List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Global phylogeography and ancient evolution of the widespread human gut virus crAssphage. Nature Microbiology, 2019, 4, 1727-1736.	13.3	184
2	Nanostructured silver–gold bimetallic SERS substrates for selective identification of bacteria in human blood. Analyst, The, 2014, 139, 1037.	3.5	110
3	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.	2.2	96
4	Metabolic modelling reveals the specialization of secondary replicons for niche adaptation in Sinorhizobium meliloti. Nature Communications, 2016, 7, 12219.	12.8	85
5	Diversity and role of plasmids in adaptation of bacteria inhabiting the Lubin copper mine in Poland, an environment rich in heavy metals. Frontiers in Microbiology, 2015, 6, 152.	3.5	83
6	Insight into heavy metal resistome of soil psychrotolerant bacteria originating from King George Island (Antarctica). Polar Biology, 2018, 41, 1319-1333.	1.2	78
7	Harnessing Rhizobia to Improve Heavy-Metal Phytoremediation by Legumes. Genes, 2018, 9, 542.	2.4	72
8	Screening for Streptomycin Resistance-Conferring Mutations in Mycobacterium tuberculosis Clinical Isolates from Poland. PLoS ONE, 2014, 9, e100078.	2.5	68
9	Plasmids of psychrophilic and psychrotolerant bacteria and their role in adaptation to cold environments. Frontiers in Microbiology, 2014, 5, 596.	3.5	61
10	Monitoring antibiotic resistance genes in wastewater environments: The challenges of filling a gap in the One-Health cycle. Journal of Hazardous Materials, 2022, 424, 127407.	12.4	60
11	Architecture and functions of a multipartite genome of the methylotrophic bacterium Paracoccus aminophilus JCM 7686, containing primary and secondary chromids. BMC Genomics, 2014, 15, 124.	2.8	51
12	The Bad and the Good—Microorganisms in Cultural Heritage Environments—An Update on Biodeterioration and Biotreatment Approaches. Materials, 2021, 14, 177.	2.9	50
13	Characterization of Halomonassp. ZM3 isolated from the Zelazny Most post-flotation waste reservoir, with a special focus on its mobile DNA. BMC Microbiology, 2013, 13, 59.	3.3	49
14	Plasmid pAMI2 of <i>Paracoccus aminophilus</i> JCM 7686 Carries <i>N</i> , <i>N</i> -Dimethylformamide Degradation-Related Genes Whose Expression Is Activated by a LuxR Family Regulator. Applied and Environmental Microbiology, 2010, 76, 1861-1869.	3.1	48
15	Genome-guided insight into the methylotrophy of Paracoccus aminophilus JCM 7686. Frontiers in Microbiology, 2015, 6, 852.	3.5	44
16	Insights into the Transposable Mobilome of Paracoccus spp. (Alphaproteobacteria). PLoS ONE, 2012, 7, e32277.	2.5	42
17	Structural and functional genomics of plasmid pSinA of Sinorhizobium sp. M14 encoding genes for the arsenite oxidation and arsenic resistance. Journal of Biotechnology, 2013, 164, 479-488.	3.8	40
18	Lifestyleâ€determining extrachromosomal replicon pAMV1 and its contribution to the carbon metabolism of the methylotrophic bacterium <i>Paracoccus aminovorans</i> JCM 7685. Environmental Microbiology, 2017, 19, 4536-4550.	3.8	40

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19	Plasmid diversity in arctic strains of Psychrobacter spp Extremophiles, 2013, 17, 433-444.	2.3	38
20	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
21	Insight Into the Diversity and Possible Role of Plasmids in the Adaptation of Psychrotolerant and Metalotolerant Arthrobacter spp. to Extreme Antarctic Environments. Frontiers in Microbiology, 2018, 9, 3144.	3.5	35
22	Molecular Characterization of a Novel Temperate Sinorhizobium Bacteriophage, ФM21, Encoding DNA Methyltransferase with CcrM-Like Specificity. Journal of Virology, 2014, 88, 13111-13124.	3.4	32
23	Novel molecular markers for the detection of methanogens and phylogenetic analyses of methanogenic communities. Frontiers in Microbiology, 2015, 6, 694.	3.5	31
