

Elena N Ilina

List of Publications by Year in descending order

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100
papers

2,719
citations

218677

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119
docs citations

119
times ranked

3969
citing authors

#	ARTICLE	IF	CITATIONS
1	Deep Functional Profiling of Wild Animal Microbiomes Reveals Probiotic <i>Bacillus pumilus</i> Strains with a Common Biosynthetic Fingerprint. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1168.	4.1	5
2	PRACTICAL ASPECTS OF THE APPLICATION OF INTRAVENOUS IMMUNOGLOBULINS FOR INTRAVENOUS ADMINISTRATION IN VARIOUS PATHOLOGIES. <i>Pediatrics</i> , 2021, 100, 174-181.	0.2	0
3	Drift of the Subgingival Periodontal Microbiome during Chronic Periodontitis in Type 2 Diabetes Mellitus Patients. <i>Pathogens</i> , 2021, 10, 504.	2.8	16
4	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
5	Novel <i>Klebsiella pneumoniae</i> K23-Specific Bacteriophages From Different Families: Similarity of Depolymerases and Their Therapeutic Potential. <i>Frontiers in Microbiology</i> , 2021, 12, 669618.	3.5	24
6	Substitutions in SurA and BamA Lead to Reduced Susceptibility to Broad Range Antibiotics in <i>Neisseria meningitidis</i> . <i>Genes</i> , 2021, 12, 1312.	2.4	0
7	The effects of <i>Levilactobacillus brevis</i> on the physiological parameters and gut microbiota composition of rats subjected to desynchronization. <i>Microbial Cell Factories</i> , 2021, 20, 226.	4.0	5
8	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
9	Genome Complexity Browser: Visualization and quantification of genome variability. <i>PLoS Computational Biology</i> , 2020, 16, e1008222.	3.2	1
10	Transcriptional Landscape of <i>Staphylococcus aureus</i> Kayvirus Bacteriophage vB_SauM-515A1. <i>Viruses</i> , 2020, 12, 1320.	3.3	10
11	Gene Networks Underlying the Resistance of <i>Bifidobacterium longum</i> to Inflammatory Factors. <i>Frontiers in Immunology</i> , 2020, 11, 595877.	4.8	5
12	Aureolic Acid Group of Agents as Potential Antituberculosis Drugs. <i>Antibiotics</i> , 2020, 9, 715.	3.7	2
13	Contribution of Podoviridae and Myoviridae bacteriophages to the effectiveness of anti-staphylococcal therapeutic cocktails. <i>Scientific Reports</i> , 2020, 10, 18612.	3.3	31
14	Metabolic Changes of <i>Mycobacterium tuberculosis</i> during the Anti-Tuberculosis Therapy. <i>Pathogens</i> , 2020, 9, 131.	2.8	11
15	Phigaro: high-throughput prophage sequence annotation. <i>Bioinformatics</i> , 2020, 36, 3882-3884.	4.1	75
16	Deep Functional Profiling Facilitates the Evaluation of the Antibacterial Potential of the Antibiotic Amicoumacin. <i>Antibiotics</i> , 2020, 9, 157.	3.7	14
17	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
18	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

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19	Genome Complexity Browser: Visualization and quantification of genome variability. , 2020, 16, e1008222.		0
20	Genome Complexity Browser: Visualization and quantification of genome variability. , 2020, 16, e1008222.		0
21	Genome Complexity Browser: Visualization and quantification of genome variability. , 2020, 16, e1008222.		0
22	Genome Complexity Browser: Visualization and quantification of genome variability. , 2020, 16, e1008222.		0
23	Proteogenomic analysis of Mycobacterium tuberculosis Beijing B0/W148 cluster strains. Journal of Proteomics, 2019, 192, 18-26.	2.4	11
24	Shifts in the Human Gut Microbiota Structure Caused by Quadruple Helicobacter pylori Eradication Therapy. Frontiers in Microbiology, 2019, 10, 1902.	3.5	39
25	The role of IS6110 in micro- and macroevolution of Mycobacterium tuberculosis lineage 2. Molecular Phylogenetics and Evolution, 2019, 139, 106559.	2.7	9
26	Global phylogeography and ancient evolution of the widespread human gut virus crAssphage. Nature Microbiology, 2019, 4, 1727-1736.	13.3	184
27	VERA: agent-based modeling transmission of antibiotic resistance between human pathogens and gut microbiota. Bioinformatics, 2019, 35, 3803-3811.	4.1	4
28	System OMICs analysis of Mycobacterium tuberculosis Beijing B0/W148 cluster. Scientific Reports, 2019, 9, 19255.	3.3	7
29	Long-term impact of fecal transplantation in healthy volunteers. BMC Microbiology, 2019, 19, 312.	3.3	55
30	Faecal Transplant in GIT Treatment (Pilot Clinical Experience). Doctor Ru, 2019, 158, 40-46.	0.3	7
31	Comparative genomics of the Escherichia coli strains AB1157, AB2463, AB2494 and AB1885. Molekuliarnaia Genetika, Mikrobiologiya i Virusologiya, 2019, 37, 134.	0.4	0
32	The Influence of Cultivation Conditions on the Proteomic Profile of Mycobacterium tuberculosis H37Rv. Biochemistry (Moscow) Supplement Series B: Biomedical Chemistry, 2018, 12, 32-38.	0.4	0
33	Draft genomes of Enterococcus faecium strains isolated from human feces before and after eradication therapy against Helicobacter pylori. Data in Brief, 2018, 16, 511-514.	1.0	5
34	Characteristics of Emergence of Mutants Resistant to Nalidixic Acid and Novobiocin in E. coli Strains with recA and lexA Mutations. Molecular Genetics, Microbiology and Virology, 2018, 33, 30-33.	0.3	4
35	Ultrahigh-throughput functional profiling of microbiota communities. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 9551-9556.	7.1	79
36	M. BOVIS BCG-1 (RUSSIA) SUB-STRAIN GENOME STABILITY INVESTIGATION WITHIN THE ENTIRE PRODUCTION PROCESS. Zhurnal Mikrobiologii Epidemiologii i Immunobiologii, 2018, 95, 58-67.	1.0	3

