

# Andrey V Mardanov

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6341342/publications.pdf>

Version: 2024-02-01

172  
papers

5,659  
citations

126708

33  
h-index

98622

67  
g-index

186  
all docs

186  
docs citations

186  
times ranked

7107  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome sequence and analysis of the tuber crop potato. <i>Nature</i> , 2011, 475, 189-195.	13.7	1,912
2	Characterization of <i>Melioribacter roseus</i> gen. nov., sp. nov., a novel facultatively anaerobic thermophilic cellulolytic bacterium from the class <i>Ignavibacteria</i> , and a proposal of a novel bacterial phylum <i>Ignavibacteriae</i> . <i>Environmental Microbiology</i> , 2013, 15, 1759-1771.	1.8	228
3	Comparative Metagenomics of Eight Geographically Remote Terrestrial Hot Springs. <i>Microbial Ecology</i> , 2015, 70, 411-424.	1.4	118
4	Complete Sequence of the Duckweed ( <i>Lemna minor</i> ) Chloroplast Genome: Structural Organization and Phylogenetic Relationships to Other Angiosperms. <i>Journal of Molecular Evolution</i> , 2008, 66, 555-564.	0.8	102
5	The 203 kbp Mitochondrial Genome of the Phytopathogenic Fungus <i>Sclerotinia borealis</i> Reveals Multiple Invasions of Introns and Genomic Duplications. <i>PLoS ONE</i> , 2014, 9, e107536.	1.1	93
6	Metabolic Versatility and Indigenous Origin of the Archaeon <i>Thermococcus sibiricus</i> , Isolated from a Siberian Oil Reservoir, as Revealed by Genome Analysis. <i>Applied and Environmental Microbiology</i> , 2009, 75, 4580-4588.	1.4	90
7	Genome sequence and analysis of methylotrophic yeast <i>Hansenula polymorpha</i> DL1. <i>BMC Genomics</i> , 2013, 14, 837.	1.2	81
8	Microbial community structure in methane hydrate-bearing sediments of freshwater Lake Baikal. <i>FEMS Microbiology Ecology</i> , 2012, 79, 348-358.	1.3	77
9	Genome of the candidate phylum Aminicenantes bacterium from a deep subsurface thermal aquifer revealed its fermentative saccharolytic lifestyle. <i>Extremophiles</i> , 2019, 23, 189-200.	0.9	74
10	Genomic Analysis of <i>Melioribacter roseus</i> , Facultatively Anaerobic Organotrophic Bacterium Representing a Novel Deep Lineage within Bacteroidetes/Chlorobi Group. <i>PLoS ONE</i> , 2013, 8, e53047.	1.1	68
11	Characterization and Genome Analysis of the First Facultatively Alkaliphilic <i>Thermodesulfovibrio</i> Isolated from the Deep Terrestrial Subsurface. <i>Frontiers in Microbiology</i> , 2016, 7, 2000.	1.5	62
12	Genome Analysis of <i>Fimbrigiobus ruber</i> SP5 <sup>T</sup> , a Planctomycete with Confirmed Chitinolytic Capability. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	59
13	Hydrolytic Capabilities as a Key to Environmental Success: Chitinolytic and Cellulolytic Acidobacteria From Acidic Sub-arctic Soils and Boreal Peatlands. <i>Frontiers in Microbiology</i> , 2018, 9, 2775.	1.5	59
14	Genome analysis of <i>Caitinivibrio alkaliphilus</i> gen. nov., sp. nov., a novel extremely haloalkaliphilic anaerobic chitinolytic bacterium from the candidate phylum <i>Termiterrum</i> group 3. <i>Environmental Microbiology</i> , 2014, 16, 1549-1565.	1.8	58
15	Respiratory Ammonification of Nitrate Coupled to Anaerobic Oxidation of Elemental Sulfur in Deep-Sea Autotrophic Thermophilic Bacteria. <i>Frontiers in Microbiology</i> , 2017, 8, 87.	1.5	55
16	Complete sequence of the mitochondrial genome of a diatom alga <i>Synedra acus</i> and comparative analysis of diatom mitochondrial genomes. <i>Current Genetics</i> , 2010, 56, 215-223.	0.8	54
17	<i>Fervidicoccus fontis</i> gen. nov., sp. nov., an anaerobic, thermophilic crenarchaeote from terrestrial hot springs, and proposal of <i>Fervidicoccaceae</i> fam. nov. and <i>Fervidicoccales</i> ord. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2010, 60, 2082-2088.	0.8	50
18	Domestication of previously uncultivated <i>Candidatus Desulforudis audaxviator</i> from a deep aquifer in Siberia sheds light on its physiology and evolution. <i>ISME Journal</i> , 2019, 13, 1947-1959.	4.4	48

