV-2 Spike on Viral Infectivity and Antigenicity. <i>Cell</i> , 2020, 182, 1284-1294.e9.	13.5	1,362
430	Response of antibiotic resistance genes in constructed wetlands during treatment of livestock wastewater with different exogenous inducers: Antibiotic and antibiotic-resistant bacteria. <i>Bioresource Technology</i> , 2020, 314, 123779.	4.8	31
431	Genome-wide association study for soybean mosaic virus SC3 resistance in soybean. <i>Molecular Breeding</i> , 2020, 40, 1.	1.0	13
432	In Vitro Cytotoxic Activity against Breast, Cervical, and Ovarian Cancer Cells and Flavonoid Content of Plant Ingredients Used in a Selected Thai Traditional Cancer Remedy: Correlation and Hierarchical Cluster Analysis. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-10.	0.5	4
433	Microbial communities and gene contributions in smokeless tobacco products. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 10613-10629.	1.7	13

#	ARTICLE	IF	CITATIONS
434	Removal of antibiotic resistance genes in pig manure composting influenced by inoculation of compound microbial agents. <i>Bioresource Technology</i> , 2020, 317, 123966.	4.8	33
435	Circular RNA ciARS regulates ferroptosis in HCC cells through interacting with RNA binding protein ALKBH5. <i>Cell Death Discovery</i> , 2020, 6, 72.	2.0	122
436	Transcriptome analysis of antennal cytochrome P450s and their transcriptional responses to plant and locust volatiles in <i>Locusta migratoria</i> . <i>International Journal of Biological Macromolecules</i> , 2020, 149, 741-753.	3.6	16
437	Genome-Wide Analysis of the Cytochromes P450 Gene Family in <i>Cordyceps militaris</i> . <i>Journal of Physics: Conference Series</i> , 2020, 1549, 032069.	0.3	1
438	Enhanced sugar accumulation and regulated plant hormone signalling genes contribute to cold tolerance in hypoploid <i>Saccharum spontaneum</i> . <i>BMC Genomics</i> , 2020, 21, 507.	1.2	19
439	MYB repressors and MBW activation complex collaborate to fine-tune flower coloration in <i>Freesia hybrida</i> . <i>Communications Biology</i> , 2020, 3, 396.	2.0	43
440	Isolation and Characterization of Novel Lytic Bacteriophages Infecting Epidemic Carbapenem-Resistant <i>Klebsiella pneumoniae</i> Strains. <i>Frontiers in Microbiology</i> , 2020, 11, 1554.	1.5	28
441	The sugar transporter system of strawberry: genome-wide identification and expression correlation with fruit soluble sugar-related traits in a <i>Fragaria</i> – <i>Ananassa</i> germplasm collection. <i>Horticulture Research</i> , 2020, 7, 132.	2.9	24
442	Transcriptomic and proteomic profiling response of methicillin-resistant <i>Staphylococcus aureus</i> (MRSA) to a novel bacteriocin, plantaricin GZ1-27 and its inhibition of biofilm formation. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 7957-7970.	1.7	21
443	Effect of Warming on Growth, Grazing, and Community Composition of Free-Living Bacterioplankton in Subtropical Coastal Waters During Winter and Summer. <i>Frontiers in Microbiology</i> , 2020, 11, 534404.	1.5	4
444	Untargeted metabolomics reveals the effect of lovastatin on steroid-induced necrosis of the femoral head in rabbits. <i>Journal of Orthopaedic Surgery and Research</i> , 2020, 15, 497.	0.9	2
445	Molecular docking-assisted screening reveals tannic acid as a natural protein disulphide isomerase inhibitor with antiplatelet and antithrombotic activities. <i>Journal of Cellular and Molecular Medicine</i> , 2020, 24, 14257-14269.	1.6	9
446	Genome-wide identification and expression patterns analysis of the RPD3/HDA1 gene family in cotton. <i>BMC Genomics</i> , 2020, 21, 643.	1.2	11
447	Discovery of chemical markers for improving the quality and safety control of <i>Sinomenium acutum</i> stem by the simultaneous determination of multiple alkaloids using UHPLC-QQQ-MS/MS. <i>Scientific Reports</i> , 2020, 10, 14182.	1.6	10
448	A Genome-Wide Survey of MATE Transporters in Brassicaceae and Unveiling Their Expression Profiles under Abiotic Stress in Rapeseed. <i>Plants</i> , 2020, 9, 1072.	1.6	9
449	Plant-PGPR interaction study of plant growth-promoting diazotrophs <i>Kosakonia radicincitans</i> BA1 and <i>Stenotrophomonas maltophilia</i> COA2 to enhance growth and stress-related gene expression in <i>Saccharum</i> spp.. <i>Journal of Plant Interactions</i> , 2020, 15, 427-445.	1.0	32
450	Downregulation of Brain Enriched Type 2 MAGEs Is Associated With Immune Infiltration and Poor Prognosis in Glioma. <i>Frontiers in Oncology</i> , 2020, 10, 573378.	1.3	10
451	Comparative transcriptome analysis of Sweetpotato ( <i>Ipomoea batatas</i> L.) and discovery of genes involved in starch biosynthesis. <i>Plant Biotechnology Reports</i> , 2020, 14, 713-723.	0.9	2

#	ARTICLE	IF	CITATIONS
452	A novel microRNA signature for pathological grading in lung adenocarcinoma based on TCGA and GEO data. <i>International Journal of Molecular Medicine</i> , 2020, 45, 1397-1408.	1.8	10
453	Genetic and Functional Diversity of <i>Pseudomonas aeruginosa</i> in Patients With Chronic Obstructive Pulmonary Disease. <i>Frontiers in Microbiology</i> , 2020, 11, 598478.	1.5	9
454	Canopy architecture and fruit microclimate, not ripening-related phytohormones, control phenylpropanoid accumulation in response to early leaf removal in 'Merlot' (Vitis vinifera L.) grapevines. <i>Plant Physiology and Biochemistry</i> , 2020, 157, 291-302.	2.8	15
455	Ubiquitinome Profiling Reveals the Landscape of Ubiquitination Regulation in Rice Young Panicles. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 305-320.	3.0	18
456	VdNPS, a Nonribosomal Peptide Synthetase, Is Involved in Regulating Virulence in <i>Verticillium dahliae</i> . <i>Phytopathology</i> , 2020, 110, 1398-1409.	1.1	5
457	Glycopeptide Biomarkers in Serum Haptoglobin for Hepatocellular Carcinoma Detection in Patients with Nonalcoholic Steatohepatitis. <i>Journal of Proteome Research</i> , 2020, 19, 3452-3466.	1.8	37
458	Genome-wide identification of the expansin gene family reveals that expansin genes are involved in fibre cell growth in cotton. <i>BMC Plant Biology</i> , 2020, 20, 223.	1.6	32
459	Electronic word-of-mouth effects on studio performance leveraging attention-based model. <i>Neural Computing and Applications</i> , 2020, 32, 17601-17622.	3.2	9
460	The Conserved and Particular Roles of the R2R3-MYB Regulator FhPAP1 from <i>Freesia hybrida</i> in Flower Anthocyanin Biosynthesis. <i>Plant and Cell Physiology</i> , 2020, 61, 1365-1380.	1.5	42
461	Comparative proteomics analysis of patients with quick development and slow development Chronic Obstructive Pulmonary Disease (COPD). <i>Life Sciences</i> , 2020, 256, 117829.	2.0	6
462	Genome-wide characterization of tea plant ( <i>Camellia sinensis</i> ) Hsf transcription factor family and role of CsHsfA2 in heat tolerance. <i>BMC Plant Biology</i> , 2020, 20, 244.	1.6	26
463	Identification and Characterization of the Expansin Genes in <i>Triticum urartu</i> in Response to Various Phytohormones. <i>Russian Journal of Genetics</i> , 2020, 56, 441-453.	0.2	0
464	Genome-wide identification, phylogeny and expression analysis of HSF gene family in barley during abiotic stress response and reproductive development. <i>Plant Gene</i> , 2020, 23, 100231.	1.4	11
465	A novel bacterial thiosulfate oxidation pathway provides a new clue about the formation of zero-valent sulfur in deep sea. <i>ISME Journal</i> , 2020, 14, 2261-2274.	4.4	76
466	Differences in pig respiratory tract and peripheral blood immune responses to <i>Actinobacillus pleuropneumoniae</i> . <i>Veterinary Microbiology</i> , 2020, 247, 108755.	0.8	9
467	Aromatic Cytokinin Arabinosides Promote PAMP-like Responses and Positively Regulate Leaf Longevity. <i>ACS Chemical Biology</i> , 2020, 15, 1949-1963.	1.6	22
468	Screening and comprehensive evaluation of rice ( <i>Oryza sativa</i> L. subsp. japonica Kato) germplasm resources for nitrogen efficiency in Xinjiang, China. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2020, 18, 179-189.	0.4	8
469	Bacterial profiles and volatile flavor compounds in commercial Suancai with varying salt concentration from Northeastern China. <i>Food Research International</i> , 2020, 137, 109384.	2.9	47

