

A complete domain-to-species taxonomy for Bacteria and

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Defining Genomic and Predicted Metabolic Features of the <i>Acetobacterium</i> Genus. <i>MSystems</i> , 2020, 5, .	1.7	11
2	The Gut Virome Database Reveals Age-Dependent Patterns of Virome Diversity in the Human Gut. <i>Cell Host and Microbe</i> , 2020, 28, 724-740.e8.	5.1	352
3	Genomic analysis of <i>Caldalkalibacillus thermarum</i> TA2.A1 reveals aerobic alkaliphilic metabolism and evolutionary hallmarks linking alkaliphilic bacteria and plant life. <i>Extremophiles</i> , 2020, 24, 923-935.	0.9	10
4	New viral biogeochemical roles revealed through metagenomic analysis of Lake Baikal. <i>Microbiome</i> , 2020, 8, 163.	4.9	43
5	Should Networks Supplant Tree Building?. <i>Microorganisms</i> , 2020, 8, 1179.	1.6	7
6	Genome-Wide Identification and Functional Characterization of Î ² -Agarases in <i>Vibrio astriarenae</i> Strain HN897. <i>Frontiers in Microbiology</i> , 2020, 11, 1404.	1.5	10
7	Catabolism and interactions of uncultured organisms shaped by eco-thermodynamics in methanogenic bioprocesses. <i>Microbiome</i> , 2020, 8, 111.	4.9	48
8	Uncovering the genomic potential of the Amazon River microbiome to degrade rainforest organic matter. <i>Microbiome</i> , 2020, 8, 151.	4.9	18
9	Genome-based Taxonomy for Bacteria: A Recent Advance. <i>Trends in Microbiology</i> , 2020, 28, 871-874.	3.5	16
10	Genomics Reveals the Metabolic Potential and Functions in the Redistribution of Dissolved Organic Matter in Marine Environments of the Genus <i>Thalassotalea</i> . <i>Microorganisms</i> , 2020, 8, 1412.	1.6	4
11	910 metagenome-assembled genomes from the phytobiomes of three urban-farmed leafy Asian greens. <i>Scientific Data</i> , 2020, 7, 278.	2.4	17
12	Characterization of Metagenome-Assembled Genomes and Carbohydrate-Degrading Genes in the Gut Microbiota of Tibetan Pig. <i>Frontiers in Microbiology</i> , 2020, 11, 595066.	1.5	34
13	Unlocking the Genomic Taxonomy of the <i>Prochlorococcus</i> Collective. <i>Microbial Ecology</i> , 2020, 80, 546-558.	1.4	12
14	Taxonomy of Bacteria and Archaea. <i>Nature Methods</i> , 2020, 17, 562-562.	9.0	1
15	Host Immune Response and Novel Diagnostic Approach to NTM Infections. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4351.	1.8	24
16	Roadmap for naming uncultivated Archaea and Bacteria. <i>Nature Microbiology</i> , 2020, 5, 987-994.	5.9	115
17	LEMMI: a continuous benchmarking platform for metagenomics classifiers. <i>Genome Research</i> , 2020, 30, 1208-1216.	2.4	11
18	Genomes OnLine Database (GOLD) v.8: overview and updates. <i>Nucleic Acids Research</i> , 2021, 49, D723-D733.	6.5	143

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19	The need to innovate sample collection and library generation in microbial drug discovery: a focus on academia. <i>Natural Product Reports</i> , 2021, 38, 292-300.	5.2	16
20	BiG-FAM: the biosynthetic gene cluster families database. <i>Nucleic Acids Research</i> , 2021, 49, D490-D497.	6.5	122
21	Evidence for non- ϵ -methanogenic metabolisms in globally distributed archaeal clades basal to the <i>Methanomassiliicoccales</i> . <i>Environmental Microbiology</i> , 2021, 23, 340-357.	1.8	19
22	Exploring Marine Planktonic Archaea: Then and Now. <i>Frontiers in Microbiology</i> , 2020, 11, 616086.	1.5	11
23	The Next Million Names for Archaea and Bacteria. <i>Trends in Microbiology</i> , 2021, 29, 289-298.	3.5	39
24	Multi-omics data integration considerations and study design for biological systems and disease. <i>Molecular Omics</i> , 2021, 17, 170-185.	1.4	85
25	Complete Genome Sequence of <i>Francisella</i> sp. Strain LA11-2445 (FDC406), a Novel <i>Francisella</i> Species Isolated from a Human Skin Lesion. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	0