#	ARTICLE	IF	CITATIONS
19	Microbial Life in the Deep Subsurface Aquifer Illuminated by Metagenomics. <i>Frontiers in Microbiology</i> , 2020, 11, 572252.	1.5	48
20	The <i>Geoglobus acetivorans</i> Genome: Fe(III) Reduction, Acetate Utilization, Autotrophic Growth, and Degradation of Aromatic Compounds in a Hyperthermophilic Archaeon. <i>Applied and Environmental Microbiology</i> , 2015, 81, 1003-1012.	1.4	46
21	The Genome Sequence of the Crenarchaeon <i>Acidilobus saccharovorans</i> Supports a New Order, <i>Acidilobales</i> , and Suggests an Important Ecological Role in Terrestrial Acidic Hot Springs. <i>Applied and Environmental Microbiology</i> , 2010, 76, 5652-5657.	1.4	43
22	Uncultured archaea dominate in the thermal groundwater of Uzon Caldera, Kamchatka. <i>Extremophiles</i> , 2011, 15, 365-372.	0.9	43
23	Comparative Genomic Analysis of <i>Mycobacterium tuberculosis</i> Drug Resistant Strains from Russia. <i>PLoS ONE</i> , 2013, 8, e56577.	1.1	42
24	Resistance of Permafrost and Modern <i>Acinetobacter lwoffii</i> Strains to Heavy Metals and Arsenic Revealed by Genome Analysis. <i>BioMed Research International</i> , 2016, 2016, 1-9.	0.9	42
25	Molecular analysis of microbial diversity in the Zavarzin Spring, Uzon Caldera, Kamchatka. <i>Microbiology</i> , 2011, 80, 244-251.	0.5	41
26	Bacterial chitin utilisation at extremely haloalkaline conditions. <i>Extremophiles</i> , 2012, 16, 883-894.	0.9	41
27	Complete Genome Sequence of <i>Vulcanisaeta moutnovskia</i> Strain 768-28, a Novel Member of the Hyperthermophilic Crenarchaeal Genus <i>Vulcanisaeta</i> . <i>Journal of Bacteriology</i> , 2011, 193, 2355-2356.	1.0	39
28	Genomic insights into a new acidophilic, copper-resistant <i>Desulfosporosinus</i> isolate from the oxidized tailings area of an abandoned gold mine. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw111.	1.3	39
29	The loss of photosynthetic pathways in the plastid and nuclear genomes of the non-photosynthetic mycoheterotrophic eudicot <i>Monotropa hypopitys</i> . <i>BMC Plant Biology</i> , 2016, 16, 238.	1.6	39
30	Genomics and biochemistry of <i>Saccharomyces cerevisiae</i> wine yeast strains. <i>Biochemistry (Moscow)</i> , 2016, 81, 1650-1668.	0.7	38
31	A metagenomic window into the 2-km-deep terrestrial subsurface aquifer revealed multiple pathways of organic matter decomposition. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	38
32	Phylogeny and physiology of candidate phylum BRC1 inferred from the first complete metagenome-assembled genome obtained from deep subsurface aquifer. <i>Systematic and Applied Microbiology</i> , 2019, 42, 67-76.	1.2	38
33	The structure of microbial communities of activated sludge of large-scale wastewater treatment plants in the city of Moscow. <i>Scientific Reports</i> , 2022, 12, 3458.	1.6	38
34	<i>Desulfurococcus kamchatkensis</i> sp. nov., a novel hyperthermophilic protein-degrading archaeon isolated from a Kamchatka hot spring. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2009, 59, 1743-1747.	0.8	37
35	Complete Genome Sequence of the Anaerobic, Protein-Degrading Hyperthermophilic Crenarchaeon <i>Desulfurococcus kamchatkensis</i> . <i>Journal of Bacteriology</i> , 2009, 191, 2371-2379.	1.0	36
36	<i>Frigoriglobus tundricola</i> gen. nov., sp. nov., a psychrotolerant cellulolytic planctomycete of the family Gemmataceae from a littoral tundra wetland. <i>Systematic and Applied Microbiology</i> , 2020, 43, 126129.	1.2	36