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470	IL-10 promotes malignant pleural effusion by regulating T <sub>H</sub> 1 response via an miR-116-5p/GPR55/ERK pathway in mice. <i>European Journal of Immunology</i> , 2020, 50, 1798-1809.	1.6	7
471	Heat map visualization for electrocardiogram data analysis. <i>BMC Cardiovascular Disorders</i> , 2020, 20, 277.	0.7	8
472	Evaluation of the cold tolerance of <i>Saccharum spontaneum</i> L. clones with different ploidy levels on the basis of morphological and physiological indices. <i>Plant Biology</i> , 2020, 22, 623-633.	1.8	3
473	Genome-wide identification and molecular evolution analysis of BPA genes in green plants. <i>Phytopathology Research</i> , 2020, 2, .	0.9	4
474	Realization of Robust and Precise Regulation of Gene Expression by Multiple Sigma Recognizable Artificial Promoters. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 92.	2.0	10
475	Comprehensive analyses of the annexin (ANN) gene family in <i>Brassica rapa</i> , <i>Brassica oleracea</i> and <i>Brassica napus</i> reveals their roles in stress response. <i>Scientific Reports</i> , 2020, 10, 4295.	1.6	39
476	Systematic analysis of ovarian cancer platinum-resistance mechanisms via text mining. <i>Journal of Ovarian Research</i> , 2020, 13, 27.	1.3	14
477	Adaptive regulation of virulence genes by microRNA-like RNAs in <i>Valsa mali</i> . <i>New Phytologist</i> , 2020, 227, 899-913.	3.5	27
478	Genome-Wide Analysis of the Shi-Related Sequence Family and Functional Identification of GmSRS18 Involving in Drought and Salt Stresses in Soybean. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1810.	1.8	12
479	Ammonium Transporter (BcAMT1.2) Mediates the Interaction of Ammonium and Nitrate in <i>Brassica campestris</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 1776.	1.7	12
480	Genomic Analysis of the SUMO-Conjugating Enzyme and Genes under Abiotic Stress in Potato ( <i>Solanum tuberosum</i> L.). <i>International Journal of Genomics</i> , 2020, 2020, 1-13.	0.8	8
481	Yield benefits from replacing chemical fertilizers with manure under water deficient conditions of the winter wheat – summer maize system in the North China Plain. <i>European Journal of Agronomy</i> , 2020, 119, 126118.	1.9	52
482	Evaluation of main post-translational modifications occurring in naturally generated peptides during the ripening of Spanish dry-cured ham. <i>Food Chemistry</i> , 2020, 332, 127388.	4.2	17
483	Cloning and functional characterization of a carotenoid cleavage dioxygenase 2 gene in safranal and crocin biosynthesis from <i>Freesia hybrida</i> . <i>Plant Physiology and Biochemistry</i> , 2020, 154, 439-450.	2.8	10
484	Pathogenic genetic variations of <i>C. acnes</i> associated with clinically relevant orthopedic shoulder infections. <i>Journal of Orthopaedic Research</i> , 2020, 38, 2731-2739.	1.2	4
485	Two hierarchical LuxR-LuxI type quorum sensing systems in <i>Novosphingobium</i> activate microcystin degradation through transcriptional regulation of the mlr pathway. <i>Water Research</i> , 2020, 183, 116092.	5.3	27
486	Characterization and Expression of KT/HAK/KUP Transporter Family Genes in Willow under Potassium Deficiency, Drought, and Salt Stresses. <i>BioMed Research International</i> , 2020, 2020, 1-12.	0.9	23
487	Foliar Spraying with Compound Amino Acid-Iron Fertilizer Increases Leaf Fresh Weight, Photosynthesis, and Fe-S Cluster Gene Expression in Peach ( <i>Prunus persica</i> (L.) Batsch). <i>BioMed Research International</i> , 2020, 2020, 1-9.	0.9	7

#	ARTICLE	IF	CITATIONS
488	Visualization of the Distance among Fishes by MALDI MS for Rapid Determination of the Taxonomic Status of Fish Fillets. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 8438-8446.	2.4	12
489	Changes of endophytic bacterial community and pathogens in pepper ( <i>Capsicum annuum</i> L.) as affected by reclaimed water irrigation. <i>Applied Soil Ecology</i> , 2020, 156, 103627.	2.1	20
490	Identification and sex-biased profiles of candidate olfactory genes in the antennal transcriptome of the parasitoid wasp <i>Cotesia vestalis</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2020, 34, 100657.	0.4	18
491	Identification of Genes Related to Clinicopathological Characteristics and Prognosis of Patients with Colorectal Cancer. <i>DNA and Cell Biology</i> , 2020, 39, 690-699.	0.9	21
492	Comparative analysis of basic helix-“loop”-helix gene family among <i>Brassica oleracea</i> , <i>Brassica rapa</i> , and <i>Brassica napus</i> . <i>BMC Genomics</i> , 2020, 21, 178.	1.2	13
493	Blood-based gene expression profile of oxidative stress and antioxidant genes for identifying surrogate markers of liver tissue injury in chronic hepatitis C patients. <i>Archives of Virology</i> , 2020, 165, 809-822.	0.9	10
494	Characterization of the bZIP Transcription Factor Family in Pepper ( <i>Capsicum annuum</i> L.): CabZIP25 Positively Modulates the Salt Tolerance. <i>Frontiers in Plant Science</i> , 2020, 11, 139.	1.7	51
495	Genome-wide analysis of a putative lipid transfer protein LTP_2 gene family reveals CsLTP_2 genes involved in response of cucumber against root-knot nematode ( <i>Meloidogyne incognita</i> ). <i>Genome</i> , 2020, 63, 225-238.	0.9	11
496	<i>Miscanthus</i> cultivation shapes rhizosphere microbial community structure and function as assessed by Illumina MiSeq sequencing combined with PICRUSt and FUNGUld analyses. <i>Archives of Microbiology</i> , 2020, 202, 1157-1171.	1.0	49
497	iTRAQ-based quantitative proteomic profiling of the immune response of the South African abalone, <i>Haliotis midae</i> . <i>Fish and Shellfish Immunology</i> , 2020, 99, 130-143.	1.6	4
498	MicroRNA expression patterns unveil differential expression of conserved miRNAs and target genes against abiotic stress in safflower. <i>PLoS ONE</i> , 2020, 15, e0228850.	1.1	31
499	Similar drivers but different effects lead to distinct ecological patterns of soil bacterial and archaeal communities. <i>Soil Biology and Biochemistry</i> , 2020, 144, 107759.	4.2	83
500	Insufficiency of prosthetic posterolateral overlap related to recurrence after laparoscopic transabdominal preperitoneal inguinal hernioplasty, as assessed by video review. <i>BMC Surgery</i> , 2020, 20, 27.	0.6	1
501	The profile of antibiotic resistance genes in pig manure composting shaped by composting stage: Mesophilic-thermophilic and cooling-maturation stages. <i>Chemosphere</i> , 2020, 250, 126181.	4.2	65
502	Airborne antibiotic resistance genes in Hong Kong kindergartens. <i>Environmental Pollution</i> , 2020, 260, 114009.	3.7	24
503	Comparative Genomics Analysis of <i>Lactobacillus mucosae</i> from Different Niches. <i>Genes</i> , 2020, 11, 95.	1.0	15
504	Comparative transcriptome analysis of differentially expressed genes in <i>Bradysia odoriphaga</i> Yang et Zhang (Diptera: Sciaridae) at different acute stress temperatures. <i>Genomics</i> , 2020, 112, 3739-3750.	1.3	4
505	Comprehensive analysis of the SLC16A gene family in pancreatic cancer via integrated bioinformatics. <i>Scientific Reports</i> , 2020, 10, 7315.	1.6	37

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506	Physiological and transcriptomic analysis of "Whangkeumbae"™ pear core browning during low-temperature storage. <i>Gene Expression Patterns</i> , 2020, 36, 119113.	0.3	9
507	Comparative transcriptome analysis of two contrasting wolfberry genotypes during fruit development and ripening and characterization of the LrMYB1 transcription factor that regulates flavonoid biosynthesis. <i>BMC Genomics</i> , 2020, 21, 295.	1.2	14
508	Analysis of rhizome colour content, bioactive compound profiling and ex-situ conservation of turmeric genotypes ( <i>Curcuma longa</i> L.) from sub-Himalayan terai region of India. <i>Industrial Crops and Products</i> , 2020, 150, 112401.	2.5	31
509	Overexpression of LITPS2 from a cultivar of lily ( <i>Lilium "Siberia"</i> ™) enhances the monoterpenoids content in tobacco flowers. <i>Plant Physiology and Biochemistry</i> , 2020, 151, 391-399.	2.8	24
510	Transcriptome-wide identification, classification, and characterization of NAC family genes in Bamboo <i>Bambusa emeiensis</i> . <i>Acta Physiologiae Plantarum</i> , 2020, 42, 1.	1.0	2
511	Exogenous melatonin improves glutathione content, redox state and increases essential oil production in two <i>Salvia</i> species under drought stress. <i>Scientific Reports</i> , 2020, 10, 6883.	1.6	62
512	Exploring the genetic base of the soybean germplasm from Africa, America and Asia as well as mining of beneficial allele for flowering and seed weight. <i>3 Biotech</i> , 2020, 10, 195.	1.1	4
513	The pH-based ecological coherence of active canonical methanotrophs in paddy soils. <i>Biogeosciences</i> , 2020, 17, 1451-1462.	1.3	22
514	Semen virome of men with HIV on or off antiretroviral treatment. <i>Aids</i> , 2020, 34, 827-832.	1.0	13
515	Biogeographic patterns of abundant and rare bacterial and microeukaryotic subcommunities in connected freshwater lake zones subjected to different levels of nutrient loading. <i>Journal of Applied Microbiology</i> , 2021, 130, 123-132.	1.4	6
516	Upregulation of Tubulointerstitial nephritis antigen like 1 promotes gastric cancer growth and metastasis by regulating multiple matrix metalloproteinase expression. <i>Journal of Gastroenterology and Hepatology (Australia)</i> , 2021, 36, 196-203.	1.4	11
517	Response of soil characteristics and bacterial communities to nitrogen fertilization gradients in a coastal salt-affected agroecosystem. <i>Land Degradation and Development</i> , 2021, 32, 338-353.	1.8	39
518	Metatranscriptomics reveals the gene functions and metabolic properties of the major microbial community during Chinese Sichuan Paocai fermentation. <i>Food Microbiology</i> , 2021, 98, 103573.	2.1	28
519	Population dynamics and interactions of <i>Noctiluca scintillans</i> and <i>Mesodinium rubrum</i> during their successive blooms in a subtropical coastal water. <i>Science of the Total Environment</i> , 2021, 755, 142349.	3.9	10
520	Genetic analyses of lodging resistance and yield provide insights into post-"Green" Revolution breeding in rice. <i>Plant Biotechnology Journal</i> , 2021, 19, 814-829.	4.1	25
521	Stage-specific protein regulation during somatic embryo development of <i>Carica papaya</i> L. "Golden"™. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2021, 1869, 140561.	1.1	10
522	Discrimination of turmeric from different origins in China by MRM-based curcuminoid profiling and multivariate analysis. <i>Food Chemistry</i> , 2021, 338, 127794.	4.2	15
523	Integrative pharmacological mechanism of vitamin C combined with glycyrrhizic acid against COVID-19: findings of bioinformatics analyses. <i>Briefings in Bioinformatics</i> , 2021, 22, 1161-1174.	3.2	51

