Nikolai V Ravin

List of Publications by Year
in descending order

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167 papers	8,527 citations	94433 37 h-index	54911 84 g-index
180 all docs	180 docs citations	180 times ranked	10640 citing authors

#	ARTICLE	IF	CITATIONS
1	Shifting the limits in wheat research and breeding using a fully annotated reference genome. Science, 2018, 361, .	12.6	2,424
2	Genome sequence and analysis of the tuber crop potato. Nature, 2011, 475, 189-195.	27.8	1,912
3	Genomic sequence and analysis of the atypical temperate bacteriophage N15 1 1Edited by M. Gottesman. Journal of Molecular Biology, 2000, 299, 53-73.	4.2	121
4	Comparative Metagenomics of Eight Geographically Remote Terrestrial Hot Springs. Microbial Ecology, 2015, 70, 411-424.	2.8	118
5	Complete Sequence of the Duckweed (Lemna minor) Chloroplast Genome: Structural Organization and Phylogenetic Relationships to Other Angiosperms. Journal of Molecular Evolution, 2008, 66, 555-564.	1.8	102
6	The 203 kbp Mitochondrial Genome of the Phytopathogenic Fungus Sclerotinia borealis Reveals Multiple Invasions of Introns and Genomic Duplications. PLoS ONE, 2014, 9, e107536.	2.5	93
7	Metabolic Versatility and Indigenous Origin of the Archaeon <i>Thermococcus sibiricus</i> , Isolated from a Siberian Oil Reservoir, as Revealed by Genome Analysis. Applied and Environmental Microbiology, 2009, 75, 4580-4588.	3.1	90
8	Linear plasmid vector for cloning of repetitive or unstable sequences in Escherichia coli. Nucleic Acids Research, 2010, 38, e88-e88.	14.5	89
9	Genome sequence and analysis of methylotrophic yeast Hansenula polymorpha DL1. BMC Genomics, 2013, 14, 837.	2.8	81
10	Microbial community structure in methane hydrate-bearing sediments of freshwater Lake Baikal. FEMS Microbiology Ecology, 2012, 79, 348-358.	2.7	77
11	Genome of the candidate phylum Aminicenantes bacterium from a deep subsurface thermal aquifer revealed its fermentative saccharolytic lifestyle. Extremophiles, 2019, 23, 189-200.	2.3	74
12	Genomic Analysis of Melioribacter roseus, Facultatively Anaerobic Organotrophic Bacterium Representing a Novel Deep Lineage within Bacteriodetes/Chlorobi Group. PLoS ONE, 2013, 8, e53047.	2.5	68
13	N15: The linear phageâ€“plasmid. Plasmid, 2011, 65, 102-109.	1.4	65
14	The Use of Transient Expression Systems for the Rapid Production of Virus-like Particles in Plants. Current Pharmaceutical Design, 2013, 19, 5564-5573.	1.9	62
15	Characterization and Genome Analysis of the First Facultatively Alkaliphilic Thermodesulfovibrio Isolated from the Deep Terrestrial Subsurface. Frontiers in Microbiology, 2016, 7, 2000.	3.5	62
16	Ancestral Absence of Electron Transport Chains in Patescibacteria and DPANN. Frontiers in Microbiology, 2020, 11, 1848.	3.5	62
17	Efficient Transient Expression of Recombinant Proteins in Plants by the Novel pEff Vector Based on the Genome of Potato Virus X. Frontiers in Plant Science, 2017, 8, 247.	3.6	60
18	Genome Analysis of Fimbriiglobus ruber SP5 ^T , a Planctomycete with Confirmed Chitinolytic Capability. Applied and Environmental Microbiology, 2018, 84, .	3.1	59

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19	Hydrolytic Capabilities as a Key to Environmental Success: Chitinolytic and Cellulolytic Acidobacteria From Acidic Sub-arctic Soils and Boreal Peatlands. Frontiers in Microbiology, 2018, 9, 2775.	3.5	59
20	Genome analysis of <i><scp>C</scp>hitinivibrio alkaliphilus</i> gen. nov., sp. nov., a novel extremely haloalkaliphilic anaerobic chitinolytic bacterium from the candidate phylum <scp>T</scp>ermite <scp>G</scp>roup 3. Environmental Microbiology, 2014, 16, 1549-1565.	3.8	58
21	Respiratory Ammonification of Nitrate Coupled to Anaerobic Oxidation of Elemental Sulfur in Deep-Sea Autotrophic Thermophilic Bacteria. Frontiers in Microbiology, 2017, 8, 87.	3.5	55
