

# Andrey V Mardanov

## List of Publications by Year in descending order

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172  
papers

5,659  
citations

126907

33  
h-index

98798

67  
g-index

186  
all docs

186  
docs citations

186  
times ranked

7107  
citing authors

#	ARTICLE	IF	CITATIONS
1	Highly Distinct Microbial Communities in Elevated Springs and Submerged Flasks in the Boreal Aapa-Type Mire. <i>Microorganisms</i> , 2022, 10, 170.	3.6	2
2	Evaluation of Antibiotic Resistance of Salmonella Serotypes and Whole-Genome Sequencing of Multiresistant Strains Isolated from Food Products in Russia. <i>Antibiotics</i> , 2022, 11, 1.	3.7	17
3	Draft Genome Sequence of <i>Acidiplasma aeolicum</i> Strain V1 <sup>T</sup> , Isolated from a Hydrothermal Pool. <i>Microbiology Resource Announcements</i> , 2022, 11, e0104621.	0.6	0
4	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.	3.3	38
5	Continuous Bioleaching of Arsenic-Containing Copper-Zinc Concentrate and Shift of Microbial Population under Various Conditions. <i>Minerals (Basel, Switzerland)</i> , 2022, 12, 592.	2.0	5
6	Two New Species of Filamentous Sulfur Bacteria of the Genus <i>Thiothrix</i> , <i>Thiothrix winogradskyi</i> sp. nov. and <i>Candidatus Thiothrix sulfatiformis</i> ™ sp. nov.. <i>Microorganisms</i> , 2022, 10, 1300.	3.6	6
7	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.	3.8	23
8	Wide distribution of <i>Phycisphaera</i> -like planctomycetes from <i>WD2101</i> soil group in peatlands and genome analysis of the first cultivated representative. <i>Environmental Microbiology</i> , 2021, 23, 1510-1526.	3.8	32
9	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, .	0.6	2
10	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.	3.6	8
11	<i>Nepenthes</i> <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.	3.6	4
12	Draft Genome Sequence of <i>Bacillus velezensis</i> BZR 277, a Prospective Biocontrol Agent against Phytoparasitic Nematodes. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	3
13	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.	3.3	18
14	Gausemycins A,B: Cyclic Lipoglycopeptides from <i>Streptomyces</i> sp.**. <i>Angewandte Chemie</i> , 2021, 133, 18842-18851.	2.0	1
15	Gausemycins A,B: Cyclic Lipoglycopeptides from <i>Streptomyces</i> sp.**. <i>Angewandte Chemie - International Edition</i> , 2021, 60, 18694-18703.	13.8	14
16	Innentitelbild: Gausemycins A,B: Cyclic Lipoglycopeptides from <i>Streptomyces</i> sp. (Angew. Chem.) Tj ETQ00000rgBT /Overl	2.0	1
17	<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, .	1.7	18
18	Sulfidogenic Microbial Communities of the Uzen High-Temperature Oil Field in Kazakhstan. <i>Microorganisms</i> , 2021, 9, 1818.	3.6	13

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19	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.	2.8	5
20	Ubiquitous Conjugative Mega-Plasmids of <i>Acinetobacter</i> Species and Their Role in Horizontal Transfer of Multi-Drug Resistance. <i>Frontiers in Microbiology</i> , 2021, 12, 728644.	3.5	11
21	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.	3.0	2
22	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.	2.2	8
23	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.	2.8	6
24	Microbial Communities Involved in Methane, Sulfur, and Nitrogen Cycling in the Sediments of the Barents Sea. <i>Microorganisms</i> , 2021, 9, 2362.	3.6	36
25	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. <i>Frontiers in Microbiology</i> , 2021, 12, 802201.	3.5	13
26	<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.	3.6	6
27	Peat-Inhabiting Verrucomicrobia of the Order Methylococcoidales Do Not Possess Methanotrophic Capabilities. <i>Microorganisms</i> , 2021, 9, 2566.	3.6	9
28	Prokaryotic community in Pleistocene ice wedges of Mammoth Mountain. <i>Extremophiles</i> , 2020, 24, 93-105.	2.3	2
29	Metabolic Diversity and Evolutionary History of the Archaeal Phylum <i>Candidatus Micrarchaeota</i> Uncovered from a Freshwater Lake Metagenome. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	22
30	<i>Acinetobacter</i> Plasmids: Diversity and Development of Classification Strategies. <i>Frontiers in Microbiology</i> , 2020, 11, 588410.	3.5	11
31	<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.	2.8	36
32	Microbial Life in the Deep Subsurface Aquifer Illuminated by Metagenomics. <i>Frontiers in Microbiology</i> , 2020, 11, 572252.	3.5	48
33	Sulfur and Methane-Oxidizing Microbial Community in a Terrestrial Mud Volcano Revealed by Metagenomics. <i>Microorganisms</i> , 2020, 8, 1333.	3.6	19
34	Metabolic Engineering of Wine Strains of <i>Saccharomyces cerevisiae</i> . <i>Genes</i> , 2020, 11, 964.	2.4	13
35	Microbial Processes and Microbial Communities in the Water Column of the Polar Meromictic Lake Bol'shie Khruslomeny at the White Sea Coast. <i>Frontiers in Microbiology</i> , 2020, 11, 1945.	3.5	14
36	Genomic and Metabolic Insights into Two Novel <i>Thiothrix</i> Species from Enhanced Biological Phosphorus Removal Systems. <i>Microorganisms</i> , 2020, 8, 2030.	3.6	20

