

Elena N Ilina

List of Publications by Year in descending order

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100
papers

2,719
citations

218677

26
h-index

206112

48
g-index

119
all docs

119
docs citations

119
times ranked

3969
citing authors

#	ARTICLE	IF	CITATIONS
1	Links of gut microbiota composition with alcohol dependence syndrome and alcoholic liver disease. <i>Microbiome</i> , 2017, 5, 141.	11.1	296
2	Global phylogeography and ancient evolution of the widespread human gut virus crAssphage. <i>Nature Microbiology</i> , 2019, 4, 1727-1736.	13.3	184
3	Microfluidic droplet platform for ultrahigh-throughput single-cell screening of biodiversity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 2550-2555.	7.1	182
4	High Interlaboratory Reproducibility of Matrix-Assisted Laser Desorption Ionization-Time of Flight Mass Spectrometry-Based Species Identification of Nonfermenting Bacteria. <i>Journal of Clinical Microbiology</i> , 2009, 47, 3732-3734.	3.9	168
5	Direct Bacterial Profiling by Matrix-Assisted Laser Desorption Ionization Time-of-Flight Mass Spectrometry for Identification of Pathogenic <i>Neisseria</i> . <i>Journal of Molecular Diagnostics</i> , 2009, 11, 75-86.	2.8	103
6	Evolutionary pathway analysis and unified classification of East Asian lineage of <i>Mycobacterium tuberculosis</i> . <i>Scientific Reports</i> , 2017, 7, 9227.	3.3	98
7	Genome-wide <i>Mycobacterium tuberculosis</i> variation (GMTV) database: a new tool for integrating sequence variations and epidemiology. <i>BMC Genomics</i> , 2014, 15, 308.	2.8	89
8	Ultrahigh-throughput functional profiling of microbiota communities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 9551-9556.	7.1	79
9	Phigaro: high-throughput prophage sequence annotation. <i>Bioinformatics</i> , 2020, 36, 3882-3884.	4.1	75
10	Molecular characteristics of rifampicin- and isoniazid-resistant <i>Mycobacterium tuberculosis</i> isolates from the Russian Federation. <i>Journal of Antimicrobial Chemotherapy</i> , 2007, 59, 1057-1064.	3.0	68
11	Discrimination between <i>Streptococcus pneumoniae</i> and <i>Streptococcus mitis</i> based on sorting of their MALDI mass spectra. <i>Clinical Microbiology and Infection</i> , 2013, 19, 1066-1071.	6.0	67
12	Chromosome 18 Transcriptome Profiling and Targeted Proteome Mapping in Depleted Plasma, Liver Tissue and HepG2 Cells. <i>Journal of Proteome Research</i> , 2013, 12, 123-134.	3.7	59
13	Emergence of carbapenemase-producing Gram-negative bacteria in Saint Petersburg, Russia. <i>International Journal of Antimicrobial Agents</i> , 2014, 44, 152-155.	2.5	55
14	Long-term impact of fecal transplantation in healthy volunteers. <i>BMC Microbiology</i> , 2019, 19, 312.	3.3	55
15	Misidentification of alpha-hemolytic streptococci by routine tests in clinical practice. <i>Infection, Genetics and Evolution</i> , 2011, 11, 1709-1715.	2.3	50
16	Chromosome 18 Transcriptoproteome of Liver Tissue and HepG2 Cells and Targeted Proteome Mapping in Depleted Plasma: Update 2013. <i>Journal of Proteome Research</i> , 2014, 13, 183-190.	3.7	44
17	Application of matrix-assisted laser desorption/ionization time-of-flight mass spectrometry for the study of <i>Helicobacter pylori</i> . <i>Rapid Communications in Mass Spectrometry</i> , 2010, 24, 328-334.	1.5	43
18	Mass spectrometry based methods for the discrimination and typing of mycobacteria. <i>Infection, Genetics and Evolution</i> , 2012, 12, 838-845.	2.3	43