#	ARTICLE	IF	CITATIONS
524	Identification, genomic organization, and expression profiles of single C2H2 zinc finger transcription factors in tomato ( <i>Solanum lycopersicum</i> ). <i>Journal of Applied Genetics</i> , 2021, 62, 1-15.	1.0	8
525	Mechanisms of the enhanced DDT removal from soils by earthworms: Identification of DDT degraders in drilosphere and non-drilosphere matrices. <i>Journal of Hazardous Materials</i> , 2021, 404, 124006.	6.5	22
526	Exploring core microbiota responsible for the production of volatile flavor compounds during the traditional fermentation of Koumiss. <i>LWT - Food Science and Technology</i> , 2021, 135, 110049.	2.5	26
527	GhAlaRP, a cotton alanine rich protein gene, involves in fiber elongation process. <i>Crop Journal</i> , 2021, 9, 313-324.	2.3	5
528	Fate of mercury and methylmercury in full-scale sludge anaerobic digestion combined with thermal hydrolysis. <i>Journal of Hazardous Materials</i> , 2021, 406, 124310.	6.5	10
529	Comprehensive Analysis of the Proteome and PTMomes of C2C12 Myoblasts Reveals that Sialylation Plays a Role in the Differentiation of Skeletal Muscle Cells. <i>Journal of Proteome Research</i> , 2021, 20, 222-235.	1.8	3
530	MMP1 3'UTR facilitates the proliferation and migration of human oral squamous cell carcinoma by sponging miR-188-5p to up-regulate SOX4 and CDK4. <i>Molecular and Cellular Biochemistry</i> , 2021, 476, 785-796.	1.4	10
531	Transcriptome-wide identification, characterization, and phylogenomic analysis of cytochrome P450s from <i>Nothapodytes nimmoniana</i> reveal candidate genes involved in the camptothecin biosynthetic pathway. <i>Genome</i> , 2021, 64, 1-14.	0.9	5
532	Identification and expression analysis of caffeoyl-coenzyme A O-methyltransferase family genes related to lignin biosynthesis in tea plant ( <i>Camellia sinensis</i> ). <i>Protoplasma</i> , 2021, 258, 115-127.	1.0	14
533	Identification and characterization of the strawberry KT/HAK/KUP transporter gene family in response to K <sup>+</sup> deficiency. <i>Acta Physiologiae Plantarum</i> , 2021, 43, 1.	1.0	7
534	Flow shear stress controls the initiation of neovascularization <i>via</i> heparan sulfate proteoglycans within a biomimetic microfluidic model. <i>Lab on A Chip</i> , 2021, 21, 421-434.	3.1	17
535	Epidemiological and co-infection characteristics of common human coronaviruses in Shanghai, 2015–2020: a retrospective observational study. <i>Emerging Microbes and Infections</i> , 2021, 10, 1660-1668.	3.0	9
536	Metabolome Analysis Revealed the Mechanism of Exogenous Glutathione to Alleviate Cadmium Stress in Maize ( <i>Zea mays</i> L.) Seedlings. <i>Plants</i> , 2021, 10, 105.	1.6	23
537	Evaluation of wetland substrates for veterinary antibiotics pollution control in lab-scale systems. <i>Environmental Pollution</i> , 2021, 269, 116152.	3.7	12
538	OsADR3 increases drought stress tolerance by inducing antioxidant defense mechanisms and regulating OsGPX1 in rice ( <i>Oryza sativa</i> L.). <i>Crop Journal</i> , 2021, 9, 1003-1017.	2.3	19
539	Distribution of Metal Resistance Genes in Estuarine Sediments and Associated Key Impact Factors. <i>Microbial Ecology</i> , 2021, 82, 581-590.	1.4	6
540	The influence of heavy metals on biological soil quality assessments in the <i>Vaccinium myrtillus</i> L. rhizosphere under different field conditions. <i>Ecotoxicology</i> , 2021, 30, 292-310.	1.1	17
541	Comprehensive analysis of AHL gene family and their expression under drought stress and ABA treatment in <i>Populus trichocarpa</i> . <i>PeerJ</i> , 2021, 9, e10932.	0.9	11

#	ARTICLE	IF	CITATIONS
542	An updated census of the maize TIFY family. PLoS ONE, 2021, 16, e0247271.	1.1	10
543	An Alternative Splicing Variant of PtRD26 Delays Leaf Senescence by Regulating Multiple NAC Transcription Factors in <i>Populus</i> . Plant Cell, 2021, 33, 1594-1614.	3.1	74
544	Comprehensive Analysis and Expression Profiling of PIN, AUX/LAX, and ABCB Auxin Transporter Gene Families in <i>Solanum tuberosum</i> under Phytohormone Stimuli and Abiotic Stresses. Biology, 2021, 10, 127.	1.3	12
545	Transcriptome Profiles of <i>Sporisorium reilianum</i> during the Early Infection of Resistant and Susceptible Maize Isogenic Lines. Journal of Fungi (Basel, Switzerland), 2021, 7, 150.	1.5	4
546	Genome-wide analysis of CBL and CIPK family genes in cotton: conserved structures with divergent interactions and expression. Physiology and Molecular Biology of Plants, 2021, 27, 359-368.	1.4	14
547	MicroRNA-20a-3p regulates the host immune response to facilitate the mycobacterium tuberculosis infection by targeting IKK $\beta$ /NF- $\kappa$ B pathway. International Immunopharmacology, 2021, 91, 107286.	1.7	10
548	In silico identification of natural products from Traditional Chinese Medicine for cancer immunotherapy. Scientific Reports, 2021, 11, 3332.	1.6	14
549	Whole Genome Analysis of Sugarcane Root-Associated Endophyte <i>Pseudomonas aeruginosa</i> B18A Plant Growth-Promoting Bacterium With Antagonistic Potential Against <i>Sporisorium scitamineum</i> . Frontiers in Microbiology, 2021, 12, 628376.	1.5	53
550	Calcineurin Immune Signaling in Response to Zinc Challenge in the Naked Carp <i>Gymnocypris eckloni</i> . Bulletin of Environmental Contamination and Toxicology, 2021, 106, 792-798.	1.3	1
551	Purkinje Neurons with Loss of STIM1 Exhibit Age-Dependent Changes in Gene Expression and Synaptic Components. Journal of Neuroscience, 2021, 41, 3777-3798.	1.7	13
553	A proteomic analysis of skeletal tissue anomaly in the brain coral <i>Platygyra carnosa</i> . Marine Pollution Bulletin, 2021, 164, 111982.	2.3	6
554	Metabolic Analysis Reveals Cry1C Gene Transformation Does Not Affect the Sensitivity of Rice to Rice Dwarf Virus. Metabolites, 2021, 11, 209.	1.3	2
555	Identification and genomic characterization of emerging goose astrovirus in central China, 2020. Transboundary and Emerging Diseases, 2022, 69, 1046-1055.	1.3	19
556	Comparative proteomics reveals mechanisms that underlie insecticide resistance in <i>Culex pipiens pallens</i> Coquillett. PLoS Neglected Tropical Diseases, 2021, 15, e0009237.	1.3	5
557	Combination of Flos Sophorae and chili pepper as a nitrite alternative improves the antioxidant, microbial communities and quality traits in Chinese sausages. Food Research International, 2021, 141, 110131.	2.9	20
558	Application of Comparative Lipidomics to Elucidate Postprandial Metabolic Excursions Following Dairy Milk Ingestion in Individuals with Prediabetes. Journal of Proteome Research, 2021, 20, 2583-2595.	1.8	3
559	Composition and co-occurrence patterns of <i>Phragmites australis</i> rhizosphere bacterial community. Aquatic Ecology, 2021, 55, 695-710.	0.7	9
560	MicroRNA-95-3p serves as a contributor to cisplatin resistance in human gastric cancer cells by targeting EMP1/PI3K/AKT signaling. Aging, 2021, 13, 8665-8687.	1.4	16



