Balázs Vajna

List of Publications by Year in descending order

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623734 552781 1,036 27 14 26 citations g-index h-index papers 28 28 28 1608 docs citations times ranked citing authors all docs

#	Article	lF	CITATIONS
1	Bacterial–fungal interactions: ecology, mechanisms and challenges. FEMS Microbiology Reviews, 2018, 42, 335-352.	8.6	468
2	DGGE and T-RFLP Analysis of Bacterial Succession during Mushroom Compost Production and Sequence-aided T-RFLP Profile of Mature Compost. Microbial Ecology, 2009, 57, 522-533.	2.8	90
3	Remarkable impact of PAHs and TPHs on the richness and diversity of bacterial species in surface soils exposed to long-term hydrocarbon pollution. World Journal of Microbiology and Biotechnology, 2013, 29, 1989-2002.	3.6	54
4	Texture and type of polymer fiber carrier determine bacterial colonization and biofilm properties in wastewater treatment. Chemical Engineering Journal, 2015, 264, 824-834.	12.7	42
5	Ferrate treatment for inactivation of bacterial community in municipal secondary effluent. Bioresource Technology, 2012, 107, 116-121.	9.6	41
6	One-year monitoring of meta-cleavage dioxygenase gene expression and microbial community dynamics reveals the relevance of subfamily I.2.C extradiol dioxygenases in hypoxic, BTEX-contaminated groundwater. Systematic and Applied Microbiology, 2013, 36, 339-350.	2.8	33
7	Diversity and seasonal dynamics of the photoautotrophic picoplankton in Lake Balaton (Hungary). Aquatic Microbial Ecology, 2011, 63, 273-287.	1.8	27
8	Thermus composti sp. nov., isolated from oyster mushroom compost. International Journal of Systematic and Evolutionary Microbiology, 2012, 62, 1486-1490.	1.7	27
9	Microbial community structure changes during oyster mushroom substrate preparation. Applied Microbiology and Biotechnology, 2010, 86, 367-375.	3.6	26
10	An Improved Sequence-aided T-RFLP Analysis of Bacterial Succession During Oyster Mushroom Substrate Preparation. Microbial Ecology, 2012, 64, 702-713.	2.8	24
11	Aboveâ€ground parts of white grapevine <scp><i>Vitis vinifera</i></scp> cv. Furmint share core members of the fungal microbiome. Environmental Microbiology Reports, 2021, 13, 509-520.	2.4	23
12	Characterisation of the large-scale production process of oyster mushroom (Pleurotus ostreatus) with the analysis of succession and spatial heterogeneity of lignocellulolytic enzyme activities. Fungal Biology, 2015, 119, 1354-1363.	2.5	20
13	Differences in planktonic microbial communities associated with three types of macrophyte stands in a shallow lake. FEMS Microbiology Ecology, 2018, 94, .	2.7	16
14	Effect of Long-Term Cropping Systems on the Diversity of the Soil Bacterial Communities. Agronomy, 2019, 9, 878.	3.0	16
15	Whole genome sequence analysis of Cupriavidus campinensis S14E4C, a heavy metal resistant bacterium. Molecular Biology Reports, 2020, 47, 3973-3985.	2.3	16
16	Phenotypic characterization and molecular taxonomic studies on Bacillus and related isolates from Phragmites australis periphyton. Aquatic Botany, 2007, 86, 243-252.	1.6	15
17	Diversity and activity of cultivable aerobic planktonic bacteria of a saline Lake located in Sovata, Romania. Folia Microbiologica, 2010, 55, 461-466.	2.3	15
18	Monitoring of soil microbial inoculants and their impact on maize (Zea mays L.) rhizosphere using T-RFLP molecular fingerprint method. Applied Soil Ecology, 2019, 138, 233-244.	4.3	15

#	Article	IF	CITATION
19	Increased incidence of genetic human prion disease in Hungary. Neurology, 2005, 65, 1666-1669.	1.1	12
20	Grazing pressure-induced shift in planktonic bacterial communities with the dominance of acIII-A1 actinobacterial lineage in soda pans. Scientific Reports, 2020, 10, 19871.	3.3	12
21	Evaluating the combined effect of biochar and PGPR inoculants on the bacterial community in acidic sandy soil. Applied Soil Ecology, 2021, 160, 103856.	4.3	12
22	Critical point analysis and biocide treatment in a microbiologically contaminated water purification system of a power plant. SN Applied Sciences, 2019, 1 , 1 .	2.9	9
23	Fertoeibacter niger gen. nov., sp. nov. a novel alkaliphilic bacterium of the family Rhodobacteraceae. International Journal of Systematic and Evolutionary Microbiology, 2019, 71, .	1.7	8
24	Succession and potential role of bacterial communities during <i>Pleurotus ostreatus</i> production. FEMS Microbiology Ecology, 2021, 97, .	2.7	6
25	Genetic Variability ofgagandenvRegions of HIV Type 1 Strains Circulating in Slovenia. AIDS Research and Human Retroviruses, 2006, 22, 109-113.	1.1	5
26	Relationships Between Chemical Defenses of Common Toad (Bufo bufo) Tadpoles and Bacterial Community Structure of their Natural Aquatic Habitat. Journal of Chemical Ecology, 2020, 46, 534-543.	1.8	3
27	Distribution of bacterial single cell parameters and their estimation from turbidity detection times. Food Microbiology, 2022, 104, 103972.	4.2	0