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19	Comparative Genomic Analysis of Mycobacterium tuberculosis Drug Resistant Strains from Russia. PLoS ONE, 2013, 8, e56577.	2.5	42
20	Mutation in ribosomal protein S5 leads to spectinomycin resistance in Neisseria gonorrhoeae. Frontiers in Microbiology, 2013, 4, 186.	3.5	40
21	Matrix-Assisted Laser Desorption Ionization-Time of Flight (Mass Spectrometry) for Hepatitis C Virus Genotyping. Journal of Clinical Microbiology, 2005, 43, 2810-2815.	3.9	39
22	Shifts in the Human Gut Microbiota Structure Caused by Quadruple Helicobacter pylori Eradication Therapy. Frontiers in Microbiology, 2019, 10, 1902.	3.5	39
23	Genome analysis of E. coli isolated from Crohn's disease patients. BMC Genomics, 2017, 18, 544.	2.8	37
24	RNA-Seq gene expression profiling of HepG2 cells: the influence of experimental factors and comparison with liver tissue. BMC Genomics, 2014, 15, 1108.	2.8	34
25	Proteome analysis of the Mycobacterium tuberculosis Beijing B0/W148 cluster. Scientific Reports, 2016, 6, 28985.	3.3	34
26	Relation between Genetic Markers of Drug Resistance and Susceptibility Profile of Clinical <i>Neisseria gonorrhoeae</i> Strains. Antimicrobial Agents and Chemotherapy, 2008, 52, 2175-2182.	3.2	31
27	Contribution of Podoviridae and Myoviridae bacteriophages to the effectiveness of anti-staphylococcal therapeutic cocktails. Scientific Reports, 2020, 10, 18612.	3.3	31
28	Comparative evaluation of new typing schemes for urogenital <i>Chlamydia trachomatis</i> isolates. FEMS Immunology and Medical Microbiology, 2010, 59, 188-196.	2.7	27
29	A MALDI TOF MS-based minisequencing method for rapid detection of TEM-type extended-spectrum beta-lactamases in clinical strains of Enterobacteriaceae. Journal of Microbiological Methods, 2008, 75, 385-391.	1.6	25
30	Novel Klebsiella pneumoniae K23-Specific Bacteriophages From Different Families: Similarity of Depolymerases and Their Therapeutic Potential. Frontiers in Microbiology, 2021, 12, 669618.	3.5	24
31	Molecular Surveillance of Clinical <i>Neisseria gonorrhoeae</i> Isolates in Russia. Journal of Clinical Microbiology, 2010, 48, 3681-3689.	3.9	23
32	State of the Art of Chromosome 18-Centric HPP in 2016: Transcriptome and Proteome Profiling of Liver Tissue and HepG2 Cells. Journal of Proteome Research, 2016, 15, 4030-4038.	3.7	23
33	Unusual Large-Scale Chromosomal Rearrangements in Mycobacterium tuberculosis Beijing B0/W148 Cluster Isolates. PLoS ONE, 2014, 9, e84971.	2.5	23
34	First detection of VIM-4 metallo- β -lactamase-producing Escherichia coli in Russia. Clinical Microbiology and Infection, 2012, 18, E214-E217.	6.0	22
35	Molecular typing of Mycobacterium tuberculosis circulated in Moscow, Russian Federation. European Journal of Clinical Microbiology and Infectious Diseases, 2011, 30, 181-191.	2.9	21
36	Spoligotyping of Mycobacterium tuberculosis complex isolates using hydrogel oligonucleotide microarrays. Infection, Genetics and Evolution, 2014, 26, 41-46.	2.3	21

