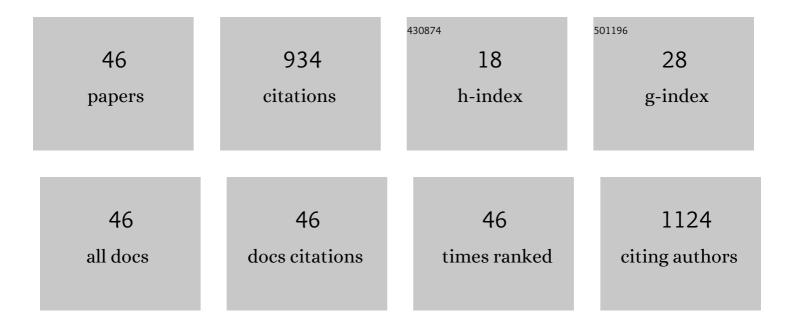
AndrÃ;s TÃ;ncsics

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2838999/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Diversity, activity, antibiotic and heavy metal resistance of bacteria from petroleum hydrocarbon contaminated soils located in Harghita County (Romania). International Biodeterioration and Biodegradation, 2012, 73, 41-49.	3.9	89
2	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
3	Investigation of catechol 2,3-dioxygenase and 16S rRNA gene diversity in hypoxic, petroleum hydrocarbon contaminated groundwater. Systematic and Applied Microbiology, 2010, 33, 398-406.	2.8	51
4	Unexpected Diversity and High Abundance of Putative Nitric Oxide Dismutase (Nod) Genes in Contaminated Aquifers and Wastewater Treatment Systems. Applied and Environmental Microbiology, 2017, 83, .	3.1	51
5	Quantification of Subfamily I.2.C Catechol 2,3-Dioxygenase mRNA Transcripts in Groundwater Samples of an Oxygen-Limited BTEX-Contaminated Site. Environmental Science & Technology, 2012, 46, 232-240.	10.0	40
6	Zoogloea oleivorans sp. nov., a floc-forming, petroleum hydrocarbon-degrading bacterium isolated from biofilm. International Journal of Systematic and Evolutionary Microbiology, 2015, 65, 274-279.	1.7	38
7	Bacterial community changes in TCE biodegradation detected in microcosm experiments. International Biodeterioration and Biodegradation, 2006, 58, 239-247.	3.9	33
8	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
9	Microaerobic conditions caused the overwhelming dominance of Acinetobacter spp. and the marginalization of Rhodococcus spp. in diesel fuel/crude oil mixture-amended enrichment cultures. Archives of Microbiology, 2020, 202, 329-342.	2.2	33
10	The detection and phylogenetic analysis of the alkane 1-monooxygenase gene of members of the genus Rhodococcus. Systematic and Applied Microbiology, 2015, 38, 1-7.	2.8	32
11	Polyphasic analysis of an Azoarcus-Leptothrix-dominated bacterial biofilm developed on stainless steel surface in a gasoline-contaminated hypoxic groundwater. Environmental Science and Pollution Research, 2016, 23, 9019-9035.	5.3	30
12	Effect of oxygen limitation on the enrichment of bacteria degrading either benzene or toluene and the identification of Malikia spinosa (Comamonadaceae) as prominent aerobic benzene-, toluene-, and ethylbenzene-degrading bacterium: enrichment, isolation and whole-genome analysis. Environmental Science and Pollution Research, 2020, 27, 31130-31142.	5.3	27
13	Aflatoxin B1 and Zearalenone-Detoxifying Profile of Rhodococcus Type Strains. Current Microbiology, 2018, 75, 907-917.	2.2	25
14	Aerobic and oxygen-limited enrichment of BTEX-degrading biofilm bacteria: dominance of Malikia versus Acidovorax species. Environmental Science and Pollution Research, 2018, 25, 32178-32195.	5.3	25
15	Stable isotope probing of hypoxic toluene degradation at the Siklós aquifer reveals prominent role of Rhodocyclaceae. FEMS Microbiology Ecology, 2018, 94, .	2.7	24
16	Saccharibacteria as Organic Carbon Sinks in Hydrocarbon-Fueled Communities. Frontiers in Microbiology, 2020, 11, 587782.	3.5	22
17	Transcriptome-Stable Isotope Probing Provides Targeted Functional and Taxonomic Insights Into Microaerobic Pollutant-Degrading Aquifer Microbiota. Frontiers in Microbiology, 2018, 9, 2696.	3.5	20
18	The single-nucleotide primer extension (SNuPE) method for the multiplex detection of various DNA sequences: from detection of point mutations to microbial ecology. Biochemical Society Transactions, 2009, 37, 454-459.	3.4	19