#	ARTICLE	IF	CITATIONS
561	A robust and flexible CRISPR/Cas9-based system for neutrophil-specific gene inactivation in zebrafish. <i>Journal of Cell Science</i> , 2021, 134, .	1.2	8
562	SARS-CoV-2 501Y.V2 variants lack higher infectivity but do have immune escape. <i>Cell</i> , 2021, 184, 2362-2371.e9.	13.5	332
563	Functional Characterization of Sex Pheromone Neurons and Receptors in the Armyworm, <i>Mythimna separata</i> (Walker). <i>Frontiers in Neuroanatomy</i> , 2021, 15, 673420.	0.9	8
564	Genome-Wide Identification, Comparison, and Expression Analysis of Transcription Factors in Ascidian <i>Styela clava</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 4317.	1.8	5
565	Inhibition of sphingosine kinase 2 down-regulates ERK/c-Myc pathway and reduces cell proliferation in human epithelial ovarian cancer. <i>Annals of Translational Medicine</i> , 2021, 9, 645-645.	0.7	3
566	Integrative proteomics and metabolomics profiling of the protective effects of <i>Phascolosoma</i> esculent ferritin on BMSCs in Cd(II) injury. <i>Ecotoxicology and Environmental Safety</i> , 2021, 212, 111995.	2.9	4
567	New Insights into the Biological Activity of Lichens: Bioavailable Secondary Metabolites of <i>Umbilicaria decussata</i> as Potential Anticoagulants. <i>Chemistry and Biodiversity</i> , 2021, 18, e2100080.	1.0	1
568	Investigating genetic drivers of juvenile dermatomyositis pathogenesis using bioinformatics methods. <i>Journal of Dermatology</i> , 2021, 48, 1007-1020.	0.6	2
569	Molecular evolution and expression analysis of ADP-ribosylation factors (ARFs) from longan embryogenic callus. <i>Gene</i> , 2021, 777, 145461.	1.0	2
570	Key wheat <i>GRF</i> genes constraining wheat tillering of mutant <i>dmc</i> . <i>PeerJ</i> , 2021, 9, e11235.	0.9	5
571	Clarifying Recent Adaptive Diversification of the Chrysanthemum-Group on the Basis of an Updated Multilocus Phylogeny of Subtribe Artemisiinae (Asteraceae: Anthemideae). <i>Frontiers in Plant Science</i> , 2021, 12, 648026.	1.7	12
572	MicroRNA-182 improves spinal cord injury in mice by modulating apoptosis and the inflammatory response via IKK $\beta$ /NF- $\kappa$ B. <i>Laboratory Investigation</i> , 2021, 101, 1238-1253.	1.7	29
573	Resolving mass fractions and congener group patterns of C8~C17 chlorinated paraffins in commercial products: Associations with source characterization. <i>Science of the Total Environment</i> , 2021, 769, 144701.	3.9	22
574	Environmental DNA of preservative ethanol performed better than water samples in detecting macroinvertebrate diversity using metabarcoding. <i>Diversity and Distributions</i> , 2021, 27, 1989-2002.	1.9	11
575	Integrated Proteomic and Metabolomic Analysis of the Testes Characterizes BDE-47-Induced Reproductive Toxicity in Mice. <i>Biomolecules</i> , 2021, 11, 821.	1.8	15
576	Genome-wide investigation and expression analysis of MACPF gene family reveals its immune role in response to bacterial challenge of Manila clam. <i>Genomics</i> , 2021, 113, 1136-1145.	1.3	7
577	Changes of gut microbiota in pregnant sows induced by 5-Aminolevulinic acid. <i>Research in Veterinary Science</i> , 2021, 136, 57-65.	0.9	5
578	Transcriptome Analysis of Light-Regulated Monoterpenes Biosynthesis in Leaves of <i>Mentha canadensis</i> L.. <i>Plants</i> , 2021, 10, 930.	1.6	10

#	ARTICLE	IF	CITATIONS
579	Genome-wide analysis of 10664 SARS-CoV-2 genomes to identify virus strains in 73 countries based on single nucleotide polymorphism. <i>Virus Research</i> , 2021, 298, 198401.	1.1	5
580	Genome-wide identification of AP2/EREBP in <i>Fragaria vesca</i> and expression pattern analysis of the FvDREB subfamily under drought stress. <i>BMC Plant Biology</i> , 2021, 21, 295.	1.6	13
581	Machine learning-based prediction of survival prognosis in cervical cancer. <i>BMC Bioinformatics</i> , 2021, 22, 331.	1.2	18
582	CaFtsH06, A Novel Filamentous Thermosensitive Protease Gene, Is Involved in Heat, Salt, and Drought Stress Tolerance of Pepper ( <i>Capsicum annuum</i> L.). <i>International Journal of Molecular Sciences</i> , 2021, 22, 6953.	1.8	5
583	Comprehensive Scanning of Prophages in <i>Lactobacillus</i> : Distribution, Diversity, Antibiotic Resistance Genes, and Linkages with CRISPR-Cas Systems. <i>MSystems</i> , 2021, 6, e0121120.	1.7	34
584	Mass cytometry and transcriptomic profiling reveal body-wide pathology induced by Loxl1 deficiency. <i>Cell Proliferation</i> , 2021, 54, e13077.	2.4	4
585	Effects of Nitrate Exposure on Nitrate Reduction Processes in the Wetland Sediments from the Yellow River Estuary. <i>Estuaries and Coasts</i> , 0, , 1.	1.0	6
586	Hybridization and introgression in sympatric and allopatric populations of four oak species. <i>BMC Plant Biology</i> , 2021, 21, 266.	1.6	8
587	Effectiveness of Selenium on Chondrocyte Glycoprotein Glycosylation Which Play Important Roles in the Pathogenesis of an Endemic Osteoarthritis, Kashinâ€œBeck Disease. <i>Biological Trace Element Research</i> , 2022, 200, 1531-1537.	1.9	0
588	Molecular Associations and Clinical Significance of RAPs in Hepatocellular Carcinoma. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 677979.	1.6	8
589	Transcriptome analysis expands the potential roles of quorum sensing in biodegradation and physiological responses to microcystin. <i>Science of the Total Environment</i> , 2021, 771, 145437.	3.9	18
590	Identification of N-linked Glycoproteins in Silkworm Serum Using Con A Lectin Affinity Chromatography and Mass Spectrometry. <i>Journal of Insect Science</i> , 2021, 21, .	0.6	0
591	Comparative proteomic profiles of resistant/susceptible cucumber leaves in response to downy mildew infection. <i>Horticultural Plant Journal</i> , 2021, 7, 327-340.	2.3	7
592	Integrated Phenotypicâ€œGenotypic Analysis of <i>Lactobacillus</i> Åsakei from Different Niches. <i>Foods</i> , 2021, 10, 1717.	1.9	10
593	A Detailed Spatial Expression Analysis of Wing Phenotypes Reveals Novel Patterns of Odorant Binding Proteins in the Soybean Aphid, <i>Aphis glycines</i> . <i>Frontiers in Physiology</i> , 2021, 12, 702973.	1.3	3
594	Genome-Wide Identification of the Early Flowering 4 (ELF4) Gene Family in Cotton and Silent GhELF4-1 and GhEFL3-6 Decreased Cotton Stress Resistance. <i>Frontiers in Genetics</i> , 2021, 12, 686852.	1.1	1
595	Arsenic or/and antimony induced mitophagy and apoptosis associated with metabolic abnormalities and oxidative stress in the liver of mice. <i>Science of the Total Environment</i> , 2021, 777, 146082.	3.9	53
596	Identification of Core Genes and Key Pathways in Gastric Cancer using Bioinformatics Analysis. <i>Russian Journal of Genetics</i> , 2021, 57, 963-971.	0.2	0

#	ARTICLE	IF	CITATIONS
597	Biocontrol potential of volatile organic compounds from <i>Pseudomonas chlororaphis</i> ZL3 against postharvest gray mold caused by <i>Botrytis cinerea</i> on Chinese cherry. <i>Biological Control</i> , 2021, 159, 104613.	1.4	20
598	Spatial distribution, radiological risk assessment and positive matrix factorization of gamma-emitting radionuclides in the sediment of the Boka Kotorska Bay. <i>Marine Pollution Bulletin</i> , 2021, 169, 112491.	2.3	10
599	Redox proteomic analysis reveals the involvement of oxidative post-translational modification in tomato fruit ripening. <i>Postharvest Biology and Technology</i> , 2021, 178, 111556.	2.9	10
600	Identification and expression profile of the soil moisture and <i>Ralstonia solanacearum</i> response CYPome in ginger ( <i>Zingiber officinale</i> ). <i>PeerJ</i> , 2021, 9, e11755.	0.9	3
601	GSK2126458 has the potential to inhibit the proliferation of pancreatic cancer uncovered by bioinformatics analysis and pharmacological experiments. <i>Journal of Translational Medicine</i> , 2021, 19, 373.	1.8	11
602	Genome-Wide Identification and Characterization of HSP90-RAR1-SGT1-Complex Members From <i>Arachis</i> Genomes and Their Responses to Biotic and Abiotic Stresses. <i>Frontiers in Genetics</i> , 2021, 12, 689669.	1.1	4
603	Genome-Wide Identification, Expression Profile, and Alternative Splicing Analysis of CAMTA Family Genes in Cucumber ( <i>Cucumis sativus</i> L.). <i>Agronomy</i> , 2021, 11, 1827.	1.3	12
604	CPLM 4.0: an updated database with rich annotations for protein lysine modifications. <i>Nucleic Acids Research</i> , 2022, 50, D451-D459.	6.5	20
605	Methane emissions and methanogenic community investigation from constructed wetlands in Chengdu City. <i>Urban Climate</i> , 2021, 39, 100956.	2.4	9
606	Comparative Transcriptome Analysis of Chemoreception Organs of <i>Laodelphax striatellus</i> in Response to Rice Stripe Virus Infection. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10299.	1.8	2
607	Capacity of soybean carbohydrate metabolism in <i>Leuconostoc mesenteroides</i> , <i>Lactococcus lactis</i> and <i>Streptococcus thermophilus</i> . <i>Food Bioscience</i> , 2021, 44, 101381.	2.0	5
608	Comparative Genomic Analysis of <i>Bifidobacterium bifidum</i> Strains Isolated from Different Niches. <i>Genes</i> , 2021, 12, 1504.	1.0	6
609	Development of a widely targeted volatilomics method for profiling volatilomes in plants. <i>Molecular Plant</i> , 2022, 15, 189-202.	3.9	49
610	De novo analysis reveals transcriptomic responses to heat stress in loquat ( <i>Eriobotrya japonica</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock	0.9	2
611	Genome-wide investigation of SQUAMOSA promoter binding protein-like transcription factor family in pearl millet ( <i>Pennisetum glaucum</i> (L) R. Br.). <i>Plant Gene</i> , 2021, 27, 100313.	1.4	6
612	Application of Tea Polyphenols and Their Effects on Ultrafiltration Effluent Disinfection and Microbial Risk. <i>Water (Switzerland)</i> , 2021, 13, 2559.	1.2	2
613	Molecular Epidemiological Analysis of ST11-K64 Extensively Drug-Resistant <i>Klebsiella pneumoniae</i> Infections Outbreak in Intensive Care and Neurosurgery Units Based on Whole-Genome Sequencing. <i>Frontiers in Microbiology</i> , 2021, 12, 709356.	1.5	4
614	Genome-wide analysis of the invertase genes in strawberry ( <i>Fragaria ananassa</i> ). <i>Journal of Integrative Agriculture</i> , 2021, 20, 2652-2665.	1.7	7

