RefSeq: expanding the Prokaryotic Genome Annotation model curation

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Citation Report

#	Article	IF	CITATIONS
1	Discovery and characterisation of an amidine-containing ribosomally-synthesised peptide that is widely distributed in nature. Chemical Science, 2021, 12, 11769-11778.	3.7	9
3	Draft Genome Sequence of Persistent Klebsiella grimontii AT013-Mero-001, Isolated from Human Feces. Microbiology Resource Announcements, 2021, 10, .	0.3	O
4	EDGAR3.0: comparative genomics and phylogenomics on a scalable infrastructure. Nucleic Acids Research, 2021, 49, W185-W192.	6.5	65
5	Genome Sequences of Neurotropic Lineage III Listeria monocytogenes Isolates UKVDL9 and 2010L-2198. Microbiology Resource Announcements, 2021, 10, .	0.3	1
6	Flagellar export apparatus and ATP synthetase: Homology evidenced by synteny predating the Last Universal Common Ancestor. BioEssays, 2021, 43, e2100004.	1.2	5
8	Complete Genome Sequence of <i>Bacillus</i> sp. Strain V3, Isolated from Mangrove Sediments in Wenzhou, China. Microbiology Resource Announcements, 2021, 10, .	0.3	O
9	Accelerating Biological Insight for Understudied Genes. Integrative and Comparative Biology, 2021, , .	0.9	2
10	Draft Genome Sequences of Four Bacterial Strains of Heterotrophic Alteromonas macleodii and <i>Marinobacter</i> , Isolated from a Nonaxenic Culture of Two Marine <i>Synechococcus</i> Strains. Microbiology Resource Announcements, 2021, 10, .	0.3	O
12	Complete Genome Sequences of Two <i>Rhodococcus</i> sp. Strains with Large and Linear Chromosomes, Isolated from Apple Rhizosphere. Microbiology Resource Announcements, 2021, 10, e0015921.	0.3	4
13	Complete Genome Sequence of Paradevosia shaoguanensis Type Strain J5-3, Obtained Using Nanopore and Illumina Sequencing Technologies. Microbiology Resource Announcements, 2021, 10, e0009921.	0.3	3
14	Draft Genome Sequence of Serratia rubidaea, a Potential Opportunistic Pathogen Isolated from Food in Italy. Microbiology Resource Announcements, 2021, 10, e0070721.	0.3	2
15	Analysis of the Taxonomy and Pathogenic Factors of Pectobacterium aroidearum L6 Using Whole-Genome Sequencing and Comparative Genomics. Frontiers in Microbiology, 2021, 12, 679102.	1.5	11
16	Closed Genome Sequence of Clostridium botulinum Strain IBCA10-7060 Type Bh. Microbiology Resource Announcements, 2021, 10, e0038321.	0.3	2
17	High-Quality Complete Genome Resource of Tomato Rhizosphere Strain <i>Pseudomonas donghuensis</i> P482, aÂRepresentative of a Species with Biocontrol Activity Against Plant Pathogens. Molecular Plant-Microbe Interactions, 2021, 34, 1450-1454.	1.4	3
18	Complete Genome Sequence and Methylome of the Type Strain of Shewanella algae. Microbiology Resource Announcements, 2021, 10, e0055921.	0.3	3
19	Genome of Serratia plymuthica UBCF_13, Insight into diverse unique traits. F1000Research, 0, 10, 826.	0.8	O
20	Complete Genome Sequence of the Secondary Alcohol-Utilizing Methanogen Methanospirillum hungatei Strain GP1. Microbiology Resource Announcements, 2021, 10, e0070821.	0.3	1
21	The Arabidopsis PeptideAtlas: Harnessing worldwide proteomics data to create a comprehensive community proteomics resource. Plant Cell, 2021, 33, 3421-3453.	3.1	36

#	Article	IF	CITATIONS
22	Draft Genome Sequences of Enterobacter spp., <i>Lelliottia</i> spp., and <i>Serratia</i> spp., Coliform Bacteria from Drinking Water Reservoirs and Lakes. Microbiology Resource Announcements, 2021, 10, e0062221.	0.3	4
24	Complete Genome Sequence of <i>Methanothermobacter</i> sp. Strain THM-1, a Thermophilic and Hydrogenotrophic Methanogen Isolated from an Anaerobic Reactor in South Korea. Microbiology Resource Announcements, 2021, 10, e0058721.	0.3	1
25	Prevalence and Specificity of Chemoreceptor Profiles in Plant-Associated Bacteria. MSystems, 2021, 6, e0095121.	1.7	20
26	Draft Genome Sequence of a Multidrug-Resistant Escherichia coli Sequence Type 1193 Pandemic Clone Isolated from Wastewater in Austria. Microbiology Resource Announcements, 2021, 10, e0076221.	0.3	2
27	Genomic Characterization of a Prophage, Smhb1, That Infects Salinivibrio kushneri BNH Isolated from a Namib Desert Saline Spring. Microorganisms, 2021, 9, 2043.	1.6	6
28	Draft Genome Sequence of the Halophilic Strain Citrobacter braakii AN-PRR1, Isolated from Rhizospheric Soil of Rice (Oryza sativa L.) from Pakistan. Microbiology Resource Announcements, 2021, 10, e0078721.	0.3	3
29	GTDB: an ongoing census of bacterial and archaeal diversity through a phylogenetically consistent, rank normalizedAand complete genome-based taxonomy. Nucleic Acids Research, 2022, 50, D785-D794.	6.5	662
30	Characterization of a new heterotrophic nitrification bacterium Pseudomonas sp. strain JQ170 and functional identification of nap gene in nitrite production. Science of the Total Environment, 2022, 806, 150556.	3.9	7
31	ViroidDB: a database of viroids and viroid-like circular RNAs. Nucleic Acids Research, 2022, 50, D432-D438.	6.5	14
32	Flavobacterium flabelliforme sp. nov. and Flavobacterium geliluteum sp. nov., Two Multidrug-Resistant Psychrotrophic Species Isolated From Antarctica. Frontiers in Microbiology, 2021, 12, 729977.	1.5	7
33	Rubber Degrading Strains: Microtetraspora and Dactylosporangium. Polymers, 2021, 13, 3524.	2.0	6
34	Genome Sequence of Escherichia coli Stbl4, a Versatile Genetic Tool for Heterologous Expression. Microbiology Resource Announcements, 2021, 10, e0082321.	0.3	3
35	Draft Genome Sequence of Rhodococcus rhodochrous Strain G38GP, Isolated from the Madagascar Hissing Cockroach. Microbiology Resource Announcements, 2021, 10, e0077721.	0.3	1
36	Application Effect and Evaluation of Two-Dimensional Speckle Tracking Imaging on Myocardial Damage in Patients with Malignant Lymphoma Treated with Anthracyclines. Evidence-based Complementary and Alternative Medicine, 2021, 2021, 1-6.	0.5	6
37	Complete Genome Sequence of Campylobacter fetus subsp. venerealis P4531 from a Rhesus Monkey. Microbiology Resource Announcements, 2021, 10, e0073921.	0.3	1
39	Hybrid Genome Assemblies of Marine Bacteria Isolated from the Sponge Sycon capricorn. Microbiology Resource Announcements, 2021, 10, e0085821.	0.3	1
40	Complete Genome Sequences of Seven Neisseria gonorrhoeae Clinical Isolates from Mucosal and Disseminated Gonococcal Infections. Microbiology Resource Announcements, 2021, 10, e0073421.	0.3	1
41	Complete Genome Sequence of a Novel <i>Dyadobacter</i> sp. Strain, NIV53, Isolated from 2-Meter Deep Subsurface Sediment. Microbiology Resource Announcements, 2021, 10, e0075421.	0.3	0