27	Complex History of Aerobic Respiration and Phototrophy in the <i>Chloroflexota</i> Class <i>Anaerolineae</i> Revealed by High-Quality Draft Genome of <i>Ca. Rosellinea mizusawaensis</i> AA3_104. <i>Microbes and Environments</i> , 2021, 36, n/a.	0.7	5
28	Identification and classification of antiviral defence systems in bacteria and archaea with PADLOC reveals new system types. <i>Nucleic Acids Research</i> , 2021, 49, 10868-10878.	6.5	92
29	The <i>Thermosynechococcus</i> Genus: Wide Environmental Distribution, but a Highly Conserved Genomic Core. <i>Microbes and Environments</i> , 2021, 36, n/a.	0.7	5
30	Defining the <i>Rhizobium leguminosarum</i> Species Complex. <i>Genes</i> , 2021, 12, 111.	1.0	48
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35	Balrog: A universal protein model for prokaryotic gene prediction. <i>PLoS Computational Biology</i> , 2021, 17, e1008727.	1.5	21
37	Quantifying the taxonomic bias in enzymology. <i>Protein Science</i> , 2021, 30, 914-921.	3.1	5
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43	Archaeal tyrosine recombinases. <i>FEMS Microbiology Reviews</i> , 2021, 45, .	3.9	5
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47	Anthropogenic and Environmental Constraints on the Microbial Methane Cycle in Coastal Sediments. <i>Frontiers in Microbiology</i> , 2021, 12, 631621.	1.5	62
48	Deep sea sediments associated with cold seeps are a subsurface reservoir of viral diversity. <i>ISME Journal</i> , 2021, 15, 2366-2378.	4.4	93
50	Rainfall Alters Permafrost Soil Redox Conditions, but Meta-Omics Show Divergent Microbial Community Responses by Tundra Type in the Arctic. <i>Soil Systems</i> , 2021, 5, 17.	1.0	5
54	Complete genomes derived by directly sequencing freshwater bloom populations emphasize the significance of the genus level ADA clade within the Nostocales. <i>Harmful Algae</i> , 2021, 103, 102005.	2.2	12
55	Estimating maximal microbial growth rates from cultures, metagenomes, and single cells via codon usage patterns. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	130
56	Recovery of complete genomes and non-chromosomal replicons from activated sludge enrichment microbial communities with long read metagenome sequencing. <i>Npj Biofilms and Microbiomes</i> , 2021, 7, 23.	2.9	29
57	Understanding the metabolome and metagenome as extended phenotypes: The next frontier in macroalgae domestication and improvement. <i>Journal of the World Aquaculture Society</i> , 2021, 52, 1009-1030.	1.2	6
59	DIAMOND+MEGAN: Fast and Easy Taxonomic and Functional Analysis of Short and Long Microbiome Sequences. <i>Current Protocols</i> , 2021, 1, e59.	1.3	55
60	Fast and sensitive taxonomic assignment to metagenomic contigs. <i>Bioinformatics</i> , 2021, 37, 3029-3031.	1.8	110
61	Genome-resolved metagenomics using environmental and clinical samples. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	18
62	Isolation and Characterization of Strain <i>Exiguobacterium</i> sp. KRL4, a Producer of Bioactive Secondary Metabolites from a Tibetan Glacier. <i>Microorganisms</i> , 2021, 9, 890.	1.6	5
64	Recent advances in culture-based gut microbiome research. <i>International Journal of Medical Microbiology</i> , 2021, 311, 151485.	1.5	15
65	Fungal taxonomy and sequence-based nomenclature. <i>Nature Microbiology</i> , 2021, 6, 540-548.	5.9	101
66	Reclassification of <i>Catabacter hongkongensis</i> as <i>Christensenella hongkongensis</i> comb. nov. based on whole genome analysis. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	11
68	Evaluation of the Microba Community Profiler for Taxonomic Profiling of Metagenomic Datasets From the Human Gut Microbiome. <i>Frontiers in Microbiology</i> , 2021, 12, 643682.	1.5	25