#	ARTICLE	IF	CITATIONS
615	Genomic organization and expression pattern of cytochrome P450 genes in the wolf spider <i>Pardosa pseudoannulata</i> . <i>Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology</i> , 2021, 248, 109118.	1.3	2
616	Multi-omics reveal the structure and function of microbial community in co-digestion of corn straw and pig manure. <i>Journal of Cleaner Production</i> , 2021, 322, 129150.	4.6	10
617	Transient expression and enzymatic assay identified uridine-diphosphate glucosyltransferases related to flavonoid glycosylation in <i>Vernonia amygdalina</i> leaves. <i>Industrial Crops and Products</i> , 2021, 172, 114005.	2.5	2
618	Successful enrichment of anammox consortium in a single-stage reactor at full-scale: The difference in response of functional genes and transcriptional expressions. <i>Chemical Engineering Journal</i> , 2021, 426, 131935.	6.6	21
619	Oral seeding and niche-adaptation of middle ear biofilms in health. <i>Biofilm</i> , 2021, 3, 100041.	1.5	4
620	Macro-composition quantification combined with metabolomics analysis uncovered key dynamic chemical changes of aging white tea. <i>Food Chemistry</i> , 2022, 366, 130593.	4.2	17
621	Exploring the typical flavours formation by combined with metatranscriptomics and metabolomics during Chinese Sichuan paocai fermentation. <i>LWT - Food Science and Technology</i> , 2022, 153, 112474.	2.5	27
622	Comparative transcriptional analyses of <i>Pleurotus ostreatus</i> mutants on beech wood and rice straw shed light on substrate-biased gene regulation. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 1175-1190.	1.7	12
623	Oxygen availability affects the synthesis of quorum sensing signal in the facultative anaerobe <i>Novosphingobium pentaromativorans</i> US6-1. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 1191-1201.	1.7	5
624	Methylome and transcriptome profiling revealed epigenetic silencing of <i>LPCAT1</i> and <i>PCYT1A</i> associated with lipidome alterations in polycystic ovary syndrome. <i>Journal of Cellular Physiology</i> , 2021, 236, 6362-6375.	2.0	13
625	Exometabolomic Analysis of Decidualizing Human Endometrial Stromal and Perivascular Cells. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 626619.	1.8	14
626	Soil Microbial Composition and <i>phoD</i> Gene Abundance Are Sensitive to Phosphorus Level in a Long-Term Wheat-Maize Crop System. <i>Frontiers in Microbiology</i> , 2020, 11, 605955.	1.5	17
627	Molecular Analysis of 14-3-3 Genes in <i>Citrus sinensis</i> and Their Responses to Different Stresses. <i>International Journal of Molecular Sciences</i> , 2021, 22, 568.	1.8	13
628	Identification of differentially expressed genes involved in spore germination of <i>Penicillium expansum</i> by comparative transcriptome and proteome approaches. <i>MicrobiologyOpen</i> , 2018, 7, e00562.	1.2	29
629	Virus-Free and Live-Cell Visualizing SARS-CoV-2 Cell Entry for Studies of Neutralizing Antibodies and Compound Inhibitors. <i>Small Methods</i> , 2021, 5, 2001031.	4.6	25
630	Insights into the aroma profiles and characteristic aroma of "Honeycrisp" apple ( <i>Malus domestica</i> ). <i>Food Chemistry</i> , 2020, 327, 127074.	4.2	50
631	Abiotic processes dominate soil organic matter mineralization: Investigating the regulatory gate hypothesis by inoculating a previously fumigated soil with increasing fresh soil inocula. <i>Geoderma</i> , 2020, 373, 114400.	2.3	6
632	Effects of exposure to ambient fine particulate matter on the heart of diet-induced obesity mouse model. <i>Science of the Total Environment</i> , 2020, 732, 139304.	3.9	14

#	ARTICLE	IF	CITATIONS
633	Grain-rich diets altered the colonic fermentation and mucosa-associated bacterial communities and induced mucosal injuries in goats. <i>Scientific Reports</i> , 2016, 6, 20329.	1.6	74
636	Transcriptome analysis and differential gene expression profiling of two contrasting quinoa genotypes in response to salt stress. <i>BMC Plant Biology</i> , 2020, 20, 568.	1.6	27
637	Metabolomic Profiling of Plasma Samples from Women with Recurrent Spontaneous Abortion. <i>Medical Science Monitor</i> , 2018, 24, 4038-4045.	0.5	30
638	Bioinformatics Analysis Identifies the Estrogen Receptor 1 (ESR1) Gene and hsa-miR-26a-5p as Potential Prognostic Biomarkers in Patients with Intrahepatic Cholangiocarcinoma. <i>Medical Science Monitor</i> , 2020, 26, e921815.	0.5	6
639	Identification and Comparison of Candidate Olfactory Genes in the Olfactory and Non-Olfactory Organs of Elm Pest <i>Ambrostoma quadriimpressum</i> (Coleoptera: Chrysomelidae) Based on Transcriptome Analysis. <i>PLoS ONE</i> , 2016, 11, e0147144.	1.1	32
640	Transcriptomic profiling of taproot growth and sucrose accumulation in sugar beet ( <i>Beta vulgaris</i> L.) at different developmental stages. <i>PLoS ONE</i> , 2017, 12, e0175454.	1.1	28
641	On the core bacterial flora of <i>Ixodes persulcatus</i> (Taiga tick). <i>PLoS ONE</i> , 2017, 12, e0180150.	1.1	18
642	RNA-sequencing analysis of fungi-induced transcripts from the bamboo wireworm <i>Melanotus cribricollis</i> (Coleoptera: Elateridae) larvae. <i>PLoS ONE</i> , 2018, 13, e0191187.	1.1	7
643	Systematic analysis of molecular mechanisms for HCC metastasis via text mining approach. <i>Oncotarget</i> , 2017, 8, 13909-13916.	0.8	6
644	Expression of miR-195 is associated with chemotherapy sensitivity of cisplatin and clinical prognosis in gastric cancer. <i>Oncotarget</i> , 2017, 8, 97260-97272.	0.8	22
645	Constructing an ovarian cancer metastasis index by dissecting medical records. <i>Oncotarget</i> , 2017, 8, 102212-102222.	0.8	4
646	The functional mechanism of miR-125b in gastric cancer and its effect on the chemosensitivity of cisplatin. <i>Oncotarget</i> , 2018, 9, 2105-2119.	0.8	29
647	A metabolomic study on early detection of steroid-induced avascular necrosis of the femoral head. <i>Oncotarget</i> , 2018, 9, 7984-7995.	0.8	17
648	Attention-based LSTM for Aspect-level Sentiment Classification. , 2016, , .		1,342
649	Identification of MicroRNAs and Their Targets Involved in <i>Paeonia rockii</i> Petal Variegation Using High-throughput Sequencing. <i>Journal of the American Society for Horticultural Science</i> , 2019, 144, 118-129.	0.5	5
650	Rhizosphere Bacterial Community Structure and Predicted Functional Analysis in the Water-Level Fluctuation Zone of the Danjiangkou Reservoir in China During the Dry Period. <i>International Journal of Environmental Research and Public Health</i> , 2020, 17, 1266.	1.2	8
651	Genome-wide identification and characterization of GRAS transcription factors in sacred lotus ( <i>Nelumbo nucifera</i> ). <i>PeerJ</i> , 2016, 4, e2388.	0.9	31
652	Genome-wide identification and characterization of GRAS transcription factors in tomato ( <i>Solanum lycopersicum</i> ). <i>PeerJ</i> , 2017, 5, e3955.	0.9	50

