

Łukasz Dziewit

List of Publications by Year in descending order

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75
papers

2,035
citations

270111

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h-index

312153

41
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76
all docs

76
docs citations

76
times ranked

2844
citing authors

#	ARTICLE	IF	CITATIONS
1	Monitoring antibiotic resistance genes in wastewater environments: The challenges of filling a gap in the One-Health cycle. <i>Journal of Hazardous Materials</i> , 2022, 424, 127407.	6.5	60
2	Development and validation of novel PCR primers for identification of plasmid-mediated colistin resistance (mcr) genes in various environmental settings. <i>Journal of Hazardous Materials</i> , 2022, 425, 127936.	6.5	5
3	Application of Psychrotolerant Antarctic Bacteria and Their Metabolites as Efficient Plant Growth Promoting Agents. <i>Frontiers in Bioengineering and Biotechnology</i> , 2022, 10, 772891.	2.0	15
4	Marginal lands and fungi – linking the type of soil contamination with fungal community composition. <i>Environmental Microbiology</i> , 2022, 24, 3809-3825.	1.8	2
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). <i>Microbiology Resource Announcements</i> , 2022, , e0022122.	0.3	0
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. <i>Applied Sciences (Switzerland)</i> , 2021, 11, 620.	1.3	10
7	Simple, Reliable, and Time-Efficient Manual Annotation of Bacterial Genomes with MAISEN. <i>Methods in Molecular Biology</i> , 2021, 2242, 221-229.	0.4	3
8	Metaplasmidome-encoded functions of Siberian low-centered polygonal tundra soils. <i>ISME Journal</i> , 2021, 15, 3258-3270.	4.4	2
9	The Bad and the Good – Microorganisms in Cultural Heritage Environments – An Update on Biodeterioration and Biotreatment Approaches. <i>Materials</i> , 2021, 14, 177.	1.3	50
10	Insight Into Ecology, Metabolic Potential, and the Taxonomic Composition of Bacterial Communities in the Periodic Water Pond on King George Island (Antarctica). <i>Frontiers in Microbiology</i> , 2021, 12, 708607.	1.5	2
11	Genome-Based Insights into the Production of Carotenoids by Antarctic Bacteria, <i>Planococcus</i> sp. ANT_H30 and <i>Rhodococcus</i> sp. ANT_H53B. <i>Molecules</i> , 2020, 25, 4357.	1.7	13
12	Effect of Clinoptilolite and Halloysite Addition on Biogas Production and Microbial Community Structure during Anaerobic Digestion. <i>Materials</i> , 2020, 13, 4127.	1.3	4
13	Molecular Characterization and Comparative Genomics of IncQ-3 Plasmids Conferring Resistance to Various Antibiotics Isolated from a Wastewater Treatment Plant in Warsaw (Poland). <i>Antibiotics</i> , 2020, 9, 613.	1.5	8
14	In vivo creation of plasmid pCRT01 and its use for the construction of carotenoid-producing <i>Paracoccus</i> spp. strains that grow efficiently on industrial wastes. <i>Microbial Cell Factories</i> , 2020, 19, 141.	1.9	8
15	Assessment of Bacterial Contamination of Air at the Museum of King John III's Palace at Wilanow (Warsaw, Poland): Selection of an Optimal Growth Medium for Analyzing Airborne Bacteria Diversity. <i>Applied Sciences (Switzerland)</i> , 2020, 10, 7128.	1.3	9
16	Identification and Characterization of the First Virulent Phages, Including a Novel Jumbo Virus, Infecting <i>Ochrobactrum</i> spp.. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2096.	1.8	3
17	Multimodal Approach to Assessment of Fecal Microbiota Donors based on Three Complementary Methods. <i>Journal of Clinical Medicine</i> , 2020, 9, 2036.	1.0	2
18	Global phylogeography and ancient evolution of the widespread human gut virus crAssphage. <i>Nature Microbiology</i> , 2019, 4, 1727-1736.	5.9	184