#	Article	IF	CITATIONS
42	RCSB Protein Data Bank resources for structure-facilitated design of mRNA vaccines for existing and emerging viral pathogens. Structure, 2022, 30, 55-68.e2.	1.6	10
44	Bakta: rapid and standardized annotation of bacterial genomes via alignment-free sequence identification. Microbial Genomics, 2021, 7, .	1.0	168
45	Complete Genome Sequence of the Methicillin-Resistant Staphylococcus aureus Strain SQL1/USA300, Used for Testing the Antimicrobial Properties of Clay Phyllosilicates and Customized Aluminosilicates. Microbiology Resource Announcements, 2021, 10, e0086121.	0.3	1
47	Undervalued Pseudo- <i>nifH</i> Sequences in Public Databases Distort Metagenomic Insights into Biological Nitrogen Fixers. MSphere, 2021, 6, e0078521.	1.3	17
48	Comparative Genomics across Three Ensifer Species Using a New Complete Genome Sequence of the Medicago Symbiont Sinorhizobium (Ensifer) meliloti WSM1022. Microorganisms, 2021, 9, 2428.	1.6	3
49	Direct RNA Sequencing Unfolds the Complex Transcriptome of Vibrio parahaemolyticus. MSystems, 2021, 6, e0099621.	1.7	9
50	Complete Genome Sequence of Bacillus badius NBPM-293, a Plant Growth-Promoting Strain Isolated from Rhizosphere Soil. Microbiology Resource Announcements, 2021, 10, e0097721.	0.3	4
51	Genome Sequence of Pseudomonas sp. Strain LAP_36, A Rhizosphere Bacterium Isolated from King George Island, Antarctica. Microbiology Resource Announcements, 2021, 10, e0073121.	0.3	O
52	Isolation, Whole-Genome Sequencing, and Annotation of Three Unclassified Antibiotic-Producing Bacteria, Enterobacter sp. Strain RIT 637, Pseudomonas sp. Strain RIT 778, and Deinococcus sp. Strain RIT 780. Microbiology Resource Announcements, 2021, 10, e0086321.	0.3	1
53	Database resources of the national center for biotechnology information. Nucleic Acids Research, 2022, 50, D20-D26.	6.5	887
54	Staphylococcus ratti sp. nov. Isolated from a Lab Rat. Pathogens, 2022, 11, 51.	1.2	7
55	Draft Genome Sequence of Ralstonia pickettii Strain NCTR106, Isolated from Milk Carton Paperboard. Microbiology Resource Announcements, 2022, 11, e0108421.	0.3	1
56	Cellular homologs of the double jelly-roll major capsid proteins clarify the origins of an ancient virus kingdom. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	26
57	Complete sequence of classic F-type plasmid pRK100 shows unique conservation over time and geographic location. Plasmid, 2022, 119-120, 102618.	0.4	0
58	Folding the unfoldable: using AlphaFold to explore spurious proteins. Bioinformatics Advances, 2022, 2, .	0.9	28
61	Genome Sequence of Bacillus velezensis P1, a Strain Isolated from a Biofilm Captured on a Pig Farm Building. Microbiology Resource Announcements, 2022, , e0121921.	0.3	1
62	Comparative genomics and proteomics of <i>Eubacterium maltosivorans</i> : functional identification of trimethylamine methyltransferases and bacterial microcompartments in a human intestinal bacterium with a versatile lifestyle. Environmental Microbiology, 2022, 24, 517-534.	1.8	8
64	KaKs_Calculator 3.0: Calculating Selective Pressure on Coding and Non-Coding Sequences. Genomics, Proteomics and Bioinformatics, 2022, 20, 536-540.	3.0	106

#	Article	IF	CITATIONS
65	Comparative Genomic Analysis of Pathogenic Factors of Pectobacterium Species Isolated in South Korea Using Whole-Genome Sequencing. Plant Pathology Journal, 2022, 38, 12-24.	0.7	1
66	Whole-Genome Sequence of Pseudomonas sp. Strain MM211, Isolated from Soil in Langenfeld, Germany. Microbiology Resource Announcements, 2022, 11, e0104821.	0.3	0
67	Genome Sequence Data of <i>Bacillus</i> sp. Strain LP16S, Which Is Capable of Inhibiting the Growth of Multiple Sorghum Fungal Pathogens. Molecular Plant-Microbe Interactions, 2022, 35, 290-292.	1.4	0
68	Draft Genome Sequences of Two <i>Streptomyces</i> Isolates Obtained from Volcanic Soils in the Philippines. Microbiology Resource Announcements, 2022, 11, e0108721.	0.3	0
69	Complete Genome Sequence of <i>Curtobacterium</i> sp. Isolated from Surface-Sterilized Germinating Alfalfa Seeds. Microbiology Resource Announcements, 2022, 11, e0090521.	0.3	0
70	Population dynamics in colonizing vancomycin-resistant Enterococcus faecium isolated from immunosuppressed patients. Journal of Global Antimicrobial Resistance, 2022, 28, 267-273.	0.9	5
72	Context-aware genomic surveillance reveals hidden transmission of a carbapenemase-producing Klebsiella pneumoniae. Microbial Genomics, 2021, 7, .	1.0	9
73	Characterization of Alistipes montrealensis sp. nov., Isolated from Human Feces of a Patient with Metastatic Melanoma Treated with Immune Checkpoint Inhibitors. Microbiology Research, 2022, 13, 140-151.	0.8	1
74	RiboGrove: a database of full-length prokaryotic 16S rRNA genes derived from completely assembled genomes. Research in Microbiology, 2022, 173, 103936.	1.0	2
75	Draft Genome Sequence of a Bacterium Isolated from Hypersaline Soil in Sonora, Mexico: <i>Halomonas</i> sp. Strain BLLS135. Microbiology Resource Announcements, 2022, 11, e0140920.	0.3	0
76	Đ"ĐμĐ½Đ¾Đ¼Đ¸Đ°Đ° Đ´Ñ€ĐμĐ²Đ½Đ¸Ñ Đ¿Đ°Ñ,Đ¾Đ³ĐμĐ½Đ¾Đ²: Đ¿ĐμÑ€Đ²Ñ‹Đμ уÑĐ¿ĐμÑи и пĐ	Ŀ ijĠ₩Ĩ Đ įĐ)μĐ9Ñ,Đ¸Đ²Ñ‹
77	<i>Paraphocaeicola brunensis</i> gen. nov., sp. nov., Carrying Two Variants of <i>nimB</i> Resistance Gene from Bacteroides fragilis, and <i>Caecibacteroides pullorum</i> gen. nov., sp. nov., Two Novel Genera Isolated from Chicken Caeca. Microbiology Spectrum, 2022, 10, e0195421.	1.2	2
78	The Complete Genome Sequence and Structure of the Oleaginous Rhodococcus opacus Strain PD630 Through Nanopore Technology. Frontiers in Bioengineering and Biotechnology, 2021, 9, 810571.	2.0	1
80	Draft Genome Sequences of a <i>Bifidobacterium</i> Strain and a <i>Bacteroides</i> Strain Isolated from a Human Stool Sample. Microbiology Resource Announcements, 2022, , e0001122.	0.3	0
81	Maritimibacter dapengensis sp. nov., a poly- \hat{l}^2 -hydroxyalkanoates-producing bacterium isolated from sediment of the Dapeng peninsula (Guangdong, China). International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	7
82	Complete Genome of Sinorhizobium meliloti AK76, a Symbiont of Wild Diploid Medicago lupulina from the Mugodgary Mountain Region. Microbiology Resource Announcements, 2022, 11, e0108821.	0.3	0
83	Draft Genome Sequence of Novel Staphylococcus epidermidis Strain EVL2000, Exhibiting Pathogenicity against Caenorhabditis elegans. Microbiology Resource Announcements, 2022, , e0123921.	0.3	0
84	Ensifer meliloti L6-AK89, an Effective Inoculant of Medicago lupulina Varieties: Phenotypic and Deep-Genome Screening. Agronomy, 2022, 12, 766.	1.3	8