69	High Diversity and Functional Potential of Undescribed "Acidobacteriota" in Danish Wastewater Treatment Plants. <i>Frontiers in Microbiology</i> , 2021, 12, 643950.	1.5	56
70	Functional genome-centric view of the CO ₂ -driven anaerobic microbiome. <i>ISME Journal</i> , 2021, 15, 2906-2919.	4.4	14

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72	Validation of the COVID-19 Indoor Testâ„¢ by Phylagen for Detection of SARS-CoV-2 Virus on Stainless-Steel Surfaces: AOAC Performance Tested MethodSM 122004. <i>Journal of AOAC INTERNATIONAL</i> , 2021, 104, 948-958.	0.7	0
73	Comparative genomics of the ADA clade within the Nostocales. <i>Harmful Algae</i> , 2021, 104, 102037.	2.2	11
74	Characterizing rumen microbiota and CAZyme profile of Indian dromedary camel (<i>Camelus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 TTS	2.6	25
75	Phylogenetic Distribution of Secondary Metabolites in the <i>Bacillus subtilis</i> Species Complex. <i>MSystems</i> , 2021, 6, .	1.7	39
78	RNase R is associated in a functional complex with the RhpA DEAD-box RNA helicase in <i>Helicobacter pylori</i> . <i>Nucleic Acids Research</i> , 2021, 49, 5249-5264.	6.5	7
79	<i>Dissulfurispira thermophila</i> gen. nov., sp. nov., a thermophilic chemolithoautotroph growing by sulfur disproportionation, and proposal of novel taxa in the phylum Nitrospirota to reclassify the genus <i>Thermodesulfovibrio</i> . <i>Systematic and Applied Microbiology</i> , 2021, 44, 126184.	1.2	48
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85	Prokaryotic taxonomy and nomenclature in the age of big sequence data. <i>ISME Journal</i> , 2021, 15, 1879-1892.	4.4	87
86	Extensive microbial diversity within the chicken gut microbiome revealed by metagenomics and culture. <i>PeerJ</i> , 2021, 9, e10941.	0.9	79
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88	Post-translational flavinylation is associated with diverse extracytosolic redox functionalities throughout bacterial life. <i>ELife</i> , 2021, 10, .	2.8	15
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92	Effect of Differences in the Microbiome of Cyp17a1-Deficient Mice on Atherosclerotic Background. <i>Cells</i> , 2021, 10, 1292.	1.8	3
93	<i>Listeria cossartiae</i> sp. nov., <i>Listeria immobilis</i> sp. nov., <i>Listeria portnoyi</i> sp. nov. and <i>Listeria rustica</i> sp. nov., isolated from agricultural water and natural environments. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	54
94	Effect of Carbon Sources in Carotenoid Production from <i>Haloarcula</i> sp. M1, <i>Halolamina</i> sp. M3 and <i>Halorubrum</i> sp. M5, Halophilic Archaea Isolated from Sonora Saltern, Mexico. <i>Microorganisms</i> , 2021, 9, 1096.	1.6	9
95	Interâ€¦domain horizontal gene transfer of nickelâ€¦binding superoxide dismutase. <i>Geobiology</i> , 2021, 19, 450-459.	1.1	11

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100	ToRQuEMaDA: tool for retrieving queried Eubacteria, metadata and dereplicating assemblies. <i>PeerJ</i> , 2021, 9, e11348.	0.9	5
101	Genomic Analysis of the Yet-Uncultured Binatota Reveals Broad Methylophilic, Alkane-Degradation, and Pigment Production Capacities. <i>MBio</i> , 2021, 12, .	1.8	13
102	<i>Pseudomonas campi</i> sp. nov., a nitrate-reducing bacterium isolated from grassland soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	10
103	Identifying biases and their potential solutions in human microbiome studies. <i>Microbiome</i> , 2021, 9, 113.	4.9	82
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106	Metagenome and analysis of metabolic potential of the microbial community in pit mud used for Chinese strong-flavor liquor production. <i>Food Research International</i> , 2021, 143, 110294.	2.9	33