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19	Genome-Wide and Functional View of Proteolytic and Lipolytic Bacteria for Efficient Biogas Production through Enhanced Sewage Sludge Hydrolysis. <i>Molecules</i> , 2019, 24, 2624.	1.7	8
20	Phenotypic plasticity of <i>Escherichia coli</i> upon exposure to physical stress induced by ZnO nanorods. <i>Scientific Reports</i> , 2019, 9, 8575.	1.6	19
21	Characterization of the virome of <i>Paracoccus</i> spp. (Alphaproteobacteria) by combined in silico and in vivo approaches. <i>Scientific Reports</i> , 2019, 9, 7899.	1.6	17
22	Literature-based, manually-curated database of PCR primers for the detection of antibiotic resistance genes in various environments. <i>Water Research</i> , 2019, 161, 211-221.	5.3	15
23	Benefits and Drawbacks of Harboring Plasmid pP32BP2, Identified in Arctic Psychrophilic Bacterium <i>Psychrobacter</i> sp. DAB_AL32B. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2015.	1.8	3
24	Diversity and Horizontal Transfer of Antarctic <i>Pseudomonas</i> spp. Plasmids. <i>Genes</i> , 2019, 10, 850.	1.0	6
25	Exploring the genome of Arctic <i>Psychrobacter</i> sp. DAB_AL32B and construction of novel <i>Psychrobacter</i> -specific cloning vectors of an increased carrying capacity. <i>Archives of Microbiology</i> , 2019, 201, 559-569.	1.0	6
26	Is bacterial microbiome from the <i>Polemonium caeruleum</i> L. (Polemoniaceae) nectar geographically variable?. <i>Acta Societatis Botanicorum Poloniae</i> , 2019, 88, .	0.8	1
27	Application of metagenomic methods for selection of an optimal growth medium for bacterial diversity analysis of microbiocenoses on historical stone surfaces. <i>International Biodeterioration and Biodegradation</i> , 2018, 131, 2-10.	1.9	20
28	Harnessing Rhizobia to Improve Heavy-Metal Phytoremediation by Legumes. <i>Genes</i> , 2018, 9, 542.	1.0	72
29	Insight Into the Diversity and Possible Role of Plasmids in the Adaptation of Psychrotolerant and Metalotolerant <i>Arthrobacter</i> spp. to Extreme Antarctic Environments. <i>Frontiers in Microbiology</i> , 2018, 9, 3144.	1.5	35
30	Plasmids of Psychrotolerant <i>Polaromonas</i> spp. Isolated From Arctic and Antarctic Glaciers – Diversity and Role in Adaptation to Polar Environments. <i>Frontiers in Microbiology</i> , 2018, 9, 1285.	1.5	38
31	Genome-Guided Characterization of <i>Ochrobactrum</i> sp. POC9 Enhancing Sewage Sludge Utilization – Biotechnological Potential and Biosafety Considerations. <i>International Journal of Environmental Research and Public Health</i> , 2018, 15, 1501.	1.2	17
32	Insight into heavy metal resistome of soil psychrotolerant bacteria originating from King George Island (Antarctica). <i>Polar Biology</i> , 2018, 41, 1319-1333.	0.5	78
33	Genomic and Biotechnological Characterization of the Heavy-Metal Resistant, Arsenic-Oxidizing Bacterium <i>Ensifer</i> sp. M14. <i>Genes</i> , 2018, 9, 379.	1.0	25
34	Description of <i>Candidatus</i> <i>Bartonella fadhilae</i> n. sp. and <i>Candidatus</i> <i>Bartonella sanaae</i> n. sp. (<i>Bartonellaceae</i>) from <i>Dipodillus dasyurus</i> and <i>Sekeetamys calurus</i> (<i>Gerbillinae</i>) from the Sinai Massif (Egypt). <i>Vector-Borne and Zoonotic Diseases</i> , 2017, 17, 483-494.	0.6	21
35	Molecular characterization of the pA3J1 plasmid from the psychrotolerant Antarctic bacterium <i>Pseudomonas</i> sp. ANT_J3. <i>Plasmid</i> , 2017, 92, 49-56.	0.4	9
36	Biostimulation and bioaugmentation of microbial community involved in the biogas production of sewage sludge. <i>Journal of Biotechnology</i> , 2017, 256, S41-S42.	1.9	0

