

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	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. <i>Nanomedicine: Nanotechnology, Biology, and Medicine</i> , 2022, 39, 102463.	3.3	9
2	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
3	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
4	Rokubacteria in Northern Peatlands: Habitat Preferences and Diversity Patterns. <i>Microorganisms</i> , 2022, 10, 11.	3.6	14
5	Phylogenetic diversity in sulphate-reducing bacterial communities from oxidised and reduced bottom sediments of the Barents Sea. <i>Antonie Van Leeuwenhoek</i> , 2022, , 1.	1.7	3
6	Two New Species of Filamentous Sulfur Bacteria of the Genus <i>Thiothrix</i> , <i>Thiothrix winogradskyi</i> sp. nov. and <i>Candidatus Thiothrix sulfatifontis</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 ^T , a Facultatively Anaerobic Acidobacterium Capable of Dissimilatory Fe(III) Reduction. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	2
10	Evolutionary stasis of a deep subsurface microbial lineage. <i>ISME Journal</i> , 2021, 15, 2830-2842.	9.8	23
11	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
12	The water column of the Yamal tundra lakes as a microbial filter preventing methane emission. <i>Biogeosciences</i> , 2021, 18, 2791-2807.	3.3	10
13	Draft Genome Sequence of <i>Bacillus velezensis</i> BZR 277, a Prospective Biocontrol Agent against Phytotoxic Nematodes. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	3
14	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
15	Gausemycins A,B: Cyclic Lipoglycopeptides from <i>Streptomyces</i> sp. **. <i>Angewandte Chemie</i> , 2021, 133, 18842-18851.	2.0	1
16	Gausemycins A,B: Cyclic Lipoglycopeptides from <i>Streptomyces</i> sp. **. <i>Angewandte Chemie - International Edition</i> , 2021, 60, 18694-18703.	13.8	14
17	Innentitelbild: Gausemycins A,B: Cyclic Lipoglycopeptides from <i>Streptomyces</i> sp. (<i>Angew. Chem.</i>) <i>TJ ETQg</i> 1 1 0.784314 rgBT 2.0 1	2.0	1
18	<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

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19	Development and Optimization of an Enzyme Immunoassay to Detect Serum Antibodies against the Hepatitis E Virus in Pigs, Using Plant-Derived ORF2 Recombinant Protein. <i>Vaccines</i> , 2021, 9, 991.	4.4	10
20	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
21	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
22	Comparative Genome Analysis of the Genus <i>Thiothrix</i> Involving Three Novel Species, <i>Thiothrix subterranea</i> sp. nov., <i>Thiothrix litoralis</i> sp. nov. AS and <i>Candidatus Thiothrix anitrata</i> 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. <i>Frontiers in Microbiology</i> , 2021, 12, 760289.	3.5	22
23	Transient expression of recombinant proteins in plants using potato virus X based vectors. <i>Methods in Enzymology</i> , 2021, 660, 205-222.	1.0	5
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	High-Yield Production of Receptor Binding Domain of SARS-CoV-2 Linked to Bacterial Flagellin in Plants Using Self-Replicating Viral Vector pEff. <i>Plants</i> , 2021, 10, 2682.	3.5	10
28	Peat-Inhabiting Verrucomicrobia of the Order Methylophilales Do Not Possess Methanotrophic Capabilities. <i>Microorganisms</i> , 2021, 9, 2566.	3.6	9
29	Rapid High-Yield Transient Expression of Swine Hepatitis E ORF2 Capsid Proteins in <i>Nicotiana benthamiana</i> Plants and Production of Chimeric Hepatitis E Virus-Like Particles Bearing the M2e Influenza Epitope. <i>Plants</i> , 2020, 9, 29.	3.5	15
30	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
31	Highly Immunogenic Nanoparticles Based on a Fusion Protein Comprising the M2e of Influenza A Virus and a Lipopeptide. <i>Viruses</i> , 2020, 12, 1133.	3.3	5
32	Microbial Life in the Deep Subsurface Aquifer Illuminated by Metagenomics. <i>Frontiers in Microbiology</i> , 2020, 11, 572252.	3.5	48
33	A plant-based transient expression system for the rapid production of highly immunogenic Hepatitis E virus-like particles. <i>Biotechnology Letters</i> , 2020, 42, 2441-2446.	2.2	10
34	Sulfur and Methane-Oxidizing Microbial Community in a Terrestrial Mud Volcano Revealed by Metagenomics. <i>Microorganisms</i> , 2020, 8, 1333.	3.6	19
35	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.	3.5	14
36	Ancestral Absence of Electron Transport Chains in Patescibacteria and DPANN. <i>Frontiers in Microbiology</i> , 2020, 11, 1848.	3.5	62