#	Article	IF	CITATIONS
85	Genomics of Ancient Pathogens: First Advances and Prospects. Biochemistry (Moscow), 2022, 87, 242-258.	0.7	3
86	Draft Genome Sequence of Polaromonas eurypsychrophila AER18D-145, Isolated from a Uranium Tailings Management Facility in Northern Saskatchewan, Canada. Microbiology Resource Announcements, 2022, 11, e0001322.	0.3	1
87	Genome Sequences of Marichromatium gracile HOL-1 and Its Purple Photosynthetic Coisolate, <i>Afifella</i> sp. H1R. Microbiology Resource Announcements, 2022, , e0003322.	0.3	1
88	Closed Genome Sequence of an Environmental Aeromonas veronii Strain from California, United States, with an IncA/C Plasmid Carrying an Extended-Spectrum β-Lactamase Gene, <i>bla</i> _{VEB-3} . Microbiology Resource Announcements, 2022, 11, e0103321.	0.3	2
89	Draft Genome Sequences of <i>Buttiauxella</i> spp. Isolates from Water and Gastropods with Putative \hat{l}^2 - <scp>d</scp> -Glucuronidase Activity. Microbiology Resource Announcements, 2022, 11, e0006422.	0.3	2
91	InÂvivo growth of Staphylococcus lugdunensis is facilitated by the concerted function of heme and non-heme iron acquisition mechanisms. Journal of Biological Chemistry, 2022, 298, 101823.	1.6	6
92	The Genome Sequence of Brucella intermedia DF13, a 2,4-Dichlorophenoxyacetic Acid-Degrading Soil Bacterium Isolated in Brazil. Microbiology Resource Announcements, 2022, , e0110521.	0.3	0
93	Streptomyces gobiensis sp. nov., an antimicrobial producing actinobacterium isolated from soil under black Gobi rocks. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	5
94	Clarification of the Dynamic Autothermal Thermophilic Aerobic Digestion Process Using Metagenomic Analysis. Microbiology Spectrum, 2022, , e0056122.	1.2	1
95	The Genome of Enterobacter hormaechei Strain MG02, a 2,4-Dichlorophenoxyacetic Acid-Degrading Bacterium Isolated from Brazilian Soil. Microbiology Resource Announcements, 2022, 11, e0110421.	0.3	0
96	Draft Genome Sequence of Riemerella anatipestifer Strain xi1. Microbiology Resource Announcements, 2022, , e0103421.	0.3	0
97	Complete Genome Sequence of Halopseudomonas aestusnigri Strain GOM5, Isolated from Asphalt Marine Sediments of the Gulf of Mexico. Microbiology Resource Announcements, 2022, , e0122221.	0.3	2
98	Metagenomic survey of the microbiome of ancient Siberian permafrost and modern Kamchatkan cryosols. MicroLife, 2022, 3, .	1.0	5
99	A Phage Foundry Framework to Systematically Develop Viral Countermeasures to Combat Antibiotic-Resistant Bacterial Pathogens. IScience, 2022, 25, 104121.	1.9	12
100	Genome sequence data of Bacillus velezensis BP1.2A and BT2.4. Data in Brief, 2022, 41, 107978.	0.5	4
103	Elioraea tepida, sp. nov., a Moderately Thermophilic Aerobic Anoxygenic Phototrophic Bacterium Isolated from the Mat Community of an Alkaline Siliceous Hot Spring in Yellowstone National Park, WY, USA. Microorganisms, 2022, 10, 80.	1.6	1
106	Complete Genome Sequences of <i>Kinneretia</i> sp. Strain XES5, <i>Shinella</i> sp. Strain XGS7, and <i>Vogesella</i> sp. Strain XCS3, Isolated from Xenopus laevis Skin. Microbiology Resource Announcements, 2021, 10, e0105021.	0.3	2
107	Draft Genome Sequences of Four Streptomycin-Sensitive Erwinia amylovora Strains Isolated from Commercial Apple Orchards in Ohio. Microbiology Resource Announcements, 2021, 10, e0089321.	0.3	2