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37	Long-Term Dissemination of CTX-M-5-Producing Hypermutable <i>Salmonella enterica</i> Serovar Typhimurium Sequence Type 328 Strains in Russia, Belarus, and Kazakhstan. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 5202-5210.	3.2	20
38	Mass-spectrometry based minisequencing method for the rapid detection of drug resistance in <i>Mycobacterium tuberculosis</i> . <i>Journal of Microbiological Methods</i> , 2007, 70, 395-405.	1.6	19
39	Mechanisms of Macrolide Resistance among <i>Streptococcus pneumoniae</i> Isolates from Russia. <i>Antimicrobial Agents and Chemotherapy</i> , 2008, 52, 2260-2262.	3.2	19
40	Fluoroquinolone-resistant <i>Neisseria gonorrhoeae</i> isolates from Russia: molecular mechanisms implicated. <i>Journal of Antimicrobial Chemotherapy</i> , 2004, 53, 653-656.	3.0	18
41	Metagenomic Analysis of Gingival Sulcus Microbiota and Pathogenesis of Periodontitis Associated with Type 2 Diabetes Mellitus. <i>Bulletin of Experimental Biology and Medicine</i> , 2017, 163, 718-721.	0.8	16
42	Drift of the Subgingival Periodontal Microbiome during Chronic Periodontitis in Type 2 Diabetes Mellitus Patients. <i>Pathogens</i> , 2021, 10, 504.	2.8	16
43	Complete Genome Sequence of <i>Mycobacterium bovis</i> Strain BCG-1 (Russia). <i>Genome Announcements</i> , 2016, 4, .	0.8	15
44	Analysis of nosocomial <i>Staphylococcus haemolyticus</i> by MLST and MALDI-TOF mass spectrometry. <i>Infection, Genetics and Evolution</i> , 2016, 39, 99-105.	2.3	15
45	Data on gut metagenomes of the patients with <i>Helicobacter pylori</i> infection before and after the antibiotic therapy. <i>Data in Brief</i> , 2017, 11, 68-71.	1.0	14
46	Deep Functional Profiling Facilitates the Evaluation of the Antibacterial Potential of the Antibiotic Amicoumacin. <i>Antibiotics</i> , 2020, 9, 157.	3.7	14
47	Species Diversity of Bifidobacteria in the Intestinal Microbiota Studied Using MALDI-TOF Mass-Spectrometry. <i>Vestnik Rossiiskoi Akademii Meditsinskikh Nauk</i> , 2015, 70, 435-440.	0.6	14
48	Detection of Fluoroquinolone Resistance Single-Nucleotide Polymorphisms in <i>Neisseria gonorrhoeae</i> <i>gyrA</i> and <i>parC</i> Using MALDI-TOF Mass Spectrometry. <i>Molecular Biology</i> , 2005, 39, 806-814.	1.3	13
49	Proteogenomic analysis of <i>Mycobacterium tuberculosis</i> Beijing B0/W148 cluster strains. <i>Journal of Proteomics</i> , 2019, 192, 18-26.	2.4	11
50	Metabolic Changes of <i>Mycobacterium tuberculosis</i> during the Anti-Tuberculosis Therapy. <i>Pathogens</i> , 2020, 9, 131.	2.8	11
51	Transcriptional Landscape of <i>Staphylococcus aureus</i> Kayvirus Bacteriophage vB_SauM-515A1. <i>Viruses</i> , 2020, 12, 1320.	3.3	10
52	Hepatitis B Virus Genetic Typing Using Mass-Spectrometry. <i>Bulletin of Experimental Biology and Medicine</i> , 2009, 147, 220-225.	0.8	9
53	The role of IS6110 in micro- and macroevolution of <i>Mycobacterium tuberculosis</i> lineage 2. <i>Molecular Phylogenetics and Evolution</i> , 2019, 139, 106559.	2.7	9
54	Application of MALDI-TOF mass spectrometry for differentiation of closely related species of the <i>Arthrobacter crystallopoietes</i> phylogenetic group. <i>Microbiology</i> , 2012, 81, 696-701.	1.2	8