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37	Mutants resistant to nalidixic acid and novobiocin. specific features of formation from E. Coli strains with RecA or LexA mutations. Molekuliarnaia Genetika, Mikrobiologija I Virusologija, 2018, 36, 26.	0.4	0
38	Data on gut metagenomes of the patients with Helicobacter pylori infection before and after the antibiotic therapy. Data in Brief, 2017, 11, 68-71.	1.0	14
39	Data on gut metagenomes of the patients with alcoholic dependence syndrome and alcoholic liver cirrhosis. Data in Brief, 2017, 11, 98-102.	1.0	6
40	Microfluidic droplet platform for ultrahigh-throughput single-cell screening of biodiversity. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 2550-2555.	7.1	182
41	Genetic Environment of the bla KPC-2 Gene in a Klebsiella pneumoniae Isolate That May Have Been Imported to Russia from Southeast Asia. Antimicrobial Agents and Chemotherapy, 2017, 61, .	3.2	8
42	Metagenomic Analysis of Gingival Sulcus Microbiota and Pathogenesis of Periodontitis Associated with Type 2 Diabetes Mellitus. Bulletin of Experimental Biology and Medicine, 2017, 163, 718-721.	0.8	16
43	Links of gut microbiota composition with alcohol dependence syndrome and alcoholic liver disease. Microbiome, 2017, 5, 141.	11.1	296
44	Evolutionary pathway analysis and unified classification of East Asian lineage of Mycobacterium tuberculosis. Scientific Reports, 2017, 7, 9227.	3.3	98
45	Genome analysis of E. coli isolated from Crohnâ€™s disease patients. BMC Genomics, 2017, 18, 544.	2.8	37
46	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. AMB Express, 2017, 7, 218.	3.0	5
47	FEATURES OF ESCHERICHIA COLI CLINICAL STRAINS, ISOLATED FROM THE PATIENTS WITH CROHNâ€™S DISEASE. Zhurnal Mikrobiologii Epidemiologii I Immunobiologii, 2017, , 42-49.	1.0	0
48	The ability of various strains of Staphylococcus to create biofilms and their effect on cells of the human body. Molecular Genetics, Microbiology and Virology, 2016, 31, 21-29.	0.3	0
49	Metagenomic analysis of taxonomic and functional changes in gut microbiota of patients with the alcohol dependence syndrome. Biochemistry (Moscow) Supplement Series B: Biomedical Chemistry, 2016, 10, 184-190.	0.4	0
50	Proteome analysis of the Mycobacterium tuberculosis Beijing B0/W148 cluster. Scientific Reports, 2016, 6, 28985.	3.3	34
51	Complete Genome Sequence of <i>Mycobacterium bovis</i> Strain BCG-1 (Russia). Genome Announcements, 2016, 4, .	0.8	15
52	1099 Changes in Taxonomy and Functions of the Gut Microbiome in Patients With Alcoholic Liver Cirrhosis: New Data. Gastroenterology, 2016, 150, S220.	1.3	0
53	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
54	Large scale analysis of amino acid substitutions in bacterial proteomics. BMC Bioinformatics, 2016, 17, 450.	2.6	2

