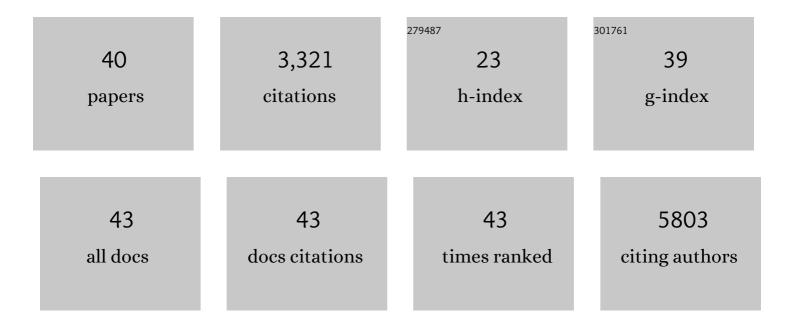
## Ekaterina Avershina

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2363452/publications.pdf Version: 2024-02-01



#	Article	lF	CITATIONS
1	Ultrafast and Cost-Effective Pathogen Identification and Resistance Gene Detection in a Clinical Setting Using Nanopore Flongle Sequencing. Frontiers in Microbiology, 2022, 13, 822402.	1.5	22
2	AMR-Diag: Neural network based genotype-to-phenotype prediction of resistance towards Î <sup>2</sup> -lactams in Escherichia coli and Klebsiella pneumoniae. Computational and Structural Biotechnology Journal, 2021, 19, 1896-1906.	1.9	38
3	Fighting Antibiotic Resistance in Hospital-Acquired Infections: Current State and Emerging Technologies in Disease Prevention, Diagnostics and Therapy. Frontiers in Microbiology, 2021, 12, 707330.	1.5	63
4	Plasmid Identification and Plasmid-Mediated Antimicrobial Gene Detection in Norwegian Isolates. Microorganisms, 2021, 9, 52.	1.6	19
5	Hybrid Assembly Provides Improved Resolution of Plasmids, Antimicrobial Resistance Genes, and Virulence Factors in Escherichia coli and Klebsiella pneumoniae Clinical Isolates. Microorganisms, 2021, 9, 2560.	1.6	26
6	Early Gut Fungal and Bacterial Microbiota and Childhood Growth. Frontiers in Pediatrics, 2020, 8, 572538.	0.9	13
7	Rapid identification of pathogens, antibiotic resistance genes and plasmids in blood cultures by nanopore sequencing. Scientific Reports, 2020, 10, 7622.	1.6	66
8	Culture dependent and independent analyses suggest a low level of sharing of endospore-forming species between mothers and their children. Scientific Reports, 2020, 10, 1832.	1.6	12
9	Exploring the Brine Microbiota of a Traditional Norwegian Fermented Fish Product (Rakfisk) from Six Different Producers during Two Consecutive Seasonal Productions. Foods, 2019, 8, 72.	1.9	20
10	Comparison of reduced metagenome and 16S rRNA gene sequencing for determination of genetic diversity and mother-child overlap of the gut associated microbiota. Journal of Microbiological Methods, 2018, 149, 44-52.	0.7	19
11	Breastfeeding-associated microbiota in human milk following supplementation with Lactobacillus rhamnosus GG, Lactobacillus acidophilus La-5, and Bifidobacterium animalis ssp. lactis Bb-12. Journal of Dairy Science, 2018, 101, 889-899.	1.4	64
12	Low Maternal Microbiota Sharing across Gut, Breast Milk and Vagina, as Revealed by 16S rRNA Gene and Reduced Metagenomic Sequencing. Genes, 2018, 9, 231.	1.0	35
13	Body fluid prediction from microbial patterns for forensic application. Forensic Science International: Genetics, 2017, 30, 10-17.	1.6	61
14	Effect of probiotics in prevention of atopic dermatitis is dependent on the intrinsic microbiota at early infancy. Journal of Allergy and Clinical Immunology, 2017, 139, 1399-1402.e8.	1.5	31
15	Diversity of vaginal microbiota increases by the time of labor onset. Scientific Reports, 2017, 7, 17558.	1.6	27
16	Early gut mycobiota and mother-offspring transfer. Microbiome, 2017, 5, 107.	4.9	138
17	Transition from infant―to adultâ€ŀike gut microbiota. Environmental Microbiology, 2016, 18, 2226-2236.	1.8	109
18	Bead-beating artefacts in the Bacteroidetes to Firmicutes ratio of the human stool metagenome. Journal of Microbiological Methods, 2016, 129, 78-80.	0.7	19