22	Mapping of Functional Domains in F Plasmid Partition Proteins Reveals a Bipartite SopB-recognition Domain in SopA. Journal of Molecular Biology, 2003, 329, 875-889.	4.2	54
23	Bidirectional replication from an internal ori site of the linear N15 plasmid prophage. Nucleic Acids Research, 2003, 31, 6552-6560.	14.5	54
24	Complete sequence of the mitochondrial genome of a diatom alga Synedra acus and comparative analysis of diatom mitochondrial genomes. Current Genetics, 2010, 56, 215-223.	1.7	54
25	The anti-immunity system of phage-plasmid N15: identification of the antirepressor gene and its control by a small processed RNA. Molecular Microbiology, 1999, 34, 980-994.	2.5	53
26	Rapid high-yield expression of a candidate influenza vaccine based on the ectodomain of M2 protein linked to flagellin in plants using viral vectors. BMC Biotechnology, 2015, 15, 42.	3.3	53
27	Protection against Multiple Influenza A Virus Strains Induced by Candidate Recombinant Vaccine Based on Heterologous M2e Peptides Linked to Flagellin. PLoS ONE, 2015, 10, e0119520.	2.5	48
28	Domestication of previously uncultivated <i>Candidatus</i> Desulforudis audaxviator from a deep aquifer in Siberia sheds light on its physiology and evolution. ISME Journal, 2019, 13, 1947-1959.	9.8	48
29	Microbial Life in the Deep Subsurface Aquifer Illuminated by Metagenomics. Frontiers in Microbiology, 2020, 11, 572252.	3.5	48
30	The Geoglobus acetivorans 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
31	Mechanisms of replication and telomere resolution of the linear plasmid prophage N15. FEMS Microbiology Letters, 2003, 221, 1-6.	1.8	45
32	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. Applied and Environmental Microbiology, 2010, 76, 5652-5657.	3.1	43
33	Uncultured archaea dominate in the thermal groundwater of Uzon Caldera, Kamchatka. Extremophiles, 2011, 15, 365-372.	2.3	43
34	Plant-produced recombinant influenza vaccine based on virus-like HBc particles carrying an extracellular domain of M2 protein. Biochemistry (Moscow), 2012, 77, 33-40.	1.5	43
35	Comparative Genomic Analysis of Mycobacterium tuberculosis Drug Resistant Strains from Russia. PLoS ONE, 2013, 8, e56577.	2.5	42
36	The protelomerase of the phage-plasmid N15 is responsible for its maintenance in linear form11Edited by I. B. Holland. Journal of Molecular Biology, 2001, 312, 899-906.	4.2	41

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37	Molecular analysis of microbial diversity in the Zavarzin Spring, Uzon Caldera, Kamchatka. Microbiology, 2011, 80, 244-251.	1.2	41
38	Complete Genome Sequence of â€œVulcanisaeta moutnovskiaâ€•Strain 768-28, a Novel Member of the Hyperthermophilic Crenarchaeal Genus Vulcanisaeta. Journal of Bacteriology, 2011, 193, 2355-2356.	2.2	39
39	Genomic insights into a new acidophilic, copper-resistant<i>Desulfosporosinus</i>isolate from the oxidized tailings area of an abandoned gold mine. FEMS Microbiology Ecology, 2016, 92, fiw111.	2.7	39
40	The loss of photosynthetic pathways in the plastid and nuclear genomes of the non-photosynthetic mycoheterotrophic eudicot Monotropa hypopitys. BMC Plant Biology, 2016, 16, 238.	3.6	39
41	A molecular assembly system for presentation of antigens on the surface of HBc virus-like particles. Virology, 2013, 435, 293-300.	2.4	38
42	A metagenomic window into the 2-km-deep terrestrial subsurface aquifer revealed multiple pathways of organic matter decomposition. FEMS Microbiology Ecology, 2018, 94, .	2.7	38
43	Phylogeny and physiology of candidate phylum BRC1 inferred from the first complete metagenome-assembled genome obtained from deep subsurface aquifer. Systematic and Applied Microbiology, 2019, 42, 67-76.	2.8	38