#	Article	IF	CITATIONS
109	Genome Sequence of <i>Lysobacter</i> sp. Strain BMK333-48F3, the Producer Strain of Potent Lipopeptide Antibiotics of the Tripropeptin Family. Microbiology Resource Announcements, 2021, 10, e0096921.	0.3	3
110	Characterization of Escherichia coli harboring colibactin genes (clb) isolated from beef production and processing systems. Scientific Reports, 2022, 12, 5305.	1.6	2
111	As(III) Exposure Induces a Zinc Scarcity Response and Restricts Iron Uptake in High-Level Arsenic-Resistant Paenibacillus taichungensis Strain NC1. Applied and Environmental Microbiology, 2022, 88, e0031222.	1.4	3
112	Genome Sequence of <i>Lelliottia</i> sp. Strain WAP21, Isolated from Soil in Canola Fields in Victoria, Australia. Microbiology Resource Announcements, 2022, 11, e0101821.	0.3	1
113	Data on complete genome sequence and annotation of two multidrug resistant atypical enteropathogenic Escherichia coli O177 serotype isolated from cattle faeces. Data in Brief, 2022, 42, 108167.	0.5	1
114	Draft Genome Sequence of the Cyanobacterium <i>Synechococcus</i> sp. Strain Nb3U1. Microbiology Resource Announcements, 2022, 11, e0025122.	0.3	2
115	Optimizing the Parametrization of Homologue Classification in the Pan-Genome Computation for a Bacterial Species: Case Study Streptococcus pyogenes. Methods in Molecular Biology, 2022, 2449, 299-324.	0.4	1
116	The Ocean Gene Atlas v2.0: online exploration of the biogeography and phylogeny of plankton genes. Nucleic Acids Research, 2022, 50, W516-W526.	6.5	26
117	Evolutionary Genome Mining for the Discovery and Engineering of Natural Product Biosynthesis. Methods in Molecular Biology, 2022, 2489, 129-155.	0.4	1
118	FUNAGE-Pro: comprehensive web server for gene set enrichment analysis of prokaryotes. Nucleic Acids Research, 2022, 50, W330-W336.	6.5	17
119	Chromohalobacter moromii sp. nov., a moderately halophilic bacterium isolated from lupine-based moromi fermentation. Systematic and Applied Microbiology, 2022, 45, 126324.	1.2	7
120	Cruciferous Weed Isolates of <i>Xanthomonas campestris</i> Yield Insight into Pathovar Genomic Relationships and Genetic Determinants of Host and Tissue Specificity. Molecular Plant-Microbe Interactions, 2022, 35, 791-802.	1.4	1
121	Streptomyces sp. AC04842: Genomic Insights and Functional Expression of Its Latex Clearing Protein Genes (lcp1 and lcp2) When Cultivated With Natural and Vulcanized Rubber as the Sole Carbon Source. Frontiers in Microbiology, 2022, 13, 854427.	1.5	3
122	Comparative Analysis and Data Provenance for 1,113 Bacterial Genome Assemblies. MSphere, 2022, 7, e0007722.	1.3	4
123	Complete Genome Sequence Resources of SixÂStrains of the Most Virulent Pathovars of <i>Xanthomonas arboricola</i> Using Long- and Short-Read Sequencing Approaches. Phytopathology, 2022, 112, 1808-1813.	1.1	3
124	<scp>HMSâ€Sâ€S</scp> : A tool for the identification of Sulphur metabolismâ€related genes and analysis of operon structures in genome and metagenome assemblies. Molecular Ecology Resources, 2022, 22, 2758-2774.	2.2	8
125	Whole-Genome Sequences of Two Klebsiella pneumoniae Strains (Sequence Types 23 and 35) from Wildlife. Microbiology Resource Announcements, 2022, 11, e0014022.	0.3	1
126	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.	0.3	0

#	Article	IF	CITATIONS
128	Description of Corynebacterium poyangense sp. nov., isolated from the feces of the greater white-fronted geese (Anser albifrons). Journal of Microbiology, 2022, 60, 668-677.	1.3	2
130	Rubinisphaera margarita sp. nov., a novel planctomycete isolated from marine sediments collected in the Portuguese north coast. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	7
131	Mutual Exclusion of <i>Methanobrevibacter</i> Species in the Human Gut Microbiota Facilitates Directed Cultivation of a <i>Candidatus</i> Methanobrevibacter Intestini Representative. Microbiology Spectrum, 2022, 10, .	1.2	6
132	Neokomagataea anthophila sp. nov., an osmotolerant acetic acid bacterium isolated in Thailand and emended description of the genus Neokomagataea. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	5
133	Developing a bioinformatics pipeline for comparative protein classification analysis. BMC Genomic Data, 2022, 23, .	0.7	1
134	To kill or to be killed: pangenome analysis of Escherichia coli strains reveals a tailocin specific for pandemic ST131. BMC Biology, 2022, 20, .	1.7	10
135	Genome sequencing data of extended-spectrum beta-lactamase-producing Escherichia coli INF191/17/A isolates of nosocomial infection. Data in Brief, 2022, 43, 108407.	0.5	1
136	Draft Genome Sequence of Pseudomonas sp. Strain RGM 3321, a Phyllosphere Endophyte from Fragaria chiloensis subsp. <i>chiloensis subsp. <i>chiloensis </i></i>	0.3	1
137	Corallococcus soli sp. Nov., a Soil Myxobacterium Isolated from Subtropical Climate, Chalus County, Iran, and Its Potential to Produce Secondary Metabolites. Microorganisms, 2022, 10, 1262.	1.6	7
138	Curation of the AMRFinderPlus databases: applications, functionality and impact. Microbial Genomics, 2022, 8, .	1.0	9
140	Emergence of plasmid-mediated tigecycline, \hat{l}^2 -lactam and florfenicol resistance genes tet(X), blaOXA-347 and floR in Riemerella anatipestifer isolated in China. Poultry Science, 2022, 101, 102057.	1.5	7
141	Complete Genome Sequences of Ezakiella coagulans C0061C1 and Fenollaria massiliensis C0061C2. Microbiology Resource Announcements, 0 , , .	0.3	1
142	Draft Genome Sequence of <i>Helicobacter</i> sp. Strain CaF467b, Isolated from a Pig Manure Storage Tank. Microbiology Resource Announcements, 0, , .	0.3	0
143	Complete Genome Sequence of a Multidrug-Resistant Klebsiella pneumoniae Environmental Isolate from Zanzibar, Tanzania, Harboring Novel Insertion Elements and Two <i>bla</i> _{CTX-M-15} Genes. Microbiology Resource Announcements, 0, , .	0.3	1
144	Two Newly Isolated Enterobacter-Specific Bacteriophages: Biological Properties and Stability Studies. Viruses, 2022, 14, 1518.	1.5	8
145	Draft Genome Sequence of Stenotrophomonas maltophilia KJ, a Clinical Isolate from Taiwan. Microbiology Resource Announcements, 0, , .	0.3	0
147	Comparison of Bioinformatic Analysis System for Antibiotic Resistance Gene Detection and Probiotics Safety Evaluation. Current Topic in Lactic Acid Bacteria and Probiotics, 2022, 8, 32-38.	0.8	1
148	Complete Genome Sequence of <i>Bradyrhizobium</i> sp. Strain C-145, a Nitrogen-Fixing Rhizobacterium Used as a Peanut Inoculant in Argentina. Microbiology Resource Announcements, 0, , .	0.3	0