#	ARTICLE	IF	CITATIONS
37	Microbial Communities Involved in Methane, Sulfur, and Nitrogen Cycling in the Sediments of the Barents Sea. <i>Microorganisms</i> , 2021, 9, 2362.	1.6	36
38	The Antirepressor Needed for Induction of Linear Plasmid-Prophage N15 Belongs to the SOS Regulon. <i>Journal of Bacteriology</i> , 2007, 189, 6333-6338.	1.0	35
39	Draft Genome Sequence of the Anoxygenic Filamentous Phototrophic Bacterium <i>Oscillochloris trichoides</i> subsp. DG-6. <i>Journal of Bacteriology</i> , 2011, 193, 321-322.	1.0	35
40	Phenotypic and Genomic Properties of <i>Chitinispirillum alkaliphilum</i> gen. nov., sp. nov., A Haloalkaliphilic Anaerobic Chitinolytic Bacterium Representing a Novel Class in the Phylum Fibrobacteres. <i>Frontiers in Microbiology</i> , 2016, 7, 407.	1.5	33
41	Wide distribution of <i>Phycisphaera</i> -like planctomycetes from WD2101 soil group in peatlands and genome analysis of the first cultivated representative. <i>Environmental Microbiology</i> , 2021, 23, 1510-1526.	1.8	32
42	Flor yeast strains from culture collection: Genetic diversity and physiological and biochemical properties. <i>Applied Biochemistry and Microbiology</i> , 2017, 53, 359-367.	0.3	31
43	Complete Genome Sequence of the Thermoacidophilic Crenarchaeon <i>Thermoproteus uzoniensis</i> 768-20. <i>Journal of Bacteriology</i> , 2011, 193, 3156-3157.	1.0	30
44	Whole-Genome Analysis of Three Yeast Strains Used for Production of Sherry-Like Wines Revealed Genetic Traits Specific to Flor Yeasts. <i>Frontiers in Microbiology</i> , 2018, 9, 965.	1.5	30
45	Genome of a Novel Bacterium <i>Candidatus Jettena ecosia</i> Reconstructed From the Metagenome of an Anammox Bioreactor. <i>Frontiers in Microbiology</i> , 2019, 10, 2442.	1.5	30
46	Microbial life in Bourlyashchy, the hottest thermal pool of Uzon Caldera, Kamchatka. <i>Extremophiles</i> , 2015, 19, 1157-1171.	0.9	29
47	The Structure of Microbial Community and Degradation of Diatoms in the Deep Near-Bottom Layer of Lake Baikal. <i>PLoS ONE</i> , 2013, 8, e59977.	1.1	29
48	Genome Analysis of <i>Thermosulfurimonas dismutans</i> , the First Thermophilic Sulfur-Disproportionating Bacterium of the Phylum Thermodesulfobacteria. <i>Frontiers in Microbiology</i> , 2016, 7, 950.	1.5	28
49	The ancient small mobilizable plasmid pALWED1.8 harboring a new variant of the non-cassette streptomycin/spectinomycin resistance gene <i>aadA27</i> . <i>Plasmid</i> , 2016, 84-85, 36-43.	0.4	28
50	First structure of archaeal branched-chain amino acid aminotransferase from <i>Thermoproteus uzoniensis</i> specific for l-amino acids and R-amines. <i>Extremophiles</i> , 2016, 20, 215-225.	0.9	28
51	Stable and Variable Parts of Microbial Community in Siberian Deep Subsurface Thermal Aquifer System Revealed in a Long-Term Monitoring Study. <i>Frontiers in Microbiology</i> , 2016, 7, 2101.	1.5	27
52	Thermostable Branched-Chain Amino Acid Transaminases From the Archaea <i>Geoglobus acetivorans</i> and <i>Archaeoglobus fulgidus</i> : Biochemical and Structural Characterization. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019, 7, 7.	2.0	26
53	Closely Located but Totally Distinct: Highly Contrasting Prokaryotic Diversity Patterns in Raised Bogs and Eutrophic Fens. <i>Microorganisms</i> , 2020, 8, 484.	1.6	25
54	Oxidative biotransformation of biotite and glauconite by alkaliphilic anaerobes: The effect of Fe oxidation on the weathering of phyllosilicates. <i>Chemical Geology</i> , 2016, 439, 98-109.	1.4	24