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124	Protein Family Content Uncovers Lineage Relationships and Bacterial Pathway Maintenance Mechanisms in DPANN Archaea. <i>Frontiers in Microbiology</i> , 2021, 12, 660052.	1.5	20

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127	Soil, senescence and exudate utilisation: characterisation of the Paragon var. spring bread wheat root microbiome. <i>Environmental Microbiomes</i> , 2021, 16, 12.	2.2	19
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130	A global metagenomic map of urban microbiomes and antimicrobial resistance. <i>Cell</i> , 2021, 184, 3376-3393.e17.	13.5	164
131	Benchmarking DNA Extraction Methods for Phylogenomic Analysis of Sub-Antarctic <i>Rhodococcus</i> and <i>Williamsia</i> Species. <i>Microorganisms</i> , 2021, 9, 1253.	1.6	7
133	Characterization and phylogenomic analysis of <i>Breznakiella homolactica</i> gen. nov. sp. nov. indicate that termite gut treponemes evolved from non-acetogenic spirochetes in cockroaches. <i>Environmental Microbiology</i> , 2021, 23, 4228-4245.	1.8	15
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136	Methane-dependent selenate reduction by a bacterial consortium. <i>ISME Journal</i> , 2021, 15, 3683-3692.	4.4	17
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140	Key Technologies for Progressing Discovery of Microbiome-Based Medicines. <i>Frontiers in Microbiology</i> , 2021, 12, 685935.	1.5	13
141	GUNC: detection of chimerism and contamination in prokaryotic genomes. <i>Genome Biology</i> , 2021, 22, 178.	3.8	94
142	Origin of symbiotic gut spirochetes as key players in the nutrition of termites. <i>Environmental Microbiology</i> , 2021, 23, 4092-4097.	1.8	2
143	Mantis: flexible and consensus-driven genome annotation. <i>GigaScience</i> , 2021, 10, .	3.3	22
144	Recent advances in the structural diversity of reaction centers. <i>Photosynthesis Research</i> , 2021, 149, 329-343.	1.6	22
149	<i>Chryseobacterium pennae</i> sp. nov., isolated from poultry feather waste. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	6

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150	Functional diversity of microbial communities in inactive seafloor sulfide deposits. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	16
151	<i>Miltoncostaea marina</i> gen. nov. sp. nov., and <i>Miltoncostaea oceani</i> sp. nov., a novel deep branching phylogenetic lineage within the class <i>Thermoleophilia</i> isolated from marine environments, and proposal of <i>Miltoncostaeaceae</i> fam. nov. and <i>Miltoncostaeales</i> ord. nov. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126216.	1.2	22
152	Reply to: "Re-evaluating the evidence for a universal genetic boundary among microbial species". <i>Nature Communications</i> , 2021, 12, 4060.	5.8	36
153	Metagenomics: a path to understanding the gut microbiome. <i>Mammalian Genome</i> , 2021, 32, 282-296.	1.0	27
154	Metagenome-Assembled Genome Sequences from Different Wastewater Treatment Stages in Germany. <i>Microbiology Resource Announcements</i> , 2021, 10, e0050421.	0.3	6
158	Development of a free radical scavenging bacterial consortium to mitigate oxidative stress in cnidarians. <i>Microbial Biotechnology</i> , 2021, 14, 2025-2040.	2.0	30
159	A genomic surveillance framework and genotyping tool for <i>Klebsiella pneumoniae</i> and its related species complex. <i>Nature Communications</i> , 2021, 12, 4188.	5.8	394
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161	Proposal of <i>Carbonactinosporaceae</i> fam. nov. within the class <i>Actinomycetia</i> . Reclassification of <i>Streptomyces thermoautotrophicus</i> as <i>Carbonactinospira thermoautotrophica</i> gen. nov., comb. nov. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126223.	1.2	20
