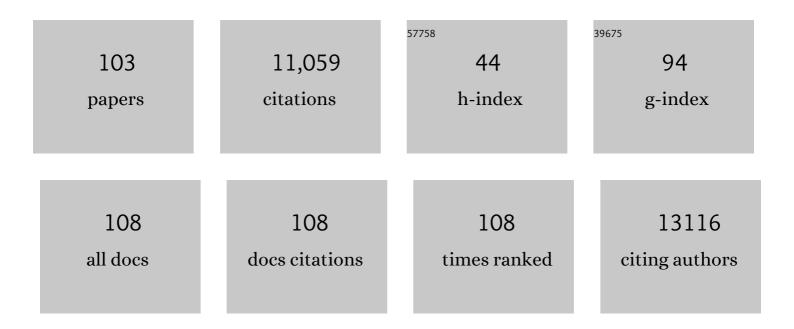
Rustam I Aminov

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/5177628/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	A Brief History of the Antibiotic Era: Lessons Learned and Challenges for the Future. Frontiers in Microbiology, 2010, 1, 134.	3.5	980
2	Occurrence and Diversity of Tetracycline Resistance Genes in Lagoons and Groundwater Underlying Two Swine Production Facilities. Applied and Environmental Microbiology, 2001, 67, 1494-1502.	3.1	674
3	Fate and Transport of Antibiotic Residues and Antibiotic Resistance Genes following Land Application of Manure Waste. Journal of Environmental Quality, 2009, 38, 1086-1108.	2.0	664
4	Diet-Dependent Shifts in the Bacterial Population of the Rumen Revealed with Real-Time PCR. Applied and Environmental Microbiology, 2001, 67, 2766-2774.	3.1	592
5	Molecular Ecology of Tetracycline Resistance: Development and Validation of Primers for Detection of Tetracycline Resistance Genes Encoding Ribosomal Protection Proteins. Applied and Environmental Microbiology, 2001, 67, 22-32.	3.1	547
6	The role of antibiotics and antibiotic resistance in nature. Environmental Microbiology, 2009, 11, 2970-2988.	3.8	490
7	Horizontal Gene Exchange in Environmental Microbiota. Frontiers in Microbiology, 2011, 2, 158.	3.5	475
8	Evolution and ecology of antibiotic resistance genes. FEMS Microbiology Letters, 2007, 271, 147-161.	1.8	414
9	Commensal gut bacteria: mechanisms of immune modulation. Trends in Immunology, 2005, 26, 326-333.	6.8	341
10	Oligonucleotide Probes That Detect Quantitatively Significant Groups of Butyrate-Producing Bacteria in Human Feces. Applied and Environmental Microbiology, 2003, 69, 4320-4324.	3.1	284
11	Predominant Role of Host Genetics in Controlling the Composition of Gut Microbiota. PLoS ONE, 2008, 3, e3064.	2.5	263
12	Monitoring and Source Tracking of Tetracycline Resistance Genes in Lagoons and Groundwater Adjacent to Swine Production Facilities over a 3-Year Period. Applied and Environmental Microbiology, 2007, 73, 4813-4823.	3.1	258
13	Rumen bacterial diversity as determined by sequence analysis of 16S rDNA libraries. FEMS Microbiology Ecology, 1999, 29, 159-169.	2.7	247
14	Rumen Bacterial Community Transition During Adaptation to High-grain Diet. Anaerobe, 2000, 6, 273-284.	2.1	243
15	Environmentally-acquired bacteria influence microbial diversity and natural innate immune responses at gut surfaces. BMC Biology, 2009, 7, 79.	3.8	228
16	Development, Validation, and Application of PCR Primers for Detection of Tetracycline Efflux Genes of Gram-Negative Bacteria. Applied and Environmental Microbiology, 2002, 68, 1786-1793.	3.1	223
17	Proposal of Roseburia faecis sp. nov., Roseburia hominis sp. nov. and Roseburia inulinivorans sp. nov., based on isolates from human faeces. International Journal of Systematic and Evolutionary Microbiology, 2006, 56, 2437-2441.	1.7	200
18	Importance of microbial colonization of the gut in early life to the development of immunity. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2007, 622, 58-69.	1.0	190