#	ARTICLE	IF	CITATIONS
653	<i>De novo</i> transcriptome sequencing and analysis of genes related to salt stress response in <i>Glehnia littoralis</i>. PeerJ, 2018, 6, e5681.	0.9	21
654	Determination of the evolutionary pressure on <i>Camellia oleifera</i> on Hainan Island using the complete chloroplast genome sequence. PeerJ, 2019, 7, e7210.	0.9	23
655	Genome-wide identification and characterization of the <i>Hsp70</i> gene family in allopolyploid rapeseed (<i>Brassica napus</i> L.) compared with its diploid progenitors. PeerJ, 2019, 7, e7511.	0.9	8
656	The R2R3-MYB transcription factor family in <i>Taxus chinensis</i>: identification, characterization, expression profiling and posttranscriptional regulation analysis. PeerJ, 2020, 8, e8473.	0.9	8
657	In silico analysis of maize HDACs with an emphasis on their response to biotic and abiotic stresses. PeerJ, 2020, 8, e8539.	0.9	12
658	Stereoselective toxicity mechanism of neonicotinoid dinotefuran in honeybees: New perspective from a spatial metabolomics study. Science of the Total Environment, 2022, 809, 151116.	3.9	18
659	Transcriptomic analysis of blackberry plant (Rubus spp.) reveals a comprehensive metabolic network involved in fruit ripening process. Biologia (Poland), 2021, 76, 3827-3840.	0.8	2
660	Transcriptome-based identification and expression profiling of AP2/ERF members in Caragana intermedia and functional analysis of CiDREB3. Molecular Biology Reports, 2021, 48, 7953-7965.	1.0	3
661	The RNA modification in Echinococcus granulosus cysts revealed by mass spectrometry. Infection, Genetics and Evolution, 2021, 96, 105124.	1.0	2
662	UPLC-QToF-MS chemical profiling and characterization of antiproliferative and anti-inflammatory compounds from seven Hypericum species in China. Industrial Crops and Products, 2021, 173, 114156.	2.5	11
664	Metabolic Profiles and High-Accuracy Diagnosis Model Based on Plasma Metabolomics of Gastric Cancer Patients. Translational Medicine Research, 2017, , 83-103.	0.0	0
671	Combined Transcriptome and Proteome Analysis to Elucidate Salt Tolerance Strategies of the Halophyte Panicum antidotale Retz. Frontiers in Plant Science, 2021, 12, 760589.	1.7	4
672	Long-term P fertilization significantly altered the diversity, composition and mycorrhizal traits of arbuscular mycorrhizal fungal communities in a wheat-maize rotation. Applied Soil Ecology, 2022, 170, 104261.	2.1	16
673	Gene Expression Profile of RNA N1-methyladenosine methyltransferases. E3S Web of Conferences, 2020, 218, 03052.	0.2	1
675	Developmental expression patterns and correlation analysis of TLR4 and its downstream genes in the intestinal and immune tissues of Meishan pigs. Revista Brasileira De Zootecnia, 2020, 49, .	0.3	0
677	Preliminary screening of intestinal barrier genes associated with porcine epidemic diarrhea virus infection in pigs. Revista Brasileira De Zootecnia, 2020, 49, .	0.3	1
679	Screening potential microRNAs associated with pancreatic cancer: Data mining based on RNA sequencing and microarrays. Experimental and Therapeutic Medicine, 2020, 20, 2705-2715.	0.8	7
680	Understanding seasonal migration of Shishamo smelt in coastal regions using environmental DNA. PLoS ONE, 2020, 15, e0239912.	1.1	2

#	ARTICLE	IF	CITATIONS
681	Predicting the Getting-on and Getting-off Points Based on the Traffic Big Data. <i>Advances in Intelligent Systems and Computing</i> , 2021, , 9-16.	0.5	0
682	microRNA-204 modulates chemosensitivity and apoptosis of prostate cancer cells by targeting zinc-finger E-box-binding homeobox 1 (ZEB1). <i>American Journal of Translational Research (discontinued)</i> , 2017, 9, 3599-3610.	0.0	27
683	Identification of hub genes associated with esophageal cancer progression using bioinformatics analysis. <i>Oncology Letters</i> , 2020, 20, 214.	0.8	1
684	Expression profiles of venom components in some social hymenopteran species over different post-capture periods. <i>Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology</i> , 2022, 253, 109247.	1.3	2
685	Reduced sensitivity of the SARS-CoV-2 Lambda variant to monoclonal antibodies and neutralizing antibodies induced by infection and vaccination. <i>Emerging Microbes and Infections</i> , 2022, 11, 18-29.	3.0	25
686	PPR proteins in the tea plant ( <i>Camellia sinensis</i> ) and their potential roles in the leaf color changes. <i>Scientia Horticulturae</i> , 2022, 293, 110745.	1.7	6
687	<i>Ilocasia fonsfrigidiae</i> NS-1 gen. nov., sp. nov., a Novel Deep-Sea Bacterium Possessing Diverse Carbohydrate Metabolic Pathways. <i>Frontiers in Microbiology</i> , 2021, 12, 725159.	1.5	2
688	Rapid Discrimination of <i>Citrus reticulata</i> "Chachi"™ by Electrospray Ionization "Ion Mobility" High-Resolution Mass Spectrometry. <i>Molecules</i> , 2021, 26, 7015.	1.7	4
689	Constructing a Defined Starter for Multispecies Vinegar Fermentation via Evaluation of the Vitality and Dominance of Functional Microbes in an Autochthonous Starter. <i>Applied and Environmental Microbiology</i> , 2022, 88, AEM0217521.	1.4	8
690	Integrated DIA proteomics and lipidomics analysis on non-small cell lung cancer patients with TCM syndromes. <i>Chinese Medicine</i> , 2021, 16, 126.	1.6	7
691	Identification of genes related to tipburn resistance in Chinese cabbage and preliminary exploration of its molecular mechanism. <i>BMC Plant Biology</i> , 2021, 21, 567.	1.6	4
692	GPS-Uber: a hybrid-learning framework for prediction of general and E3-specific lysine ubiquitination sites. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	10
693	A Novel and Green Method for Turning Food Waste into Environmentally-Friendly Organic Deicing Salts: Enhanced VFA Production through AnMBR. <i>Separations</i> , 2022, 9, 11.	1.1	2
694	Antibiotic resistance genes and antibiotic sensitivity in bacterial aerosols and their comparisons with known respiratory pathogens. <i>Journal of Aerosol Science</i> , 2022, 161, 105931.	1.8	11
695	Metagenomics revealed the mobility and hosts of antibiotic resistance genes in typical pesticide wastewater treatment plants. <i>Science of the Total Environment</i> , 2022, 817, 153033.	3.9	26
696	Ethnopharmacological nexus between the traditional Thai medicine theory and biologically based cancer treatment. <i>Journal of Ethnopharmacology</i> , 2022, 287, 114932.	2.0	2
697	Heterotrophy-coordinated diazotrophy is associated with significant changes of rare taxa in soil microbiome. <i>Pedosphere</i> , 2022, 32, 402-413.	2.1	3
698	Identification of hub genes associated with esophageal cancer progression using bioinformatics analysis. <i>Oncology Letters</i> , 2020, 20, 1-1.	0.8	3

#	ARTICLE	IF	CITATIONS
699	Evaluation of lodging resistance in rice based on an optimized parameter from lodging index. <i>Crop Science</i> , 2022, 62, 1318-1332.	0.8	11
700	Evolution and Stress Responses of CLO Genes and Potential Function of the GhCLO06 Gene in Salt Resistance of Cotton. <i>Frontiers in Plant Science</i> , 2021, 12, 801239.	1.7	3
701	Application of the hydrothermally treated oxytetracycline fermentation residue in agriculture: concentrations of antibiotic and resistance genes in soil and plant. <i>Journal of Soils and Sediments</i> , 2022, 22, 1095-1104.	1.5	3
702	Machine learning analysis for the noninvasive prediction of lymphovascular invasion in gastric cancer using PET/CT and enhanced CT-based radiomics and clinical variables. <i>Abdominal Radiology</i> , 2022, 47, 1209-1222.	1.0	17
703	Sedimentary and Source-to-Sink Evolution of Intracontinental Basins: Implications for tectonic and Climate Evolution in the Late Mesozoic (Southern Junggar Basin, NW China). <i>Frontiers in Earth Science</i> , 2022, 9, .	0.8	2
704	Rv1258c acts as a drug efflux pump and growth controlling factor in <i>Mycobacterium tuberculosis</i> . <i>Tuberculosis</i> , 2022, 133, 102172.	0.8	4
705	Aggregation of high-frequency RBD mutations of SARS-CoV-2 with three VOCs did not cause significant antigenic drift. <i>Journal of Medical Virology</i> , 2022, , .	2.5	5
706	A Deep-Sea Bacterium Senses Blue Light via a BLUF-Dependent Pathway. <i>MSystems</i> , 2022, 7, e0127921.	1.7	6
707	Genome-wide Identification, Characterization and Expression profile of TALE gene family in ( <i>Juglans</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.7	8
708	Metagenomics insights into the profiles of antibiotic resistome in combined sewage overflows from reads to metagenome assembly genomes. <i>Journal of Hazardous Materials</i> , 2022, 429, 128277.	6.5	20
709	Nutrients, temperature, and oxygen mediate microbial antibiotic resistance in sea bass ( <i>Lateolabrax</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	3.9	10
711	Cloning and functional analysis of the promoter of allergen gene Ara h 1 from peanut. <i>Oil Crop Science</i> , 2022, , .	0.9	0
712	Metabolite Characteristics Analysis of Siliques and Effects of Lights on the Accumulation of Glucosinolates in Siliques of Rapeseed. <i>Frontiers in Plant Science</i> , 2022, 13, 817419.	1.7	0
713	Overexpression of GhKT112 Enhances Seed Yield and Biomass Production in <i>Nicotiana Tabacum</i> . <i>Genes</i> , 2022, 13, 426.	1.0	3
714	Transcriptome analysis and differential gene expression profiling of wucaï ( <i>Brassica campestris</i> L.) in response to cold stress. <i>BMC Genomics</i> , 2022, 23, 137.	1.2	11
715	Dual RNA Sequencing Reveals the Genome-Wide Expression Profiles During the Compatible and Incompatible Interactions Between <i>Solanum tuberosum</i> and <i>Phytophthora infestans</i> . <i>Frontiers in Plant Science</i> , 2022, 13, 817199.	1.7	2
716	Identification of the LOX Gene Family in Peanut and Functional Characterization of AhLOX29 in Drought Tolerance. <i>Frontiers in Plant Science</i> , 2022, 13, 832785.	1.7	16
717	Rapid and Selective Absorption of Plant Defense Compounds From the Gut of a Sequestering Insect. <i>Frontiers in Physiology</i> , 2022, 13, 846732.	1.3	4