163	Five Metagenome-Assembled Genomes of the Rare Phylum <i>CSSD10-310</i> from Zodletone Spring (Oklahoma, USA). <i>Microbiology Resource Announcements</i> , 2021, 10, e0041421.	0.3	0
164	Release LTP_12_2020, featuring a new ARB alignment and improved 16S rRNA tree for prokaryotic type strains. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126218.	1.2	44
165	Re-evaluating the evidence for a universal genetic boundary among microbial species. <i>Nature Communications</i> , 2021, 12, 4059.	5.8	35
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167	Archaea Are Rare and Uncommon Members of the Mammalian Skin Microbiome. <i>MSystems</i> , 2021, 6, e0064221.	1.7	7
169	Linking 16S rRNA Gene Classification to <i>amoA</i> Gene Taxonomy Reveals Environmental Distribution of Ammonia-Oxidizing Archaeal Clades in Peatland Soils. <i>MSystems</i> , 2021, 6, e0054621.	1.7	9
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173	Characterizing rhizosphere microbiota of peanut (<i>Arachis hypogaea</i> L.) from pre-sowing to post-harvest of crop under field conditions. <i>Scientific Reports</i> , 2021, 11, 17457.	1.6	10
176	Post-weaning shifts in microbiome composition and metabolism revealed by over 25,000 pig gut metagenome-assembled genomes. <i>Microbial Genomics</i> , 2021, 7, .	1.0	9

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179	Structural determinants and distribution of phosphate specificity in ribonucleotide reductases. <i>Journal of Biological Chemistry</i> , 2021, 297, 101008.	1.6	4
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181	Comparative genomics provides structural and functional insights into <i>Bacteroides</i> RNA biology. <i>Molecular Microbiology</i> , 2022, 117, 67-85.	1.2	5
185	Distribution of Denitrification among Haloarchaea: A Comprehensive Study. <i>Microorganisms</i> , 2021, 9, 1669.	1.6	6
186	Spatial and Temporal Dynamics of Prokaryotic and Viral Community Assemblages in a Lotic System (Manatee Springs, Florida). <i>Applied and Environmental Microbiology</i> , 2021, 87, e0064621.	1.4	10
187	Expanding Archaeal Diversity and Phylogeny: Past, Present, and Future. <i>Annual Review of Microbiology</i> , 2021, 75, 359-381.	2.9	34
188	Characterizing the Uncultivated Microbial Minority: towards Understanding the Roles of the Rare Biosphere in Microbial Communities. <i>MSystems</i> , 2021, 6, e0077321.	1.7	7
189	Recovery of small plasmid sequences via Oxford Nanopore sequencing. <i>Microbial Genomics</i> , 2021, 7, .	1.0	44
192	Living to the High Extreme: Unraveling the Composition, Structure, and Functional Insights of Bacterial Communities Thriving in the Arsenic-Rich Salar de Huasco Altiplanic Ecosystem. <i>Microbiology Spectrum</i> , 2021, 9, e0044421.	1.2	16
193	Tricycler: consensus long-read assemblies for bacterial genomes. <i>Genome Biology</i> , 2021, 22, 266.	3.8	175
194	Genomes of Novel <i>Myxococcota</i> Reveal Severely Curtailed Machineries for Predation and Cellular Differentiation. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0170621.	1.4	28
198	Comparative genomic analysis reveals metabolic flexibility of Woesearchaeota. <i>Nature Communications</i> , 2021, 12, 5281.	5.8	25
199	Identification of FadT as a Novel Quorum Quenching Enzyme for the Degradation of Diffusible Signal Factor in <i>Cupriavidus pinatubonensis</i> Strain HN-2. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9862.	1.8	7
200	The nasal mutualist <i>Dolosigranulum pigrum</i> AMBR11 supports homeostasis via multiple mechanisms. <i>IScience</i> , 2021, 24, 102978.	1.9	15
201	The Hidden Genomic Diversity, Specialized Metabolite Capacity, and Revised Taxonomy of <i>Burkholderia</i> <i>Sensu Lato</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 726847.	1.5	16
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