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37	Lifestyleâ€determining extrachromosomal replicon pAMV1 and its contribution to the carbon metabolism of the methylotrophic bacterium <i>Paracoccus aminovorans</i> JCM 7685. <i>Environmental Microbiology</i> , 2017, 19, 4536-4550.	1.8	40
38	Genome content, metabolic pathways and biotechnological potential of the psychrophilic Arctic bacterium <i>Psychrobacter</i> sp. DAB_AL43B, a source and a host of novel <i>Psychrobacter</i> -specific vectors. <i>Journal of Biotechnology</i> , 2017, 263, 64-74.	1.9	21
39	Molecular characterization of the pSinB plasmid of the arsenite oxidizing, metallotolerant <i>Sinorhizobium</i> sp. M14 â€“ insight into the heavy metal resistome of sinorhizobial extrachromosomal replicons. <i>FEMS Microbiology Ecology</i> , 2017, 93, fiw215.	1.3	9
40	Genome-based insights into the resistome and mobilome of multidrug-resistant <i>Aeromonas</i> sp. ARM81 isolated from wastewater. <i>Archives of Microbiology</i> , 2017, 199, 177-183.	1.0	15
41	Analysis of the Genome and Mobilome of a Dissimilatory Arsenate Reducing <i>Aeromonas</i> sp. O23A Reveals Multiple Mechanisms for Heavy Metal Resistance and Metabolism. <i>Frontiers in Microbiology</i> , 2017, 8, 936.	1.5	20
42	Characterization of <i>Sinorhizobium</i> sp. LM21 Prophages and Virus-Encoded DNA Methyltransferases in the Light of Comparative Genomic Analyses of the Sinorhizobial Virome. <i>Viruses</i> , 2017, 9, 161.	1.5	16
43	Application of Metagenomic Analyses in Dentistry as a Novel Strategy Enabling Complex Insight into Microbial Diversity of the Oral Cavity. <i>Polish Journal of Microbiology</i> , 2017, 66, 9-15.	0.6	4
44	Periapical abscess â€“ etiology, pathogenesis and epidemiology. <i>Przegląd Epidemiologiczny</i> , 2017, 71, 417-428.	0.4	1
45	Metabolic modelling reveals the specialization of secondary replicons for niche adaptation in <i>Sinorhizobium meliloti</i> . <i>Nature Communications</i> , 2016, 7, 12219.	5.8	85
46	Identification of miniature plasmids in psychrophilic Arctic bacteria of the genus <i>Variovorax</i> . <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw043.	1.3	24
47	Two novel temperate bacteriophages co-existing in <i>Aeromonas</i> sp. ARM81 â€“ characterization of their genomes, proteomes and DNA methyltransferases. <i>Journal of General Virology</i> , 2016, 97, 2008-2022.	1.3	14
48	Two Inducible Prophages of an Antarctic <i>Pseudomonas</i> sp. ANT_H14 Use the Same Capsid for Packaging Their Genomes â€“ Characterization of a Novel Phage Helper-Satellite System. <i>PLoS ONE</i> , 2016, 11, e0158889.	1.1	11
49	Heavy Metals Resistance, Metabolism and Transformation: Genomic, Metagenomic and Metatranscriptomic Studies. , 2016, , 13-26.		3
50	Identification and Characterization of Putative Integron-Like Elements of the Heavy-Metal-Hypertolerant Strains of <i>Pseudomonas</i> spp.. <i>Journal of Microbiology and Biotechnology</i> , 2016, 26, 1983-1992.	0.9	1
51	Diversity of the Epsilonproteobacteria Dsb (disulfide bond) systems. <i>Frontiers in Microbiology</i> , 2015, 6, 570.	1.5	17
52	Novel molecular markers for the detection of methanogens and phylogenetic analyses of methanogenic communities. <i>Frontiers in Microbiology</i> , 2015, 6, 694.	1.5	31
53	Genome-guided insight into the methylotrophy of <i>Paracoccus aminophilus</i> JCM 7686. <i>Frontiers in Microbiology</i> , 2015, 6, 852.	1.5	44
54	Diversity and Global Distribution of IncL/M Plasmids Enabling Horizontal Dissemination of β -Lactam Resistance Genes among the Enterobacteriaceae. <i>BioMed Research International</i> , 2015, 2015, 1-12.	0.9	31