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55	Genetic Environment of the bla KPC-2 Gene in a Klebsiella pneumoniae Isolate That May Have Been Imported to Russia from Southeast Asia. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	3.2	8
56	System OMICs analysis of Mycobacterium tuberculosis Beijing B0/W148 cluster. <i>Scientific Reports</i> , 2019, 9, 19255.	3.3	7
57	Identification of Clinically Significant Prostate Cancer by Combined PCA3 and AMACR mRNA Detection in Urine Samples. <i>Research and Reports in Urology</i> , 2020, Volume 12, 403-413.	1.0	7
58	Faecal Transplant in GIT Treatment (Pilot Clinical Experience). <i>Doctor Ru</i> , 2019, 158, 40-46.	0.3	7
59	Analysis of genetic markers of N. Gonorrhoeae resistance to β -lactam antibiotics. <i>Bulletin of Experimental Biology and Medicine</i> , 2006, 141, 610-615.	0.8	6
60	Analysis of the contribution of molecular mechanisms into formation of gonococcal resistance to tetracycline. <i>Bulletin of Experimental Biology and Medicine</i> , 2007, 144, 432-437.	0.8	6
61	Molecular mechanisms of formation of drug resistance in Neisseria gonorrhoeae: History and prospects. <i>Molecular Genetics, Microbiology and Virology</i> , 2015, 30, 132-140.	0.3	6
62	Data on gut metagenomes of the patients with alcoholic dependence syndrome and alcoholic liver cirrhosis. <i>Data in Brief</i> , 2017, 11, 98-102.	1.0	6
63	Analysis of the genetic determinants of multidrug and extensive drug resistance in Mycobacterium tuberculosis with the use of an oligonucleotide microchip. <i>Molecular Biology</i> , 2014, 48, 214-226.	1.3	5
64	The mystery of the fourth clone: comparative genomic analysis of four non-typeable Streptococcus pneumoniae strains with different susceptibilities to optochin. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2016, 35, 119-130.	2.9	5
65	Inhibitory effect of streptococci on the growth of M. catarrhalis strains and the diversity of putative bacteriocin-like gene loci in the genomes of S. pneumoniae and its relatives. <i>AMB Express</i> , 2017, 7, 218.	3.0	5
66	Draft genomes of Enterococcus faecium strains isolated from human feces before and after eradication therapy against Helicobacter pylori. <i>Data in Brief</i> , 2018, 16, 511-514.	1.0	5
67	Gene Networks Underlying the Resistance of Bifidobacterium longum to Inflammatory Factors. <i>Frontiers in Immunology</i> , 2020, 11, 595877.	4.8	5
68	Deep Functional Profiling of Wild Animal Microbiomes Reveals Probiotic Bacillus pumilus Strains with a Common Biosynthetic Fingerprint. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1168.	4.1	5
69	The effects of Levilactobacillus brevis on the physiological parameters and gut microbiota composition of rats subjected to desynchronization. <i>Microbial Cell Factories</i> , 2021, 20, 226.	4.0	5
70	Molecular typing of N. gonorrhoeae strains prevalent in the Russian Federation. <i>Bulletin of Experimental Biology and Medicine</i> , 2003, 136, 179-182.	0.8	4
71	Characteristics of Emergence of Mutants Resistant to Nalidixic Acid and Novobiocin in E. coli Strains with recA and lexA Mutations. <i>Molecular Genetics, Microbiology and Virology</i> , 2018, 33, 30-33.	0.3	4
72	VERA: agent-based modeling transmission of antibiotic resistance between human pathogens and gut microbiota. <i>Bioinformatics</i> , 2019, 35, 3803-3811.	4.1	4

