MichaÅ, Kalita

List of Publications by Year in descending order

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ΜΙCHAΔ ΚΛΙΙΤΑ

#	Article	IF	CITATIONS
1	Phylogeny of nodulation genes and symbiotic properties of Genista tinctoria bradyrhizobia. Archives of Microbiology, 2006, 186, 87-97.	2.2	38
2	Phylogeny of Symbiotic Genes and the Symbiotic Properties of Rhizobia Specific to Astragalus glycyphyllos L PLoS ONE, 2015, 10, e0141504.	2.5	30
3	Phenotypic characterization of Astragalus glycyphyllos symbionts and their phylogeny based on the 16S rDNA sequences and RFLP of 16S rRNA gene. Antonie Van Leeuwenhoek, 2014, 105, 1033-1048.	1.7	21
4	Diversity and plant growth promoting properties of rhizobia isolated from root nodules of Ononis arvensis. Antonie Van Leeuwenhoek, 2017, 110, 1087-1103.	1.7	21
5	Host-dependent symbiotic efficiency of Rhizobium leguminosarum bv. trifolii strains isolated from nodules of Trifolium rubens. Antonie Van Leeuwenhoek, 2017, 110, 1729-1744.	1.7	19
6	Molecular phylogeny of Bradyrhizobium bacteria isolated from root nodules of tribe Genisteae plants growing in southeast Poland. Systematic and Applied Microbiology, 2017, 40, 482-491.	2.8	19
7	Phenotypic and Genomic Characteristics of Rhizobia Isolated From Genista tinctoria Root Nodules. Systematic and Applied Microbiology, 2004, 27, 707-715.	2.8	16
8	New taxonomic markers for identification of Rhizobium leguminosarum and discrimination between closely related species. Archives of Microbiology, 2009, 191, 207-219.	2.2	15
9	Genista tinctoria microsymbionts from Poland are new members of Bradyrhizobium japonicum bv. genistearum. Systematic and Applied Microbiology, 2010, 33, 252-259.	2.8	14
10	Insight into the evolutionary history of symbiotic genes of Robinia pseudoacacia rhizobia deriving from Poland and Japan. Archives of Microbiology, 2010, 192, 341-350.	2.2	12
11	Analysis of genetic relationship of Sarothamnus scoparius microsymbionts and Bradyrhizobium sp. by hybridization in microdilution wells. Journal of Bioscience and Bioengineering, 2004, 97, 158-161.	2.2	11
12	Isolation of Cultivable Microorganisms from Polish Notes and Coins. Polish Journal of Microbiology, 2013, 62, 281-286.	1.7	11
13	Phylogenetic Diversity of Rhizobia Associated with Horsegram [Macrotyloma uniflorum (Lam.) Verdc.] Grown in South India Based on gInII, recA and 16S-23S Intergenic Sequence Analyses. Current Microbiology, 2011, 62, 1230-1238.	2.2	9
14	Putative novel Bradyrhizobium and Phyllobacterium species isolated from root nodules of Chamaecytisus ruthenicus. Systematic and Applied Microbiology, 2020, 43, 126056.	2.8	8
15	The ftsA gene as a molecular marker for phylogenetic studies in Bradyrhizobium and identification of Bradyrhizobium japonicum. Journal of Applied Genetics, 2019, 60, 123-126.	1.9	7
16	Root nodules of Genista germanica harbor Bradyrhizobium and Rhizobium bacteria exchanging nodC and nodZ genes. Systematic and Applied Microbiology, 2020, 43, 126026.	2.8	6
17	Genetic diversity of microsymbionts nodulating Trifolium pratense in subpolar and temperate climate regions. Scientific Reports, 2022, 12,	3.3	6
18	Application of the AFLP method to differentiate Genista tinctoria microsymbionts. Journal of General and Applied Microbiology, 2006, 52, 321-328.	0.7	5

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19	Insight into the genomic diversity and relationship of Astragalus glycyphyllos symbionts by RAPD, ERIC-PCR, and AFLP fingerprinting. Journal of Applied Genetics, 2015, 56, 551-554.	1.9	5
20	Numerical analysis of phenotypic properties, genomic fingerprinting, and multilocus sequence analysis of Bradyrhizobium strains isolated from root nodules of Lembotropis nigricans of the tribe Genisteae. Annals of Microbiology, 2019, 69, 1123-1134.	2.6	5
21	Multilocus sequence analysis supports the taxonomic position of Astragalus glycyphyllos symbionts based on DNA–DNA hybridization. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 1906-1912.	1.7	5
22	Protein Profiles from Intact Cells as a Tool in Bifidobacterium Characteristics. Polish Journal of Microbiology, 2012, 61, 305-310.	1.7	1
23	Contamination of the urban environment with excrements of companion animals as an underestimated source of Staphylococcus species posing a threat to public health. Acta Veterinaria Hungarica, 2020, 68, 12-19.	0.5	1