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19	Sphingobium aquiterrae sp. nov., a toluene, meta- and para-xylene-degrading bacterium isolated from petroleum hydrocarbon-contaminated groundwater. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 2807-2812.	1.7	19
20	<i>De Novo</i> Genome Project of Cupriavidus basilensis OR16. Journal of Bacteriology, 2012, 194, 2109-2110.	2.2	18
21	Enrichment of dissimilatory Fe(III)-reducing bacteria from groundwater of the Siklós BTEX-contaminated site (Hungary). Folia Microbiologica, 2017, 62, 63-71.	2.3	18
22	Rhodococcus sovatensis sp. nov., an actinomycete isolated from the hypersaline and heliothermal Lake Ursu. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 190-196.	1.7	18
23	De Novo Genome Project for the Aromatic Degrader Rhodococcus pyridinivorans Strain AK37. Journal of Bacteriology, 2012, 194, 1247-1248.	2.2	16
24	Genome analysis provides insights into microaerobic toluene-degradation pathway of Zoogloea oleivorans BucT. Archives of Microbiology, 2020, 202, 421-426.	2.2	16
25	Siphonobacter aquaeclarae gen. nov., sp. nov., a novel member of the family †Flexibacteraceae', phylum Bacteroidetes. International Journal of Systematic and Evolutionary Microbiology, 2010, 60, 2567-2571.	1.7	16
26	Potential of Variovorax paradoxus isolate BFB1_13 for bioremediation of BTEX contaminated sites. AMB Express, 2021, 11, 126.	3.0	15
27	Evaluation of Single-Nucleotide Primer Extension for Detection and Typing of Phylogenetic Markers Used for Investigation of Microbial Communities. Applied and Environmental Microbiology, 2009, 75, 2850-2860.	3.1	13
28	Availability of Nitrite and Nitrate as Electron Acceptors Modulates Anaerobic Toluene-Degrading Communities in Aquifer Sediments. Frontiers in Microbiology, 2020, 11, 1867.	3.5	13
29	Aerobic and oxygen-limited naphthalene-amended enrichments induced the dominance of Pseudomonas spp. from a groundwater bacterial biofilm. Applied Microbiology and Biotechnology, 2020, 104, 6023-6043.	3.6	13
30	Cloning, Expression and Biochemical Characterization of Endomannanases from Thermobifida Species Isolated from Different Niches. PLoS ONE, 2016, 11, e0155769.	2.5	13
31	Evaluating the aerobic xylene-degrading potential of the intrinsic microbial community of a legacy BTEX-contaminated aquifer by enrichment culturing coupled with multi-omics analysis: uncovering the role of Hydrogenophaga strains in xylene degradation. Environmental Science and Pollution Research, 2022, 29, 28431-28445.	5.3	12
32	Hydrogenophaga aromaticivorans sp. nov., isolated from a para-xylene-degrading enrichment culture, capable of degrading benzene, meta- and para-xylene. International Journal of Systematic and Evolutionary Microbiology, 2019, 71, .	1.7	11
33	Nocardioides carbamazepini sp. nov., an ibuprofen degrader isolated from a biofilm bacterial community enriched on carbamazepine. Systematic and Applied Microbiology, 2022, 45, 126339.	2.8	10
34	Pinisolibacter aquiterrae sp. nov., a novel aromatic hydrocarbon-degrading bacterium isolated from benzene-, and xylene-degrading enrichment cultures, and emended description of the genus Pinisolibacter. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	1.7	9
35	Analysis of biofilm bacterial communities responsible for carbon removal through a reactor cascade treating wastewater. World Journal of Microbiology and Biotechnology, 2014, 30, 977-987.	3.6	8
36	Sphingobacterium pedocola sp. nov. a novel halotolerant bacterium isolated from agricultural soil. Antonie Van Leeuwenhoek, 2021, 114, 1575-1584.	1.7	7

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37	Planktonic and Benthic Bacterial Communities of the Largest Central European Shallow Lake, Lake Balaton and Its Main Inflow Zala River. Current Microbiology, 2020, 77, 4016-4028.	2.2	6
38	Cellvibrio polysaccharolyticus sp. nov., a cellulolytic bacterium isolated from agricultural soil. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	1.7	6
39	Development of a bacterial consortium from Variovorax paradoxus and Pseudomonas veronii isolates applicable in the removal of BTEX. AMB Express, 2022, 12, 4.	3.0	6
40	Flavobacterium hungaricum sp. nov. a novel soil inhabitant, cellulolytic bacterium isolated from plough field. Archives of Microbiology, 2022, 204, 301.	2.2	6
41	Microaerobic enrichment of benzene-degrading bacteria and description of Ideonella benzenivorans sp. nov., capable of degrading benzene, toluene and ethylbenzene under microaerobic conditions. Antonie Van Leeuwenhoek, 2022, 115, 1113-1128.	1.7	6
42	Sphingobacterium hungaricum sp. nov. a novel species on the borderline of the genus Sphingobacterium. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	1.7	5
43	The role of Beta-Proteobacteria in aromatic hydrocarbon degradation: fingerprinting of 16S rRNA gene and catechol 2,3-dioxygenase gene by T-RFLP in BTEX degradative bacterial communities. , 2009, , .		3
44	Editorial: New Insights Into the Biodegradation of Organic Contaminants in Subsurface Ecosystems: Approaches and Achievements of the Multiomics Era. Frontiers in Microbiology, 2021, 12, 650615.	3.5	2
45	Talajmikrobiológiai paraméterek változása szántóként és rétként hasznosÃŧott réti szolonyec talajokban. Agrokemia Es Talajtan, 2019, 68, 155-175.	0.2	2

The Ecology of Microbial Contaminant Degradation in Groundwater. , 2022, , 428-436.