#	Article	IF	CITATIONS
19	History of antimicrobial drug discovery: Major classes and health impact. Biochemical Pharmacology, 2017, 133, 4-19.	4.4	184
20	Analysis of the Rumen Bacterial Diversity under two Different Diet Conditions using Denaturing Gradient Gel Electrophoresis, Random Sequencing, and Statistical Ecology Approaches. Anaerobe, 2001, 7, 119-134.	2.1	173
21	Phylogenetic analysis of archaeal 16S rRNA libraries from the rumen suggests the existence of a novel group of archaea not associated with known methanogens. FEMS Microbiology Letters, 2001, 200, 67-72.	1.8	165
22	Editorial: Phage Therapy: Past, Present and Future. Frontiers in Microbiology, 2017, 8, 981.	3.5	163
23	Tetracycline Residues and Tetracycline Resistance Genes in Groundwater Impacted by Swine Production Facilities. Animal Biotechnology, 2006, 17, 157-176.	1.5	156
24	Mechanisms of antibiotic resistance. Frontiers in Microbiology, 2015, 6, 34.	3.5	150
25	Molecular Ecological Analysis of the Succession and Diversity of Sulfate-Reducing Bacteria in the Mouse Gastrointestinal Tract. Applied and Environmental Microbiology, 2000, 66, 2166-2174.	3.1	140
26	Potential Effects of Horizontal Gene Exchange in the Human Gut. Frontiers in Immunology, 2017, 8, 1630.	4.8	140
27	Ecology of Uncultivated Oscillospira Species in the Rumen of Cattle, Sheep, and Reindeer as Assessed by Microscopy and Molecular Approaches. Applied and Environmental Microbiology, 2003, 69, 6808-6815.	3.1	137
28	Phenotypic Characterization of Polysaccharidases Produced by Four Prevotella Type Strains. Current Microbiology, 2000, 41, 45-49.	2.2	131
29	Influence of high temperature and humidity on rumen bacterial diversity in Holstein heifers. Anaerobe, 2007, 13, 57-64.	2.1	128
30	Human Gut Symbiont Roseburia hominis Promotes and Regulates Innate Immunity. Frontiers in Immunology, 2017, 8, 1166.	4.8	128
31	Establishment of Normal Gut Microbiota Is Compromised under Excessive Hygiene Conditions. PLoS ONE, 2011, 6, e28284.	2.5	120
32	Restricting Microbial Exposure in Early Life Negates the Immune Benefits Associated with Gut Colonization in Environments of High Microbial Diversity. PLoS ONE, 2011, 6, e28279.	2.5	118
33	Molecular Diversity, Cultivation, and Improved Detection by Fluorescent In Situ Hybridization of a Dominant Group of Human Gut Bacteria Related to Roseburia spp. or Eubacterium rectale. Applied and Environmental Microbiology, 2006, 72, 6371-6376.	3.1	113
34	Unravelling the genetic diversity of ruminal bacteria belonging to the CFB phylum. FEMS Microbiology Ecology, 2000, 33, 69-79.	2.7	97
35	Tetracycline Resistome of the Organic Pig Gut. Applied and Environmental Microbiology, 2009, 75, 1717-1722.	3.1	83
36	Dysbiosis May Trigger Autoimmune Diseases via Inappropriate Post-Translational Modification of Host Proteins. Frontiers in Microbiology, 2016, 7, 84.	3.5	79

#	Article	IF	CITATIONS
37	A novel class of CoA-transferase involved in short-chain fatty acid metabolism in butyrate-producing human colonic bacteria. Microbiology (United Kingdom), 2006, 152, 179-185.	1.8	76
38	Update on Pyrin Functions and Mechanisms of Familial Mediterranean Fever. Frontiers in Microbiology, 2016, 7, 456.	3.5	67