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19	Diet-Dependent Modular Dynamic Interactions of the Equine Cecal Microbiota. Microbes and Environments, 2016, 31, 378-386.	0.7	15
20	Over-represented pairwise 16S rRNA gene sequence distance levels among prokaryotes. Annals of Microbiology, 2016, 66, 489-493.	1.1	0
21	The commensal infant gut meta-mobilome as a potential reservoir for persistent multidrug resistance integrons. Scientific Reports, 2015, 5, 15317.	1.6	32
22	Shifts in the Midgut/Pyloric Microbiota Composition within a Honey Bee Apiary throughout a Season. Microbes and Environments, 2015, 30, 235-244.	0.7	67
23	Confusion about the species richness of human gut microbiota. Beneficial Microbes, 2015, 6, 657-659.	1.0	18
24	Potential association of vacuum cleaning frequency with an altered gut microbiota in pregnant women and their 2-year-old children. Microbiome, 2015, 3, 65.	4.9	9
25	Gut microbiota diversity predicts immune status in HIV-1 infection. Aids, 2015, 29, 2409-2418.	1.0	238
26	Does Maternal Perinatal Probiotic Supplementation Alter the Intestinal Microbiota of Mother and Child?. Journal of Pediatric Gastroenterology and Nutrition, 2015, 61, 200-207.	0.9	88
27	High nutrient availability reduces the diversity and stability of the equine caecal microbiota. Microbial Ecology in Health and Disease, 2015, 26, 27216.	3.8	20
28	The composition of the gut microbiota throughout life, with an emphasis on early life. Microbial Ecology in Health and Disease, 2015, 26, 26050.	3.8	766
29	High-Resolution Analyses of Overlap in the Microbiota Between Mothers and Their Children. Current Microbiology, 2015, 71, 283-290.	1.0	31
30	Dominant short repeated sequences in bacterial genomes. Genomics, 2015, 105, 175-181.	1.3	8
31	Integrons in the Intestinal Microbiota as Reservoirs for Transmission of Antibiotic Resistance Genes. Pathogens, 2014, 3, 238-248.	1.2	58
32	Gut Microbiota in HIV Infection: Implication for Disease Progression and Management. Gastroenterology Research and Practice, 2014, 2014, 1-6.	0.7	35
33	Major faecal microbiota shifts in composition and diversity with age in a geographically restricted cohort of mothers and their children. FEMS Microbiology Ecology, 2014, 87, 280-290.	1.3	144
34	Correlation between the human fecal microbiota and depression. Neurogastroenterology and Motility, 2014, 26, 1155-1162.	1.6	765
35	Bifidobacterial Succession and Correlation Networks in a Large Unselected Cohort of Mothers and Their Children. Applied and Environmental Microbiology, 2013, 79, 497-507.	1.4	81
36	Dominant Fecal Microbiota in Newly Diagnosed Untreated Inflammatory Bowel Disease Patients. Gastroenterology Research and Practice, 2013, 2013, 1-13.	0.7	46

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37	Age-Dependent Fecal Bacterial Correlation to Inflammatory Bowel Disease for Newly Diagnosed Untreated Children. Gastroenterology Research and Practice, 2013, 2013, 1-7.	0.7	12
38	Diversity of intestinal microbiota in infancy and the risk of allergic disease in childhood. Current Opinion in Allergy and Clinical Immunology, 2013, 13, 257-262.	1.1	17
39	<i>De novo</i> Semi-alignment of 16S rRNA Gene Sequences for Deep Phylogenetic Characterization of Next Generation Sequencing Data. Microbes and Environments, 2013, 28, 211-216.	0.7	76
40	ls it who you are or what you do that is important in the human gut?. Beneficial Microbes, 2013, 4, 219-222.	1.0	10