

# Ksenia Klimina

## List of Publications by Year in descending order

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Version: 2024-02-01

33  
papers

820  
citations

687363

13  
h-index

501196

28  
g-index

34  
all docs

34  
docs citations

34  
times ranked

1426  
citing authors

#	ARTICLE	IF	CITATIONS
1	GABA production and structure of <i>gadB</i> / <i>gadC</i> genes in <i>Lactobacillus</i> and <i>Bifidobacterium</i> strains from human microbiota. <i>Anaerobe</i> , 2016, 42, 197-204.	2.1	238
2	Microbial Community Structure of Activated Sludge in Treatment Plants with Different Wastewater Compositions. <i>Frontiers in Microbiology</i> , 2016, 7, 90.	3.5	160
3	Long-term impact of fecal transplantation in healthy volunteers. <i>BMC Microbiology</i> , 2019, 19, 312.	3.3	55
4	HK3 overexpression associated with epithelial-mesenchymal transition in colorectal cancer. <i>BMC Genomics</i> , 2018, 19, 113.	2.8	45
5	Identification, Expression Analysis, and Target Prediction of Flax Genotroph MicroRNAs Under Normal and Nutrient Stress Conditions. <i>Frontiers in Plant Science</i> , 2016, 7, 399.	3.6	43
6	Downregulation of OGDHL expression is associated with promoter hypermethylation in colorectal cancer. <i>Molecular Biology</i> , 2015, 49, 608-617.	1.3	37
7	Effect of lentivirus-mediated shRNA inactivation of HK1, HK2, and HK3 genes in colorectal cancer and melanoma cells. <i>BMC Genetics</i> , 2016, 17, 156.	2.7	33
8	Identification and characterization of toxin-antitoxin systems in strains of <i>Lactobacillus rhamnosus</i> isolated from humans. <i>Anaerobe</i> , 2013, 22, 82-89.	2.1	21
9	Differentially Expressed Genes Associated With Prognosis in Locally Advanced Lymph Node-Negative Prostate Cancer. <i>Frontiers in Genetics</i> , 2019, 10, 730.	2.3	21
10	Complete Genome Sequence of <i>Bifidobacterium longum</i> GT15: Identification and Characterization of Unique and Global Regulatory Genes. <i>Microbial Ecology</i> , 2015, 70, 819-834.	2.8	19
11	Upregulation of NETO2 gene in colorectal cancer. <i>BMC Genetics</i> , 2017, 18, 117.	2.7	16
12	The effects of desynchronization on the gut microbiota composition and physiological parameters of rats. <i>BMC Microbiology</i> , 2019, 19, 160.	3.3	15
13	Expression of the toxin-antitoxin genes <i>yefM<sub>Lrh</sub></i> , <i>yoeB<sub>Lrh</sub></i> in human <i>Lactobacillus rhamnosus</i> isolates. <i>Journal of Basic Microbiology</i> , 2015, 55, 982-991.	3.3	14
14	Metabolic Changes of <i>Mycobacterium tuberculosis</i> during the Anti-Tuberculosis Therapy. <i>Pathogens</i> , 2020, 9, 131.	2.8	11
15	Transcriptional Landscape of <i>Staphylococcus aureus</i> Kayvirus Bacteriophage vB_SauM-515A1. <i>Viruses</i> , 2020, 12, 1320.	3.3	10
16	Draft Genome Sequence of <i>Streptomyces fradiae</i> ATCC 19609, a Strain Highly Sensitive to Antibiotics. <i>Genome Announcements</i> , 2014, 2, .	0.8	9
17	Complete Genome Sequence of <i>Bifidobacterium longum</i> GT15: Unique Genes for Russian Strains. <i>Genome Announcements</i> , 2014, 2, .	0.8	7
18	System OMICs analysis of <i>Mycobacterium tuberculosis</i> Beijing B0/W148 cluster. <i>Scientific Reports</i> , 2019, 9, 19255.	3.3	7

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19	Draft Genome Sequences of <i>Bifidobacterium angulatum</i> GT102 and <i>Bifidobacterium adolescentis</i> 150: Focusing on the Genes Potentially Involved in the Gut-Brain Axis. <i>Genome Announcements</i> , 2015, 3, .	0.8	6
20	Draft Genome Sequences of Two Pyrazinamide-Resistant Clinical Isolates, <i>Mycobacterium tuberculosis</i> 13-4152 and 13-2459. <i>Genome Announcements</i> , 2015, 3, .	0.8	6
21	Toxin-Antitoxin Systems: A Tool for Taxonomic Analysis of Human Intestinal Microbiota. <i>Toxins</i> , 2020, 12, 388.	3.4	6
22	Bacterial toxin-antitoxin systems: Properties, functional significance, and possibility of use (Review). <i>Applied Biochemistry and Microbiology</i> , 2017, 53, 494-505.	0.9	5
23	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
24	Genetic diversity of the genus <i>Lactobacillus</i> bacteria from the human gastrointestinal microbiome. <i>Russian Journal of Genetics</i> , 2010, 46, 1399-1406.	0.6	4
25	Employing toxin-antitoxin genome markers for identification of <i>Bifidobacterium</i> and <i>Lactobacillus</i> strains in human metagenomes. <i>PeerJ</i> , 2019, 7, e6554.	2.0	4
26	16S rRNA gene sequencing data of the upper respiratory tract microbiome in the SARS-CoV-2 infected patients. <i>Data in Brief</i> , 2022, 40, 107770.	1.0	4
27	Global Transcriptomic Response of <i>Staphylococcus aureus</i> to Virulent Bacteriophage Infection. <i>Viruses</i> , 2022, 14, 567.	3.3	4
28	Revised classification of native probiotic strains of <i>Lactobacillus</i> used in Russian Federation. <i>Russian Journal of Genetics</i> , 2010, 46, 1306-1313.	0.6	3
29	Draft Genome Sequences of <i>Lactobacillus plantarum</i> Strain 90sk and <i>Lactobacillus brevis</i> Strain 15f: Focusing on Neurotransmitter Genes. <i>Genome Announcements</i> , 2015, 3, .	0.8	3
30	Draft Genome Sequence of <i>Mycobacterium tuberculosis</i> Strain E186hv of Beijing B0/W Lineage with Reduced Virulence. <i>Genome Announcements</i> , 2015, 3, .	0.8	3
31	Draft genome sequence of <i>Mycobacterium tuberculosis</i> strain B9741 of Beijing B0/W lineage from HIV positive patient from Siberia. <i>Genomics Data</i> , 2016, 10, 61-62.	1.3	2
32	Aureolic Acid Group of Agents as Potential Antituberculosis Drugs. <i>Antibiotics</i> , 2020, 9, 715.	3.7	2
33	Transcriptomic dataset of <i>Mycobacterium smegmatis</i> exposed to an imidazo[1,2-b][1,2,4,5]tetrazine. <i>Data in Brief</i> , 2020, 31, 105805.	1.0	1