Shuang-Quan Zou

List of Publications by Year
in descending order

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35 papers	549 citations	933447 10 h-index	677142 22 g-index
36 all docs	36 docs citations	36 times ranked	657 citing authors

#	Article	IF	Citations
1	The camphor tree genome enhances the understanding of magnoliid evolution. Journal of Genetics and Genomics, 2022, 49, 249-253.	3.9	7
2	Field-applied biochar-based MgO and sepiolite composites possess CO2 capture potential and alter organic C mineralization and C-cycling bacterial structure in fertilized soils. Science of the Total Environment, 2022, 813, 152495.	8.0	17
3	Comparative Impact of Bacillus spp. on Long-Term N Supply and N-Cycling Bacterial Distribution Under Biochar and Manure Amendment. Journal of Soil Science and Plant Nutrition, 2022, 22, 882.	3.4	2
4	High-Throughput Sequencing Analysis of the Composition and Diversity of the Bacterial Community in Cinnamomum camphora Soil. Microorganisms, 2022, 10, 72.	3.6	6
5	Genomes of leafy and leafless Platanthera orchids illuminate the evolution of mycoheterotrophy. Nature Plants, 2022, 8, 373-388.	9.3	36
6	A New Flavonoid From Leaves of Ormosia xylocarpa. Natural Product Communications, 2022, 17, 1934578X2211020.	0.5	0
7	Orchid Bsister gene PeMADS28 displays conserved function in ovule integument development. Scientific Reports, 2021, 11, 1205.	3.3	8
8	Genome-wide identification, evolution and expression analysis of the aspartic protease gene family during rapid growth of moso bamboo (Phyllostachys edulis) shoots. BMC Genomics, 2021, 22, 45.	2.8	9
9	Wolfberry genomes and the evolution of LyciumÂ(Solanaceae). Communications Biology, 2021, 4, 671.	4.4	40
10	Genetic diversity and population structure of Euscaphis japonica, a monotypic species. PeerJ, 2021, 9, e12024.	2.0	2
11	The Euscaphis japonica genome and the evolution of malvids. Plant Journal, 2021, 108, 1382-1399.	5.7	6
12	Genome-Wide Identification and Co-Expression Analysis of ARF and IAA Family Genes in Euscaphis konishii: Potential Regulators of Triterpenoids and Anthocyanin Biosynthesis. Frontiers in Genetics, 2021, 12, 737293.	2.3	1
13	Shifts in Microbial Biomass C/N/P Stoichiometry and Bacterial Community Composition in Subtropical Estuarine Tidal Marshes Along a Gradient of Freshwaterâ€“Oligohaline Water. Ecosystems, 2020, 23, 1265-1280.	3.4	3
14	The complete mitochondrial genome of Monochamus alternatus alternatus (Coleoptera:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 222 Td (	0.4	2
15	The complete chloroplast genome sequence of Tapiscia sinensis (Staphyleaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 2658-2660.	0.4	1
16	Terpenoids and Their Biological Activities from Cinnamomum: A Review. Journal of Chemistry, 2020, 2020, 1-14.	1.9	20
17	The complete chloroplast genome sequence of Turpinia montana (Staphyleaceae). Mitochondrial DNA Part B: Resources, 2020, 5, 3354-3356.	0.4	0
18	The Phoebe genome sheds light on the evolution of magnoliids. Horticulture Research, 2020, 7, 146.	6.3	41

#	Article	IF	Citations
19	Characterization of Bacterial Communities Associated with Rhynchophorus ferrugineus Olivier (Coleoptera: Curculionidae) and its Host Phoenix sylvestris. Current Microbiology, 2020, 77, 3321-3329.	2.2	1
20	Chromosome-scale assembly of the Kandelia obovata genome. Horticulture Research, 2020, 7, 75.	6.3	38
21	Total phenolic extract of Euscaphis konishii hayata Pericarp attenuates carbon tetrachloride (CCl4)-induced liver fibrosis in mice. Biomedicine and Pharmacotherapy, 2020, 125, 109932.	5.6	11
22	Comprehensive transcriptome analysis of reference genes for fruit development ofEuscaphis konishii. PeerJ, 2020, 8, e8474.	2.0	4
23	Multivariate analysis reveals phenotypic diversity of Euscaphis japonica population. PLoS ONE, 2019, 14, e0219046.	2.5	13
24	The complete chloroplast genome sequence of Euscaphis japonica (Staphyleaceae). Mitochondrial DNA Part B: Resources, 2019, 4, 3484-3485.	0.4	6
25	The complete chloroplast genome sequence of Kandelia obovata (Rhizophoraceae). Mitochondrial DNA Part B: Resources, 2019, 4, 3494-3495.	0.4	4
26	Chemical Constituents of Euscaphis konishii and Their Inhibitory Activities. Chemistry of Natural Compounds, 2019, 55, 832-834.	0.8	4
27	Protective Effect of the Total Triterpenes ofEuscaphis konishiiHayata Pericarp on Bacillus Calmette-GuÃ©rin Plus Lipopolysaccharide-Induced Liver Injury. Evidence-based Complementary and Alternative Medicine, 2019, 2019, 1-15.	1.2	4
28	The complete chloroplast genome sequence of Brasenia schreberi (Cabombaceae). Mitochondrial DNA Part B: Resources, 2019, 4, 3842-3843.	0.4	2
29	Comparative transcriptome among Euscaphis konishii Hayata tissues and analysis of genes involved in flavonoid biosynthesis and accumulation. BMC Genomics, 2019, 20, 24.	2.8	29
30	Sequencing of Euscaphis konishii Endocarp Transcriptome Points to Molecular Mechanisms of Endocarp Coloration. International Journal of Molecular Sciences, 2018, 19, 3209.	4.1	5
31	Selection and evaluation of reference genes for qRT-PCR analysis in Euscaphis konishii Hayata based on transcriptome data. Plant Methods, 2018, 14, 42.	4.3	42
32	Effect of proteolytic and detoxification enzyme inhibitors on Bacillus thuringiensis var. israelensis tolerance in the mosquito Aedes aegypti. Biocontrol Science and Technology, 2017, 27, 169-179.	1.3	1
33	Physiological and biochemical response ofAedes aegyptitolerance toBacillus thuringiensis. Biocontrol Science and Technology, 2016, 26, 227-238.	1.3	3
34	Identification of Genes Relevant to Pesticides and Biology from Global Transcriptome Data of Monochamus alternatus Hope (Coleoptera: Cerambycidae) Larvae. PLoS ONE, 2016, 11, e0147855.	2.5	19
35	The dynamic response of soil respiration to landâ€use changes in subtropical China. Global Change Biology, 2010, 16, 1107-1121.	9.5	162