39	Molecular Ecology Of Macrolide–Lincosamide–Streptogramin B Methylases in Waste Lagoons and Subsurface Waters Associated with Swine Production. Microbial Ecology, 2010, 59, 487-498.	2.8	59
40	Biochemical and Microbiological Evidence for Fermentative Digestion in Free‣iving Land Iguanas (Conolophus pallidus) and Marine Iguanas (Amblyrhynchus cristatus) on the Galápagos Archipelago. Physiological and Biochemical Zoology, 2004, 77, 127-138.	1.5	58
41	Cytokine profile of Armenian patients with Familial Mediterranean fever. Clinical Biochemistry, 2008, 41, 920-922.	1.9	58
42	Silk route to the acceptance and reâ€implementation of bacteriophage therapy. Biotechnology Journal, 2016, 11, 595-600.	3.5	54
43	Transglutaminases in Dysbiosis As Potential Environmental Drivers of Autoimmunity. Frontiers in Microbiology, 2017, 8, 66.	3.5	52
44	Validation of a Bioinformatics Workflow for Routine Analysis of Whole-Genome Sequencing Data and Related Challenges for Pathogen Typing in a European National Reference Center: Neisseria meningitidis as a Proof-of-Concept. Frontiers in Microbiology, 2019, 10, 362.	3.5	51
45	Silk Route to the Acceptance and Re-Implementation of Bacteriophage Therapy—Part II. Antibiotics, 2018, 7, 35.	3.7	46
46	Omics of antimicrobials and antimicrobial resistance. Expert Opinion on Drug Discovery, 2019, 14, 455-468.	5.0	46
47	Desulfotomaculum genus- and subgenus-specific 16S rRNA hybridization probes for environmental studies. Environmental Microbiology, 2000, 2, 143-159.	3.8	43
48	Systemic Concentrations of Short Chain Fatty Acids Are Elevated in Salmonellosis and Exacerbation of Familial Mediterranean Fever. Frontiers in Microbiology, 2016, 7, 776.	3.5	40
49	Environmental Triggers of Autoreactive Responses: Induction of Antiphospholipid Antibody Formation. Frontiers in Immunology, 2019, 10, 1609.	4.8	39
50	Role of archaea in human disease. Frontiers in Cellular and Infection Microbiology, 2013, 3, 42.	3.9	37
51	Evolution in action: dissemination of tet(X) into pathogenic microbiota. Frontiers in Microbiology, 2013, 4, 192.	3.5	36
52	Biotic acts of antibiotics. Frontiers in Microbiology, 2013, 4, 241.	3.5	32
53	Elevated Systemic Antibodies towards Commensal Gut Microbiota in Autoinflammatory Condition. PLoS ONE, 2008, 3, e3172.	2.5	27
54	Profiles of Microbial Fatty Acids in the Human Metabolome are Disease-Specific. Frontiers in Microbiology, 2010, 1, 148.	3.5	25

#	Article	IF	CITATIONS
55	Antimicrobial resistance in mollicutes: known and newly emerging mechanisms. FEMS Microbiology Letters, 2018, 365, .	1.8	24
56	Fermented liquid feed enhances bacterial diversity in piglet intestine. Anaerobe, 2010, 16, 6-11.	2.1	22
57	Editorial: Microbial and Environmental Factors in Autoimmune and Inflammatory Diseases. Frontiers in Immunology, 2017, 8, 243.	4.8	20
58	Acquisition and Spread of Antimicrobial Resistance: A tet(X) Case Study. International Journal of Molecular Sciences, 2021, 22, 3905.	4.1	20
59	Molecular Analysis of Archaea, Bacteria and Eucarya Communities in the Rumen - Review Asian-Australasian Journal of Animal Sciences, 1999, 12, 129-138.	2.4	19