#	ARTICLE	IF	CITATIONS
55	A new technique for obtaining whole pathogen transcriptomes from infected host tissues. <i>BioTechniques</i> , 2010, 48, 139-144.	0.8	23
56	A novel uncultured bacterium of the family Gallionellaceae: Description and genome reconstruction based on metagenomic analysis of microbial community in acid mine drainage. <i>Microbiology</i> , 2016, 85, 449-461.	0.5	23
57	Targeted isolation based on metagenome-assembled genomes reveals a phylogenetically distinct group of thermophilic spirochetes from deep biosphere. <i>Environmental Microbiology</i> , 2021, 23, 3585-3598.	1.8	23
58	Complete Genome of a Member of a New Bacterial Lineage in the Microgenomates Group Reveals an Unusual Nucleotide Composition Disparity Between Two Strands of DNA and Limited Metabolic Potential. <i>Microorganisms</i> , 2020, 8, 320.	1.6	23
59	Complete Genome Sequence of the Hyperthermophilic Cellulolytic Crenarchaeon <i>Thermogladus cellulolyticus</i> 1633. <i>Journal of Bacteriology</i> , 2012, 194, 4446-4447.	1.0	22
60	A Novel highly thermostable branched-chain amino acid aminotransferase from the crenarchaeon <i>Vulcanisaeta moutnovskia</i> . <i>Enzyme and Microbial Technology</i> , 2017, 96, 127-134.	1.6	22
61	Adaptive dif Modules in Permafrost Strains of <i>Acinetobacter lwoffii</i> and Their Distribution and Abundance Among Present Day <i>Acinetobacter</i> Strains. <i>Frontiers in Microbiology</i> , 2019, 10, 632.	1.5	22
62	Metabolic Diversity and Evolutionary History of the Archaeal Phylum <i>Candidatus</i> <i>Micrarchaeota</i> Uncovered from a Freshwater Lake Metagenome. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	22
63	Characterization of a Thermostable Short-Chain Alcohol Dehydrogenase from the Hyperthermophilic Archaeon <i>Thermococcus sibiricus</i> . <i>Applied and Environmental Microbiology</i> , 2010, 76, 4096-4098.	1.4	21
64	Metagenomics as a tool for the investigation of uncultured microorganisms. <i>Russian Journal of Genetics</i> , 2015, 51, 431-439.	0.2	21
65	The complete chloroplast genome of parasitic flowering plant <i>Monotropa hypopitys</i> : extensive gene losses and size reduction. <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 212-213.	0.2	21
66	Complete Genome Sequence of Strain 1860, a Crenarchaeon of the Genus <i>Pyrobaculum</i> Able To Grow with Various Electron Acceptors. <i>Journal of Bacteriology</i> , 2012, 194, 727-728.	1.0	20
67	Experimental and computational studies on the unusual substrate specificity of branched-chain amino acid aminotransferase from <i>Thermoproteus uzoniensis</i> . <i>Archives of Biochemistry and Biophysics</i> , 2016, 607, 27-36.	1.4	20
68	Genomic and Metabolic Insights into Two Novel Thiobacillus Species from Enhanced Biological Phosphorus Removal Systems. <i>Microorganisms</i> , 2020, 8, 2030.	1.6	20
69	Functional characterization of the repA replication gene of linear plasmid prophage N15. <i>Research in Microbiology</i> , 2006, 157, 176-183.	1.0	19
70	Effect of metal concentration on the microbial community in acid mine drainage of a polysulfide ore deposit. <i>Microbiology</i> , 2016, 85, 745-751.	0.5	19
71	Lignite coal burning seam in the remote Altai Mountains harbors a hydrogen-driven thermophilic microbial community. <i>Scientific Reports</i> , 2018, 8, 6730.	1.6	19
72	Sulfur and Methane-Oxidizing Microbial Community in a Terrestrial Mud Volcano Revealed by Metagenomics. <i>Microorganisms</i> , 2020, 8, 1333.	1.6	19

#	ARTICLE	IF	CITATIONS
73	Microbial sulfate reduction by <i>Desulfovibrio</i> is an important source of hydrogen sulfide from a large swine finishing facility. <i>Scientific Reports</i> , 2021, 11, 10720.	1.6	18
74	<i>Desulfosporosinus metallidurans</i> sp. nov., an acidophilic, metal-resistant sulfate-reducing bacterium from acid mine drainage. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	18
75	Draft Genome Sequence of the Wine Yeast Strain <i>Saccharomyces cerevisiae</i> I-328. <i>Genome Announcements</i> , 2018, 6, .	0.8	17
76	Evaluation of Antibiotic Resistance of <i>Salmonella</i> Serotypes and Whole-Genome Sequencing of Multiresistant Strains Isolated from Food Products in Russia. <i>Antibiotics</i> , 2022, 11, 1.	1.5	17
77	Tightly regulated, high-level expression from controlled copy number vectors based on the replicon of temperate phage N15. <i>Gene</i> , 2007, 395, 15-21.	1.0	16
78	ATP-dependent DNA ligase from <i>Thermococcus</i> sp. 1519 displays a new arrangement of the OB-fold domain. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1440-1447.	0.7	16
79	Specific features of telomerase RNA from <i>Hansenula polymorpha</i> . <i>Rna</i> , 2013, 19, 1563-1574.	1.6	16
80	Draft Genome Sequence of <i>Sclerotinia borealis</i> , a Psychrophilic Plant Pathogenic Fungus. <i>Genome Announcements</i> , 2014, 2, .	0.8	16
81	Draft genome sequence of the first acid-tolerant sulfate-reducing <i>deltaproteobacterium</i> <i>Desulfovibrio</i> sp. TomC having potential for minewater treatment. <i>FEMS Microbiology Letters</i> , 2015, 362, 1-3.	0.7	16
82	Microbial communities involved in the methane cycle in the near-bottom water layer and sediments of the meromictic subarctic Lake Svetloe. <i>Antonie Van Leeuwenhoek</i> , 2019, 112, 1801-1814.	0.7	16
83	Conversion of Linear DNA with Hairpin Telomeres into a Circular Molecule in the Course of Phage N15 Lytic Replication. <i>Journal of Molecular Biology</i> , 2009, 391, 261-268.	2.0	15
84	Analysis of the complete genome of <i>Fervidococcus fontis</i> confirms the distinct phylogenetic position of the order <i>Fervidococcales</i> and suggests its environmental function. <i>Extremophiles</i> , 2014, 18, 295-309.	0.9	15
85	Uncultured bacteria and methanogenic archaea predominate in the microbial community of Western Siberian deep subsurface aquifer. <i>Microbiology</i> , 2017, 86, 412-415.	0.5	15
86	Complete mitochondrial genomes of three <i>Saccharomyces cerevisiae</i> flor strains. <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 849-850.	0.2	15
87	Microbial diversity in acidic thermal pools in the Uzon Caldera, Kamchatka. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 35-43.	0.7	15
88	Complete sequence and analysis of the mitochondrial genome of the methylotrophic yeast <i>Hansenula polymorpha</i> DL-1. <i>FEMS Yeast Research</i> , 2011, 11, 464-472.	1.1	14
89	Microbial Processes and Microbial Communities in the Water Column of the Polar Meromictic Lake Bolshie Khruslomeny at the White Sea Coast. <i>Frontiers in Microbiology</i> , 2020, 11, 1945.	1.5	14
90	Gausemycins A,B: Cyclic Lipoglycopeptides from <i>Streptomyces</i> sp.**. <i>Angewandte Chemie - International Edition</i> , 2021, 60, 18694-18703.	7.2	14