44	The structure of microbial communities of activated sludge of large-scale wastewater treatment plants in the city of Moscow. Scientific Reports, 2022, 12, 3458.	3.3	38
45	Complete Genome Sequence of the Anaerobic, Protein-Degrading Hyperthermophilic Crenarchaeon <i>Desulfurococcus kamchatkensis</i>. Journal of Bacteriology, 2009, 191, 2371-2379.	2.2	36
46	Methane as an Organic Matter Source and the Trophic Basis of a Laptev Sea Cold Seep Microbial Community. Geomicrobiology Journal, 2018, 35, 411-423.	2.0	36
47	Microbial Communities Involved in Methane, Sulfur, and Nitrogen Cycling in the Sediments of the Barents Sea. Microorganisms, 2021, 9, 2362.	3.6	36
48	The Antirepressor Needed for Induction of Linear Plasmid-Prophage N15 Belongs to the SOS Regulon. Journal of Bacteriology, 2007, 189, 6333-6338.	2.2	35
49	Draft Genome Sequence of the Anoxygenic Filamentous Phototrophic Bacterium <i>Oscillochloris trichoides</i> subsp. DG-6. Journal of Bacteriology, 2011, 193, 321-322.	2.2	35
50	Development of a candidate influenza vaccine based on virus-like particles displaying influenza M2e peptide into the immunodominant region of hepatitis B core antigen: Broad protective efficacy of particles carrying four copies of M2e. Vaccine, 2015, 33, 3398-3406.	3.8	33
51	Phenotypic and Genomic Properties of Chitinispirillum alkaliphilum gen. nov., sp. nov., A Haloalkaliphilic Anaerobic Chitinolytic Bacterium Representing a Novel Class in the Phylum Fibrobacteres. Frontiers in Microbiology, 2016, 7, 407.	3.5	33
52	Development of a candidate influenza vaccine based on virus-like particles displaying influenza M2e peptide into the immunodominant loop region of hepatitis B core antigen: Insertion of multiple copies of M2e increases immunogenicity and protective efficiency. Vaccine, 2015, 33, 3392-3397.	3.8	32
53	Wide distribution of <i>Phycisphaera</i>â€•like planctomycetes from <scp>WD2101</scp> soil group in peatlands and genome analysis of the first cultivated representative. Environmental Microbiology, 2021, 23, 1510-1526.	3.8	32
54	Flagellin-fused protein targeting M2e and HA2 induces potent humoral and T-cell responses and protects mice against various influenza viruses a subtypes. Journal of Biomedical Science, 2018, 25, 33.	7.0	31

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55	Complete Genome Sequence of the Thermoacidophilic Crenarchaeon Thermoproteus uzoniensis 768-20. Journal of Bacteriology, 2011, 193, 3156-3157.	2.2	30
56	Whole-Genome Analysis of Three Yeast Strains Used for Production of Sherry-Like Wines Revealed Genetic Traits Specific to Flor Yeasts. Frontiers in Microbiology, 2018, 9, 965.	3.5	30
57	Genome of a Novel Bacterium â€œCandidatus Jettenia ecosiâ€•Reconstructed From the Metagenome of an Anammox Bioreactor. Frontiers in Microbiology, 2019, 10, 2442.	3.5	30
58	The Structure of Microbial Community and Degradation of Diatoms in the Deep Near-Bottom Layer of Lake Baikal. PLoS ONE, 2013, 8, e59977.	2.5	29
59	Replication and Maintenance of Linear Phage-Plasmid N15. Microbiology Spectrum, 2015, 3, PLAS-0032-2014.	3.0	28
60	Genome Analysis of Thermosulfurimonas dismutans, the First Thermophilic Sulfur-Disproportionating Bacterium of the Phylum Thermodesulfobacteria. Frontiers in Microbiology, 2016, 7, 950.	3.5	28
61	First structure of archaeal branched-chain amino acid aminotransferase from Thermoproteus uzoniensis specific for l-amino acids and R-amines. Extremophiles, 2016, 20, 215-225.	2.3	28
62	Stable and Variable Parts of Microbial Community in Siberian Deep Subsurface Thermal Aquifer System Revealed in a Long-Term Monitoring Study. Frontiers in Microbiology, 2016, 7, 2101.	3.5	27
63	The 5â€² untranslated region of the maize alcohol dehydrogenase gene contains an internal ribosome entry site. Gene, 2008, 420, 11-16.	2.2	26