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55	The mystery of the fourth clone: comparative genomic analysis of four non-typeable <i>Streptococcus pneumoniae</i> strains with different susceptibilities to optochin. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2016, 35, 119-130.	2.9	5
56	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
57	Molecular mechanisms of formation of drug resistance in <i>Neisseria gonorrhoeae</i> : History and prospects. <i>Molecular Genetics, Microbiology and Virology</i> , 2015, 30, 132-140.	0.3	6
58	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
59	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
60	RNA-Seq gene expression profiling of HepG2 cells: the influence of experimental factors and comparison with liver tissue. <i>BMC Genomics</i> , 2014, 15, 1108.	2.8	34
61	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
62	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
63	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
64	Analysis of the genetic determinants of multidrug and extensive drug resistance in <i>Mycobacterium tuberculosis</i> with the use of an oligonucleotide microchip. <i>Molecular Biology</i> , 2014, 48, 214-226.	1.3	5
65	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
66	Spoligotyping of <i>Mycobacterium tuberculosis</i> complex isolates using hydrogel oligonucleotide microarrays. <i>Infection, Genetics and Evolution</i> , 2014, 26, 41-46.	2.3	21
67	Unusual Large-Scale Chromosomal Rearrangements in <i>Mycobacterium tuberculosis</i> Beijing B0/W148 Cluster Isolates. <i>PLoS ONE</i> , 2014, 9, e84971.	2.5	23
68	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
69	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
70	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
71	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
72	Comparative Genomic Analysis of <i>Mycobacterium tuberculosis</i> Drug Resistant Strains from Russia. <i>PLoS ONE</i> , 2013, 8, e56577.	2.5	42

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73	Mutation in ribosomal protein S5 leads to spectinomycin resistance in <i>Neisseria gonorrhoeae</i> . <i>Frontiers in Microbiology</i> , 2013, 4, 186.	3.5	40
74	First detection of VIM-4 metallo- β -lactamase-producing <i>Escherichia coli</i> in Russia. <i>Clinical Microbiology and Infection</i> , 2012, 18, E214-E217.	6.0	22
75	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
76	Mass spectrometry based methods for the discrimination and typing of mycobacteria. <i>Infection, Genetics and Evolution</i> , 2012, 12, 838-845.	2.3	43
77	Misidentification of alpha-hemolytic streptococci by routine tests in clinical practice. <i>Infection, Genetics and Evolution</i> , 2011, 11, 1709-1715.	2.3	50
78	Molecular typing of <i>Mycobacterium tuberculosis</i> circulated in Moscow, Russian Federation. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2011, 30, 181-191.	2.9	21
79	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
80	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
81	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
82	Comparative evaluation of new typing schemes for urogenital <i>Chlamydia trachomatis</i> isolates. <i>FEMS Immunology and Medical Microbiology</i> , 2010, 59, 188-196.	2.7	27
83	Molecular Surveillance of Clinical <i>Neisseria gonorrhoeae</i> Isolates in Russia. <i>Journal of Clinical Microbiology</i> , 2010, 48, 3681-3689.	3.9	23
84	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
85	Hepatitis B Virus Genetic Typing Using Mass-Spectrometry. <i>Bulletin of Experimental Biology and Medicine</i> , 2009, 147, 220-225.	0.8	9
86	Mass spectrometry of nucleic acids in molecular medicine. <i>Russian Journal of Bioorganic Chemistry</i> , 2009, 35, 135-149.	1.0	3
87	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
88	A MALDI TOF MS-based minisequencing method for rapid detection of TEM-type extended-spectrum beta-lactamases in clinical strains of Enterobacteriaceae. <i>Journal of Microbiological Methods</i> , 2008, 75, 385-391.	1.6	25
89	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
90	Relation between Genetic Markers of Drug Resistance and Susceptibility Profile of Clinical <i>Neisseria gonorrhoeae</i> Strains. <i>Antimicrobial Agents and Chemotherapy</i> , 2008, 52, 2175-2182.	3.2	31

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91	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
92	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
93	Direct evaluation of drug resistance parameters in gonococcus. <i>Bulletin of Experimental Biology and Medicine</i> , 2007, 144, 227-230.	0.8	2
94	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
95	Analysis of genetic markers of <i>N. Gonorrhoeae</i> resistance to β -lactam antibiotics. <i>Bulletin of Experimental Biology and Medicine</i> , 2006, 141, 610-615.	0.8	6
96	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
97	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
98	Matrix-Assisted Laser Desorption Ionization-Time of Flight (Mass Spectrometry) for Hepatitis C Virus Genotyping. <i>Journal of Clinical Microbiology</i> , 2005, 43, 2810-2815.	3.9	39
99	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
100	Molecular typing of <i>N. gonorrhoeae</i> strains prevalent in the Russian Federation. <i>Bulletin of Experimental Biology and Medicine</i> , 2003, 136, 179-182.	0.8	4