#	ARTICLE	IF	CITATIONS
91	Molecular analysis of the intestinal microbiome composition of mammoth and woolly rhinoceros. Doklady Biochemistry and Biophysics, 2012, 445, 203-206.	0.3	13
92	A Novel Highly Thermostable Multifunctional Beta-Glycosidase from Crenarchaeon <i>Acidilobus saccharovorans</i> . Archaea, 2015, 2015, 1-6.	2.3	13
93	Dynamics of the composition of a microbial consortium during start-up of a single-stage constant flow laboratory nitrification/anammox setup. Microbiology, 2016, 85, 681-692.	0.5	13
94	Plastid Genomes of Carnivorous Plants <i>Drosera rotundifolia</i> and <i>Nepenthes ventrata</i> Reveal Evolutionary Patterns Resembling Those Observed in Parasitic Plants. International Journal of Molecular Sciences, 2019, 20, 4107.	1.8	13
95	Metabolic Engineering of Wine Strains of <i>Saccharomyces cerevisiae</i> . Genes, 2020, 11, 964.	1.0	13
96	Sulfidogenic Microbial Communities of the Uzen High-Temperature Oil Field in Kazakhstan. Microorganisms, 2021, 9, 1818.	1.6	13
97	New Insight Into the Interspecies Shift of Anammox Bacteria <i>Ca. Brocadia</i> and <i>Ca. Jettenia</i> in Reactors Fed With Formate and Folate. Frontiers in Microbiology, 2021, 12, 802201.	1.5	13
98	Draft Genome Sequence of <i>Magnetospirillum</i> sp. Strain SO-1, a Freshwater Magnetotactic Bacterium Isolated from the Ol'khovka River, Russia. Genome Announcements, 2014, 2, .	0.8	12
99	De novo transcriptome assembly of the mycoheterotrophic plant <i>Monotropa hypopitys</i> . Genomics Data, 2017, 11, 60-61.	1.3	12
100	Composition of the microbial communities of bituminous constructions at natural oil seeps at the bottom of Lake Baikal. Microbiology, 2013, 82, 373-382.	0.5	11
101	Characterization of the structure of the prokaryotic complex of Antarctic permafrost by molecular genetic techniques. Microbiology, 2016, 85, 102-108.	0.5	11
102	Acinetobacter Plasmids: Diversity and Development of Classification Strategies. Frontiers in Microbiology, 2020, 11, 588410.	1.5	11
103	Transcriptome Profile of Yeast Strain Used for Biological Wine Aging Revealed Dynamic Changes of Gene Expression in Course of Flor Development. Frontiers in Microbiology, 2020, 11, 538.	1.5	11
104	Ubiquitous Conjugative Mega-Plasmids of <i>Acinetobacter</i> Species and Their Role in Horizontal Transfer of Multi-Drug Resistance. Frontiers in Microbiology, 2021, 12, 728644.	1.5	11
105	Complete Chloroplast Genome Sequence of Freshwater Araphid Pennate Diatom Alga <i>Synedra acus</i> from Lake Baikal. International Journal of Biology, 2011, 4, .	0.1	10
106	Diversity of bacteria of the genus <i>Bacillus</i> on board of international space station. Doklady Biochemistry and Biophysics, 2015, 465, 347-350.	0.3	10
107	Overexpression, purification and crystallization of a thermostable DNA ligase from the archaeon <i>Thermococcus</i> sp. 1519. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 368-371.	0.7	9
108	Metagenome of the Siberian Underground Water Reservoir. Genome Announcements, 2017, 5, .	0.8	9