64	Thermostable Branched-Chain Amino Acid Transaminases From the Archaea Geoglobus acetivorans and Archaeoglobus fulgidus: Biochemical and Structural Characterization. Frontiers in Bioengineering and Biotechnology, 2019, 7, 7.	4.1	26
65	Closely Located but Totally Distinct: Highly Contrasting Prokaryotic Diversity Patterns in Raised Bogs and Eutrophic Fens. Microorganisms, 2020, 8, 484.	3.6	25
66	Structural insight into the molecular basis of polyextremophilicity of short-chain alcohol dehydrogenase from the hyperthermophilic archaeon Thermococcus sibiricus. Biochimie, 2012, 94, 2628-2638.	2.6	23
67	A novel uncultured bacterium of the family Gallionellaceae: Description and genome reconstruction based on metagenomic analysis of microbial community in acid mine drainage. Microbiology, 2016, 85, 449-461.	1.2	23
68	Combination of M2e peptide with stalk HA epitopes of influenza A virus enhances protective properties of recombinant vaccine. PLoS ONE, 2018, 13, e0201429.	2.5	23
69	Targeted isolation based on metagenomeâ€assembled genomes reveals a phylogenetically distinct group of thermophilic spirochetes from deep biosphere. Environmental Microbiology, 2021, 23, 3585-3598.	3.8	23
70	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. Microorganisms, 2020, 8, 320.	3.6	23
71	Evolutionary stasis of a deep subsurface microbial lineage. ISME Journal, 2021, 15, 2830-2842.	9.8	23
72	Complete Genome Sequence of the Hyperthermophilic Cellulolytic Crenarchaeon â€œThermogladius cellulolyticusâ€•1633. Journal of Bacteriology, 2012, 194, 4446-4447.	2.2	22

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73	Metabolic Diversity and Evolutionary History of the Archaeal Phylum â€œ <i>Candidatus</i> Micrarchaeotaâ€•Uncovered from a Freshwater Lake Metagenome. Applied and Environmental Microbiology, 2020, 86, .	3.1	22
74	Comparative Genome Analysis of the Genus Thiothrix Involving Three Novel Species, Thiothrix subterranea sp. nov. Ku-5, Thiothrix litoralis sp. nov. AS and â€œCandidatus Thiothrix anitrataâ€•sp. nov. A52, Revealed the Conservation of the Pathways of Dissimilatory Sulfur Metabolism and Variations in the Genetic Inventory for Nitrogen Metabolism and Autotrophic Carbon Fixation. Frontiers in Microbiology, 2021, 12, 760289.	3.5	22
75	Recombineering linear DNA that replicate stably in E. coli. Plasmid, 2008, 59, 63-71.	1.4	21
76	Characterization of a Thermostable Short-Chain Alcohol Dehydrogenase from the Hyperthermophilic Archaeon Thermococcus sibiricus. Applied and Environmental Microbiology, 2010, 76, 4096-4098.	3.1	21
77	Metagenomics as a tool for the investigation of uncultured microorganisms. Russian Journal of Genetics, 2015, 51, 431-439.	0.6	21
78	The complete chloroplast genome of parasitic flowering plant Monotropa hypopitys: extensive gene losses and size reduction. Mitochondrial DNA Part B: Resources, 2016, 1, 212-213.	0.4	21
79	Complete Genome Sequence of Strain 1860, a Crenarchaeon of the Genus Pyrobaculum Able To Grow with Various Electron Acceptors. Journal of Bacteriology, 2012, 194, 727-728.	2.2	20
80	Experimental and computational studies on the unusual substrate specificity of branched-chain amino acid aminotransferase from Thermoproteus uzoniensis. Archives of Biochemistry and Biophysics, 2016, 607, 27-36.	3.0	20
81	High immunogenicity of plant-produced candidate influenza vaccine based on the M2e peptide fused to flagellin. Bioengineered, 2016, 7, 28-32.	3.2	20
82	Genomic and Metabolic Insights into Two Novel Thiothrix Species from Enhanced Biological Phosphorus Removal Systems. Microorganisms, 2020, 8, 2030.	3.6	20
83	Functional characterization of the repA replication gene of linear plasmid prophage N15. Research in Microbiology, 2006, 157, 176-183.	2.1	19
84	Effect of metal concentration on the microbial community in acid mine drainage of a polysulfide ore deposit. Microbiology, 2016, 85, 745-751.	1.2	19