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149	Systematic whole-genome sequencing reveals an unexpected diversity among actinomycetoma pathogens and provides insights into their antibacterial susceptibilities. PLoS Neglected Tropical Diseases, 2022, 16, e0010128.	1.3	4
150	Complete Genome Sequence of a Psychrophilic Bacterium, <i>Pseudoalteromonas</i> sp. Strain APM04, Isolated from the Seafloor of the South Mariana Trough, Pacific Ocean. Microbiology Resource Announcements, 0, , .	0.3	0
152	An automated $13.5 \hat{a} \in \%$ hour system for scalable diagnosis and acute management guidance for genetic diseases. Nature Communications, 2022, 13, .	5.8	35
154	Rhodococcus pseudokoreensis sp. nov. isolated from the rhizosphere of young M26 apple rootstocks. Archives of Microbiology, 2022, 204, .	1.0	3
155	Desulfoferrobacter suflitae gen. nov., sp. nov., a novel sulphate-reducing bacterium in the Deltaproteobacteria capable of autotrophic growth with hydrogen or elemental iron. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	5
156	Complete Genome Sequence of Flavobacterium sediminilitoris YSM-43 ^T , Isolated from Tidal Sediment in Yeosu. Microbiology Resource Announcements, 0, , .	0.3	1
157	Genome Sequence of $\langle i \rangle$ Erysipelothrix $\langle i \rangle$ sp. Strain Poltava, Isolated from Acute Septic Erysipelas of Swine in Ukraine. Microbiology Resource Announcements, 2022, 11, .	0.3	1
158	Genome-Scale Metabolic Modeling Combined with Transcriptome Profiling Provides Mechanistic Understanding of Streptococcus thermophilus CH8 Metabolism. Applied and Environmental Microbiology, 2022, 88, .	1.4	6
159	Designing a synthetic microbial community devoted to biological control: The case study of Fusarium wilt of banana. Frontiers in Microbiology, $0,13,13$	1.5	15
161	In silico analysis reveals the co-existence of CRISPR-Cas type I-F1 and type I-F2 systems and its association with restricted phage invasion in Acinetobacter baumannii. Frontiers in Microbiology, 0, 13 , .	1.5	5
162	Genome Sequence of a Potent Biosurfactant-Producing Bacterium, <i>Franconibacter</i> sp. Strain IITDAS19. Microbiology Resource Announcements, 2022, 11, .	0.3	0
163	Complete Genome Sequence of Providencia stuartii CMC-4104, Isolated from a Human Splenic Abscess, Containing Multiple Copies of NDM-1 and PER-1 Carbapenem Resistance Genes. Microbiology Resource Announcements, 0, , .	0.3	0
164	Complete Genome Sequences of the Soil Oxalotrophic Bacterium Cupriavidus oxalaticus Strain Ox1 and Its Derived mCherry-Tagged Strain. Microbiology Resource Announcements, 0, , .	0.3	0
165	Genomic and transcriptomic variation in <i>Bordetella</i> spp. following induction of erythromycin resistance. Journal of Antimicrobial Chemotherapy, 2022, 77, 3016-3025.	1.3	3
166	Comparative Genomics Reveal the High Conservation and Scarce Distribution of Nitrogen Fixation nif Genes in the Plant-Associated Genus Herbaspirillum. Microbial Ecology, 0, , .	1.4	0
167	A roadmap for the functional annotation of protein families: a community perspective. Database: the Journal of Biological Databases and Curation, 2022, 2022, .	1.4	14
168	Functional characterization of prokaryotic dark matter: the road so far and what lies ahead. Current Research in Microbial Sciences, 2022, 3, 100159.	1.4	2
171	Draft Genome Sequence of Pseudomonas mandelii Strain 29, Isolated from the Desert Truffle Terfezia claveryi. Microbiology Resource Announcements, 0, , .	0.3	0

#	Article	IF	CITATIONS
172	Draft Genome Sequences of Three Streptomycetes Isolated from Frobisher Bay Marine Sediments. Microbiology Resource Announcements, 0, , .	0.3	0
173	Draft Genome Sequences of <i>Chromobacterium</i> Strains Isolated from Water Systems in Central Western Brazil. Microbiology Resource Announcements, 2022, 11 , .	0.3	1
174	Draft Genome Sequence of Cupriavidus basilensis SRS, a Bacterium Isolated from Stream Sediments. Microbiology Resource Announcements, 0, , .	0.3	0
176	Whole-Genome Sequencing of the Tropical Marine Bacterium Nocardiopsis dassonvillei NCIM 5124, Containing the Ectoine Biosynthesis Gene Cluster <i>ectABC</i> . Microbiology Resource Announcements, 2022, 11, .	0.3	4
177	Complete Genome of Sphingomonas aerolata PDD-32b-11, Isolated from Cloud Water at the Summit of Puy de D $ ilde{A}$ me, France. Microbiology Resource Announcements, 0, , .	0.3	0
178	Apilactobacillus apisilvae sp. nov., Nicolia spurrieriana gen. nov. sp. nov., Bombilactobacillus folatiphilus sp. nov. and Bombilactobacillus thymidiniphilus sp. nov., four new lactic acid bacterial isolates from stingless bees Tetragonula carbonaria and Austroplebeia australis. International lournal of Systematic and Evolutionary Microbiology, 2022, 72	0.8	11
179	Complete Genome Sequence of Glutamicibacter mysorens NBNZ-009, Isolated from Jin Lake Sediment. Microbiology Resource Announcements, 2022, 11, .	0.3	2
180	Characterization and genome analysis of a psychrophilic methanotroph representing a ubiquitous <i>Methylobacter</i> spp. cluster in boreal lake ecosystems. ISME Communications, 2022, 2, .	1.7	6
181	Complete Genome Sequence of <i>Rhizobium</i> sp. Strain RCAM05350 from Shulgan-Tash Karst Cave. Microbiology Resource Announcements, 0, , .	0.3	0
182	Complete Genome Sequence of the Uropathogenic Methicillin-Resistant Staphylococcus aureus Strain MRSA-1369. Microbiology Resource Announcements, 2022, 11, .	0.3	2
183	Pan-genome Analysis Reveals Comparative Genomic Features of Central Metabolic Pathways in Methylorubrum extorquens. Biotechnology and Bioprocess Engineering, 2023, 28, 990-1004.	1.4	0
184	A bacterial pan-genome makes gene essentiality strain-dependent and evolvable. Nature Microbiology, 2022, 7, 1580-1592.	5.9	38
185	Complete Genome Sequence of Campylobacter coli Strain P4581, a Hybrid Carrying Campylobacter jejuni Genomic Content, Isolated from Rhesus Monkey, Macaca mulatta. Microbiology Resource Announcements, 2022, 11, .	0.3	1
186	Role of Bifidobacterium pseudocatenulatum in Degradation and Consumption of Xylan-Derived Carbohydrates. Applied and Environmental Microbiology, 2022, 88, .	1.4	6
189	Genome analysis of a plastisphere-associated Oceanimonas sp. NSJ1 sequenced on Nanopore MinION platform. IOP SciNotes, 2022, 3, 044601.	0.4	2
190	Draft genome of Pseudomonas sp. RGM 2987 isolated from Stevia philippiana roots reveals its potential as a plant biostimulant and potentially constitutes a novel species. Electronic Journal of Biotechnology, 2023, 61, 9-13.	1.2	4
191	Complete Genome Sequence of Mesorhizobium ciceri Strain R30, a Rhizobium Used as a Commercial Inoculant for Chickpea in Argentina. Microbiology Resource Announcements, 2022, 11, .	0.3	2
192	Unveiling the complete genome sequence of <i>Alicyclobacillus acidoterrestris</i> DSM 3922T, a taint-producing strain. G3: Genes, Genomes, Genetics, 0, , .	0.8	0