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37	Genomic and Metabolic Insights into Two Novel Thiothrix Species from Enhanced Biological Phosphorus Removal Systems. <i>Microorganisms</i> , 2020, 8, 2030.	3.6	20
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	Plant-Produced Recombinant Influenza A Virus Candidate Vaccine Based on Flagellin Linked to Conservative Fragments of M2 Protein and Hemagglutinin. <i>Plants</i> , 2020, 9, 162.	3.5	14
40	Hiding in Plain Sight: The Globally Distributed Bacterial Candidate Phylum PAUC34f. <i>Frontiers in Microbiology</i> , 2020, 11, 376.	3.5	5
41	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
42	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
43	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
44	A novel narnavirus from a <i>Saccharomyces cerevisiae</i> flor strain. <i>Archives of Virology</i> , 2020, 165, 789-791.	2.1	4
45	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
46	Phage N15 protelomerase resolves its <i>tos</i> recognition site into hairpin telomeres within mammalian cells. <i>Analytical Biochemistry</i> , 2019, 583, 113361.	2.4	4
47	Genome of a Novel Bacterium <i>Candidatus</i> <i>Jettenia ecosi</i> Reconstructed From the Metagenome of an Anammox Bioreactor. <i>Frontiers in Microbiology</i> , 2019, 10, 2442.	3.5	30
48	Plastid Genomes of Carnivorous Plants <i>Drosera rotundifolia</i> and <i>Nepenthes</i> <i>ventrata</i> Reveal Evolutionary Patterns Resembling Those Observed in Parasitic Plants. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4107.	4.1	13
49	Genomes of three bacteriophages from the deep subsurface aquifer. <i>Data in Brief</i> , 2019, 22, 488-491.	1.0	5
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	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
54	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

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55	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
56	Genome Analysis of <i>Fimbrigiobus ruber</i> SP5 ^T , a Planctomycete with Confirmed Chitinolytic Capability. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	59
57	Methane as an Organic Matter Source and the Trophic Basis of a Laptev Sea Cold Seep Microbial Community. <i>Geomicrobiology Journal</i> , 2018, 35, 411-423.	2.0	36
58	Microbial diversity in acidic thermal pools in the Uzon Caldera, Kamchatka. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 35-43.	1.7	15
59	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
60	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
61	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
62	The YABBY Genes of Leaf and Leaf-Like Organ Polarity in Leafless Plant <i>Monotropa hypopitys</i> . <i>International Journal of Genomics</i> , 2018, 2018, 1-16.	1.6	9
63	Flagellin-fused protein targeting M2e and HA2 induces potent humoral and T-cell responses and protects mice against various influenza viruses a subtypes. <i>Journal of Biomedical Science</i> , 2018, 25, 33.	7.0	31
64	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
65	Combination of M2e peptide with stalk HA epitopes of influenza A virus enhances protective properties of recombinant vaccine. <i>PLoS ONE</i> , 2018, 13, e0201429.	2.5	23
66	Shifting the limits in wheat research and breeding using a fully annotated reference genome. <i>Science</i> , 2018, 361, .	12.6	2,424
67	Plant-produced Recombinant Influenza A Vaccines Based on the M2e Peptide. <i>Current Pharmaceutical Design</i> , 2018, 24, 1317-1324.	1.9	13
68	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
69	De novo transcriptome assembly of the mycoheterotrophic plant <i>Monotropa hypopitys</i> . <i>Genomics Data</i> , 2017, 11, 60-61.	1.3	12
70	Metagenome of the Microbial Community of Anammox Granules in a Nitritation/Anammox Wastewater Treatment System. <i>Genome Announcements</i> , 2017, 5, .	0.8	7
71	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
72	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

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73	Efficient Transient Expression of Recombinant Proteins in Plants by the Novel pEff Vector Based on the Genome of Potato Virus X. <i>Frontiers in Plant Science</i> , 2017, 8, 247.	3.6	60
74	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
75	Metagenome of the Siberian Underground Water Reservoir. <i>Genome Announcements</i> , 2017, 5, .	0.8	9
76	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
77	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
78	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
79	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
80	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
81	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
82	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
83	Internal initiation of translation of mRNA in the methylotrophic yeast <i>Hansenula polymorpha</i> . <i>Biochemistry (Moscow)</i> , 2016, 81, 521-529.	1.5	1
84	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
85	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
86	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
87	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
88	High immunogenicity of plant-produced candidate influenza vaccine based on the M2e peptide fused to flagellin. <i>Bioengineered</i> , 2016, 7, 28-32.	3.2	20
89	Replication and Maintenance of Linear Phage-Plasmid N15. <i>Microbiology Spectrum</i> , 2015, 3, PLAS-0032-2014.	3.0	28
90	Protection against Multiple Influenza A Virus Strains Induced by Candidate Recombinant Vaccine Based on Heterologous M2e Peptides Linked to Flagellin. <i>PLoS ONE</i> , 2015, 10, e0119520.	2.5	48