85	Sulfur and Methane-Oxidizing Microbial Community in a Terrestrial Mud Volcano Revealed by Metagenomics. Microorganisms, 2020, 8, 1333.	3.6	19
86	Microbial sulfate reduction by Desulfovibrio is an important source of hydrogen sulfide from a large swine finishing facility. Scientific Reports, 2021, 11, 10720.	3.3	18
87	Desulfosporosinus metallidurans sp. nov., an acidophilic, metal-resistant sulfate-reducing bacterium from acid mine drainage. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	1.7	18
88	Tightly regulated, high-level expression from controlled copy number vectors based on the replicon of temperate phage N15. Gene, 2007, 395, 15-21.	2.2	16
89	Specific features of telomerase RNA from Hansenula polymorpha. Rna, 2013, 19, 1563-1574.	3.5	16
90	Draft genome sequence of the first acid-tolerant sulfate-reducing deltaproteobacterium Desulfovibrio sp. TomC having potential for minewater treatment. FEMS Microbiology Letters, 2015, 362, 1-3.	1.8	16

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91	Microbial communities involved in the methane cycle in the near-bottom water layer and sediments of the meromictic subarctic Lake Svetloe. Antonie Van Leeuwenhoek, 2019, 112, 1801-1814.	1.7	16
92	Conversion of Linear DNA with Hairpin Telomeres into a Circular Molecule in the Course of Phage N15 Lytic Replication. Journal of Molecular Biology, 2009, 391, 261-268.	4.2	15
93	Analysis of the complete genome of Fervidococcus fontis confirms the distinct phylogenetic position of the order Fervidicoccales and suggests its environmental function. Extremophiles, 2014, 18, 295-309.	2.3	15
94	Microbial diversity in acidic thermal pools in the Uzon Caldera, Kamchatka. Antonie Van Leeuwenhoek, 2018, 111, 35-43.	1.7	15
95	Rapid High-Yield Transient Expression of Swine Hepatitis E ORF2 Capsid Proteins in Nicotiana benthamiana Plants and Production of Chimeric Hepatitis E Virus-Like Particles Bearing the M2e Influenza Epitope. Plants, 2020, 9, 29.	3.5	15
96	Complete sequence and analysis of the mitochondrial genome of the methylotrophic yeast Hansenula polymorpha DL-1. FEMS Yeast Research, 2011, 11, 464-472.	2.3	14
97	Microbial Processes and Microbial Communities in the Water Column of the Polar Meromictic Lake Bolâ€™shie Khruslomeny at the White Sea Coast. Frontiers in Microbiology, 2020, 11, 1945.	3.5	14
98	Plant-Produced Recombinant Influenza A Virus Candidate Vaccine Based on Flagellin Linked to Conservative Fragments of M2 Protein and Hemagglutintin. Plants, 2020, 9, 162.	3.5	14
99	Gausemycinsâ€…A,B: Cyclic Lipoglycopeptides from<i>Streptomyces</i>sp.**. Angewandte Chemie - International Edition, 2021, 60, 18694-18703.	13.8	14
100	Rokubacteria in Northern Peatlands: Habitat Preferences and Diversity Patterns. Microorganisms, 2022, 10, 11.	3.6	14
101	A Novel Highly Thermostable Multifunctional Beta-Glycosidase from Crenarchaeon<i>Acidilobus saccharovorans</i>. Archaea, 2015, 2015, 1-6.	2.3	13
102	Plastid Genomes of Carnivorous Plants Drosera rotundifolia and Nepenthes Ã— ventrata Reveal Evolutionary Patterns Resembling Those Observed in Parasitic Plants. International Journal of Molecular Sciences, 2019, 20, 4107.	4.1	13
103	Plant-produced Recombinant Influenza A Vaccines Based on the M2e Peptide. Current Pharmaceutical Design, 2018, 24, 1317-1324.	1.9	13
104	New Insight Into the Interspecies Shift of Anammox Bacteria Ca. â€œBrocadiaâ€•and Ca. â€œJetteniaâ€•in Reactors Fed With Formate and Folate. Frontiers in Microbiology, 2021, 12, 802201.	3.5	13
105	Recombination between linear double-stranded DNA substrates in vivo. Analytical Biochemistry, 2009, 387, 139-141.	2.4	12
106	De novo transcriptome assembly of the mycoheterotrophic plant Monotropa hypopitys. Genomics Data, 2017, 11, 60-61.	1.3	12