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55	Diversity and role of plasmids in adaptation of bacteria inhabiting the Lubin copper mine in Poland, an environment rich in heavy metals. <i>Frontiers in Microbiology</i> , 2015, 6, 152.	1.5	83
56	Maintenance and genetic load of plasmid pKON1 of <i>Paracoccus kondratievae</i> , containing a highly efficient toxin-antitoxin module of the hipAB family. <i>Plasmid</i> , 2015, 80, 45-53.	0.4	13
57	Comparative Analyses of Extrachromosomal Bacterial Replicons, Identification of Chromids, and Experimental Evaluation of Their Indispensability. <i>Methods in Molecular Biology</i> , 2015, 1231, 15-29.	0.4	7
58	Plasmids of psychrophilic and psychrotolerant bacteria and their role in adaptation to cold environments. <i>Frontiers in Microbiology</i> , 2014, 5, 596.	1.5	61
59	Architecture and functions of a multipartite genome of the methylotrophic bacterium <i>Paracoccus aminophilus</i> JCM 7686, containing primary and secondary chromids. <i>BMC Genomics</i> , 2014, 15, 124.	1.2	51
60	Molecular Characterization of a Novel Temperate <i>Sinorhizobium</i> Bacteriophage, Φ LM21, Encoding DNA Methyltransferase with CcrM-Like Specificity. <i>Journal of Virology</i> , 2014, 88, 13111-13124.	1.5	32
61	Nanostructured silver-gold bimetallic SERS substrates for selective identification of bacteria in human blood. <i>Analyst</i> , 2014, 139, 1037.	1.7	110
62	Screening for Streptomycin Resistance-Confering Mutations in <i>Mycobacterium tuberculosis</i> Clinical Isolates from Poland. <i>PLoS ONE</i> , 2014, 9, e100078.	1.1	68
63	Structural and functional genomics of plasmid pSinA of <i>Sinorhizobium</i> sp. M14 encoding genes for the arsenite oxidation and arsenic resistance. <i>Journal of Biotechnology</i> , 2013, 164, 479-488.	1.9	40
64	Characterization of <i>Halomonas</i> sp. ZM3 isolated from the Zelazny Most post-flotation waste reservoir, with a special focus on its mobile DNA. <i>BMC Microbiology</i> , 2013, 13, 59.	1.3	49
65	Plasmid diversity in arctic strains of <i>Psychrobacter</i> spp.. <i>Extremophiles</i> , 2013, 17, 433-444.	0.9	38
66	Sequence determination and analysis of three plasmids of <i>Pseudomonas</i> sp. GLE121, a psychrophile isolated from surface ice of Ecology Glacier (Antarctica). <i>Plasmid</i> , 2013, 70, 254-262.	0.4	24
67	Plasmids of Carotenoid-Producing <i>Paracoccus</i> spp. (Alphaproteobacteria) - Structure, Diversity and Evolution. <i>PLoS ONE</i> , 2013, 8, e80258.	1.1	24
68	Plasmid pP62BP1 isolated from an Arctic <i>Psychrobacter</i> sp. strain carries two highly homologous type II restriction-modification systems and a putative organic sulfate metabolism operon. <i>Extremophiles</i> , 2012, 16, 363-376.	0.9	8
69	Insights into the Transposable Mobilome of <i>Paracoccus</i> spp. (Alphaproteobacteria). <i>PLoS ONE</i> , 2012, 7, e32277.	1.1	42
70	DIY series of genetic cassettes useful in construction of versatile vectors specific for Alphaproteobacteria. <i>Journal of Microbiological Methods</i> , 2011, 86, 166-174.	0.7	24
71	Functional characterization of the type II Pml restriction-modification system derived from plasmid pAMI7 of <i>Paracoccus aminophilus</i> JCM 7686. <i>FEMS Microbiology Letters</i> , 2011, 324, 56-63.	0.7	23
72	Plasmid pAMI2 of <i>Paracoccus aminophilus</i> JCM 7686 Carries , , -Dimethylformamide Degradation-Related Genes Whose Expression Is Activated by a LuxR Family Regulator. <i>Applied and Environmental Microbiology</i> , 2010, 76, 1861-1869.	1.4	48

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73	Transposable Modules Generated by a Single Copy of Insertion Sequence IS <i>Pme1</i> and Their Influence on Structure and Evolution of Natural Plasmids of <i>Paracoccus methylutens</i> DM12. Journal of Bacteriology, 2008, 190, 3306-3313.	1.0	25
74	The SXT Conjugative Element and Linear Prophage N15 Encode Toxin-Antitoxin-Stabilizing Systems Homologous to the tad-ata Module of the Paracoccus aminophilus Plasmid pAMI2. Journal of Bacteriology, 2007, 189, 1983-1997.	1.0	96
75	Fresh Versus Frozen Stool for Fecal Microbiota Transplantation—Assessment by Multimethod Approach Combining Culturing, Flow Cytometry, and Next-Generation Sequencing. Frontiers in Microbiology, 0, 13, .	1.5	6