#	Article	IF	CITATIONS
193	Whole genome sequence data of Stenotrophomonas maltophilia SCAID WND1-2022 (370). Data in Brief, 2022, , 108694.	0.5	0
194	PAT: a comprehensive database of prokaryotic antimicrobial toxins. Nucleic Acids Research, 2023, 51, D452-D459.	6.5	3
195	Draft Genome Sequences for 6 Isolates of Endospore-Forming Class <i>Bacilli</i> Species Isolated from Soil from a Suburban, Wooded, Developed Space. Microbiology Resource Announcements, 2022, 11, .	0.3	1
196	Natural language processing approach to model the secretion signal of type III effectors. Frontiers in Plant Science, $0,13,.$	1.7	6
197	Draft Genome of <i>Acidovorax kalamii</i> Strain JM16, Isolated from Skin Mucus of Zebrafish (Danio) Tj ETQq0	0 8.rgBT /	Overlock 10
198	Complete Genome Sequence of Terrisporobacter glycolicus Strain WW3900, Isolated from Influent Wastewater at a Research Center with Multiple-Species Research Animal Facilities. Microbiology Resource Announcements, 0, , .	0.3	0
199	Draft Genome Sequence of a Multidrug-Resistant Strain of Salmonella enterica Serovar Typhimurium Isolated from a Pine Siskin (Spinus pinus). Microbiology Resource Announcements, 0, , .	0.3	0
201	Draft Genome Sequence of Delftia tsuruhatensis Strain 45.2.2, Colonizer of Zebrafish, Danio rerio, Skin Mucus. Microbiology Resource Announcements, 2022, 11, .	0.3	1
202	<i>binny</i> : an automated binning algorithm to recover high-quality genomes from complex metagenomic datasets. Briefings in Bioinformatics, 2022, 23, .	3.2	5
203	Atopomonas sediminilitoris sp. nov., isolated from beach sediment of Zhairuo Island, China. Antonie Van Leeuwenhoek, 2023, 116, 97-107.	0.7	1
204	DoriC 12.0: an updated database of replication origins in both complete and draft prokaryotic genomes. Nucleic Acids Research, 2023, 51, D117-D120.	6.5	9
205	Sketching and sampling approaches for fast and accurate long read classification. BMC Bioinformatics, 2022, 23, .	1.2	0
206	Draft Genome Sequence of Bacillus halotolerans IcBac2.1, a Strain with Potential as a Phytopathogen Control Agent. Microbiology Resource Announcements, 2022, 11 , .	0.3	1
207	Genomic Characterization of a Carbapenemase-Producing, Extensively Drug-Resistant Klebsiella michiganensis Strain from a Renal Abscess Patient. Microbiology Resource Announcements, 0, , .	0.3	0
209	A Catalog of over 5,000 Metagenome-Assembled Microbial Genomes from the Caprinae Gut Microbiota. Microbiology Spectrum, 2022, 10, .	1.2	3
210	Twenty-five years of Genomes OnLine Database (GOLD): data updates and new features in v.9. Nucleic Acids Research, 2023, 51, D957-D963.	6.5	31
211	Citrobacter portucalensis Sb-2 contains a metalloid resistance determinant transmitted by Citrobacter phage Chris1. Journal of Hazardous Materials, 2023, 443, 130184.	6.5	5
212	Draft Genome Sequence of a Ketoprofen Degrader, Rhodococcus erythropolis IEGM 746. Microbiology Resource Announcements, 0, , .	0.3	0

#	ARTICLE	IF	CITATIONS
213	The STRING database in 2023: protein–protein association networks and functional enrichment analyses for any sequenced genome of interest. Nucleic Acids Research, 2023, 51, D638-D646.	6.5	848
214	Effect of conditioned media from Aeromonas caviae on the transcriptomic changes of the porcine isolates of Pasteurella multocida. BMC Microbiology, 2022, 22, .	1.3	0
215	InterPro in 2022. Nucleic Acids Research, 2023, 51, D418-D427.	6.5	623
216	Globally Disseminated Multidrug Resistance Plasmids Revealed by Complete Assembly of Multidrug Resistant Escherichia coli and KlebsiellaÂpneumoniae Genomes from Diarrheal Disease in Botswana. Applied Microbiology, 2022, 2, 934-949.	0.7	3
217	Complete Genome Sequence of Xanthomonas arboricola pv. <i>pruni</i> Strain Xcp1 Isolated in 1984 from a Bacterial Spot Spring Canker on Prunus persica var. <i>nucipersica</i> cv. "Redgold― Microbiology Resource Announcements, 2022, 11, .	0.3	1
218	Distribution, inducibility, and characterisation of prophages in Latilactobacillus sakei. BMC Microbiology, 2022, 22, .	1.3	4
219	Type IV Pili Are a Critical Virulence Factor in Clinical Isolates of Paenibacillus thiaminolyticus. MBio, 2022, 13, .	1.8	2
220	Genome sequence analysis of halophilic Luteibacter sp. CQ10 to prospect its dual roles in antioxidants production and lignocellulose degradation. Gene Reports, 2022, 29, 101708.	0.4	O
221	eggNOG 6.0: enabling comparative genomics across 12Â535 organisms. Nucleic Acids Research, 2023, 51, D389-D394.	6.5	55
222	Complete Genome Sequence of <i>Brachybacterium</i> sp. Strain NBEC-018, Isolated from Nematode-Infected Potatoes. Microbiology Resource Announcements, 0, , .	0.3	0
223	Genomic analysis of Marinimicrobium sp. C6131 reveals its genetic potential involved in chitin metabolism. Marine Genomics, 2023, 67, 101007.	0.4	0
224	Consumption of N2O by Flavobacterium azooxidireducens sp. nov. Isolated from Decomposing Leaf Litter of Phragmites australis (Cav.). Microorganisms, 2022, 10, 2304.	1.6	3
227	Genomes of Vibrio cholerae O1 Serotype Ogawa Associated with Current Cholera Activity in Pakistan. Microbiology Resource Announcements, 2023, 12, .	0.3	3
228	Unexpected absence of ribosomal protein genes from metagenome-assembled genomes. ISME Communications, 2022, 2, .	1.7	13
230	A large-scale benchmark study of tools for the classification of protein-coding and non-coding RNAs. Nucleic Acids Research, 2022, 50, 12094-12111.	6.5	2
231	The conserved domain database in 2023. Nucleic Acids Research, 2023, 51, D384-D388.	6.5	68
232	Genome-Based Analysis of Virulence Factors and Biofilm Formation in Novel P. aeruginosa Strains Isolated from Household Appliances. Microorganisms, 2022, 10, 2508.	1.6	1
233	Genomic Characterization of Aureimonas altamirensis C2P003—A Specific Member of the Microbiome of Fraxinus excelsior Trees Tolerant to Ash Dieback. Plants, 2022, 11, 3487.	1.6	4

