## PrzemysÅ, aw Decewicz

List of Publications by Year in descending order

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687363 642732 33 652 13 23 citations g-index h-index papers 35 35 35 995 docs citations times ranked citing authors all docs

#	Article	IF	Citations
1	Development and validation of novel PCR primers for identification of plasmid-mediated colistin resistance (mcr) genes in various environmental settings. Journal of Hazardous Materials, 2022, 425, 127936.	12.4	5
2	Application of Psychrotolerant Antarctic Bacteria and Their Metabolites as Efficient Plant Growth Promoting Agents. Frontiers in Bioengineering and Biotechnology, 2022, 10, 772891.	4.1	15
3	Marginal lands and fungi – linking the type of soil contamination with fungal community composition. Environmental Microbiology, 2022, 24, 3809-3825.	3.8	2
4	Characterization of Three Novel Virulent Aeromonas Phages Provides Insights into the Diversity of the Autographiviridae Family. Viruses, 2022, 14, 1016.	3.3	3
5	Draft Genome Sequence of Arctic, Heavy Metal-Resistant <i>Agrococcus</i> sp. Strain ARC_14 Isolated from Active Layer of Permafrost from Spitsbergen (Norway). Microbiology Resource Announcements, 2022, , e0022122.	0.6	O
6	Diversity of Biodeteriorative Bacterial and Fungal Consortia in Winter and Summer on Historical Sandstone of the Northern Pergola, Museum of King John III's Palace at Wilanow, Poland. Applied Sciences (Switzerland), 2021, 11, 620.	2.5	10
7	Simple, Reliable, and Time-Efficient Manual Annotation of Bacterial Genomes with MAISEN. Methods in Molecular Biology, 2021, 2242, 221-229.	0.9	3
8	Plasmidome of Listeria spp.â€"The repA-Family Business. International Journal of Molecular Sciences, 2021, 22, 10320.	4.1	7
9	Genome Study of a Novel Virulent Phage vB_SspS_KASIA and Mu-like Prophages of Shewanella sp. M16 Provides Insights into the Genetic Diversity of the Shewanella Virome. International Journal of Molecular Sciences, 2021, 22, 11070.	4.1	2
10	Prototheca-ID: a web-based application for molecular identification of Prototheca species. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	3.0	6
11	Effect of Clinoptilolite and Halloysite Addition on Biogas Production and Microbial Community Structure during Anaerobic Digestion. Materials, 2020, 13, 4127.	2.9	4
12	Identification, Characterization, and Genomic Analysis of Novel Serratia Temperate Phages from a Gold Mine. International Journal of Molecular Sciences, 2020, 21, 6709.	4.1	11
13	Identification and Characterization of the First Virulent Phages, Including a Novel Jumbo Virus, Infecting Ochrobactrum spp International Journal of Molecular Sciences, 2020, 21, 2096.	4.1	3
14	Characterization of a Unique Bordetella bronchiseptica vB_BbrP_BB8 Bacteriophage and Its Application as an Antibacterial Agent. International Journal of Molecular Sciences, 2020, 21, 1403.	4.1	16
15	Global phylogeography and ancient evolution of the widespread human gut virus crAssphage. Nature Microbiology, 2019, 4, 1727-1736.	13.3	184
16	Genome-Wide and Functional View of Proteolytic and Lipolytic Bacteria for Efficient Biogas Production through Enhanced Sewage Sludge Hydrolysis. Molecules, 2019, 24, 2624.	3.8	8
17	Phenotypic plasticity of Escherichia coli upon exposure to physical stress induced by ZnO nanorods. Scientific Reports, 2019, 9, 8575.	3.3	19
18	Characterization of the virome of Paracoccus spp. (Alphaproteobacteria) by combined in silico and in vivo approaches. Scientific Reports, 2019, 9, 7899.	3.3	17

#	Article	IF	CITATIONS
19	Literature-based, manually-curated database of PCR primers for the detection of antibiotic resistance genes in various environments. Water Research, 2019, 161, 211-221.	11.3	15
20	Diversity and Horizontal Transfer of Antarctic Pseudomonas spp. Plasmids. Genes, 2019, 10, 850.	2.4	6
21	Is bacterial microbiome from the Polemonium caeruleum L. (Polemoniaceae) nectar geographically variable?. Acta Societatis Botanicorum Poloniae, 2019, 88, .	0.8	1
22	Application of metagenomic methods for selection of an optimal growth medium for bacterial diversity analysis of microbiocenoses onÂhistorical stone surfaces. International Biodeterioration and Biodegradation, 2018, 131, 2-10.	3.9	20
23	Genome Structure of the Opportunistic Pathogen Paracoccus yeei (Alphaproteobacteria) and Identification of Putative Virulence Factors. Frontiers in Microbiology, 2018, 9, 2553.	3.5	37
24	<i>cytb</i> as a New Genetic Marker for Differentiation of Prototheca Species. Journal of Clinical Microbiology, 2018, 56, .	3.9	36
25	Plasmids of Psychrotolerant Polaromonas spp. Isolated From Arctic and Antarctic Glaciers – Diversity and Role in Adaptation to Polar Environments. Frontiers in Microbiology, 2018, 9, 1285.	3.5	38
26	Genome-Guided Characterization of Ochrobactrum sp. POC9 Enhancing Sewage Sludge Utilization—Biotechnological Potential and Biosafety Considerations. International Journal of Environmental Research and Public Health, 2018, 15, 1501.	2.6	17
27	Insight into heavy metal resistome of soil psychrotolerant bacteria originating from King George Island (Antarctica). Polar Biology, 2018, 41, 1319-1333.	1.2	78
28	Molecular characterization of the pA3J1 plasmid from the psychrotolerant Antarctic bacterium Pseudomonas sp. ANT_J3. Plasmid, 2017, 92, 49-56.	1.4	9
29	Genome content, metabolic pathways and biotechnological potential of the psychrophilic Arctic bacterium Psychrobacter sp. DAB_AL43B, a source and a host of novel Psychrobacter -specific vectors. Journal of Biotechnology, 2017, 263, 64-74.	3.8	21
30	Molecular characterization of the pSinB plasmid of the arsenite oxidizing, metallotolerantSinorhizobiumsp. M14 – insight into the heavy metal resistome of sinorhizobial extrachromosomal replicons. FEMS Microbiology Ecology, 2017, 93, fiw215.	2.7	9
31	Analysis of the Genome and Mobilome of a Dissimilatory Arsenate Reducing Aeromonas sp. O23A Reveals Multiple Mechanisms for Heavy Metal Resistance and Metabolism. Frontiers in Microbiology, 2017, 8, 936.	3 <b>.</b> 5	20
32	Characterization of Sinorhizobium sp. LM21 Prophages and Virus-Encoded DNA Methyltransferases in the Light of Comparative Genomic Analyses of the Sinorhizobial Virome. Viruses, 2017, 9, 161.	3.3	16
33	Application of Metagenomic Analyses in Dentistry as a Novel Strategy Enabling Complex Insight into Microbial Diversity of the Oral Cavity. Polish Journal of Microbiology, 2017, 66, 9-15.	1.7	4