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37	Natural Yeast Strains of <i>Saccharomyces cerevisiae</i> that are Promising for Sherry Production. <i>Applied Biochemistry and Microbiology</i> , 2020, 56, 329-335.	0.9	2
38	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.	3.6	23
39	Complete Genome Sequence of <i>Candidatus</i> <i>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, .	0.6	1
40	Closely Located but Totally Distinct: Highly Contrasting Prokaryotic Diversity Patterns in Raised Bogs and Eutrophic Fens. <i>Microorganisms</i> , 2020, 8, 484.	3.6	25
41	Transcriptome Profile of Yeast Strain Used for Biological Wine Aging Revealed Dynamic Changes of Gene Expression in Course of Flor Development. <i>Frontiers in Microbiology</i> , 2020, 11, 538.	3.5	11
42	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.	1.7	16
43	Adaptive <i>dif</i> 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.	3.5	22
44	Genome of a Novel Bacterium <i>Candidatus</i> <i>Jettenia ecosia</i> Reconstructed From the Metagenome of an Anammox Bioreactor. <i>Frontiers in Microbiology</i> , 2019, 10, 2442.	3.5	30
45	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.	1.0	5
46	Plastid Genomes of Carnivorous Plants <i>Drosera rotundifolia</i> and <i>Nepenthes ventrata</i> Reveal Evolutionary Patterns Resembling Those Observed in Parasitic Plants. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4107.	4.1	13
47	Genomes of three bacteriophages from the deep subsurface aquifer. <i>Data in Brief</i> , 2019, 22, 488-491.	1.0	5
48	Mitochondrial Genomes of Flor Yeast Strains Are Characterized by Low Genetic Variability. <i>Russian Journal of Genetics</i> , 2019, 55, 649-652.	0.6	0
49	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.	1.2	4
50	Domestication of previously uncultivated <i>Candidatus</i> <i>Desulforudis audaxviator</i> from a deep aquifer in Siberia sheds light on its physiology and evolution. <i>ISME Journal</i> , 2019, 13, 1947-1959.	9.8	48
51	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.	4.1	26
52	Complete Genome Sequences of Endophytic Bacilli Isolated from Grapevine Plants. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	4
53	A Novel Phosphate-Accumulating Bacterium Identified in a Bioreactor for Phosphate Removal from Wastewater. <i>Microbiology</i> , 2019, 88, 751-755.	1.2	6
54	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.	2.8	38

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55	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.	2.3	74
56	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.	2.0	5
57	Draft Genome Sequence of the Wine Yeast Strain <i>Saccharomyces cerevisiae</i> I-328. <i>Genome Announcements</i> , 2018, 6, .	0.8	17
58	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.	5.1	3
59	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, .	3.1	59
60	Novel design and optimisation of a nitrification/anammox set-up for ammonium removal from filtrate of digested sludge. <i>Environmental Technology (United Kingdom)</i> , 2018, 39, 593-606.	2.2	8
61	Microbial diversity in acidic thermal pools in the Uzon Caldera, Kamchatka. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 35-43.	1.7	15
62	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.	0.4	7
63	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.	3.5	59
64	Structural characterization of geranylgeranyl pyrophosphate synthase GACE1337 from the hyperthermophilic archaeon <i>Geoglobus acetivorans</i> . <i>Extremophiles</i> , 2018, 22, 877-888.	2.3	7
65	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, .	2.7	38
66	Lignite coal burning seam in the remote Altai Mountains harbors a hydrogen-driven thermophilic microbial community. <i>Scientific Reports</i> , 2018, 8, 6730.	3.3	19
67	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.	3.5	30
68	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
69	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 Transbaikalian area. <i>Genomics Data</i> , 2017, 11, 106-108.	1.3	8
70	Uncultured bacteria and methanogenic archaea predominate in the microbial community of Western Siberian deep subsurface aquifer. <i>Microbiology</i> , 2017, 86, 412-415.	1.2	15
71	Flor yeast strains from culture collection: Genetic diversity and physiological and biochemical properties. <i>Applied Biochemistry and Microbiology</i> , 2017, 53, 359-367.	0.9	31
72	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