107	Highly efficient expression of Escherichia coli heat-labile enterotoxin B subunit in plants using potato virus X-based vector. Biochemistry (Moscow), 2008, 73, 1108-1113.	1.5	11
108	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

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109	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.	3.5	11
110	Partition operon expression in the linear plasmid prophage N15 is controlled by both Sop proteins and protelomerase. Molecular Microbiology, 2003, 50, 713-721.	2.5	10
111	A plant-based transient expression system for the rapid production of highly immunogenic Hepatitis E virus-like particles. Biotechnology Letters, 2020, 42, 2441-2446.	2.2	10
112	The water column of the Yamal tundra lakes as a microbial filter preventing methane emission. Biogeosciences, 2021, 18, 2791-2807.	3.3	10
113	Development and Optimization of an Enzyme Immunoassay to Detect Serum Antibodies against the Hepatitis E Virus in Pigs, Using Plant-Derived ORF2 Recombinant Protein. Vaccines, 2021, 9, 991.	4.4	10
114	High-Yield Production of Receptor Binding Domain of SARS-CoV-2 Linked to Bacterial Flagellin in Plants Using Self-Replicating Viral Vector pEff. Plants, 2021, 10, 2682.	3.5	10
115	A study of the effect of expression of the gene encoding the membrane H+-pyrophosphatase of Rhodospirillum rubrum on salt resistance of transgenic tobacco plants. Doklady Biological Sciences, 2006, 409, 346-348.	0.6	9
116	The 5â€²-untranslated region of the maize alcohol dehydrogenase gene provides efficient translation of mRNA in plants under stress conditions. Molecular Biology, 2007, 41, 914-919.	1.3	9
117	Understanding and Engineering Thermostability in DNA Ligase from <i>Thermococcus</i> sp. 1519. Biochemistry, 2015, 54, 3076-3085.	2.5	9
118	Metagenome of the Siberian Underground Water Reservoir. Genome Announcements, 2017, 5, .	0.8	9
119	TheYABBYGenes of Leaf and Leaf-Like Organ Polarity in Leafless PlantMonotropa hypopitys. International Journal of Genomics, 2018, 2018, 1-16.	1.6	9
120	Nanoparticles based on artificial self-assembling peptide and displaying M2e peptide and stalk HA epitopes of influenza A virus induce potent humoral and T-cell responses and protect against the viral infection. Nanomedicine: Nanotechnology, Biology, and Medicine, 2022, 39, 102463.	3.3	9
121	Peat-Inhabiting Verrucomicrobia of the Order Methylacidiphilales Do Not Possess Methanotrophic Capabilities. Microorganisms, 2021, 9, 2566.	3.6	9
122	Extended Function of Plasmid Partition Genes: the Sop System of Linear Phage-Plasmid N15 Facilitates Late Gene Expression. Journal of Bacteriology, 2008, 190, 3538-3545.	2.2	8
123	The impact of genomics on research in diversity and evolution of archaea. Biochemistry (Moscow), 2012, 77, 799-812.	1.5	8
124	Genome sequence of the copper resistant and acid-tolerant Desulfosporosinus sp. BG isolated from the tailings of a molybdenum-tungsten mine in the Transbaikal area. Genomics Data, 2017, 11, 106-108.	1.3	8
125	Thermophilic Chloroflexi Dominate in the Microbial Community Associated with Coal-Fire Gas Vents in the Kuznetsk Coal Basin, Russia. Microorganisms, 2021, 9, 948.	3.6	8
126	Reclassification of Sphaerotilus natans subsp. sulfidivorans Gridneva et al. 2011 as Sphaerotilus sulfidivorans sp. nov. and comparative genome analysis of the genus Sphaerotilus. Archives of Microbiology, 2021, 203, 1595-1599.	2.2	8

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127	Contribution of internal initiation to translation of cellular mRNAs containing IRESs. Biochemical Society Transactions, 2008, 36, 694-697.	3.4	7
128	The optimization of viral vector translation improves the production of recombinant proteins in plants. Molecular Biology, 2009, 43, 524-527.	1.3	7