#	ARTICLE	IF	CITATIONS
109	Peat-Inhabiting Verrucomicrobia of the Order Methylophilales Do Not Possess Methanotrophic Capabilities. <i>Microorganisms</i> , 2021, 9, 2566.	1.6	9
110	The impact of genomics on research in diversity and evolution of archaea. <i>Biochemistry (Moscow)</i> , 2012, 77, 799-812.	0.7	8
111	Nicotinamidase from the thermophilic archaeon <i>Acidilobus saccharovorans</i> : Structural and functional characteristics. <i>Biochemistry (Moscow)</i> , 2014, 79, 54-61.	0.7	8
112	Genome sequence of the copper resistant and acid-tolerant <i>Desulfosporosinus</i> sp. BG isolated from the tailings of a molybdenum-tungsten mine in the Transbaikal area. <i>Genomics Data</i> , 2017, 11, 106-108.	1.3	8
113	Novel design and optimisation of a nitritation/anammox set-up for ammonium removal from filtrate of digested sludge. <i>Environmental Technology (United Kingdom)</i> , 2018, 39, 593-606.	1.2	8
114	Thermophilic Chloroflexi Dominate in the Microbial Community Associated with Coal-Fire Gas Vents in the Kuznetsk Coal Basin, Russia. <i>Microorganisms</i> , 2021, 9, 948.	1.6	8
115	Reclassification of <i>Sphaerotilus natans</i> subsp. <i>sulfidivorans</i> Gridneva et al. 2011 as <i>Sphaerotilus sulfidivorans</i> sp. nov. and comparative genome analysis of the genus <i>Sphaerotilus</i> . <i>Archives of Microbiology</i> , 2021, 203, 1595-1599.	1.0	8
116	Characteristic of biodiversity of thermophilic microbial community by parallel pyrosequencing method. <i>Doklady Biochemistry and Biophysics</i> , 2010, 432, 110-113.	0.3	7
117	Complete mitochondrial genome of the cephalosporin-producing fungus <i>Acremonium chrysogenum</i> . <i>Mitochondrial DNA</i> , 2015, 26, 943-944.	0.6	7
118	Metagenome of the Microbial Community of Anammox Granules in a Nitritation/Anammox Wastewater Treatment System. <i>Genome Announcements</i> , 2017, 5, .	0.8	7
119	The complete mitochondrial genome of the carnivorous flowering plant <i>Nepenthes X Ventrata</i> . <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 1259-1260.	0.2	7
120	Structural characterization of geranylgeranyl pyrophosphate synthase GACE1337 from the hyperthermophilic archaeon <i>Geoglobus acetivorans</i> . <i>Extremophiles</i> , 2018, 22, 877-888.	0.9	7
121	Complete mitochondrial genome of compactin-producing fungus <i>Penicillium solitum</i> and comparative analysis of Trichocomaceae mitochondrial genomes. <i>FEMS Microbiology Letters</i> , 2012, 329, 9-17.	0.7	6
122	A Novel Phosphate-Accumulating Bacterium Identified in a Bioreactor for Phosphate Removal from Wastewater. <i>Microbiology</i> , 2019, 88, 751-755.	0.5	6
123	Complete genome sequence of the cellulolytic planctomycete <i>Telmatocola sphagniphila</i> SP2T and characterization of the first cellulolytic enzyme from planctomycetes. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126276.	1.2	6
124	<i>Desulfovibrio desulfuricans</i> AY5 Isolated from a Patient with Autism Spectrum Disorder Binds Iron in Low-Soluble Greigite and Pyrite. <i>Microorganisms</i> , 2021, 9, 2558.	1.6	6
125	Two New Species of Filamentous Sulfur Bacteria of the Genus <i>Thiothrix</i> , <i>Thiothrix winogradskyi</i> sp. nov. and <i>Candidatus Thiothrix sulfatfontis</i> sp. nov.. <i>Microorganisms</i> , 2022, 10, 1300.	1.6	6
126	Metrological support for DNA sequencing. <i>Measurement Techniques</i> , 2012, 55, 345-350.	0.2	5