24	Diversity and Global Distribution of IncL/M Plasmids Enabling Horizontal Dissemination of <i>¹/₂</i> -Lactam Resistance Genes among the Enterobacteriaceae. BioMed Research International, 2015, 2015, 1-12.	1.9	31
25	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.	2.2	25
26	Genomic and Biotechnological Characterization of the Heavy-Metal Resistant, Arsenic-Oxidizing Bacterium Ensifer sp. M14. Genes, 2018, 9, 379.	2.4	25
27	DIY series of genetic cassettes useful in construction of versatile vectors specific for Alphaproteobacteria. Journal of Microbiological Methods, 2011, 86, 166-174.	1.6	24
28	Sequence determination and analysis of three plasmids of Pseudomonas sp. GLE121, a psychrophile isolated from surface ice of Ecology Glacier (Antarctica). Plasmid, 2013, 70, 254-262.	1.4	24
29	Identification of miniature plasmids in psychrophilic Arctic bacteria of the genus <i>Variovorax</i> . FEMS Microbiology Ecology, 2016, 92, fiw043.	2.7	24
30	Plasmids of Carotenoid-Producing Paracoccus spp. (Alphaproteobacteria) - Structure, Diversity and Evolution. PLoS ONE, 2013, 8, e80258.	2.5	24
31	Functional characterization of the type II PamI restriction-modification system derived from plasmid pAMI7 of Paracoccus aminophilusJCM 7686. FEMS Microbiology Letters, 2011, 324, 56-63.	1.8	23
32	Description of <i>Candidatus</i> Bartonella fadhilae n. sp. and <i>Candidatus</i> Bartonella sanaae n. sp. (<i>Bartonellaceae</i>) from <i>Dipodillus dasyurus</i> and <i>Sekeetamys calurus</i> (<i>Gerbillinae)</i> from the Sinai Massif (Egypt). Vector-Borne and Zoonotic Diseases, 2017, 17 483-494	1.5	21
33	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
34	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.	3.5	20
35	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
36	Phenotypic plasticity of Escherichia coli upon exposure to physical stress induced by ZnO nanorods. Scientific Reports, 2019, 9, 8575.	3.3	19

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37	Diversity of the Epsilonproteobacteria Dsb (disulfide bond) systems. Frontiers in Microbiology, 2015, 6, 570.	3.5	17
38	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
39	Characterization of the virome of Paracoccus spp. (Alphaproteobacteria) by combined in silico and in vivo approaches. Scientific Reports, 2019, 9, 7899.	3.3	17
40	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
41	Genome-based insights into the resistome and mobilome of multidrug-resistant Aeromonas sp. ARM81 isolated from wastewater. Archives of Microbiology, 2017, 199, 177-183.	2.2	15
42	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
43	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
44	Two novel temperate bacteriophages co-existing in Aeromonas sp. ARM81 – characterization of their genomes, proteomes and DNA methyltransferases. Journal of General Virology, 2016, 97, 2008-2022.	2.9	14
45	Maintenance and genetic load of plasmid pKON1 of Paracoccus kondratievae, containing a highly efficient toxin–antitoxin module of the hipAB family. Plasmid, 2015, 80, 45-53.	1.4	13
46	Genome-Based Insights into the Production of Carotenoids by Antarctic Bacteria, Planococcus sp. ANT_H30 and Rhodococcus sp. ANT_H53B. Molecules, 2020, 25, 4357.	3.8	13
47	Two Inducible Prophages of an Antarctic Pseudomonas sp. ANT_H14 Use the Same Capsid for Packaging Their Genomes – Characterization of a Novel Phage Helper-Satellite System. PLoS ONE, 2016, 11, e0158889.	2.5	11
48	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
49	Molecular characterization of the pA3J1 plasmid from the psychrotolerant Antarctic bacterium Pseudomonas sp. ANT_J3. Plasmid, 2017, 92, 49-56.	1.4	9
50	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