60	Structural Organization of pRAM4, a Cryptic Plasmid fromPrevotella ruminicola. Plasmid, 1996, 35, 91-97.	1.4	18
61	Application of bacteriophages. Microbiology Australia, 2017, 38, 63.	0.4	18
62	Antimicrobial drug discovery: lessons of history and future strategies. Expert Opinion on Drug Discovery, 2018, 13, 983-985.	5.0	17
63	Role and prevalence of antibiosis and the related resistance genes in the environment. Frontiers in Microbiology, 2014, 5, 520.	3.5	16
64	Unravelling the genetic diversity of ruminal bacteria belonging to the CFB phylum. FEMS Microbiology Ecology, 2000, 33, 69-79.	2.7	16
65	Enumeration of transconjugated Ruminococcus albus and its survival in the goat rumen microcosm. Applied and Environmental Microbiology, 1995, 61, 2030-2032.	3.1	16
66	Low-dose antibiotics: current status and outlook for the future. Frontiers in Microbiology, 2014, 5, 478.	3.5	15
67	Sequence Analysis of Small Cryptic Plasmids Isolated from Selenomonas ruminantium S20. Current Microbiology, 1999, 38, 107-112.	2.2	14
68	Comparative analysis of cytokine profiles in autoinflammatory and autoimmune conditions. Cytokine, 2010, 50, 146-151.	3.2	14
69	Comparative Microbial Diversity in the Gastrointestinal Tracts of Food Animal Species. Integrative and Comparative Biology, 2002, 42, 327-331.	2.0	13
70	Molecular cloning, nucleotide sequence and characteristics of a xylanase gene (xyn A) from Ruminococcus albus 7. Animal Science Journal, 2002, 73, 347-352.	1.4	13
71	Characterization of the gene encoding glutamate dehydrogenase (gdhA) from the ruminal bacterium Ruminococcus flavefaciens FD-1. Archives of Microbiology, 2003, 179, 184-190.	2.2	13
72	Construction of genetically marked Ruminococcus albus strains and conjugal transfer of plasmid pAMβ1 into them. Journal of Bioscience and Bioengineering, 1994, 78, 1-5.	0.9	12

#	Article	IF	CITATIONS
73	Detection of Tetracycline Resistance Genes by PCR Methods. , 2004, 268, 003-014.		12
74	Construction of a Fibrobacter succinogenes Genomic Map and Demonstration of Diversity at the Genomic Level. Current Microbiology, 1997, 35, 22-27.	2.2	11
75	Editorial: Shaping of Human Immune System and Metabolic Processes by Viruses and Microorganisms. Frontiers in Microbiology, 2019, 10, 816.	3.5	11
76	A small cryptic plasmid fromRuminobacter amylophilusNIAH-3 possesses functional mobilization properties. FEMS Microbiology Letters, 1999, 181, 41-48.	1.8	10
77	Accelerated Apoptosis of Neutrophils in Familial Mediterranean Fever. Frontiers in Immunology, 2015, 6, 239.	4.8	10
78	Extended-Spectrum β-Lactamases in Human Isolates of Multidrug-Resistant Non-typhoidal Salmonella enterica. Frontiers in Microbiology, 2020, 11, 592223.	3.5	10
79	Antimicrobial drug resistance mechanisms among Mollicutes. International Journal of Antimicrobial Agents, 2021, 57, 106253.	2.5	10
80	Expression of a celE gene from Clostridium thermocellum in Bacillus. Journal of Bioscience and Bioengineering, 1995, 79, 530-537.	0.9	9
81	Management of familial Mediterranean fever by colchicine does not normalize the altered profile of microbial long chain fatty acids in the human metabolome. Frontiers in Cellular and Infection Microbiology, 2013, 3, 2.	3.9	9