129	On the role of centromere dispersion in stability of linear bacterial plasmids. Plasmid, 2010, 64, 51-59.	1.4	7
130	Complete mitochondrial genome of the cephalosporin-producing fungusAcremonium chrysogenum. Mitochondrial DNA, 2015, 26, 943-944.	0.6	7
131	Metagenome of the Microbial Community of Anammox Granules in a Nitritation/Anammox Wastewater Treatment System. Genome Announcements, 2017, 5, .	0.8	7
132	The complete mitochondrial genome of the carnivorous flowering plant <i>Nepenthes X Ventrata</i>. Mitochondrial DNA Part B: Resources, 2018, 3, 1259-1260.	0.4	7
133	Novel Endoxylanases of the Moderately Thermophilic Polysaccharide-Degrading Bacterium Melioribacter roseus. Journal of Microbiology and Biotechnology, 2015, 25, 1476-1484.	2.1	7
134	Complete mitochondrial genome of compactin-producing fungus Penicillium solitum and comparative analysis of Trichocomaceae mitochondrial genomes. FEMS Microbiology Letters, 2012, 329, 9-17.	1.8	6
135	Desulfovibrio desulfuricans AY5 Isolated from a Patient with Autism Spectrum Disorder Binds Iron in Low-Soluble Greigite and Pyrite. Microorganisms, 2021, 9, 2558.	3.6	6
136	Two New Species of Filamentous Sulfur Bacteria of the Genus Thiothrix, Thiothrix winogradskyi sp. nov. and â€˜Candidatus Thiothrix sulfatifontisâ€™ sp. nov.. Microorganisms, 2022, 10, 1300.	3.6	6
137	Isolation and functional characterization of lipase from the thermophilic alkali-tolerant bacterium Thermosyntropha lipolytica. Applied Biochemistry and Microbiology, 2012, 48, 338-343.	0.9	5
138	Structures of Î²-glycosidase from Acidilobus saccharovorans in complexes with tris and glycerol. Doklady Biochemistry and Biophysics, 2013, 449, 99-101.	0.9	5
139	Metagenome Sequence of a Microbial Community from the Gold Mine Tailings in the Kuzbass Area, Russia. Genome Announcements, 2017, 5, .	0.8	5
140	Genomes of three bacteriophages from the deep subsurface aquifer. Data in Brief, 2019, 22, 488-491.	1.0	5
141	Highly Immunogenic Nanoparticles Based on a Fusion Protein Comprising the M2e of Influenza A Virus and a Lipopeptide. Viruses, 2020, 12, 1133.	3.3	5
142	Hiding in Plain Sight: The Globally Distributed Bacterial Candidate Phylum PAUC34f. Frontiers in Microbiology, 2020, 11, 376.	3.5	5
143	Extensive plastome reduction and loss of photosynthesis genes in Diphelypaea coccinea, a holoparasitic plant of the family Orobanchaceae. PeerJ, 2019, 7, e7830.	2.0	5
144	Transient expression of recombinant proteins in plants using potato virus X based vectors. Methods in Enzymology, 2021, 660, 205-222.	1.0	5

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145	Expression of genes involved in DNA repair and telomere maintenance in the yeast Hansenula polymorpha DL1 under heat stress. Doklady Biochemistry and Biophysics, 2015, 462, 185-188.	0.9	4
146	Phage N15 protelomerase resolves its tos recognition site into hairpin telomeres within mammalian cells. Analytical Biochemistry, 2019, 583, 113361.	2.4	4
147	Complete Genome Sequences of Endophytic Bacilli Isolated from Grapevine Plants. Microbiology Resource Announcements, 2019, 8, .	0.6	4
148	A novel narnavirus from a Saccharomyces cerevisiae flor strain. Archives of Virology, 2020, 165, 789-791.	2.1	4
149	The genome-wide transcription response to telomerase deficiency in the thermotolerant yeast Hansenula polymorpha DL-1. BMC Genomics, 2017, 18, 492.	2.8	3
150	Draft Genome Sequence of Bacillus velezensis BZR 277, a Prospective Biocontrol Agent against Phytoparasitic Nematodes. Microbiology Resource Announcements, 2021, 10, .	0.6	3
151	Phylogenetic diversity in sulphate-reducing bacterial communities from oxidised and reduced bottom sediments of the Barents Sea. Antonie Van Leeuwenhoek, 2022, , 1.	1.7	3
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