51	Assessment of Bacterial Contamination of Air at the Museum of King John Ill's Palace at Wilanow (Warsaw, Poland): Selection of an Optimal Growth Medium for Analyzing Airborne Bacteria Diversity. Applied Sciences (Switzerland), 2020, 10, 7128.	2.5	9
52	Plasmid pP62BP1 isolated from an Arctic Psychrobacter sp. strain carries two highly homologous type Il restriction-modification systems and a putative organic sulfate metabolism operon. Extremophiles, 2012, 16, 363-376.	2.3	8
53	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
54	Molecular Characterization and Comparative Genomics of IncQ-3 Plasmids Conferring Resistance to Various Antibiotics Isolated from a Wastewater Treatment Plant in Warsaw (Poland). Antibiotics, 2020, 9, 613.	3.7	8

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55	In vivo creation of plasmid pCRT01 and its use for the construction of carotenoid-producing Paracoccus spp. strains that grow efficiently on industrial wastes. Microbial Cell Factories, 2020, 19, 141.	4.0	8
56	Comparative Analyses of Extrachromosomal Bacterial Replicons, Identification of Chromids, and Experimental Evaluation of Their Indispensability. Methods in Molecular Biology, 2015, 1231, 15-29.	0.9	7
57	Diversity and Horizontal Transfer of Antarctic Pseudomonas spp. Plasmids. Genes, 2019, 10, 850.	2.4	6
58	Exploring the genome of Arctic Psychrobacter sp. DAB_AL32B and construction of novel Psychrobacter-specific cloning vectors of an increased carrying capacity. Archives of Microbiology, 2019, 201, 559-569.	2.2	6
59	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, .	3.5	6
60	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
61	Effect of Clinoptilolite and Halloysite Addition on Biogas Production and Microbial Community Structure during Anaerobic Digestion. Materials, 2020, 13, 4127.	2.9	4
62	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
63	Benefits and Drawbacks of Harboring Plasmid pP32BP2, Identified in Arctic Psychrophilic Bacterium Psychrobacter sp. DAB_AL32B. International Journal of Molecular Sciences, 2019, 20, 2015.	4.1	3
64	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
65	Simple, Reliable, and Time-Efficient Manual Annotation of Bacterial Genomes with MAISEN. Methods in Molecular Biology, 2021, 2242, 221-229.	0.9	3
66	Heavy Metals Resistance, Metabolism and Transformation: Genomic, Metagenomic and Metatranscriptomic Studies. , 2016, , 13-26.		3
67	Multimodal Approach to Assessment of Fecal Microbiota Donors based on Three Complementary Methods. Journal of Clinical Medicine, 2020, 9, 2036.	2.4	2
68	Metaplasmidome-encoded functions of Siberian low-centered polygonal tundra soils. ISME Journal, 2021, 15, 3258-3270.	9.8	2
69	Insight Into Ecology, Metabolic Potential, and the Taxonomic Composition of Bacterial Communities in the Periodic Water Pond on King George Island (Antarctica). Frontiers in Microbiology, 2021, 12, 708607.	3.5	2
70	Marginal lands and fungi – linking the type of soil contamination with fungal community composition. Environmental Microbiology, 2022, 24, 3809-3825.	3.8	2
71	Identification and Characterization of Putative Integron-Like Elements of the Heavy-Metal-Hypertolerant Strains of Pseudomonas spp Journal of Microbiology and Biotechnology, 2016, 26, 1983-1992.	2.1	1
72	Is bacterial microbiome from the Polemonium caeruleum L. (Polemoniaceae) nectar geographically variable?. Acta Societatis Botanicorum Poloniae, 2019, 88, .	0.8	1

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73	Periapical abscess – etiology, pathogenesis and epidemiology. Przeglad Epidemiologiczny, 2017, 71, 417-428.	0.2	1
74	Biostimulation and bioaugmentation of microbial community involved in the biogas production of sewage sludge. Journal of Biotechnology, 2017, 256, S41-S42.	3.8	0
75	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	0