#	Article	IF	CITATIONS
234	Draft Genome Sequences of Probiotic Candidate Schleiferilactobacillus harbinensis Isolated from Fermented Milk $\hat{a} \in \mathbb{C} (i)$ Aban (i) $\hat{a} \in \mathbb{C} (i)$ Microbiology Resource Announcements, $0,$	0.3	0
235	Genomic Investigation of Desert Streptomyces huasconensis D23 Reveals Its Environmental Adaptability and Antimicrobial Activity. Microorganisms, 2022, 10, 2408.	1.6	5
236	Complete Genome Sequences of Eight <i>Faecalibacterium</i> sp. Strains Isolated from Healthy Human Stool. Microbiology Resource Announcements, 0, , .	0.3	0
237	Complete Genome Sequence of Antibiotic-Producing Bacillus velezensis H208, Isolated from Ginger Rhizosphere in Laifeng County, China. Microbiology Resource Announcements, 0, , .	0.3	0
238	Current Scenario of Exogenously Induced RNAi for Lepidopteran Agricultural Pest Control: From dsRNA Design to Topical Application. International Journal of Molecular Sciences, 2022, 23, 15836.	1.8	3
239	Draft Genome Sequence of Enterococcus dispar CoE-457-22, Isolated from Traditionally Produced Montenegrin Dry Sausage. Microbiology Resource Announcements, 2023, 12, .	0.3	1
240	Comparative Genomic and Metagenomic Investigations of the Corynebacterium tuberculostearicum Species Complex Reveals Potential Mechanisms Underlying Associations To Skin Health and Disease. Microbiology Spectrum, 2023, 11, .	1.2	5
241	Characteristics and adaptability of Flavobacterium panici BSSL-CR3 in tidal flat revealed by comparative genomic and enzymatic analysis. Archives of Microbiology, 2023, 205, .	1.0	2
242	Complete Genome Sequence of <i>Xanthomonas citri</i> subsp. <i>citri</i> CQ13, an Alternative Model Strain to Study Citrus Bacterial Canker in China. PhytoFrontiers, 2023, 3, 484-486.	0.8	2
243	Draft Genome Sequence and Annotation of Priestia aryabhattai Strain BD1 Isolated from a Dye Sediment. Microbiology Resource Announcements, 2023, 12, .	0.3	2
244	Novel Plant-Associated Brevibacillus and Lysinibacillus Genomospecies Harbor a Rich Biosynthetic Potential of Antimicrobial Compounds. Microorganisms, 2023, 11, 168.	1.6	7
245	Complete Genome Sequence of Vibrio natriegens Strain PWH3a. Microbiology Resource Announcements, 0, , .	0.3	0
246	Complete Genome Sequences of $\langle i \rangle$ Massilia $\langle i \rangle$ sp. Strains B-10 and H-1, Isolated from the Water in the Shulgan-Tash Cave. Microbiology Resource Announcements, 0, , .	0.3	0
247	Complete genome sequencing of three clade-1 xanthomonads reveals genetic determinants for a lateral flagellin and the biosynthesis of coronatine-like molecules in Xanthomonas. Phytopathology, 0 , , .	1.1	3
248	Complete Genome Sequence of Phormidium yuhuli AB48, Isolated from an Industrial Photobioreactor Environment. Microbiology Resource Announcements, 0, , .	0.3	0
249	TransAAP: an automated annotation pipeline for membrane transporter prediction in bacterial genomes. Microbial Genomics, 2023, 9, .	1.0	2
250	Eight Unexpected Selenoprotein Families in Organometallic Biochemistry in Clostridium difficile, in ABC Transport, and in Methylmercury Biosynthesis. Journal of Bacteriology, 2023, 205, .	1.0	1
251	Draft Genome Sequences of 20 Clostridium botulinum Type A Isolates from Foodborne Botulism Outbreaks. Microbiology Resource Announcements, 2023, 12, .	0.3	1

#	Article	IF	CITATIONS
253	OpenGenomeBrowser: a versatile, dataset-independent and scalable web platform for genome data management and comparative genomics. BMC Genomics, 2022, 23, .	1.2	1
254	EVIncRNA-Dpred: improved prediction of experimentally validated IncRNAs by deep learning. Briefings in Bioinformatics, 2023, 24, .	3.2	4
255	Flavobacterium potami sp. nov., a multi-metal resistance genes harbouring bacterium isolated from shallow river silt. Antonie Van Leeuwenhoek, 2023, 116, 265-280.	0.7	1
257	Collection and curation of prokaryotic genome assemblies from type strains at NCBI. International Journal of Systematic and Evolutionary Microbiology, 2023, 73, .	0.8	7
258	Complete Genome Sequences of Extraintestinal Pathogenic Escherichia coli Clinical Isolates from Danish Ulcerative Colitis Patients. Microbiology Resource Announcements, 0, , .	0.3	0
259	EBR-5, a Novel Variant of Metallo- \hat{l}^2 -Lactamase EBR from Multidrug-Resistant Empedobacter stercoris. Microbiology Spectrum, 2023, 11 , .	1.2	1
260	Genome sequences of BCG Pasteur ATCC 35734 and its derivative, the vaccine candidate BCGî"BCG1419c. BMC Genomics, 2023, 24, .	1.2	2
261	Staphylococcus aureus Prophage-Encoded Protein Causes Abortive Infection and Provides Population Immunity against Kayviruses. MBio, 2023, 14, .	1.8	2
262	Industry Adoption of Organoids and Organsâ€onâ€Chip Technology: Toward a Paradox of Choice. Advanced Biology, 2023, 7, .	1.4	4
263	Genome Sequences of Bordetella pertussis Isolates from Outbreaks in Northeastern Mexico. Microbiology Resource Announcements, 0, , .	0.3	0
264	Govania unica gen. nov., sp. nov., a rare biosphere bacterium that represents a novel family in the class Alphaproteobacteria. Systematic and Applied Microbiology, 2023, 46, 126405.	1.2	0
265	Complete genome sequence of Pseudoalteromonas sp. PS1M3, a psychrotrophic bacterium isolated from deep-sea sediment off the Boso Peninsula, Japan Trench. Marine Genomics, 2023, 69, 101028.	0.4	0
266	Methylomonas rapida sp. nov., a novel species of fast-growing, carotenoid-producing obligate methanotrophs with high biotechnological potential. Systematic and Applied Microbiology, 2023, 46, 126398.	1.2	7
267	Set of Small Molecule Polyurethane (PU) Model Substrates: Ecotoxicity Evaluation and Identification of PU Degrading Biocatalysts. Catalysts, 2023, 13, 278.	1.6	3
268	Elucidating the functional roles of prokaryotic proteins using big data and artificial intelligence. FEMS Microbiology Reviews, 2023, 47, .	3.9	4
269	Tychonema sp. BBK16 Characterisation: Lifestyle, Phylogeny and Related Phages. Viruses, 2023, 15, 442.	1.5	2
271	Capsular Polysaccharide Is Essential for the Virulence of the Antimicrobial-Resistant Pathogen Enterobacter hormaechei. MBio, 2023, 14, .	1.8	2
272	Complete Genome Sequences of Mycobacterium bovis Strains Affiliated with Bovine Tuberculosis Outbreaks in Canada in 2016 and 2018. Microbiology Resource Announcements, 2023, 12, .	0.3	1