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718	Tissue specificity and responses to abiotic stresses and hormones of PIN genes in rice. <i>Biologia (Poland)</i> , 2022, 77, 1459-1470.	0.8	7
719	The impacts of allopolyploidization on Methyl-CpG-Binding Domain (MBD) gene family in <i>Brassica napus</i> . <i>BMC Plant Biology</i> , 2022, 22, 103.	1.6	3
720	Genome-wide identification, characterisation, and expression of C3HC4-type RING finger gene family in <i>Capsicum annuum</i> L. <i>Journal of Horticultural Science and Biotechnology</i> , 2022, 97, 603-614.	0.9	3
721	Genome-Wide Analysis of Invertase Gene Family, and Expression Profiling under Abiotic Stress Conditions in Potato. <i>Biology</i> , 2022, 11, 539.	1.3	23
722	Genome-wide identification and expression of SAUR gene family in peanut ( <i>Arachis hypogaea</i> L.) and functional identification of AhSAUR3 in drought tolerance. <i>BMC Plant Biology</i> , 2022, 22, 178.	1.6	5
723	Comparative Metabolomic Profiling of Compatible and Incompatible Interactions Between Potato and <i>Phytophthora infestans</i> . <i>Frontiers in Microbiology</i> , 2022, 13, 857160.	1.5	3
724	Characterization and quantification of ginsenosides from the root of <i>Panax quinquefolius</i> L. by integrating untargeted metabolites and targeted analysis using UPLC-Triple TOF-MS coupled with UFLC-ESI-MS/MS. <i>Food Chemistry</i> , 2022, 384, 132466.	4.2	18
725	Comprehensive evaluation and analysis of the salinity stress response mechanisms based on transcriptome and metabolome of <i>Staphylococcus aureus</i> . <i>Archives of Microbiology</i> , 2022, 204, 28.	1.0	8
726	Genetic diversity and population structure analysis of rice false smut pathogen in North India using molecular markers. <i>Journal of Phytopathology</i> , 2022, 170, 124-140.	0.5	0
727	Whole genome duplication and dispersed duplication characterize the evolution of the plant PINOID gene family across plant species. <i>Gene</i> , 2022, 829, 146494.	1.0	6
728	Optimization of a pheromone lure by analyzing the peripheral coding of sex pheromones of <i>Spodoptera frugiperda</i> in China. <i>Pest Management Science</i> , 2022, 78, 2995-3004.	1.7	13
729	Esophageal squamous cell carcinoma: Integrated bioinformatics analysis for differential gene expression with identification of hub genes and lncRNA. <i>Biochemistry and Biophysics Reports</i> , 2022, 30, 101262.	0.7	1
844	Genome-wide Characterization of the JmjC Domain-Containing Histone Demethylase Gene Family Reveals GhJM24 and GhJM49 Involving in Somatic Embryogenesis Process in Cotton. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 888983.	1.6	0
845	Identification of PP2C Genes in Tibetan Hulless Barley ( <i>Hordeum vulgare</i> var. <i>nudum</i> ) Under Dehydration Stress and Initiatory Expression and Functional Analysis of HvPP2C59. <i>Plant Molecular Biology Reporter</i> , 2022, 40, 611-627.	1.0	3
846	Biodiversity and seasonal variation of microzooplankton contaminating pilot-scale cultures of <i>Chlorella sorokiniana</i> . <i>Algal Research</i> , 2022, 64, 102722.	2.4	5
847	Metabolic Profiling Analysis of the Effect and Mechanism of Gushiling Capsule in Rabbits With Glucocorticoid-Induced Osteonecrosis of the Femoral Head. <i>Frontiers in Pharmacology</i> , 2022, 13, 845856.	1.6	2
848	Network Pharmacology Approach for Medicinal Plants: Review and Assessment. <i>Pharmaceuticals</i> , 2022, 15, 572.	1.7	99
849	Insights into Prokaryotic Community and Its Potential Functions in Nitrogen Metabolism in the Bay of Bengal, a Pronounced Oxygen Minimum Zone. <i>Microbiology Spectrum</i> , 2022, 10, e0089221.	1.2	9

#	ARTICLE	IF	CITATIONS
850	Novel Thermostable Heparinase Based on the Genome of Bacteroides Isolated from Human Gut Microbiota. <i>Foods</i> , 2022, 11, 1462.	1.9	1
851	Heterologous expression of ISU1 gene from <i>Fragaria vesca</i> enhances plant tolerance to Fe depletion in <i>Arabidopsis</i> . <i>Plant Physiology and Biochemistry</i> , 2022, 184, 65-74.	2.8	3
853	HemI 2.0: an online service for heatmap illustration. <i>Nucleic Acids Research</i> , 2022, 50, W405-W411.	6.5	24
854	Genome-wide investigation of histone acetyltransferase gene family and its responses to biotic and abiotic stress in foxtail millet ( <i>Setaria italica</i> [L.] P. Beauv). <i>BMC Plant Biology</i> , 2022, 22, .	1.6	8
855	Comparison of <i>SWEET</i> gene family between maize and foxtail millet through genomic, transcriptomic, and proteomic analyses. <i>Plant Genome</i> , 2022, 15, .	1.6	10
856	iPCD: A Comprehensive Data Resource of Regulatory Proteins in Programmed Cell Death. <i>Cells</i> , 2022, 11, 2018.	1.8	0
857	Physiological, epigenetic, and proteomic responses in <i>Pfaffia glomerata</i> growth in vitro under salt stress and 5-azacytidine. <i>Protoplasma</i> , 0, , .	1.0	2
858	A 16S rRNA Sequencing Study Describing the Environmental Microbiota of Two Powdered Infant Formula Built Facilities. <i>Foodborne Pathogens and Disease</i> , 2022, 19, 473-484.	0.8	1
859	Genome-Wide Analysis of the Rice Gibberellin Dioxygenases Family Genes. <i>Agronomy</i> , 2022, 12, 1627.	1.3	4
860	Genome-Wide Analysis of Multidrug and Toxic Compound Extrusion Transporters in Grape. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
861	Wheat heat shock factor TaHsfA2d contributes to plant responses to phosphate deficiency. <i>Plant Physiology and Biochemistry</i> , 2022, 185, 178-187.	2.8	7
862	The Analysis of the Ubiquitylomic Responses to <i>Streptococcus agalactiae</i> Infection in Bovine Mammary Gland Epithelial Cells. <i>Journal of Inflammation Research</i> , 0, Volume 15, 4331-4343.	1.6	1
863	Comprehensive deciphering prophages in genus <i>Acetobacter</i> on the ecology, genomic features, toxin-antitoxin system, and linkage with CRISPR-Cas system. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
864	Systematic analysis of CNGCs in cotton and the positive role of GhCNGC32 and GhCNGC35 in salt tolerance. <i>BMC Genomics</i> , 2022, 23, .	1.2	2
865	The potential of mineral weathering of halophilic-endophytic bacteria isolated from <i>Suaeda salsa</i> and <i>Spartina anglica</i> . <i>Archives of Microbiology</i> , 2022, 204, .	1.0	3
866	Profiles of Microbial Community and Antibiotic Resistome in Wild Tick Species. <i>MSystems</i> , 2022, 7, .	1.7	4
867	Identification of receptor-like proteins induced by <i>Sclerotinia sclerotiorum</i> in <i>Brassica napus</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
868	Identification of the WRKY Gene Family and Characterization of Stress-Responsive Genes in <i>Taraxacum kok-saghyz</i> Rodin. <i>International Journal of Molecular Sciences</i> , 2022, 23, 10270.	1.8	11

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869	24-epibrassinolide promotes selenium uptake in grapevine under selenium stress. <i>Scientia Horticulturae</i> , 2023, 308, 111564.	1.7	12
870	Spatial Distributions and Intrinsic Influence Analysis of Cr, Ni, Cu, Zn, As, Cd and Pb in Sediments from the Wuliangshuai Wetland, China. <i>International Journal of Environmental Research and Public Health</i> , 2022, 19, 10843.	1.2	4
871	Functional characterization of powdery mildew resistance-related genes HbSGT1a and HbSGT1b in <i>Hevea brasiliensis</i> Muell. Arg.. <i>European Journal of Plant Pathology</i> , 2023, 165, 153-161.	0.8	3
872	ERIC-PCR-based molecular typing of multidrug-resistant <i>Escherichia coli</i> isolated from houseflies ( <i>Musca domestica</i> ) in the environment of milk and meat shops. <i>Letters in Applied Microbiology</i> , 2022, 75, 1549-1558.	1.0	2
873	Temperature-Responsive Nanocarrier-Regulated Alternative Release of Cargos for a Multiplex Photoelectrochemical Bioassay of Antibiotic-Resistant Genes. <i>Analytical Chemistry</i> , 2022, 94, 14061-14070.	3.2	7
874	Comparative chloroplast genome and phylogenetic analyses of Chinese <i>Polyspora</i> . <i>Scientific Reports</i> , 2022, 12, .	1.6	5
875	Sediment provenances of a Mesozoic intracontinental basin enclosed by multiple orogenic belts, Junggar Basin, NW China: insights from detrital ilmenite, Cr-spinel geochemistry, and zircon U-Pb geochronology. <i>International Geology Review</i> , 0, , 1-26.	1.1	1
876	Genome-Wide Analysis and Expression Profiles of the VOZ Gene Family in Quinoa ( <i>Chenopodium</i> ) Tj ETQq1 1 0.784314 rgBT 4 Overload	1.0	4
877	Systematic Characterization of the OSCA Family Members in Soybean and Validation of Their Functions in Osmotic Stress. <i>International Journal of Molecular Sciences</i> , 2022, 23, 10570.	1.8	6
878	Proteomic analysis of rat colonic mucosa following acupuncture treatment for irritable bowel syndrome with diarrhea. <i>PLoS ONE</i> , 2022, 17, e0273853.	1.1	1
879	A deep-sea sulfate-reducing bacterium generates zero-valent sulfur via metabolizing thiosulfate. , 2022, 1, 257-271.		2
880	Function and Evolution of C1-2i Subclass of C2H2-Type Zinc Finger Transcription Factors in POPLAR. <i>Genes</i> , 2022, 13, 1843.	1.0	2
881	A plant-based mutant huntingtin model-driven discovery of impaired expression of GTPCH and DHFR. <i>Cellular and Molecular Life Sciences</i> , 2022, 79, .	2.4	2
882	MIKC-type MADS-box transcription factor gene family in peanut: Genome-wide characterization and expression analysis under abiotic stress. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	6
883	Histological characteristics, cell wall hydrolytic enzyme activity, and transcriptome analysis with seed shattering of <i>Stylosanthes</i> accessions. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
884	Genome-Wide Identification and Evolution Analysis of R2R3-MYB Gene Family Reveals S6 Subfamily R2R3-MYB Transcription Factors Involved in Anthocyanin Biosynthesis in Carrot. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11859.	1.8	6
885	The polysaccharides from the fruits of <i>Lycium barbarum</i> L. modify the gut community profile and alleviate dextran sulfate sodium-induced colitis in mice. <i>International Journal of Biological Macromolecules</i> , 2022, 222, 2244-2257.	3.6	6
886	Characterization of WOX genes revealed drought tolerance, callus induction, and tissue regeneration in <i>Gossypium hirsutum</i> . <i>Frontiers in Genetics</i> , 0, 13, .	1.1	7