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91	A Novel Highly Thermostable Multifunctional Beta-Glycosidase from Crenarchaeon <i>Acidilobus saccharovorans</i> . <i>Archaea</i> , 2015, 2015, 1-6.	2.3	13
92	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. <i>Vaccine</i> , 2015, 33, 3398-3406.	3.8	33
93	Metagenomics as a tool for the investigation of uncultured microorganisms. <i>Russian Journal of Genetics</i> , 2015, 51, 431-439.	0.6	21
94	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
95	Comparative Metagenomics of Eight Geographically Remote Terrestrial Hot Springs. <i>Microbial Ecology</i> , 2015, 70, 411-424.	2.8	118
96	Understanding and Engineering Thermostability in DNA Ligase from <i>Thermococcus</i> sp. 1519. <i>Biochemistry</i> , 2015, 54, 3076-3085.	2.5	9
97	Draft genome sequence of the first acid-tolerant sulfate-reducing deltaproteobacterium <i>Desulfovibrio</i> sp. TomC having potential for minewater treatment. <i>FEMS Microbiology Letters</i> , 2015, 362, 1-3.	1.8	16
98	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. <i>Vaccine</i> , 2015, 33, 3392-3397.	3.8	32
99	Rapid high-yield expression of a candidate influenza vaccine based on the ectodomain of M2 protein linked to flagellin in plants using viral vectors. <i>BMC Biotechnology</i> , 2015, 15, 42.	3.3	53
100	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.	3.1	46
101	Complete mitochondrial genome of the cephalosporin-producing fungus <i>Acremonium chrysogenum</i> . <i>Mitochondrial DNA</i> , 2015, 26, 943-944.	0.6	7
102	Novel Endoxylanases of the Moderately Thermophilic Polysaccharide-Degrading Bacterium <i>Melioribacter roseus</i> . <i>Journal of Microbiology and Biotechnology</i> , 2015, 25, 1476-1484.	2.1	7
103	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.	2.5	93
104	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
105	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>Terrimicrobia</i> group 3. <i>Environmental Microbiology</i> , 2014, 16, 1549-1565.	3.8	58
106	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.	2.3	15
107	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.	0.5	0
108	Composition of the microbial communities of bituminous constructions at natural oil seeps at the bottom of Lake Baikal. <i>Microbiology</i> , 2013, 82, 373-382.	1.2	11

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109	Specific features of telomerase RNA from <i>Hansenula polymorpha</i> . <i>Rna</i> , 2013, 19, 1563-1574.	3.5	16
110	Structures of Î²-glycosidase from <i>Acidilobus saccharovorans</i> in complexes with tris and glycerol. <i>Doklady Biochemistry and Biophysics</i> , 2013, 449, 99-101.	0.9	5
111	Genome sequence and analysis of methylotrophic yeast <i>Hansenula polymorpha</i> DL1. <i>BMC Genomics</i> , 2013, 14, 837.	2.8	81
112	The Use of Transient Expression Systems for the Rapid Production of Virus-like Particles in Plants. <i>Current Pharmaceutical Design</i> , 2013, 19, 5564-5573.	1.9	62
113	A molecular assembly system for presentation of antigens on the surface of HBc virus-like particles. <i>Virology</i> , 2013, 435, 293-300.	2.4	38
114	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.	2.5	68
115	Comparative Genomic Analysis of <i>Mycobacterium tuberculosis</i> Drug Resistant Strains from Russia. <i>PLoS ONE</i> , 2013, 8, e56577.	2.5	42
116	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.	2.5	29
117	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.	2.2	20
118	Complete Genome Sequence of the Hyperthermophilic Cellulolytic Crenarchaeon <i>Thermogladius cellulolyticus</i> 1633. <i>Journal of Bacteriology</i> , 2012, 194, 4446-4447.	2.2	22
119	The impact of genomics on research in diversity and evolution of archaea. <i>Biochemistry (Moscow)</i> , 2012, 77, 799-812.	1.5	8
120	Structural insight into the molecular basis of polyextremophilicity of short-chain alcohol dehydrogenase from the hyperthermophilic archaeon <i>Thermococcus sibiricus</i> . <i>Biochimie</i> , 2012, 94, 2628-2638.	2.6	23
121	Plant-produced recombinant influenza vaccine based on virus-like HBc particles carrying an extracellular domain of M2 protein. <i>Biochemistry (Moscow)</i> , 2012, 77, 33-40.	1.5	43
122	Microbial community structure in methane hydrate-bearing sediments of freshwater Lake Baikal. <i>FEMS Microbiology Ecology</i> , 2012, 79, 348-358.	2.7	77
123	Complete mitochondrial genome of compactin-producing fungus <i>Penicillium solitum</i> and comparative analysis of <i>Trichocomaceae</i> mitochondrial genomes. <i>FEMS Microbiology Letters</i> , 2012, 329, 9-17.	1.8	6
124	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.	0.9	5
125	Genome sequence and analysis of the tuber crop potato. <i>Nature</i> , 2011, 475, 189-195.	27.8	1,912
126	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.	2.2	35

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127	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.	2.3	14
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