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73	Sulfate-reducing bacteria in the microbial community of acidic drainage from a gold deposit tailing storage. <i>Microbiology</i> , 2017, 86, 286-288.	1.2	2
74	De novo transcriptome assembly of the mycoheterotrophic plant <i>Monotropa hypopitys</i> . <i>Genomics Data</i> , 2017, 11, 60-61.	1.3	12
75	Metagenome of the Microbial Community of Anammox Granules in a Nitrification/Anammox Wastewater Treatment System. <i>Genome Announcements</i> , 2017, 5, .	0.8	7
76	Microorganisms associated with microscopic insects <i>Megaphragma amalphantum</i> and <i>Scydosella musawasensis</i> . <i>Microbiology</i> , 2017, 86, 533-535.	1.2	0
77	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
78	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.	2.8	3
79	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.	3.2	22
80	Complete mitochondrial genomes of three <i>Saccharomyces cerevisiae</i> flor strains. <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 849-850.	0.4	15
81	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.	3.5	55
82	Metagenome of the Siberian Underground Water Reservoir. <i>Genome Announcements</i> , 2017, 5, .	0.8	9
83	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.	1.9	42
84	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.	3.5	33
85	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.	3.5	28
86	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.	3.5	62
87	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.	3.5	27
88	Dynamics of the composition of a microbial consortium during start-up of a single-stage constant flow laboratory nitrification/anammox setup. <i>Microbiology</i> , 2016, 85, 681-692.	1.2	13
89	The complete mitochondrial genome of the acid-tolerant fungus <i>Penicillium ShG4C</i> . <i>Genomics Data</i> , 2016, 10, 141-143.	1.3	3
90	Genomics and biochemistry of <i>Saccharomyces cerevisiae</i> wine yeast strains. <i>Biochemistry (Moscow)</i> , 2016, 81, 1650-1668.	1.5	38

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91	Effect of metal concentration on the microbial community in acid mine drainage of a polysulfide ore deposit. <i>Microbiology</i> , 2016, 85, 745-751.	1.2	19
92	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.	0.4	21
93	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.	2.7	39
94	The ancient small mobilizable plasmid pALWED1.8 harboring a new variant of the non-cassette streptomycin/spectinomycin resistance gene aadA27. <i>Plasmid</i> , 2016, 84-85, 36-43.	1.4	28
95	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.	1.2	23
96	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.	3.0	20
97	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.	3.6	39
98	Nucleotide sequence and structural analysis of cryptic plasmid pBL90 from <i>Brevibacterium lactofermentum</i> . <i>Russian Journal of Genetics</i> , 2016, 52, 1131-1136.	0.6	0
99	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.	3.3	24
100	Characterization of the structure of the prokaryotic complex of Antarctic permafrost by molecular genetic techniques. <i>Microbiology</i> , 2016, 85, 102-108.	1.2	11
101	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.	2.3	28
102	Diversity of bacteria of the genus <i>Bacillus</i> on board of international space station. <i>Doklady Biochemistry and Biophysics</i> , 2015, 465, 347-350.	0.9	10
103	A Novel Highly Thermostable Multifunctional Beta-Glycosidase from Crenarchaeon <i>Acidilobus saccharovorans</i> . <i>Archaea</i> , 2015, 2015, 1-6.	2.3	13
104	Metagenomics as a tool for the investigation of uncultured microorganisms. <i>Russian Journal of Genetics</i> , 2015, 51, 431-439.	0.6	21
105	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.	0.9	4
106	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.	0.9	5
107	Comparative Metagenomics of Eight Geographically Remote Terrestrial Hot Springs. <i>Microbial Ecology</i> , 2015, 70, 411-424.	2.8	118
108	Active sulfate reduction in acidic sediments of gold mine tailings. <i>Microbiology</i> , 2015, 84, 453-455.	1.2	1