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73	Separation of Donor and Recipient Microbial Diversity Allows Determination of Taxonomic and Functional Features of Gut Microbiota Restructuring following Fecal Transplantation. <i>MSystems</i> , 2021, 6, e0081121.	3.8	4
74	Mass spectrometry of nucleic acids in molecular medicine. <i>Russian Journal of Bioorganic Chemistry</i> , 2009, 35, 135-149.	1.0	3
75	M. BOVIS BCG-1 (RUSSIA) SUB-STRAIN GENOME STABILITY INVESTIGATION WITHIN THE ENTIRE PRODUCTION PROCESS. <i>Zhurnal Mikrobiologii Epidemiologii I Immunobiologii</i> , 2018, 95, 58-67.	1.0	3
76	Direct evaluation of drug resistance parameters in gonococcus. <i>Bulletin of Experimental Biology and Medicine</i> , 2007, 144, 227-230.	0.8	2
77	Molecular genetic characterization of methicillin-resistant <i>Staphylococcus aureus</i> isolates recovered from Moscow clinics. <i>Molecular Genetics, Microbiology and Virology</i> , 2010, 25, 66-70.	0.3	2
78	Multiple-locus variable number tandem repeat analysis of <i>Neisseria gonorrhoeae</i> isolates in Russia. <i>Infection, Genetics and Evolution</i> , 2013, 14, 8-14.	2.3	2
79	Large scale analysis of amino acid substitutions in bacterial proteomics. <i>BMC Bioinformatics</i> , 2016, 17, 450.	2.6	2
80	Aureolic Acid Group of Agents as Potential Antituberculosis Drugs. <i>Antibiotics</i> , 2020, 9, 715.	3.7	2
81	A2144G Is the Main Mutation in the 23S rRNA Gene of <i>Helicobacter pylori</i> Associated with Clarithromycin Resistance. <i>Russian Journal of Genetics</i> , 2005, 41, 1095-1100.	0.6	1
82	Mass-spectrometry analysis of genetic markers of <i>S. pneumoniae</i> resistance to β -lactam antibiotics. <i>Molecular Genetics, Microbiology and Virology</i> , 2010, 25, 106-117.	0.3	1
83	Strain differentiation of <i>Staphylococcus aureus</i> by means of direct MALDI TOF mass spectrometry profiling. <i>Biochemistry (Moscow) Supplement Series B: Biomedical Chemistry</i> , 2013, 7, 70-78.	0.4	1
84	Genome Complexity Browser: Visualization and quantification of genome variability. <i>PLoS Computational Biology</i> , 2020, 16, e1008222.	3.2	1
85	Evaluation of the Levels of Metabolites in Feces of Patients with Inflammatory Bowel Diseases. <i>Biochemistry (Moscow) Supplement Series B: Biomedical Chemistry</i> , 2020, 14, 312-319.	0.4	1
86	Variability in the relative human DNA content during metagenomic analysis of gut microbiota. <i>Biochemistry (Moscow) Supplement Series B: Biomedical Chemistry</i> , 2015, 9, 290-295.	0.4	0
87	The ability of various strains of <i>Staphylococcus</i> to create biofilms and their effect on cells of the human body. <i>Molecular Genetics, Microbiology and Virology</i> , 2016, 31, 21-29.	0.3	0
88	Metagenomic analysis of taxonomic and functional changes in gut microbiota of patients with the alcohol dependence syndrome. <i>Biochemistry (Moscow) Supplement Series B: Biomedical Chemistry</i> , 2016, 10, 184-190.	0.4	0
89	1099 Changes in Taxonomy and Functions of the Gut Microbiome in Patients With Alcoholic Liver Cirrhosis: New Data. <i>Gastroenterology</i> , 2016, 150, S220.	1.3	0
90	The Influence of Cultivation Conditions on the Proteomic Profile of <i>Mycobacterium tuberculosis</i> H37Rv. <i>Biochemistry (Moscow) Supplement Series B: Biomedical Chemistry</i> , 2018, 12, 32-38.	0.4	0

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91	PRACTICAL ASPECTS OF THE APPLICATION OF INTRAVENOUS IMMUNOGLOBULINS FOR INTRAVENOUS ADMINISTRATION IN VARIOUS PATHOLOGIES. <i>Pediatrics</i> , 2021, 100, 174-181.	0.2	0
92	Substitutions in SurA and BamA Lead to Reduced Susceptibility to Broad Range Antibiotics in <i>Gonococci</i> . <i>Genes</i> , 2021, 12, 1312.	2.4	0
93	FEATURES OF ESCHERICHIA COLI CLINICAL STRAINS, ISOLATED FROM THE PATIENTS WITH CROHN'S DISEASE. <i>Zhurnal Mikrobiologii Epidemiologii I Immunobiologii</i> , 2017, , 42-49.	1.0	0
94	Mutants resistant to nalidixic acid and novobiocin. specific features of formation from E. Coli strains with RecA or LexA mutations. <i>Molekuliarnaia Genetika, Mikrobiologiya I Virusologiya</i> , 2018, 36, 26.	0.4	0
95	Comparative genomics of the Escherichia coli strains AB1157, AB2463, AB2494 and AB1885. <i>Molekuliarnaia Genetika, Mikrobiologiya I Virusologiya</i> , 2019, 37, 134.	0.4	0
96	Gut microbiota assessment in Moscow long-livers using next generation sequencing. <i>Bulletin of Russian State Medical University</i> , 2020, , 16-20.	0.2	0
97	Genome Complexity Browser: Visualization and quantification of genome variability. , 2020, 16, e1008222.		0
98	Genome Complexity Browser: Visualization and quantification of genome variability. , 2020, 16, e1008222.		0
99	Genome Complexity Browser: Visualization and quantification of genome variability. , 2020, 16, e1008222.		0
100	Genome Complexity Browser: Visualization and quantification of genome variability. , 2020, 16, e1008222.		0