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887	<scp>ZmEREB92</scp> interacts with <scp>ZmMYC2</scp> to activate maize terpenoid phytoalexin biosynthesis upon <i>Fusarium graminearum</i> infection through jasmonic acid/ethylene signaling. <i>New Phytologist</i> , 2023, 237, 1302-1319.	3.5	3
888	Castration alters the cecal microbiota and inhibits growth in Holstein cattle. <i>Journal of Animal Science</i> , 2022, 100, .	0.2	2
889	Identification of sex-specific splicing via comparative transcriptome analysis of gonads from sea cucumber <i>Apostichopus japonicus</i> . <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2023, 45, 101031.	0.4	0
890	Dynamic change of oligopeptides and free amino acids composition in five types of tea with different fermentation degree processed from the same batch of fresh tea ( <i>Camellia Sinensis</i> . L.) leaves. <i>Food Chemistry</i> , 2023, 404, 134608.	4.2	2
891	Systematical Characterization of the Cotton Di19 Gene Family and the Role of GhDi19-3 and GhDi19-4 as Two Negative Regulators in Response to Salt Stress. <i>Antioxidants</i> , 2022, 11, 2225.	2.2	3
892	Validation of suitable reference genes by various algorithms for gene expression analysis in <i>Isodon rubescens</i> under different abiotic stresses. <i>Scientific Reports</i> , 2022, 12, .	1.6	8
893	Transcriptome and Regional Association Analyses Reveal the Effects of Oleosin Genes on the Accumulation of Oil Content in <i>Brassica napus</i> . <i>Plants</i> , 2022, 11, 3140.	1.6	5
894	Identification and expression analysis of maize <i>NF-YA</i> subunit genes. <i>PeerJ</i> , 0, 10, e14306.	0.9	2
895	Comparative analysis of differentially expressed miRNAs in leaves of three sugarcanes ( <i>Saacharum</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.0	1
896	The role of Connexin26 regulated by MiR-2114-3p in the pathogenesis of ovarian cancer. <i>Biochemical and Biophysical Research Communications</i> , 2023, 640, 105-116.	1.0	0
897	Heterogeneous selection dominated the temporal variation of the planktonic prokaryotic community during different seasons in the coastal waters of Bohai Bay. <i>Scientific Reports</i> , 2022, 12, .	1.6	0
898	Comprehensive Analysis of Codon Usage in <i>Quercus</i> Chloroplast Genome and Focus on psbA Gene. <i>Genes</i> , 2022, 13, 2156.	1.0	9
899	Comparative Transcriptome Analysis of MeJA Responsive Enzymes Involved in Phillyrin Biosynthesis of <i>Forsythia suspensa</i> . <i>Metabolites</i> , 2022, 12, 1143.	1.3	1
900	Identification of candidate genes regulating seed oil content by QTL mapping and transcriptome sequencing in <i>Brassica napus</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
901	Genome-wide investigation and expression pattern of <i>PHR</i> family genes in cotton under low phosphorus stress. <i>PeerJ</i> , 0, 10, e14584.	0.9	0
902	Genome-wide investigation and expression analysis of TLR gene family reveals its immune role in <i>Vibrio</i> tolerance challenge of Manila clam. <i>Fish and Shellfish Immunology Reports</i> , 2022, 3, 100072.	0.5	0
903	Analyzing the Therapeutic Mechanism of Mongolian Medicine Zhonglun-5 in Rheumatoid Arthritis Using a Bagging Algorithm with Serum Metabonomics. <i>Evidence-based Complementary and Alternative Medicine</i> , 2022, 2022, 1-9.	0.5	1
904	Multiparametric MRI-based radiomics nomogram for early prediction of pathological response to neoadjuvant chemotherapy in locally advanced gastric cancer. <i>European Radiology</i> , 2023, 33, 2746-2756.	2.3	5

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905	Toxic mechanism of the Mongolian medicine "Hunqile-7" based on metabonomics and the metabolism of intestinal flora. <i>Toxicology Research</i> , 0, , .	0.9	0
906	Genome-Wide Identification and Expression Analysis of the 4-Coumarate: CoA Ligase Gene Family in <i>Solanum tuberosum</i> . <i>International Journal of Molecular Sciences</i> , 2023, 24, 1642.	1.8	8
907	Understanding the Sensitivity of Grape Terpenes to Jasmonates Using <i>In Vitro</i> Culture and <i>In Vivo</i> Vineyard Experiments. <i>Journal of Agricultural and Food Chemistry</i> , 2023, 71, 3141-3151.	2.4	1
908	The Histone H3K27 Demethylase REF6 Is a Positive Regulator of Light-Initiated Seed Germination in <i>Arabidopsis</i> . <i>Cells</i> , 2023, 12, 295.	1.8	1
909	Characterization of the key odorants and investigation of the effects of drying methods on the aroma, taste, color and volatile profiles of the fruit of <i>Clausena anisum-olens</i> (Blanco) Merr.. <i>LWT - Food Science and Technology</i> , 2023, 175, 114476.	2.5	2
910	Pepper heat shock transcription factor A1d contributes to seed thermotolerance and germination vigor. <i>Scientia Horticulturae</i> , 2023, 311, 111786.	1.7	1
911	Genome-wide characterization of phospholipase D family genes in allotetraploid peanut and its diploid progenitors revealed their crucial roles in growth and abiotic stress responses. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	3
912	Metabolic Pathway of Monounsaturated Lipids Revealed by In-Depth Structural Lipidomics by Mass Spectrometry. <i>Research</i> , 2023, 6, .	2.8	2
913	UPLC-QTOF-MS-based metabolomics and chemometrics studies of geographically diverse <i>Acer truncatum</i> leaves: A traditional herbal tea in Northern China. <i>Food Chemistry</i> , 2023, 417, 135873.	4.2	3
914	The composition, function and assembly mechanism of epiphytic microbial communities on <i>Gracilariopsis lemaneiformis</i> . <i>Journal of Experimental Marine Biology and Ecology</i> , 2023, 564, 151909.	0.7	1
915	Iron oxide (Fe <sub>2</sub> O <sub>3</sub> ) nanoparticles alleviate PEG-simulated drought stress in grape ( <i>Vitis vinifera</i> L.) plants by regulating leaf antioxidants. <i>Scientia Horticulturae</i> , 2023, 312, 111847.	1.7	8
916	Catechins prevent obesity-induced kidney damage by modulating PPAR <sup>α</sup> /CD36 pathway and gut-kidney axis in rats. <i>Life Sciences</i> , 2023, 316, 121437.	2.0	3
918	Development of a New Sex Attractant via the Peripheral Coding of Pheromones in <i>Mythimna loreyi</i> . <i>Journal of Agricultural and Food Chemistry</i> , 2023, 71, 2795-2803.	2.4	2
919	PIP5K1C phosphoinositide kinase deficiency distinguishes PIKFYVE-dependent cancer cells from non-malignant cells. <i>Autophagy</i> , 2023, 19, 2464-2484.	4.3	2
920	Genetic-Phenotype Analysis of <i>Bifidobacterium bifidum</i> and Its Glycoside Hydrolase Gene Distribution at Different Age Groups. <i>Foods</i> , 2023, 12, 922.	1.9	2
921	Lutein Prevents Liver Injury and Intestinal Barrier Dysfunction in Rats Subjected to Chronic Alcohol Intake. <i>Nutrients</i> , 2023, 15, 1229.	1.7	2
922	Genome-wide analysis of bromodomain gene family in <i>Arabidopsis</i> and rice. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	1
923	The <i>Phaseolus vulgaris</i> Receptor-Like Kinase PvFER1 and the Small Peptides PvRALF1 and PvRALF6 Regulate Nodule Number as a Function of Nitrate Availability. <i>International Journal of Molecular Sciences</i> , 2023, 24, 5230.	1.8	4

#	ARTICLE	IF	CITATIONS
924	Bacillus subtilis DSM29784 attenuates Clostridium perfringens-induced intestinal damage of broilers by modulating intestinal microbiota and the metabolome. <i>Frontiers in Microbiology</i> , 0, 14, .	1.5	1
925	DT-109 ameliorates nonalcoholic steatohepatitis in nonhuman primates. <i>Cell Metabolism</i> , 2023, 35, 742-757.e10.	7.2	10
926	Evolution of soil texture in mid-subtropical forests in the past 32 years: taking Fanjing mountain in Southwest China as an example. <i>Tropical Ecology</i> , 0, , .	0.6	0
927	Bifidobacterium and Lactobacillus improve inflammatory bowel disease in zebrafish of different ages by regulating the intestinal mucosal barrier and microbiota. <i>Life Sciences</i> , 2023, 324, 121699.	2.0	14
928	Tridepsides as potential bioactives: a review on their chemistry and the global distribution of their lichenic and non-lichenic natural sources. <i>Frontiers in Fungal Biology</i> , 0, 4, .	0.9	1