#	Article	IF	Citations
273	The genome sequence of <i>Synechocystis</i> sp. PCC 6803 substrain GT†and its implications for the evolution of PCC 6803 substrains. FEBS Open Bio, 2023, 13, 701-712.	1.0	2
274	Optimization and elucidation of organophosphorus and pyrethroid degradation pathways by a novel bacterial consortium C3 using RSM and GC-MS-based metabolomics. Journal of the Taiwan Institute of Chemical Engineers, 2023, 144, 104744.	2.7	9
275	Unfolding the Bacterial Transcriptome Landscape Using Oxford Nanopore Technology Direct RNA Sequencing. Methods in Molecular Biology, 2023, , 269-279.	0.4	0
277	Draft Genome Assembly of <i>Stutzerimonas</i> sp. Strain S1 and Achromobacter spanius Strain S4, Two Syringol-Metabolizing Bacteria Isolated from Compost Soil. Microbiology Resource Announcements, 2023, 12, .	0.3	1
278	Exploring microbial functional biodiversity at the protein family levelâ€"From metagenomic sequence reads to annotated protein clusters. Frontiers in Bioinformatics, 0, 3, .	1.0	2
279	Complete genome sequence resource of Pseudomonas koreensis FP1691, a plant growth-promoting rhizobacterium isolated from cowpea. PhytoFrontiers, 0, , .	0.8	0
280	Isolation and characterization of a novel Tenacibaculum species and a corresponding bacteriophage from a Mediterranean fish hatchery: Description of Tenacibaculum larymnensis sp. nov. and Tenacibaculum phage Larrie. Frontiers in Microbiology, $0,14,.$	1.5	1
281	A Genome-Scale Atlas Reveals Complex Interplay of Transcription and Translation in an Archaeon. MSystems, 2023, 8, .	1.7	4
282	<i>Escherichia coli</i> transcriptome assembly from a compendium of RNA-seq data sets. RNA Biology, 2023, 20, 77-84.	1.5	1
283	Complete Genome Sequence of <i>Bacillus velezensis</i> strain ZY1, a Potential Biological Control Agent for Bacterial Fruit Blotch. PhytoFrontiers, 0, , .	0.8	0
285	Whole genome characterization of thermophilic Campylobacter species isolated from dairy manure in small specialty crop farms of Northeast Ohio. Frontiers in Microbiology, $0,14,.$	1.5	3
286	Pynteny: a Python package to perform synteny-aware, profile HMM-based searches in sequence databases. Journal of Open Source Software, 2023, 8, 5289.	2.0	O
287	Genomics assisted characterization of plant growth-promoting and metabolite producing psychrotolerant Himalayan Chryseobacterium cucumeris PCH239. Archives of Microbiology, 2023, 205,	1.0	1
288	Draft genome sequence of Enterobacter chengduensis ECC445, isolated from fresh water in the West Indies. BMC Genomic Data, 2023, 24, .	0.7	1
289	Genome mining to identify valuable secondary metabolites and their regulation in Actinobacteria from different niches. Archives of Microbiology, 2023, 205, .	1.0	1
290	Complete Genome Sequence of the Carboxydotrophic Knallgas Bacterium Pseudomonas carboxydohydrogena Strain DSM 1083. Microbiology Resource Announcements, 2023, 12, .	0.3	0
291	ViroProfiler: a containerized bioinformatics pipeline for viral metagenomic data analysis. Gut Microbes, 2023, 15, .	4.3	10
294	Draft Genome Sequence of Lactobacillus oris BE7N, Isolated from a Healthy Centenarian in Hainan, China. Microbiology Resource Announcements, 0, , .	0.3	0

#	Article	IF	CITATIONS
295	Whole-Genome Sequence of Burkholderia ambifaria Strain Q53, a Potential Plant Growth Promoter Isolated from the Rhizosphere of Peanut. Microbiology Resource Announcements, 0, , .	0.3	0
296	Engineering osmolysis susceptibility in Cupriavidus necator and Escherichia coli for recovery of intracellular products. Microbial Cell Factories, 2023, 22, .	1.9	4
297	Genome sequencing and multifaceted taxonomic analysis of novel strains of violacein-producing bacteria and non-violacein-producing close relatives. Microbial Genomics, 2023, 9, .	1.0	0
298	Complete Genome Sequence of an Endemic Mycobacterium bovis Strain from Wood Bison in Wood Buffalo National Park, Canada. Microbiology Resource Announcements, 0, , .	0.3	0
299	Unexplored diversity and ecological functions of transposable phages. ISME Journal, 2023, 17, 1015-1028.	4.4	2
300	Genome Sequences of Seven Clade B2 Escherichia coli Strains Associated with Recurrent Urinary Tract Infections in Postmenopausal Women. Microbiology Resource Announcements, 0, , .	0.3	1
301	Complete Genome Sequence of Citrobacter braakii GW-lmi- $1b1$, Isolated from Hospital Wastewater in Greifswald, Germany. Microbiology Resource Announcements, 0 , , .	0.3	0
302	Aeoliella straminimaris sp. nov., a novel member of the phylum Planctomycetota with an unusual filamentous structure. International Journal of Systematic and Evolutionary Microbiology, 2023, 73, .	0.8	1