#	ARTICLE	IF	CITATIONS
127	Isolation and functional characterization of lipase from the thermophilic alkali-tolerant bacterium <i>Thermosyntropha lipolytica</i> . <i>Applied Biochemistry and Microbiology</i> , 2012, 48, 338-343.	0.3	5
128	Reconstruction of iron metabolism pathways of bacteria <i>Magnetospirillum aberrantis</i> SpK spp. based on sequenced genome analysis. <i>Doklady Biological Sciences</i> , 2012, 444, 202-205.	0.2	5
129	Cephalosporin-acid synthetase of <i>Escherichia coli</i> strain VKPM B-10182: Genomic context, gene identification, producer strain production. <i>Applied Biochemistry and Microbiology</i> , 2015, 51, 505-510.	0.3	5
130	Genome sequencing and annotation of <i>Geobacillus</i> sp. 1017, a hydrocarbon-oxidizing thermophilic bacterium isolated from a heavy oil reservoir (China). <i>Genomics Data</i> , 2017, 11, 95-97.	1.3	5
131	Metagenome Sequence of a Microbial Community from the Gold Mine Tailings in the Kuzbass Area, Russia. <i>Genome Announcements</i> , 2017, 5, .	0.8	5
132	Metagenomic data of the microbial community of lab-scale nitrification-anammox sequencing-batch bioreactor performing nitrogen removal from synthetic wastewater. <i>Data in Brief</i> , 2019, 27, 104722.	0.5	5
133	Genomes of three bacteriophages from the deep subsurface aquifer. <i>Data in Brief</i> , 2019, 22, 488-491.	0.5	5
134	Genome Analysis of <i>Acinetobacter lwoffii</i> Strains Isolated from Permafrost Soils Aged from 15 Thousand to 1.8 Million Years Revealed Their Close Relationships with Present-Day Environmental and Clinical Isolates. <i>Biology</i> , 2021, 10, 871.	1.3	5
135	Extensive plastome reduction and loss of photosynthesis genes in <i>Diphelypaea coccinea</i> , a holoparasitic plant of the family Orobanchaceae. <i>PeerJ</i> , 2019, 7, e7830.	0.9	5
136	Continuous Bioleaching of Arsenic-Containing Copper-Zinc Concentrate and Shift of Microbial Population under Various Conditions. <i>Minerals (Basel, Switzerland)</i> , 2022, 12, 592.	0.8	5
137	Characterization of a novel M42 aminopeptidase from crenarchaeon <i>Desulfurococcus kamchatkensis</i> . <i>Doklady Biochemistry and Biophysics</i> , 2012, 442, 30-32.	0.3	4
138	Expression of genes involved in DNA repair and telomere maintenance in the yeast <i>Hansenula polymorpha</i> DL1 under heat stress. <i>Doklady Biochemistry and Biophysics</i> , 2015, 462, 185-188.	0.3	4
139	Polymorphism of the Iron Homeostasis Genes and Iron Sensitivity in <i>Saccharomyces cerevisiae</i> Flor and Wine Strains. <i>Microbiology</i> , 2019, 88, 200-205.	0.5	4
140	Complete Genome Sequences of Endophytic Bacilli Isolated from Grapevine Plants. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	4
141	<i>Nepenthes</i> $\tilde{A}$ - <i>ventrata</i> Transcriptome Profiling Reveals a Similarity Between the Evolutionary Origins of Carnivorous Traps and Floral Organs. <i>Frontiers in Plant Science</i> , 2021, 12, 643137.	1.7	4
142	Isolation and characteristics of new thermostable DNA ligase from archaea of the genus <i>Thermococcus</i> . <i>Applied Biochemistry and Microbiology</i> , 2008, 44, 473-477.	0.3	3
143	The complete mitochondrial genome of the acid-tolerant fungus <i>Penicillium ShG4C</i> . <i>Genomics Data</i> , 2016, 10, 141-143.	1.3	3
144	Genome sequence of the acid-tolerant <i>Desulfovibrio</i> sp. DV isolated from the sediments of a Pb-Zn mine tailings dam in the Chita region, Russia. <i>Genomics Data</i> , 2017, 11, 125-127.	1.3	3