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109	Draft genome sequence of the first acid-tolerant sulfate-reducing deltaproteobacterium <i>Desulfovibrio</i> sp. TomC having potential for minewater treatment. FEMS Microbiology Letters, 2015, 362, 1-3.	1.8	16
110	Microbial life in Bourlyashchy, the hottest thermal pool of Uzon Caldera, Kamchatka. Extremophiles, 2015, 19, 1157-1171.	2.3	29
111	The <i>Geoglobus acetivorans</i> Genome: Fe(III) Reduction, Acetate Utilization, Autotrophic Growth, and Degradation of Aromatic Compounds in a Hyperthermophilic Archaeon. Applied and Environmental Microbiology, 2015, 81, 1003-1012.	3.1	46
112	Complete mitochondrial genome of the cephalosporin-producing fungus <i>Acremonium chrysogenum</i> . Mitochondrial DNA, 2015, 26, 943-944.	0.6	7
113	The 203 kbp Mitochondrial Genome of the Phytopathogenic Fungus <i>Sclerotinia borealis</i> Reveals Multiple Invasions of Introns and Genomic Duplications. PLoS ONE, 2014, 9, e107536.	2.5	93
114	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
115	Draft Genome Sequence of <i>Sclerotinia borealis</i> , a Psychrophilic Plant Pathogenic Fungus. Genome Announcements, 2014, 2, .	0.8	16
116	Draft Genome Sequence of <i>Escherichia coli</i> Strain VKPM B-10182, Producing the Enzyme for Synthesis of Cephalosporin Acids. Genome Announcements, 2014, 2, .	0.8	1
117	Genome analysis of <i>Candidatus</i> <i>hitinivibrio alkaliphilus</i> gen. nov., sp. nov., a novel extremely haloalkaliphilic anaerobic chitinolytic bacterium from the candidate phylum <i>Candidatus</i> <i>Termitibacter</i> group 3. Environmental Microbiology, 2014, 16, 1549-1565.	3.8	58
118	Nicotinamidase from the thermophilic archaeon <i>Acidilobus saccharovorans</i> : Structural and functional characteristics. Biochemistry (Moscow), 2014, 79, 54-61.	1.5	8
119	Analysis of the complete genome of <i>Fervidococcus fontis</i> confirms the distinct phylogenetic position of the order Fervidococcales and suggests its environmental function. Extremophiles, 2014, 18, 295-309.	2.3	15
120	Metrological Support for Real-Time Polymerase Chain Reaction Amplifiers. Measurement Techniques, 2014, 57, 97-102.	0.6	0
121	Characteristics of the new plasmid, pMTB1, from the metagenome of the microbial community of underground thermal waters of Western Siberia. Biology Bulletin, 2014, 41, 223-227.	0.5	0
122	Composition of the microbial communities of bituminous constructions at natural oil seeps at the bottom of Lake Baikal. Microbiology, 2013, 82, 373-382.	1.2	11
123	Specific features of telomerase RNA from <i>Hansenula polymorpha</i> . Rna, 2013, 19, 1563-1574.	3.5	16
124	Genome sequence and analysis of methylotrophic yeast <i>Hansenula polymorpha</i> DL1. BMC Genomics, 2013, 14, 837.	2.8	81
125	Sodium Chloride-Induced Modulation of the Activity and Thermal Stability of Short-Chain Oxidoreductase from the Archaeon <i>Thermococcus sibiricus</i> . Applied Biochemistry and Biotechnology, 2013, 171, 1877-1889.	2.9	1
126	Characterization of <i>Candidatus</i> <i>Melioribacter roseus</i> gen. nov., sp. nov., a novel facultatively anaerobic thermophilic cellulolytic bacterium from the class <i>Candidatus</i> <i>Ignavibacteria</i> , and a proposal of a novel bacterial phylum <i>Candidatus</i> <i>Ignavibacteriia</i> . Environmental Microbiology, 2013, 15, 1759-1771.	3.8	228



#	ARTICLE	IF	CITATIONS
127	New low-copy plasmid in cyanobacterium <i>Anabaena variabilis</i> . Russian Journal of Genetics, 2013, 49, 798-805.	0.6	1
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