82	Bacteriophage therapy: coping with the growing antibiotic resistance problem. Microbiology Australia, 2019, 40, 5.	0.4	9
83	Phylogenetic analysis of archaeal 16S rRNA libraries from the rumen suggests the existence of a novel group of archaea not associated with known methanogens. FEMS Microbiology Letters, 2001, 200, 67-72.	1.8	9
84	Segmented filamentous bacteria are a major group in terminal ileum of piglets. Anaerobe, 2013, 23, 109-111.	2.1	8
85	Complete Genome Sequence of the Human Gut Symbiont Roseburia hominis. Genome Announcements, 2015, 3, .	0.8	8
86	Structure and Function of a Nonruminant Gut: A Porcine Model. , 2015, , 47-75.		8
87	Construction of Prevotella ruminicola-Escherichia coli shuttle vector pRAM45 and transformation of P. ruminicola strains by electroporation. Journal of Bioscience and Bioengineering, 1999, 88, 316-318.	2.2	7
88	MULTIDRUG-RESISTANCE AND PRESENCE OF CLASS 1 INTEGRONS IN CLINICAL ISOLATES OF SALMONELLA ENTERICA SEROTYPE ENTERITIDIS, CIRCULATING IN ARMENIA. Russian Journal of Infection and Immunity, 2014, 3, 355.	0.7	7
89	Cloning, sequencing and complementation analysis of therecAgene fromPrevotella ruminicola. FEMS Microbiology Letters, 1996, 144, 53-59.	1.8	6
90	Transcriptional Regulation of the Prevotella ruminicola recA Gene. Current Microbiology, 1998, 36, 259-265.	2.2	6

#	Article	IF	CITATIONS
91	Inflammatory Responses to Salmonella Infections Are Serotype-Specific. International Journal of Bacteriology, 2013, 2013, 1-7.	1.0	6
92	Potential Involvement of Salmonella Infection in Autoimmunity. Pathogens, 2019, 8, 96.	2.8	6
93	Differential induction of total IgE by two Salmonella enterica serotypes. Frontiers in Cellular and Infection Microbiology, 2015, 5, 43.	3.9	5
94	Method for Preparation of RNA from Ruminococcus albus. BioTechniques, 1997, 22, 406-408.	1.8	3
95	16S/18S ribosomal DNA clone library analysis of rumen microbial diversity. , 2005, , 163-174.		3
96	Analysis of evolving lysogenized products of spontaneous zygogenesis in <i>Escherichia coli</i> . FEMS Microbiology Letters, 2017, 364, fnw290.	1.8	2
97	Gut Health, Microbiota and Immunity. Recent Advances in Animal Nutrition, 2009, 2008, 195-210.	0.1	1
98	Antibiotic Resistance and Occurrence of Class 1 Integrons in Clinical Isolates of Salmonella enterica. Global Journal of Immunology and Allergic Diseases, 0, , .	0.7	1
99	Erratum to "Cloning, sequencing and complementation analysis of the recA gene from Prevotella ruminicola―[FEMS Microbiol. Lett. 144 (1996) 53–59]1. FEMS Microbiology Letters, 1996, 145, 473.	1.8	0
100	P-005: Mechanism of action of potential live biotherapeutics for the treatment of inflammatory bowel disease. Journal of Crohn's and Colitis, 2014, 8, S395.	1.3	0
101	Cloning, Expression, and Characterization of a Cellulase Gene from Prevotella ruminicola. Nihon Chikusan Gakkaiho, 2001, 72, 421-426.	0.2	0
102	Editorial: Antimicrobials in Wildlife and the Environment. Frontiers in Microbiology, 2021, 12, 783118.	3.5	0
103	A small cryptic plasmid from Ruminobacter amylophilus NIAH-3 possesses functional mobilization properties. FEMS Microbiology Letters, 1999, 181, 41-48.	1.8	0