#	ARTICLE	IF	CITATIONS
145	The genome-wide transcription response to telomerase deficiency in the thermotolerant yeast <i>Hansenula polymorpha</i> DL-1. <i>BMC Genomics</i> , 2017, 18, 492.	1.2	3
146	Transcriptome-Wide Characterization of the MADS-Box Family in Pinesap <i>Monotropa hypopitys</i> Reveals Flowering Conservation in Non-photosynthetic Myco-Heterotrophs. <i>Journal of Plant Growth Regulation</i> , 2018, 37, 768-783.	2.8	3
147	Draft Genome Sequence of <i>Bacillus velezensis</i> BZR 277, a Prospective Biocontrol Agent against Phytoparasitic Nematodes. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	3
148	RepA Protein of the Bacteriophage N15 Exhibits Activity of DNA Helicase. <i>Doklady Biochemistry and Biophysics</i> , 2004, 397, 217-219.	0.3	2
149	Expression, purification and crystallization of a thermostable short-chain alcohol dehydrogenase from the archaeon <i>Thermococcus sibiricus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 655-657.	0.7	2
150	Sulfate-reducing bacteria in the microbial community of acidic drainage from a gold deposit tailing storage. <i>Microbiology</i> , 2017, 86, 286-288.	0.5	2
151	Prokaryotic community in Pleistocene ice wedges of Mammoth Mountain. <i>Extremophiles</i> , 2020, 24, 93-105.	0.9	2
152	Natural Yeast Strains of <i>Saccharomyces cerevisiae</i> that are Promising for Sherry Production. <i>Applied Biochemistry and Microbiology</i> , 2020, 56, 329-335.	0.3	2
153	Complete Genome Sequence of <i>Paludibaculum fermentans</i> P105 <sup>T</sup> , a Facultatively Anaerobic Acidobacterium Capable of Dissimilatory Fe(III) Reduction. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	2
154	Stress Resistance and Adhesive Properties of Commercial Flor and Wine Strains, and Environmental Isolates of <i>Saccharomyces cerevisiae</i> . <i>Fermentation</i> , 2021, 7, 188.	1.4	2
155	Highly Distinct Microbial Communities in Elevated Strings and Submerged Flarks in the Boreal Aapa-Type Mire. <i>Microorganisms</i> , 2022, 10, 170.	1.6	2
156	Sop proteins can cause transcriptional silencing of genes located close to the centromere sites of linear plasmid N15. <i>Molecular Biology</i> , 2010, 44, 262-267.	0.4	1
157	Iron-dependent superoxide dismutase from novel thermoacidophilic crenarchaeon <i>Acidilobus saccharovorans</i> : from gene to active enzyme. <i>Biochemistry (Moscow)</i> , 2012, 77, 1368-1376.	0.7	1
158	Sodium Chloride-Induced Modulation of the Activity and Thermal Stability of Short-Chain Oxidoreductase from the Archaeon <i>Thermococcus sibiricus</i> . <i>Applied Biochemistry and Biotechnology</i> , 2013, 171, 1877-1889.	1.4	1
159	New low-copy plasmid in cyanobacterium <i>Anabaena variabilis</i> . <i>Russian Journal of Genetics</i> , 2013, 49, 798-805.	0.2	1
160	Draft Genome Sequence of <i>Escherichia coli</i> Strain VKPM B-10182, Producing the Enzyme for Synthesis of Cephalosporin Acids. <i>Genome Announcements</i> , 2014, 2, .	0.8	1
161	Active sulfate reduction in acidic sediments of gold mine tailings. <i>Microbiology</i> , 2015, 84, 453-455.	0.5	1
162	Complete Genome Sequence of <i>Candidatus Syntrophocurvum alkaliphilum</i> Strain B(2M), Obtained from the Metagenome of a Salt-Tolerant Alkaliphilic Anaerobic Syntrophic Butyrate-Degrading Consortium. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	1

#	ARTICLE	IF	CITATIONS
163	Gausemycins A, B: Cyclic Lipoglycopeptides from <i>Streptomyces</i> sp.**. <i>Angewandte Chemie</i> , 2021, 133, 18842-18851.	1.6	1
164	Innentitelbild: Gausemycins A, B: Cyclic Lipoglycopeptides from <i>Streptomyces</i> sp. ( <i>Angew. Chem.</i> )	1.6	1
165	Initiator protein DnaA of <i>Escherichia coli</i> is a negative replication regulator of linear phage-plasmid N15. <i>Russian Journal of Genetics</i> , 2007, 43, 35-40.	0.2	0
166	Determination of complete nucleotide sequence of the genome of hyperthermophilic microorganism. <i>Doklady Biochemistry and Biophysics</i> , 2008, 421, 204-206.	0.3	0
167	Metrological Support for Real-Time Polymerase Chain Reaction Amplifiers. <i>Measurement Techniques</i> , 2014, 57, 97-102.	0.2	0
168	Characteristics of the new plasmid, pMTB1, from the metagenome of the microbial community of underground thermal waters of Western Siberia. <i>Biology Bulletin</i> , 2014, 41, 223-227.	0.1	0
169	Nucleotide sequence and structural analysis of cryptic plasmid pBL90 from <i>Brevibacterium lactofermentum</i> . <i>Russian Journal of Genetics</i> , 2016, 52, 1131-1136.	0.2	0
170	Microorganisms associated with microscopic insects <i>Megaphragma amalphantum</i> and <i>Scydosella musawasensis</i> . <i>Microbiology</i> , 2017, 86, 533-535.	0.5	0
171	Mitochondrial Genomes of Flor Yeast Strains Are Characterized by Low Genetic Variability. <i>Russian Journal of Genetics</i> , 2019, 55, 649-652.	0.2	0
172	Draft Genome Sequence of <i>Acidiplasma aeolicum</i> Strain V1, Isolated from a Hydrothermal Pool. <i>Microbiology Resource Announcements</i> , 2022, 11, e0104621.	0.3	0